Sow herd typologies based on biosecurity, productivity, antimicrobial and

Kruse, Amanda Brinch; Nielsen, Liza Rosenbaum; Alban, Lis Marianne

ISVEE 15

12 – 16 November 2018
Chiang Mai, Thailand

The 15th International Symposium of Veterinary Epidemiology and Economics

Abstract Book

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CONTENTS

WELCOME MESSAGE FROM THE THAI VETERINARY MEDICAL ASSOCIATION UNDER ROYAL PATRONAGE

Dear colleagues and participants,

Welcome all of you at ISVEE; the 15th International Symposium on Veterinary Epidemiology and Economics. Welcome you to Chiangmai, Thailand.

Decision makers dealing with animal health, human health and the ecosystem problems, at the herd, national, regional or global level are increasingly faced with new challenges. In the face of growing world human and animal populations and rapid environmental change, the linkages between human, animal, and environmental health are becoming more evident. Furthermore, human and animal health professionals must overcome specific barriers to interprofessional collaboration to implement needed multidisciplinary strategies.

The five-day conference program focuses on a broad range of issues and challenges in the field of Veterinary Epidemiology and Economics which will be weaved through the keynote speakers, plenary speakers, distinguished session speakers, epidemiologists, scientists, practitioners and researchers.

As the host country of ISVEE 15, I believe that the success of the conference depends heavily on the people who have worked hard in planning and organizing the conference program. It has been our greatest hope that this conference will serve as an international platform for the exchange of knowledge and expertise in Veterinary Epidemiology and Economics researches and practices, at the same time to explore the potential collaborations in future research. We hope that the conference will be a stimulating, engaging and fulfilling experience to all the participants.

We thank the organizing committee and the scientific committee for their invaluable assistance in designing a very interesting program. Moreover, we wish to thank our sponsors for making this conference possible. Most of all we thank you, participants of ISVEE, for your contributions and your presence at ISVEE 2018. We wish you an inspiring conference.

Somchuan Ratanamungklanon
President
The Thai Veterinary Medical Association under Royal Patronage (TVMA)

WELCOME MESSAGE FROM THE DEPARTMENT OF LIVESTOCK DEVELOPMENT

Dear ISVEE participants and colleagues,

It is a great honour and pleasure for me to welcome you to Chiangmai, Thailand at the 15th International Symposium on Veterinary Epidemiology and Economics (ISVEE 15).

This international seminar will focus special attention on the epidemiologic studies, animal health economics, animal and human health policy, One Health, disease surveillance and etc.

These issues of animal health, human health, and ecosystem have a significant societal dimension. Efforts towards ensuring that the population is in good health must be a result of dynamic and mutually complementary collaboration among all the parties involved.

In the field of Veterinary Epidemiology and Economics, it is absolutely essential that we focus on the quality of animal health, human health, and food safety related issues. The Department of Livestock Development, Ministry of Agriculture and Cooperatives of Thailand is greatly supportive of this conference and is working hard to ensure food security and food safety standards across all branches of veterinary medicine.

I believe that the conference will be of benefit to one and all, and that you will exchange with one another the useful experience that you have gained in your work with epidemiologists, practitioners, scientists and researchers.

I thank the organizing committee, the scientific committee, the keynote speakers, the plenary speakers, the distinguished session speakers, and all participants for their invaluable contribution and support to ISVEE 15 in Chiangmai, Thailand. Finally, I wish you all fruitful deliberations, I wish the meeting all success, and I wish you all an enjoyable stay in Thailand.

Sorravis Thaneto
Director General
Department of Livestock Development, Thailand

WELCOME MESSAGE FROM THE LOCAL ORGANIZING COMMITTEE OF ISVEE 15

Dear Colleagues,

It is my great pleasure to invite you to take part of The 15th International Symposium of Veterinary Epidemiology and Economics (ISVEE 15) during 12 – 16 November 2018 in Chiang Mai, Thailand.

It has been an enormous challenge for the Thai committees as we have prepared ad developed this coming premier event, ISVEE 15, where science, knowledge, expertise, experiences, leadership and communication meet for advancing all facets of our collective efforts to better understanding in recent veterinary epidemiology and economics.

Nor only the academic shares, Chiang Mai, a famous norther province of Thailand is also fully facilitated by modern conveniences with combination of natural resources and rich cultures, this ISVEE 15 venue will be a memorable place for all delegates.

I do hope you will accept our invitation to join the symposium, share your experiences and contribute to the discussion. Then enjoy staying and creating friendship in the magnificent surrounding of Chiang Mai, Thailand.

With best regards,

Assoc. Prof. Dr. Sudson Sirivaidyapong, D.V.M., Ph.D.,
Diplomate-Thai Board of Theriogenology
President of ISVEE 15

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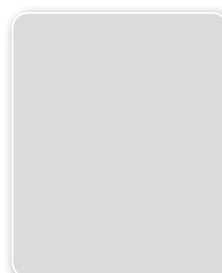
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ACKNOWLEDGEMENTS

GENERAL INFORMATION

THE VENUE
The Empress Convention Centre & The Empress Chiang Mai Hotel
199/42 Chang Klan Road
Chiang Mai 50100, Thailand
Phone: +66 53 253 199 / +66 53 270 240
http://empresshotels.com/.

REGISTRATION DESK HOURS
The registration desk will be located on Level 1, The Empress Convention Centre and will open as follows:

Sunday, 11 November 2018	14:00 – 17:00 hrs.
Monday, 12 November 2018	7:30 – 17:00 hrs.
Tuesday, 13 November 2018	7:30 – 17:00 hrs.
Wednesday, 14 November 2018	8:00 – 17:00 hrs.
Thursday, 15 November 2018	8:00 – 17:00 hrs.
Friday, 16 November 2018	8:00 – 12:00 hrs.

EXHIBITION HOURS
The exhibition hall is located on Level 2, The Empress Convention Centre and will be open as follows:

Monday, 12 November 2018	9:00 – 17:00 hrs.
Tuesday, 13 November 2018	9:00 – 17:00 hrs.
Wednesday, 14 October 2018	9:00 – 17:00 hrs.
Thursday, 15 November 2018	9:00 – 17:00 hrs.
Friday, 16 November 2018	9:00 – 15:30 hrs.

POSTER SESSION
Poster session will be at poster area which is located on Level 3, **The Empress Convention Centre,** scheduled as follows:

Monday, 12 November 2018	16:30 – 17:30 hrs. Poster session I
Tuesday, 13 November 2018	16:30 – 17:30 hrs. Poster session II
Wednesday, 14 November 2018	13.20 – 15.00 hrs. and 16:30 – 17:30 hrs. Poster session III
Thursday, 15 November 2018	16:30 – 17:30 hrs. Poster session IV

***Poster will be displayed all day from 8:30-18.00 hrs

SCIENTIFIC PROGRAM
A full interactive Scientific Program is available on the Congress website via the following link: http://isvee. net/scientific-information/program-at-a-glance/. Presenters are encouraged to visit this link and verify their presentation schedule as it may have changed.

CERTIFICATE OF ATTENDANCE / PRESENTATION
Please note that certificates of attendance / poster presentation / oral presentation will NOT be printed onsite. Certificates of Attendance will be issued to all attendees electronically after the Congress.

REFRESHMENTS AND LUNCH
Refreshments and lunch will be provided daily according to the time indicated in the program.

GENERAL INFORMATION

OPENING CEREMONY
Registered participants are invited to attend the Opening Ceremony on Monday 12 November 2018 from 8:30-9:15 hrs at Grand Hall, Level 3, The Empress Convention Centre.

GALA DINNER
Registered participants are invited to attend the Gala Dinner at Royal Flora Ratchapruek on Wednesday 14 November 2018 from 18:00-22:00 hrs.
17:30 and 17:45 hrs: buses leave from The Empress Hotel to Royal Flora Ratchapruek
21:45 and 22:00 hrs: buses leave from Royal Flora Ratchapruek back to The Empress Hotel
(RSVP is required at the registration counter)

FAREWELL COFFEE
Registered participants are invited to the Farewell Coffee on Friday 16 November 2018 from 15.00-15.30 hrs.

SMOKING POLICY
Smoking is prohibited at all times in the meeting halls, exhibit halls and restrooms. Your compliance is appreciated.

LIABILITY AND INSURANCE
The Congress Secretariat and Organizers cannot accept liability for personal accidents or loss of or damage to private property of participants and accompanying persons. Participants are advised to take out their own personal travel and health insurance for their trip.

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ORAL PRESENTATION

A. Epidemiologic studies in specific species/topics

Assessment of the analgesic efficacy of ketoprofen and meloxicam when compounded with iron dextran and administered to piglets at the time of castration

K. Reynolds[1]; R. Johnson[2]; R. Friendship[1]; J. Brown[3]; T. O'Sullivan[1*]

[1]Department of Population Medicine, University of Guelph, Canada
[2]Department of Biomedical Sciences, University of Guelph, Canada
[3]Prairie Swine Center, University of Saskatchewan, Canada

ABSTRACT

It has been documented that castration of neonatal piglets is a painful procedure. The Canadian Code of Practice for Care and Handling of Piglets requires swine producers to provide pigs with analgesia to control post-procedural pain. There is interest in mixing iron dextran (ID), already given to piglets to prevent anemia, with non-steroidal anti-inflammatory drugs (NSAIDs) at the time of processing. This has the potential to decrease piglet handling, reduce injections piglets receive, and reduce labour and materials costs. The objectives of this study were to determine if the analgesic efficacies of the NSAIDs meloxicam (M) and ketoprofen (K) are altered after mixing with ID and administered at the time of castration.

Materials and methods: Piglets (n=175) from 25 litters were assigned to 1 of 7 treatment groups: M or K alone, compounded M+ID, compounded K+ID, or 1 of 3 control groups; sham handled, ID+castration (ID+C), ID and no castration (ID-C). Piglets navigated a chute at 7 time-points ranging from 15-minutes prior to 30-hours post-castration and chute navigation time (seconds) was recorded and compared.

Results: After controlling for the effect of time-point, all treatments groups had faster chute navigation times versus the ID+C group ($P < 0.01$). There was no difference between the chute navigation times of any other treatment groups comparisons (all, P > 0.05). The results indicate that the compounding of ID with M or K did not decrease the efficacy of the NSAIDs when compared to the NSAID alone.

Conclusion: This supports the utilization of these NSAIDs compounded with ID in a commercial setting and hence the practice has the potential to improve pig welfare around the time of castration. Further studies on tissue drug depletion of compounded formulations are needed to ensure food safety.

Key words: Swine, castration, analgesia, iron dextran, welfare

Evaluation of welfare and cow comfort through a controlled field trial on smallholder dairy farms in Central Kenya

S. Richards[1,] J. VanLeeuwen[1], S. McKenna[1], C. Kamunde[2], F. Uehlinger[3], J. Wichtel[4]

[1] Centre for Veterinary Epidemiologic Research, Department of Health Management
Atlantic Veterinary College, University of Prince Edward Island
[2] Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island
[3] Department of Large Animal Clinical Sciences, Faculty of Veterinary Medicine University of Saskatchewan
[4] Ontario Veterinary College, University of Guelph

ABSTRACT

Objective: Through the use of a controlled field trial, a welfare-based intervention was evaluated on zero-grazing, smallholder dairy farms in Kenya. The intervention was: 1) training on the importance and best management practices of good cow comfort; and 2) low-cost modifications of cow stalls (eg. improved stall base or rails).

Materials and methods: Fifty farms were randomly allocated to intervention or control farms, with cow comfort measures taken pre-intervention, as well as one month and one year post-intervention. Objective measurements at each of these visits included daily milk production and accelerometer readings to evaluate the lying behaviours of all cows (n=75). Subjective measures included stall base hardness and wetness, and cow hygiene and lesion scoring. Factors associated with continuous outcomes, such as accelerometer readings and daily milk production, were evaluated using mixed models accounting for repeated measures, while Chi-squared tests were used to compare subjective outcomes between groups at each time period.

Results: Soft stalls were associated with an additional 45 minutes/day of lying time, an extra 0.63 lying bouts/day in shorter bout durations, and 0.76 kg/day higher daily milk production than cows with hard stalls. Cows with dry stalls had 0.47 more lying bouts/day compared to cows with wet stalls. Intervention cow hygiene scores on hocks and udders were significantly better than for control cows at one month post-intervention, and this result was maintained one year post-intervention.

Conclusion: These results indicate the relative benefits of low cost interventions on cow welfare and comfort on smallholder dairy farms in Kenya.

Key words: Dairy cattle, welfare, smallholder dairy farms, accelerometer data

Effects of local anesthetic and/or systemic analgesia on pain associated with cautery disbudding in calves: A systematic review and meta-analysis

C.B. Winder[1*], C.L. Miltenburg[1], J.M. Sargeant[1,2], S.J. LeBlanc[1], D.B. Haley[1], K.D. Lissemore[1],
M.A. Godkin[3], T.F. Duffield[1]

[1] Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada,
[2] Centre for Public Health and Zoonoses, University of Guelph, Guelph, Ontario, Canada,
[3] Ontario Ministry of Agriculture, Food, and Rural Affairs, Elora, Ontario, Canada

ABSTRACT

Objective: Disbudding is a common management procedure performed on dairy farms, and when done without pain mitigation is a key welfare issue. Although pain control use is increasing, full adoption of anesthesia/analgesia has not been achieved. The objective of this systematic review was to examine the effects of pain control for cautery disbudding on outcomes associated with pain: plasma cortisol concentration, pressure sensitivity of the horn bud, and pain behaviors.

Materials and methods: Eligible intervention studies described cautery disbudding in calves ≤12 weeks of age, provided they compared local anesthesia, non-steroidal anti-inflammatory drug (NSAID), or both, to one or more of local anesthesia, NSAID, or no treatment. Of the 4394 records identified, 21 articles comprising 23 studies were eligible for qualitative synthesis. Meta-analysis was performed for all outcomes measured at similar time points with >2 comparator groups.

Results: Local anesthetic was associated with reduced plasma cortisol until 2 h post-disbudding (30 min, n=7 studies; 1 h, n=8; 2 h, n=5); however, a rise in cortisol was observed in the meta-analysis of studies reporting at 4 h (n=5). The addition of NSAID to local anesthetic showed reduction in plasma cortisol at 4 h (n=6), and reduction in pressure sensitivity and pain behaviors in some analyses from 3-6 h (n=3-6). Heterogeneity was present in several meta-analyses, including many examining pain behavior. This may reflect variation in measurement periods, and/or differences among NSAIDs. Local anesthetic showed a protective effect on acute pain, and NSAID use mitigated the delayed cortisol rise, which also reduced pressure sensitivity and pain behaviors.

Conclusion: These findings support the use of local anesthetic and an NSAID, but the magnitude and duration of the effect of NSAID treatment was not possible to deduce from the literature. We recommend adherence to reporting guidelines and consideration of more standardized outcome measurements, particularly for pain behaviours.

Key words: Pain, calf, disbudding, systematic review

Antimicrobial usage in organic pig production with reference to in-door conventional production in Denmark

J.T. Sørensen[1], H. Kongsted[1], C.L. Nielsen[1]

[1] Department of Animal Science, Aarhus University, Denmark

ABSTRACT

Objective: The organic pig production, which is less than 1% of the total Danish pig production, differs from in-door conventional pig production. Organic piglets are weaned at 7 weeks, weaners and finishers are kept in-door with an out-door run at a lower animal density and provided roughage. Organic sows and piglets are kept out-door. Disease treatment rules are more restrictive in organic than in conventional pig production. The objective of this study is to describe antimicrobial usage in organic pig production with reference to in-door conventional pig production in Denmark.

Materials and methods: In Denmark, antimicrobial usage is registered centrally specified on three groups of pigs; sows and piglets, weaners and finishers. Based on data from 2014-2016 the Animal Daily Doses (ADD*) per 100 animal per day was calculated for organic and conventional pigs for each animal group.

Results: It appears from Fig. 1 that conventional weaners receive 10 ADD/100 animal days compared to, 0.7 ADD/100 animals per day in organic production. The level of antimicrobial usage in Denmark in organic production relative to the same conventional animal group is 7% for weaners, 12% for sows and piglets and 42% for finishers.

Conclusions: The lower antimicrobial usage in organic pig production – especially with respect to weaners – may reflect that organic systems supports the production of more robust animals. However, the disease threshold for treatment in organic herds may be higher than in conventional herds.
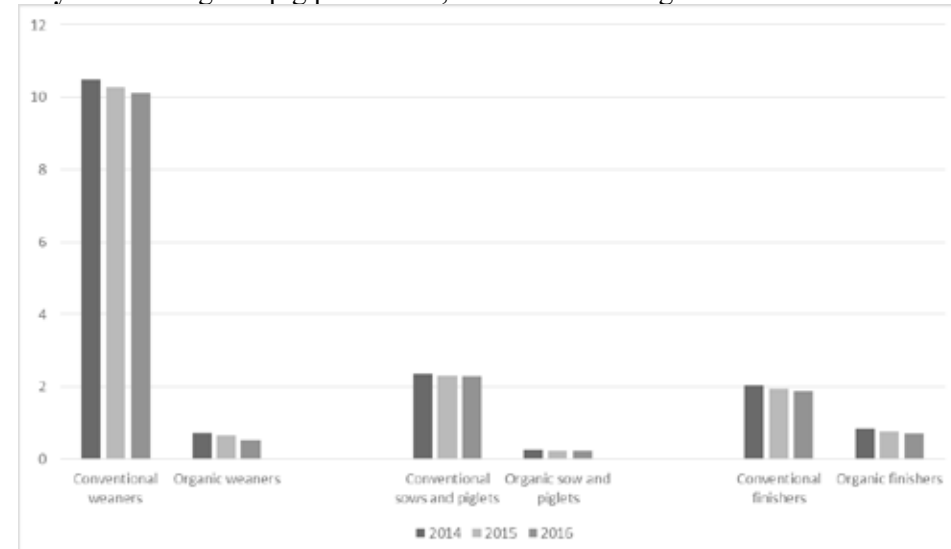
Key words: Organic pig production, antimicrobial usage

Figure 1. Antimicrobial usages in organic and conventional pig production during three years (ADD/100 animals per day)

* Defined as the average daily maintenance dose for a drug for its main indication in a specified animal species. The dose is defined for a „standard animal", i.e. an animal with an estimated average weight within a specified age group.

Big Data approach in swine production system: effect of transport conditions on carcass quality

C. Faverjon[1*], C. Sarasua[2], M. Vargas[2,3], M. Sterchi[2,3,6], C. Nathues[4], R. Grütter[3], A. Bernstein[2], H. Nathues[5], J. Berezowski[1]

[1] Veterinary Public Health Institute / University of Bern, Bern, Switzerland;
[2] Department for Informatics / University of Zurich, Zürich, Switzerland;
[3] Swiss Federal Research Institute WSL, Birmensdorf, Switzerland;
[4] Federal Food Safety and Veterinary Office, Bern, Switzerland;
[5] Clinic for Swine / University of Bern, Bern, Switzerland;
[6] University of Applied Sciences and Arts Northwestern Switzerland, Olten, Switzerland

ABSTRACT

Objective: Big Data approaches have not been broadly implemented in livestock production and health, even though it is certain that they would be of benefit. For example, it is already known that transport conditions in slaughterhouses affect carcass quality. However, traditional study designs used to assess these effects can only look at a limited number of animals and risk factors. This, they could fail to identify small effects that could be used to improve livestock production and health. The purpose of this study was to implement Big Data approaches to assess the effect of transport conditions on swine carcass quality.

Materials and methods: Using a transdisciplinary approach, we collected data generated at each stage of the swine production chain, and we developed a centralized data store allowing for the inclusion of these heterogeneous data, and the unearthing of their systematic bias. We obtained valid information on 567'195 pigs slaughtered in Switzerland between 2014 and 2017. We used mixed models to assess the effect of many variables (e.g., duration of transport and lairage, farm of origin, weather) on 6 carcass quality parameters (iodine value, polyunsaturated fatty acids (PUFA), lean meat, cold weight, cannibalism, and skin lesions).

Results: Our main results were that transport duration only affected the iodine value (+0.02/hour), the cold weight (-0.05kg/hour) and the risk of skin lesions (1.2times higher/hour). The lairage duration, the season and the category of pigs affected all meat parameters. Differences between farms also explained part of the parameters' variance (e.g., 71% for PUFA, 22% for cold weight).

Conclusion: Our approach allowed us to identify with statistical significance small effects which are however of high relevance for the Swiss swine industry. All the carcass quality parameters considered in our study influenced the economic value of the carcass. Approaches such as this offer great opportunity for improving livestock production management and health.

Key words: Big data, pig, meat quality, animal transport

Using network analysis to evaluate the role of feed suppliers during the early months of the 2014 porcine epidemic diarrhea Canadian outbreak

T.L. O'Sullivan[1]*, A. M. Perri[1], C. Dewey[1], J.C.S. Harding[2], Z. Poljak[1]

[1] Department of Population Medicine, University of Guelph, Canada
[2] Large Animal Clinical Sciences, University of Saskatchewan, Canada

ABSTRACT

Objectives: Network analysis can be used to visualize and characterize networks and for identifying important nodes involved in the transmission of infectious pathogens. The objectives were to describe the contact structure of porcine epidemic diarrhea (PED) case herds and matched control herds with feed suppliers; and to evaluate possible mechanisms of PED spread during the early phase of the 2014 Canadian outbreak through random permutations of the observed two- mode networks.

Materials and methods: A questionnaire was used to gather information on contact patterns with feed suppliers between Dec 2013 and Feb 2014. The full network was divided into case and control directed networks. The point-source hypothesis was evaluated by comparing the observed proportion of PED cases in a maximum network of a single feed supplier in a two-mode network consisting of feed suppliers and herds (cases and controls), to the expected proportion obtained through the random permutation of the network.

Results: The spread of porcine epidemic diarrhea virus (PEDV) in the early phase of the outbreak could most likely be attributed to the point source outbreak through feed-related connections. This finding was based on the fact that the observed proportion of cases in the largest network of a single feed company was unusually high compared to randomly permuted networks. The outgoing contact chain (OCC) of the case network (n=9) was longer than the OCC of the control network (n=4) with the origin of the OCC in the case network being a single feed supplier (FS). The case herd network also had a higher mean out-degree (1.83; range: 1-8), compared to the control herd network (1.43; range: 1-3). Therefore, the early phase of the 2014 Canadian outbreak was likely due to point-source transmission through feed, and more specifically, a single FS was found to be the most important member for PEDV transmission.

Key words: Network analysis, porcine epidemic diarrhea virus, case-control, point-source hypothesis, feed suppliers

Viral co-infections affect hepatitis E virus (HEV) infection dynamics in pigs and increase the risk of contaminated livers at slaughter

Morgane Salines[1]*, Marine Dumarest[2], Mathieu Andraud[1], Sophie Mahé[1], Maelan Cineux[1], Cécilia Bernard[1], Eric Eveno[1], Florent Eono[1], Virginie Dorenlor[1], Béatrice Grasland[1], Olivier Bourry[1], Nicole Pavio[2], Nicolas Rose[1]

[1]ANSES, French Agency for Food, Environmental and Occupational Health & Safety, Ploufragan/Plouzané Laboratory, Ploufragan, France
[2] ANSES Animal Health Laboratory, UMR 1161 Virology, INRA, ENVA, Maisons-Alfort, France

ABSTRACT

Objectives: Hepatitis E virus (HEV) is a zoonotic pathogen mainly transmitted through the consumption of contaminated pork products. This study aimed at describing HEV infection patterns in pig farms and at assessing the impact of factors related to intercurrent viral co-infections, HEV immunity status and litters' characteristics on HEV dynamics in field conditions.

Material and methods: A longitudinal follow-up was conducted in three HEV-infected farrow-to-finish farms. Forty piglets in three batches per farm were randomly sampled and individually monitored from birth to slaughter. Blood and fecal samples were taken at 1, 6, 10, 14, 18 and 22 weeks of age; blood and liver samples were collected at slaughterhouse. Virological and serological analyses were performed to assess HEV, Porcine Circovirus type 2 (PCV2) and Porcine Reproductive and Respiratory Syndrome virus (PRRSV) dynamics. The links between 12 explanatory variables and four outcomes describing HEV dynamics were explored using survival analysis and logistic regression considering within-farm piglets' clustering.

Results: HEV infection dynamics was highly variable between farms and in a lower magnitude between batches. HEV positive livers were more likely related to short time-intervals between HEV infection and slaughter (OR=4.07 [3.72-4.45]). In addition to an influence of piglets' sex and sows' parity, the sequence of co-infections strongly affected HEV dynamics. Prior or concomitant infection by PRRSV or PCV2/PRRSV significantly delayed the age at HEV shedding (Hazard Ratio = 0.28 [0.17-0.47], HR=0.26 [0.15-0.46], respectively). The age at HEV seroconversion was delayed (HR=0.43 [0.25-0.74]) in PCV2/PRRSV co-infected piglets, also showing a longer shedding period (HR=0.50 [0.32-0.79]). Consequently, a PRRSV or PCV2/PRRSV pre- or co-infection dramatically increased the risk of positive livers at slaughter (OR=4.10 [1.87-8.97], OR=6.49 [3.18-13.23], respectively).

Conclusions: Co-infections with immunosuppressive viruses, mainly PRRSV, affected HEV dynamics. Controlling these pathogens may be a major lever to mitigate the risk for public health.

Key words: hepatitis E virus, public health risk, longitudinal follow-up, co-infection (5 max)

Data-driven predictions and novel hypotheses about outbreaks of porcine epidemic diarrhea virus based on neighboring farms and disease intelligence

G. Machado*, C. Vilalta, C. Corzo , M. Recamonde-Mendoza, A.M. Perez, K. VanderWaal

ABSTRACT

Objective: Understanding factors that distinguish between when and where a disease outbreak occurs from where outbreaks do not occur is a critical component of disease mitigation. This study aims to integrate animal movements into neighboring farms (farms within 10 km of the focal farm) and the environmental characteristic of the neighborhood to identify what most contributes to porcine epidemic diarrhea virus (PEDv) outbreaks in the United States.

Materials and methods: We use a novel machine learning set of algorithms to interrogate animal movement and environmental variables with the ultimate goal of predicting the occurrence of new outbreaks. We analyzed a total of 15 million pigs transported between swine sites.

Results: Our best classifier, Random Forest, was selected and predicted PEDv outbreaks with more than 83% accuracy, with a sensitivity and specificity of 83.33 (± 2.27) and 79.57 (±2.52). The distinguishing characteristics associated with PEDv outbreaks included the number of pigs moved into neighboring farms followed by environment characteristics. We suggest that outbreaks are likely to be dependent mostly on the number of pigs moved into neighboring (within 10 km) farms, followed by neighborhood attributes predictors included hog density, environmental and weather factors such as vegetation, wind speed, temperature, and precipitation, and topographical features such as slope.

Conclusion: Our results suggest that the use of multiple machine learning algorithms provide a better performance for disease prediction and identified particular environmental conditions that PEDv outbreaks. Our neighborhood-based approach allowed us to simultaneously capture disease risks associated with long-distance animal movement as well as local spatial dynamics, which are nearly always overlooked in analyses of livestock movement data. The predictive model presented here will advance disease surveillance and control for endemic swine pathogens in the United States.

Key words: Animal Movement, big data, neighborhood, network analysis, machine learning, spatial epidemiology, environment, landscape

Characterization of temporal and spatial patterns of clinical respiratory episodes in growing pigs using continuous sound monitoring and an algorithm-based respiratory distress index

D. D. Polson[1], S. Playter[1], D. Berckmans[2], Z. Y. Cui[2], B. Quinn[1], M. Genzow[1]

[1]Boehringer Ingelheim Animal Health, Ingelheim, Germany;
[2]SoundTalks NV, Leuven, Belgium

ABSTRACT

Objective: The purpose of this analysis was to characterize the temporal and spatial patterns of clinical episodes of swine respiratory diseases of growing pigs under large-scale commercial production conditions using a continuous audio monitoring system.

Materials and methods: Audio monitoring devices (SOMO+ Respiratory Distress Monitor, SoundTalks NV, Leuven, Belgium) were obtained and installed in a large 25 meter wide by 75 meter long commercial single airspace wean-to-finish facility designed to house 2400 pigs from weaning to market. In total, 11 devices were installed representing 11 zones in the airspace, with four devices over the middle of the pens on each side of the building spaced equidistant from each other and three in the central alleyway spaced equidistant from each other. Pigs were placed into the facility per normal practice. An algorithm-based respiratory distress index (RDI) was continuously generated from recorded sound files and uploaded to a cloud-based database. RDI's were continuously monitored and alerts were automatically sent to pre-determined personnel when a significant rise in RDI was detected by the system. When an RDI alert was generated, diagnostic samples were collected and tested by PCR for PRRS, IAV-S, Mycoplasma hyopneumoniae, PCV2 and parainfluenza.

Results: RDI episodes were detected in the animal cohort at this site, including: IAV-S (H1N1), IAV-S (H3N2), and Mycoplasma hyopneumoniae. Distinct differences in the temporal RDI patterns were observed between IAV-S and Mycoplasma hyopneumoniae. Spatial patterns indicated RDI episode onset occurred in specific zones and subsequently spread throughout the airspace.

Conclusion: An audio monitoring system can be used to detect the onset and location of clinical respiratory events in commercial growing pig cohorts, enabling more targeted and timely interventions.

Key words: Temporal, spatial, sound, respiratory, monitoring

The effect of PRRS outbreak season on time to stability

J.M. Sanhueza*, C. Vilalta, C. Corzo, A. Arruda

ABSTRACT

Objective: The time from Porcine Reproductive and Respiratory Syndrome (PRRS) outbreak occurrence to weaning PCR-negative piglets is called time to stability (TTS). Anecdotal reports suggested that summer outbreaks have a longer TTS compared to those occurring during autumn/winter but no formal assessment had been conducted. The objective of this study was to assess whether TTS was affected by the season in which the PRRS outbreak had occurred.

Materials and methods: Seven years of data (2011-2017) from 86 farms in six systems that participate in the Morrison's Swine Health Monitoring Project (MSHMP) were used in the analysis. TTS was calculated as the time difference between the outbreak reporting date and the date at which four consecutive PCR tests in due-to-wean piglets, 30 days apart, was achieved. A mixed-effects Cox model was used to model the effect of PRRS outbreak season and recorded predictors on TTS. Farm and system were included in the model as random effects.

Results: The median TTS was 41.5 weeks (1st quartile 31 weeks-3rd quartile 55 weeks). The final multivariable mixed model results showed that farms in which the outbreak had occurred during winter (hazard ratio (HR) 2.3, 95% confidence interval (CI) 1.2-4.1) and autumn (HR 1.8, 95% CI 1.0-3.1) achieved stability sooner than farms in which the outbreak occurred during summer. No significant difference was observed between TTS of summer and spring outbreaks. Additionally, farms that were using field virus inoculation when the PRRS outbreak occurred achieved stability sooner (HR 3.7, 95% CI 1.8-7.6) than farms that were using a modified live vaccine.

Conclusion: Our results suggest that PRRS outbreaks that occur during summer/spring take significantly longer to stabilize than outbreaks that occur during winter/autumn. Outbreak season may be an important factor to consider when planning herd closure and managing expectation of weaning negative piglets.

Key words: PRRS, stability, season

Descriptive epidemiology of porcine reproductive and respiratory syndrome summer outbreaks in US sow farms

J.M. Sanhueza*, C. Vilalta, C. Corzo, M. Stevenson

ABSTRACT

Objective: Porcine reproductive and respiratory syndrome (PRRS) is endemic in US pig herds. Although most PRRS outbreaks occur during the autumn and winter, an unquantified percentage of outbreaks occur during the summer. We describe the incidence of PRRS summer outbreaks over calendar time and identify geographical areas where there is a high and low incidence of PRRS summer outbreaks.

Materials and methods: PRRS incidence data from 2009 to 2017 shared by participants of the Morrison's Swine Health Monitoring Project (MSHMP) were used for the analysis. A summer outbreak was defined as an outbreak reported between June 21st and September 21st in any given year. The yearly incidence risk of summer outbreaks was estimated by dividing the number of PRRS outbreaks by the total number of farms at risk in each time period. The Mann-Kendall test was used to evaluate the incidence trend over the years. Adaptive kernel smoothing was used to estimate the density of farms that did or did not have an outbreak during the summer. The ratio of these two densities was used to identify geographical areas of high and low incidence of summer PRRSV outbreaks.

Results: Since 2009, 182 out of 1329 PRRS outbreaks (13.7% of total outbreaks) were recorded during summer. The incidence risk of PRRS outbreaks during summer averaged 3.2% (min 1.2% - max 4.4%) between 2009 and 2017. No significant increasing or decreasing trend was detected over the years (p=0.47). Geographical areas of significantly high (OR=3.7) and low (OR=0.4) risk of summer outbreaks were observed.

Conclusion: Our results show that PRRS outbreaks continue to occur during the summer without any trend across the years that were assessed. Swine producers should maintain biosecurity measures throughout the year, particularly for those farms located in areas with a higher risk of PRRS summer outbreaks.

Key words: PRRS, summer, outbreak, spatial, risk

Modelling the economic efficiency of using different strategies to control Porcine Reproductive & Respiratory Syndrome at herd level

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ABSTRACT

Objective: PRRS is among the diseases with the highest economic impact in pig production worldwide. The broad variety of available intervention strategies makes it difficult to decide on the most cost-efficient strategy for a given farm situation, as it depends on many farm-individual factors. Aim of this study was to create a simulation tool to estimate the cost-efficiency of different control strategies at individual farm level.

Materials and methods: Baseline is a model that estimates the costs of PRRS, based on changes in health and productivity, in a specific farm setting. The model evaluates different intervention scenarios: depopulation/repopulation (D/R), close & roll-over (C&R), mass vaccination of sows (MS), mass vaccination of sows and vaccination of piglets (MS+piglets), improvements in internal biosecurity (BSM), and combinations of vaccinations with BSM. The economic efficiency of the different strategies was assessed over 5 years through investment appraisals: the resulting expected value (EV) indicated the most cost-effective strategy. Calculations were performed for 5 example scenarios with varying farm type (farrow-to-finish – breeding herd), disease severity (slightly – moderately – severely affected) and PRRSV detection (yes – no).

Results: The assumed herd size was 1000 sows with farm and price structure as commonly found in Germany. In a moderately affected (moderate deviations in health and productivity parameters from what could be expected in an average negative herd), unstable farrow-to-finish herd, the most cost-efficient strategies according to their median EV were C&R (€1′126′807) and MS+piglets (€ 1′114′649). In a slightly affected farrow-to-finish herd, no virus detected, the highest median EV was for MS+piglets (€ 721′745) and MS (€ 664′111).

Conclusion: Results indicate that the expected benefits of interventions and the most efficient strategy depend on the individual farm situation, e.g. disease severity. The model is a valuable tool for farmers and veterinarians to estimate expected economic consequences of an intervention and thus enables a better informed decision.

Inferring within-herd transmission parameters for African swine fever outbreaks using mortality data

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ABSTRACT

Objectives: Since 2007, the pig industry in Eastern Europe has experienced severe African swine fever (ASF) outbreaks. Knowledge gaps remain on how fast and extensive ASF virus (ASFV) spread is within herds, although this is important when assessing the effectiveness of intervention strategies. The objective of this study was to estimate within-herd transmission parameters for ASFV using mortality data.

Materials and methods: The transmission of ASFV within pig herds was modelled by a stochastic compartmental susceptible-infected-infectious-dead (SEIR) model. This model was fitted to daily mortality data collected in nine infected herds of the Russian Federation and a posterior distribution for the model parameters was obtained through Approximate Bayesian Computation (ABC) rejection sampling. Sampled parameters were accepted or rejected on the basis of the level of difference between simulated and observed mortality. This allowed us to approximate the posterior distributions with the distribution of parameter values associated with accepted simulations.

Results: Results show that parameter estimates, such as the basic reproduction number, varied amongst herds, ranging from 4.4 to 17.3. This was primarily a consequence of differences in transmission rate (range: 0.7–2.2), but also differences in the mean infectious period (range: 4.5–8.3 days). We also found differences amongst herds in the mean latent period (range: 5.8–9.7 days). Dates of introduction were estimated for each herd.

Conclusion: Results suggest that ASFV could be circulating in a herd for several weeks before an increase in mortality is observed in a herd, limiting the usefulness of mortality data as a means of early detection of an outbreak. However, results also show that mortality data are a potential source of data from which to infer transmission parameters, at least for diseases which cause high mortality. These results will be used to inform between-farm transmission models of ASFV, which aim at optimising control strategies for ASF.

Key words: African swine fever, approximate Bayesian computation, mortality data, pigs, disease control, modelling

Evaluation of Gross Thoracic Lesions in Pigs from Selected Slaughterhouses in the Provinces of Batangas and Albay in the Philippines using Latent Class Analysis

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ABSTRACT

Objective: Respiratory disease is one of the most important disease syndromes pigs in the Philippines. Lung scoring is a widely accepted technique to evaluate thoracic lesions and can be used for respiratory disease surveillance. This study aimed to estimate the prevalence of thoracic lesions in slaughter-age pigs in two provinces in the Philippines (Batangas and Albay) and identify patterns of co-occurrence of lesions in these populations.

Materials and methods: A total of 560 pigs from nine slaughterhouses were included in the study. Lungs were scored for cranio-ventral pneumonia using a scale of 0 to 55 and for pleurisy from 0 to 3. Presence or absence of pericarditis was recorded.

Results: The median lung score was 7 in Batangas and 0 in Albay with interquartile ranges 2-19 and 0-2. Using a threshold of ≥7, 51.9% and 13.7% pigs had a high lung score from Batangas and Albay, respectively. Similarly, 56.9% and 5.0% had a pleurisy score of ≥1 and 24.6% and 1.7% had pericarditis. Latent class analysis identified four classes based on thoracic lesions: 1) "healthy pigs" unlikely to have any thoracic lesion, 2) "multi-lesion pigs" likely to have a moderate-high lung score, pleurisy score of ≥1 and pericarditis and two intermediate classes, 3) one likely to have a mild-moderate lung score and possible pleurisy, and 4) the other a moderate-high lung score but lower likelihood of pleurisy. The relative frequency of these classes differed between the two provinces and between smallholder and commercially raised pigs within provinces. Most pigs from Albay were "healthy pigs", whereas most pigs from commercial farms in Batangas were "multi-lesion pigs".

Conclusion: This study has provided baseline data for these provinces and identified patterns of co-occurrence of lesions. Targeting areas where "multi-lesion pigs" are most common should maximize impact of future control measures.

Key words: lung scoring, respiratory diseases, Philippines

Dog days and dingo nights: cross-species interactions to inform rabies spread modelling

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ABSTRACT

Objective: determine abundance of wild dogs surrounding indigenous communities in northern Australia and estimate frequency of contact with domestic dogs.

Materials and methods: sites surrounding 5 indigenous communities in the Northern Peninsula Area, Queensland were purposively selected. A motion-and-heat activated camera was established at each site. Data were screened for dog photos. Dogs were classified as dingo-type, supervised or unsupervised domestic and unsure. Activity was estimated as dogs per camera-trap night (CTN; a 24 hour period of camera-trap activity). Cross-species interactions within 2 hour and 30 minute windows were counted.

Results: During a 6-month period, 55,473 photo series were captured at 19 camera-trap sites (2,951 CTN). Dogs were observed in 2.21% of photo-series: 538 (43.8%) dingo-type, 502 (40.9%) unsupervised domestic, 122 (9.9%) supervised domestic and 66 (5.4%) unsure. Dingo-type dogs were most active at one site, an unofficial waste dumping area close to one community: 57 cross-category pairs within 2 hours were observed at this site, and the frequency at which cross-category pairs were observed within 30 minutes and 2 hour windows were 0.06 and 0.30 pairs/CTN, respectively. Dingo activity was also frequently observed between two other communities, and near the official refuse-dump, but rarely at the camp-ground or beach sites. The activity of unsupervised domestic dogs followed a similar spatial pattern to dingo-type dogs (R_{sp} 0.64, P = 0.003).

Conclusion: Preliminary data suggest that dingoes are abundant (up to 1.02/CTN), and potential interaction with unsupervised domestic dogs appears to greatest around locations at which waste is dumped; it is less likely in areas with high human activity. This information will be incorporated into a rabies spread model to identify effective surveillance (including *proof of freedom* assessment) and response strategies that can inform policy for a rabies outbreak response in this region.

Key words: Wild dogs, domestic dogs, contact, interface, Australia

Epidemiology of wild marine mammal mortalities in the UK- 25 years of strandings surveillance

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ABSTRACT

Objective: Systematic and coordinated surveillance of marine animal strandings around the UK coast has been in operation since 1992. Funded by the UK governments, the schemes collate reports of marine animal strandings and a subset of cases are necropsied to establish causes of mortality. Here we present a summary of this long term dataset and highlight some of the patterns and conclusions it has been possible to draw about the health of, and threats to, cetacean populations around the UK coastline

Materilas and methods: In the 27-year period between 1991 and 2017, 19,186 marine strandings were reported; 14927 cetaceans, 4152 pinnipeds, 75 basking shark and 37 marine turtles. Systematic necropsy was undertaken on 4285 cases during this period.

Results: Twenty-nine species were necropsied comprising; Phocoenidae (n=2369); Delphinidae (n=1369); Balaenopteridae (n=91); Ziphiidae (n=61); Physeteridae (n=30); and Kogiidae (n=9). Traumatic causes of mortality, or those where the animal was otherwise healthy formed 53% of those examined. Common direct anthropogenic drivers of mortality included by-catch and/or entanglement (n=718) and ship strike (n=35). Additional factors for mortality included infectious disease related mortality (n=664), live stranding (n=506), starvation (n=448, of which 141 were neonatal starvation cases) and interspecific aggression (n=388). Eleven large mass stranding events (MSE), involving ten or more cetaceans occurred during this period. Two of the MSE's investigated had potential acoustic drivers. Although evidence of marine debris ingestion was noted in some individuals, only one case of fatal impact from debris ingestion was recorded in the 3924 cetaceans examined during this 27-year period. However, several cases of chronic entanglement were diagnosed likely caused by marine debris or fisheries interactions.

Conclusion: This work highlights the value, and potential biases, associated with using opportunistic data for wildlife surveillance and suggests how approaches employed successfully in this program could potentially be applicable to epidemiological investigations of other wildlife taxa.

Anthropozoonotic parasites in urban dwelling marsupials in the greater Perth region, Australia

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ABSTRACT

Objectives: Wildlife living in urban areas are at risk of acquiring infections from humans and domestic pets. This is of concern regarding the impact on wildlife population health, and the creation of wildlife reservoirs of infection. This research investigated the presence and epidemiologic features of gastrointestinal and macroscopic ecto- parasitic infections in the marsupials quenda (*Isoodon obesulus*) and brushtail possums (*Trichosurus vulpecula*) in the greater Perth region, Australia. This was undertaken with a focus on anthropozoonotic parasites, and investigating differences in infection epidemiology between marsupials living in urbanised environments and bushland.

Materials and Methods: A cross-sectional study was undertaken, sampling 287 quenda and 33 possums across 35 urbanised and 29 bushland sites. Faeces were tested for gastrointestinal parasites using immunofluorescence, faecal flotations and PCR and sequencing; blood samples were tested for *T. gondii* antibodies using modified agglutination testing; ectoparasites were differented morphologically. Data were analysed using multivariable logistic and linear regression.

Results and conclusions: Identified parasitic infections, which included two previously undescribed species and 11 new host records, were overwhelmingly of native taxa that are not known to, or considered highly unlikely to, infect humans or domestic animals. However, *Giardia duodenalis* and *Giardia canis* were identified in quenda, both at 0.4% prevalence (95% CI 0.1 – 1.9%); prevalence of infection with stick-fast fleas (*Echidnophaga gallinacea* and/or *E. myrmecobii*) was 4.5% (2.7 – 7.6%) in quenda and 6.06% (1.7 – 19.6%) in possums; and eggs of the poultry nematode *Ascaridia* spp. were identified in quenda faeces, suggesting that they are capable of acting as a vector of this infection. The odds of or intensity of certain parasitic infections varied between animals trapped in bushland and urbanised environments. Results suggest that in quenda, this was attributable to the exceptionally high population densities observed in urbanised environments.

Infectious disease transmission at the wild dog – domestic dog interface in remote indigenous communities in northern Australia

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ABSTRACT

Objective(s): Remote Indigenous communities in northern Australia contain large populations of free-roaming domestic dogs and are surrounded by wild dogs. Australia, which is a canine-rabies free country, is threatened by the current spread of the disease across Indonesia, leaving only 300 kilometers between northern Australia and infected Islands. The incursion of rabies into wild dog populations in Australia would make disease control very challenging. The objective of this study is to evaluate potential rabies spread within wild dogs using a disease spread model based on parameters relevant to the north Australian wild dog context.

Materials and methods: Multiple approaches were used to estimate wild dog density and home range and the extent of interactions between wild and community dogs in northern Australia: 1) camera-traps; 2) scoping review on wild dog ecology and biology; 3) interviews with local residents who use community dogs for pig hunting activities. An integrated approach combining these methodologies is being used to parameterize a stochastic spatial simulation model of rabies spread in wild dogs, incorporating the wild-domestic dog interface.

Results: Twenty-eight cameras deployed along trails and at focal points captured 1.374 million photographs over one year. Dogs were identified in 2.4% of these photographs, which are used to calculate wild dog density estimates in northern Australia. Results from the scoping review has revealed that wild dog home range is a well-researched area in which pooled estimates can be calculated using a meta-analysis. According to interviews with hunters, hunting trips provide opportunities for encounters between hunting and wild dogs, highlighting the possibility of disease transmission between both populations. Further analyses in relation to the stochastic rabies spread model will be presented.

Conclusions: Using this information, the model developed will help provide recommendations for controlling a potential outbreak of rabies impacting Indigenous communities, wildlife populations and the ecosystem in Australia.

Key words: Disease modelling, wild dogs, Australia, wild-domestic interface, rabies

Factors affecting incidental koala sightings in Queensland, Australia

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ABSTRACT

Objective: To describe and identify factors associated with incidental koala sightings in South-East Queensland (SEQ), Australia.

Materials and methods: Koala sightings reported by members of the public (n = 42,000) between 1997 and 2014 were analysed using spatial cluster analysis, adaptive kernel smoothing and boosted regression trees (BRT).

Results: Over 17 years, a total of 14,252 of koalas were sighted in trees (87%, n = 11,251), on the ground (6%, n = 792), in other locations (6%, n = 805) or in captivity (0.39%, n = 50).
Sightings showed a strong seasonal trend with highest numbers reported during the koala breeding period (September-November) during July to November. Sightings were observed mostly in residential land (63%), followed by agricultural land (15%) and parklands (12%). Longitudinal analysis showed that koalas were present in all land categories during all months of the year without any specific temporal pattern. Spatial clusters were identified (p <0.05) in the east coast and central region, throughout the study period and a few clusters in new areas from 2010 onwards in the center of the study area. Adaptive kernel smoothing showed high intensities of koalas in two east coast areas. Using BRT, we identified contribution of distance variables to the probability of detection; cycle paths (32%) and residential roads (27%) followed by footways (15%), motorways (11%) and other road types (13%).

Conclusion: Incidental sightings of koalas are consistently reported by members of the public and provide a valuable passive surveillance dataset for koala health and abundance estimates. Sighting data have inherent biases that have to be taken into account if used as a basis for decision making.

Key words: Koala, Queensland, sighting

Where do bats go? Shedding light on virus exposure pathways and surveillance strategies by tracking bats

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ABSTRACT

Objectives: Our objective was to track the movement of African straw-colored fruit bats (*Eidolon helvum*) in Tanzania to study their foraging patterns and implications for disease transmission to other species. *E. helvum*, is a widely distributed and gregarious species, which plays a critical role in seed dispersal and pollination.

Materials and methods: GPS data loggers (satellite: n = 15, and UHF: n = 10) were deployed on 25 adult *E. helvum* bats captured at their roosting locations in two areas: Morogoro Municipal and Kilombero District near the Udzungwa Mountains of Tanzania. Foraging and roosting sites were determined from collected movement data and characterized according to their proximity to urban and protected areas via geostatistical analyses. Areas for virus shedding and environmental sampling were determined, and potential locations for setting up camera traps to record the presence of other animal species near bat foraging sites were identified.

Results: Tracking data from 7 of the 10 UHF tags revealed variability between individual bat movements and a fidelity to foraging areas on consecutive nights. While the majority of the foraging areas were in or near urban areas, bats fed in protected areas as well, Udzungwa Mountains National Park (UMNP) being the most frequented out of these. The GPS information from the satellite tags led to researchers identifying specific types of orchards for environmental sampling and setting of camera traps.

Conclusion: Movement patterns of *E. helvum* bats in Tanzania reveal that there is the possibility of contact between bats, non-human primates, livestock, and humans in bat foraging areas around human dwellings and horticulture, as well as an opportunity for viral sharing to occur between bats and other wild species in protected areas. Thus, while these bats are important for pollination and seed dispersal within protected areas, they may also serve as bridges for interspecific viral transmission.

Key words: Bats, tracking, movement, spillover, zoonoses

Towards diagnosing tuberculosis in pachyderms: the contribution of species-specific interferon gamma assays

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ABSTRACT

Objectives: To investigate the potential of species-specific interferon-gamma (IFNg) assays to detect infection with *Mycobacterium tuberculosis* complex (MTBC) bacteria in captive elephants and free-ranging rhinoceroses.

Materials and methods: Fifty African elephants in safari facilities in Zimbabwe and Zambia were tested using the elephant-specific IFNg assay, of which 17 animals were re-tested after >12 months. Three white rhinoceroses experimentally infected with *M. bovis* were tested in the rhinoceros specific IFNg assay in monthly intervals from 3 months prior to 20 months after infection (p.i.). In addition, 67 white rhinoceroses, 56 from Tb negative properties and 11 from KNP as well as 19 black rhinoceroses from KNP were tested. Whole blood stimulation for the IFNg assays was done with bovine and avian tuberculin, mitogen, medium as negative control and in the case of the e-IFNg assay including ESAT-6 and CFP10.

Results: Cut-off values were determined for both assays. Thirteen elephants (26%) were considered test positive following cut-off determination. Re-testing of 17 elephants >12 months later detected six test positive animals which included 4 previously test positive elephants. No animal was found to have converted from previously test positive to test negative. All rhinoceroses from Tb negative properties as well as nine individuals from KNP with confirmed negative *M. bovis* status yielded negative rh-IFNg results..Among the three experimentally infected rhinoceroses positive test results were obtained between four and eleven weeks p.i. but not at any other sampling occasion. Two white rhinoceroses euthanized due to injuries tested positive in the rh-IFNg assay followed by positive *M. bovis* culture. All 19 black rhinoceroses tested negative in the rh-IFNg assay.

Conclusion: Application of species-specific IFNg assays in elephants and rhinoceroses has shown the ability of these tests to a) detect IFNg released in response to infection with MTBC and b) be highly specific.

Key words: Bovine tuberculosis, cell mediated immune response, elephants, interferon gamma, rhinoceros

Molecular epidemiology of foot-and-mouth disease virus in rangelands shared by African buffalo and cattle in Kenya

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ABSTRACT

Objective: The role of wild African buffalo (*Syncerus caffer*) as reservoirs for foot-and-mouth disease virus (FMDV) is poorly understood in eastern Africa, a region where cattle and wildlife populations regularly intermix. Here, we use epidemiological and molecular genetic methods to evaluate the frequency of buffalo-cattle FMDV transmission in central Kenya.

Materials and methods: We collected samples from 92 buffalo and 98 cattle from in and around Ol Pejeta Conservancy (OPC) in Laikipia County. Blood samples were analyzed for detection of antibodies to FMDV non-structural proteins, and oropharyngeal samples were used for genetic sequencing of the VP1 region. 21 samples from cattle outbreaks in central Kenya were analyzed.

Results: Seroprevalence in cattle and buffalo was 93% and 77%, respectively. We recovered 16 sequences from cattle (serotypes A, O, SAT1, and SAT2), and 75 sequences from buffalo (SAT1 and SAT2). NGS revealed dual infection by both serotypes in six buffalo. Despite extensive contact with infected buffalo populations, no SAT1 or SAT2 viruses were found in OPC cattle, suggesting that cross-species transmission is rare. An FMDV outbreak in OPC cattle was associated with serotype A. At a broader scale, SAT1 and SAT2 viruses found in buffalo showed close phylogenetic relationships with sequences associated with several outbreaks of FMDV in cattle elsewhere in Kenya, suggesting that viral populations found in buffalo and cattle are intermixed but that buffalo do not tend to be the source of infection for cattle.

Conclusion: Viruses found in buffalo and in some cattle outbreaks were genetically distinct from current vaccine strains, suggesting that the vaccine may not be a good match to circulating FMDV strains. Results of our study significantly advance current knowledge of FMD within buffalo in east Africa, thus filling a knowledge gap for control measures in areas where buffalo and cattle populations share rangelands extensively.

Key words: Wildlife-livestock interfaces, Foot-and-mouth disease, molecular epidemiology

The impact of elephant endotheliotropic herpesvirus hemorrhagic disease on the European captive population of Asian elephant (Elephas maximus)

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ABSTRACT

Objective: Elephant Endotheliotropic Herpesvirus (EEHV) is considered the major cause of calf mortality in the captive Asian elephant population and is presently the most important infectious disease, threatening not only North American and European zoological institutions but also wild populations. The disease presents itself as an acute haemorrhagic syndrome due to vast endothelial destruction, causing sudden death. In captivity, there are breeding facilities which are highly affected by this hemorrhagic disease (HD) and others which are not or just minimally affected. In diseased elephants, the treatment with the human anti-herpetic drug Famciclovir was first described in 1998, which represents until today the most used antiviral treatment. More than 50.000 euros were invested in antiviral drugs in European breeding institutions, and despite its high costs shows a rather low efficacy, ranging between 20 and 50 per cent. To better understand and quantify the impact of EEHV-HD in the Asian elephant EEP (European Endangered species Program) population, a case-controlled study was conducted.

Materials and methods: A 30-year lifetime case-controlled study was conducted (1st Jan1985 – 1st January 2015), based on retrospective data reported by the European EEP Studbook, including 72 institutions holding 298 (84.214) Asian elephants. All captive-born individuals living in Europe (n=232) were included in the study.

Results: EEHV-HD is responsible for the death of nearly one-third of all captive born Asian elephants in Europe, which is further aggravated inasmuch as 75% of fatal cases occur between 1,4 and 3,2 year of age, presenting a serious risk to the conservation breeding efforts made by Zoos.

Conclusion: Currently, there are 41 calves at risk living in Europe, and as the world Asian elephant population continues to decline, finding and understanding the trigger elements on the onset of EEHV-HD becomes critical.

Key words: Elephant, Herpesvirus, EEHV, hemorrhagic disease, European population

Between roost contact is essential for maintenance of European bat lyssavirus type-2 in Myotis daubentonii bat reservoir: 'The Swarming Hypothesis'

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ABSTRACT

Objective: Many high-consequence human and animal pathogens persist in wildlife reservoirs. An understanding of the dynamics of these pathogens in their reservoir hosts is crucial to inform the risk of spill-over events, yet our understanding of these dynamics is frequently insufficient. Viral persistence in a wild bat population was investigated by combining empirical data and in-silico analyses to test hypotheses on mechanisms for viral persistence.

Materials and methods: A fatal zoonotic virus, European Bat Lyssavirus type 2 (EBLV-2), in Daubenton's bats (*Myotis daubentonii*) was used as a model system. A total of 1839 *M. daubentonii* were sampled for evidence of virus exposure and excretion during a prospective nine year serial cross-sectional survey. Multivariate statistical models demonstrated age-related differences in seroprevalence, with significant variation in seropositivity over time and among roosts. An Approximate Bayesian Computation approach was used to model the infection dynamics incorporating the known host ecology.

Results: The results demonstrate that EBLV-2 is endemic in the study population, and suggest that mixing between roosts during seasonal swarming events is necessary to maintain EBLV-2 in the population.

Conclusion: These findings contribute to understanding how bat viruses can persist despite low prevalence of infection, and why infection is constrained to certain bat species in multispecies roosts and ecosystems.

Key words: Lyssavirus, infection dynamics, wildlife reservoir, rabies, seroepidemiology

Chicken or the egg, or neither? Wildlife-livestock multi-host prevalence surveys of infectious abortion in interface areas of the SE Lowveld of Zimbabwe 2008-2017

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ABSTRACT

Objective: Infectious causes of abortion are a major constraint to livestock productions throughout the world, especially for ruminants in developping countries. Major knowledge gaps hindering the improvement of the management of these diseases include a poor understanding of the risk factors associated with the spread and maintenance of the infections between herds. This is especially true in areas where livestock interact with wildlife that may be infected by the same pathogens, thus potentially playing a role in the transmission to domestic hosts, while also suffering from the impacts of these pathogens. This paper compiles the results of several serological studies on brucellosis, chlamydiosis and Rift Valley Fever carried out over the past decade in three contrasted interface areas of South-Eastern Zimbabwe.

Materials and methods: Six sero-surveys conducted between 2008-2016 on the same three sites located in the Great Limpopo TFCA: no interface/porous interface/fenced interface (see Table 1 for details of methods, samples size and reference).

Results: Table 1 summarizes the prevalence estimates in livestock (cattle, goats) and wildlife (buffalo, greater kudu and impala) for three abortive contagious diseases in SE lowveld of Zimbabwe

Conclusions: We acknowledge possible biases associated with small sample sizes and non-validated diagnostic tests for some wildlife species. The conclusions differ markedly depending on the pathogens and the sympatric host-species considered: cattle and buffalo may both act as reservoir for all three diseases, including RVF, whereas only Chlamydia apparently circulates in impala and goats, and no serological evidence was found for the three pathogens in kudu. No clear pattern regarding the type of interface and disease prevalence in livestock was found. Further molecular studies are needed to assess the frequency and direction of pathogen spill-over in these complex wildlife-livestock multi-host communities.

Key words: Infectious disease, Maintenance, Abortion, Wildlife, Zoonosis

Table 1: Prevalence of selected infectious abortive diseases of ruminants in livestock and wildlife with contrasted levels of direct and indirect interactions in the SE lowveld of Zimbabwe (studies 2008-2017; see legend for references and tests).

Species	Interface	Brucellosis		Chlamydiosis		Rift Valley Fever	
		Samples (n+/N)	Prevalence (%/ [95%CI])	Samples (n+/N)	Prevalence (%/ [95%CI])	Samples (n+/N)	Prevalence (%/ [95%CI])
Cattle	0	19/180[a] 33/254[c]	10.5 [6.0-15.1][a] 13.0 [9.2-17.9][c]	92/254[d]	36.2 [30.4-42.5][d]	4/52[b]	7.7 [0.4-15.0][b]
	1	55/575[a] 92/472[c]	9.6 [7.25-12.0][a] 19.5 [16.1-23.4][c]	14/472[d]	24.2 [20.4-28.3][d]	13/71[b]	18.8 [9.2-27.4][b]
	2	0/60[a] 44-285[c]	0.0 [0-4.9][a] 15.4 [11.6-20.3][c]	121/285[d]	42.5 [36.7-48.4][d]	5/59[b]	8.5 [1.3-15.6][b]
Goat	0	0/196[e]	0.0 [0.0-1.5][e]	17/196[e]	8.7 [5.3-13.8][e]	0/10[f]	0.0 [0.0-25.9][f]
	1	0/228[e]	0.0 [0.0-1.3][e]	43/228[e]	18.9 [14.1-24.7][e]	1/18[f]	5.6 [0.1-27.3][f]
	2	0/175[e]	0.0 [0.0-1.7][e]	64/157[e]	36.6 [29.5-44.2][e]	0/13[f]	0.0 [0.0-20.6][f]
Buffalo	PA	0/38[a] 33/111[c]	0.0 [0.0-7.6][a] 20.7 [13.9-29.7][c]	53/111[d]	47.7 [38.2-57.4][d]	2/38[b]	5.3 [0-12.5][b]
Greater Kudu	PA	0/16[a] 0/18[c]	0.0 [0.0-17.1][a] 0.0 [0.0-15.3][c]	0/18[d]	0.0 [0.0-15.3][d]	0/22[f]	0.0 [0.0-12.7][f]
Impala	PA	0/33[a] 0/32[c]	0.0 [0.0-8.7][a] 0.0 [0.0-8.9][c]	14/32[d]	43.8 [26.8-62.1][d]	0/23[f]	0.0 [0.0-12.2][f]

Interface: 0=no wildlife; 1=porous; 2=fenced interface; PA: Gonarezhou NP-Malilangwe Cons.

References: [a] Gomo et al 2012; [b] Caron et al 2013; [c] Ndengu et al 2017; [d] Ndengu et al 2018; [e] Bhandi et al in prep; [f] Morton-Knight unpublished

Serological tests : Brucellosis/RBT +/- CFT or C-ELISA; Chlamydia/CFT; RVF/IgG I-ELISA

Avian Influenza Outbreak Response in US Zoos and Aquariums

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ABSTRACT

Objective: The objective of this project was to detail actions taken by state and federal animal health officials and zoological industry personnel in response to the 2014-2015 HPAI in the US and to identify strategies for improvement of the response in this sector.

Materials and methods: Detailed searches of web pages, media, literature, and personal discussions with stakeholders from HPAI affected and unaffected areas were conducted to identify patterns of disease response across stakeholder groups.

Results: Awareness of the importance of FAD preparedness for zoos and aquariums in the US has increased substantially in the past three decades. Several events have inspired new efforts to enhance the capacity of zoos and animal exhibitors to respond to an FAD event impacting their facility. In December of 2014, HPAI was diagnosed in wild birds in the State of Washington. The subsequent epidemic lasted until June of 2015 becoming the single largest US animal disease outbreak. There were 211 commercial premises and 21 backyard flocks located in 15 US states identified as having cases of HPAI. In excess of 50 million birds were affected. It is estimated that economic losses attributed to this outbreak exceeded $3.3 billion USD.

Conclusion: Responses varied across jurisdictions including: quarantine, surveillance, movement restrictions and imposition of requirements for enhanced biosecurity at facilities. Communication chains between state and federal regulatory agencies with the zoological facilities varied in their approach to disseminating information about disease risk, surveillance, and mitigation strategies. Zoological facilities in HPAI impacted states varied in their implementation of new operating procedures and increased biosecurity.

Key words: Avian Influenza, Zoological facility, Highly Pathogenic Avian Influenza

Baseline exposure to rabies and targeted vaccination of a large population of free-roaming African wild dogs in the Kruger National Park, South Africa

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ABSTRACT

Objective: Since 2008, rabies re-emerged in the domestic dog population in the areas surrounding the Kruger National Park (KNP), with domestic dogs entering the reserve having a very high probability of being rabies infected. This poses a threat to the endangered African wild dog (*Lycaon pictus*). Objectives of this study were to: 1) Measure baseline exposure to rabies in the African wild dog population of the Kruger National Park, South Africa; 2) Vaccinate 30-40% of adult dogs with an inactivated rabies vaccine; 3) Measure the immune response of a selected number of individuals over time; and 4) Assess the practicality of rabies vaccination in a large free-ranging population of and endangered species.

Materials and methods: AWD were chemically immobilised and vaccinated subcutaneously with 2ml inactivated rabies vaccine (Rabisin, Merial or Defensor 3, Zoetis) after collection of blood samples between 2016-08-06 and 2017-04-12 One dose of recombinant canine distemper vaccine (Recombitek CDV, Merial) was administered concurrently. A commercial BioPro ELISA rabies antibody kit (O.K. SERVIS BIOPRO, 2014) was used to determine previous exposure and response to vaccination through percentage blocking ELISA.

Results: Seventy-seven AWD, originating from 23 packs/dispersal groups were sampled. Of these, 73 (constituting 43.8% of the adult population) were vaccinated. Of these vaccinated AWD, 84.9% (62/73) were given a similar secondary vaccination at median 50 (range 22-150) days post primary vaccination. 3.9% (3/77) of the AWD tested had antibodies against rabies prior to vaccination. Of the animals tested post vaccination (46/77 by 2018-03-01), only 3 did not show detectable rabies antibodies, even though all animals showed an increase in their ELISA blocking percentage. About half (6/13) AWD monitored beyond one year post vaccination still had high antibody levels.

Conclusion: Targeted vaccination of AWD against rabies in a large, free-roaming environment is feasible and lasting, albeit requiring massive effort.

Key words: Rabies, African wild dog, free-ranging, vaccination, immunity

City zoos in Mediterranean countries: a safe haven for Leishmania infantum?

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ABSTRACT

Objective: To investigate abundance, host-feeding preferences and *Leishmania infantum* infection in Phlebotomine sand fly vectors in a zoological park in the outskirts of Murcia City in Southeast Spain.

Materials and methods: Sand flies were collected using eight CDC light traps placed close to wildlife enclosures during nine days in July 2016 and 2017 coinciding with the highest sand fly abundance in the area. They were morphologically identified, DNA was extracted from female vectors and PCRs were used to detect *L. infantum* kinetoplast sequences and to identify the blood meal source by amplifying and sequencing the vertebrate cytochrome c oxidase subunit 1 gene.

Results: Overall, 4027 sand flies were collected and 25% were *Phlebotomus perniciosus* and *P. ariasi* females, vectors of *L. infantum* in Western Europe. None of 202 specimens examined so far were *L. infantum* PCR-positive. Further analysis focusing on females engorged with fresh blood will allow a more precise estimation of *L. infantum* infection rate and feeding preferences.

Conclusion: Zoological gardens provide ideal breeding environments for sand flies however their importance as a reservoir of *L. infantum* may be scarce, depending on host susceptibility to infection and this is presently being investigated.

Key words: Sandflies, *Leishmania infantum*, wildlife, host-feeding preferences

Emergence of tick-borne diseases at northern latitudes in Europe: a comparative approach

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ABSTRACT

Objectives: The factors that drive the emergence of vector-borne diseases are difficult to identify due to the complexity of the pathogen-vector-host triad. The objective was to separate general (shared vector) and specific (different pathogen reservoir hosts) limiting factors of tick-borne diseases, as well as to address the role of exposure (shared and non-shared pathogens in different hosts), by utilizing a comparative approach.

Materials and methods: Four long-term datasets (1995–2015) on the occurrence and incidence of tick-borne diseases in humans (Lyme disease) and livestock (anaplasmosis and babesiosis) over a geographic area that covered the whole of Norway, were analysed by mixed effects regression analyses.

Results: We found broadly similar patterns of emergence across the four tick-borne diseases. Following initial increases during the first decade of the time series, the numbers of cases peaked at slightly different years and then stabilized or declined. Contrasting spatial patterns of disease incidence were consistent with exposure to ticks being an important factor influencing disease incidence in livestock. Uncertainty regarding the reservoir host(s) of the pathogens causing anaplasmosis and babesiosis prevented a firm conclusion regarding the role of the reservoir host-pathogen distribution.

Conclusion: Our study shows that the emergence of tick-borne diseases at northern latitudes is linked to the shared tick vector and that variation in host-pathogen distribution and exposure causes considerable variation in emergence.

Key words: *Anaplasma phagocytophilum, Babesia divergens, Borrelia burgdorferi* sensu lato complex, *Ixodes ricinus*, mixed-effects models

Trophic behavior of Japanese Encephalitis vectors in Cambodia

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ABSTRACT

Objectives: Japanese Encephalitis (JE) is the most important cause of human encephalitis in Southeast Asia. It is a zoonosis, transmitted from pigs, the amplifying hosts, to human by mosquito bites. Culex mosquitoes are opportunistic feeders and may adapt their behavior to environmental conditions. An improved knowledge of mosquito feeding behavior is crucial to identify risky areas and focus vector control strategies.

Materials and methods: To assess feeding behavior of mosquitoes in a rural Cambodian area where JE circulates, we performed 4 sessions of trapping (March, May, September, December), during 5 consecutive nights, collecting 4 times a night (6pm to 6am), and simultaneously using 5 baited traps , ie cow, chicken, pig, human and control. Abundances were adjusted according to body surface areas. For each species, effects on abundance of trap type, season, trapping time and site were assessed using generalized linear mixed models, with either trap, season, site or collection time as random effect.

Results: JE vectors were present throughout the year demonstrating that JE may be transmitted even during dry season, and that bed mosquito nets are not sufficient to protect humans. 36,599 individuals were trapped, with 66.8% of *Culex vishnui*, 14% of *Cx. tritaeniorynchus*, 6.7% of *Cx. gelidus*, 1.7% of *Cx. quinquefasciatus*, these latter four species being major vectors of JE, and 12,4% of Anopheles sp. Statistical analyses showed that *Culex vishnui, Cx. tritaeniorynchus*, and *Cx. gelidus* were mainly ornithophilic. *Cx. vishnui* was more abundant in December and less abundant from 3 to 6 am. *Cx. tritaeniorynchus* was more abundant during the dry season, in March and May; *Cx. gelidus* and *Cx. quinquefasciatus* were also more abundant in May.

Conclusion: This study confirmed a preferred ornithophilic and also opportunistic behavior, but mainly highlighted the high relative density all the year, that can explain the important circulation of JEV in the Southeast Asian area.

Key words: Japanese Encephalitis Virus, trophic Behavior;mosquitoes, vector, *Culex vishnui*

Use of entomology surveillance data for modeling Culicoides abundance in mainland France

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ABSTRACT

Objective: In France, *Culicoides* surveillance was implemented in 2002 in specific areas (Corsica and Mediterranean coastal mainland) and in the whole metropolitan France during 2009-2012 to monitor vectors activity during bluetongue epizootics. The national-scale surveillance was implemented again following the re-emergence in 2015. The purpose of this study was to model the abundance of *Culicoides* using surveillance data.

Materials and methods: Since 2016, the *Culicoides* surveillance network operates in 24 eco-climatic zones, with one night trapping per week in one site per eco-climatic zone. Eco-climatic zones were delineated by analyzing the catch data collected in France during 2009-2011, and are homogenous in terms of *Culicoides* abundance, diversity and phenology (start and end of activity period). Minimum and maximum temperature data at each trap location were obtained from Météo France, the French national meteorological service. We applied a specific count model for every eco-climatic zone using a spline transformation of the week number, the minimum and maximum temperature as fixed effects, and the catch site and the year of trapping as random effects. Model fit was evaluated by root mean standard error and mean absolute error.

Result(s): Overall, the model provided a good fit to the data for the 24 eco-climatic zones. They showed that the annual distribution of *Culicoides* varied in terms of abundance, duration, onset and end of activity period, and shape (one or two peaks, with or without plateaus).

Conclusion: Although data were collected for surveillance purposes, our modelling approach integrating minimum and maximum temperatures, which are known to be major drivers for *Culicoides* activity, allowed us to predict annual variations in abundance in each zone. Our results may be used to predict at-risk period within each eco-climatic zone and to model bluetongue dynamics and spread in mainland France. This information is essential to define risk-based surveillance programs.

Key words: Culicoides, Abundance modelling, Bluetongue spread, Surveillance and control evaluation

Modelling the Spatial Distribution of the Bluetongue Vector Culicoides brevitarsis in Australia

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ABSTRACT

Objective: Effective decision making in emergency animal disease outbreaks requires an understanding of the potential for disease transmission appropriate for local conditions. Disease models are tools to prepare for such risks. The Australian Animal Disease (AADIS) model has been developed to support foot-and-mouth disease preparedness and response. In this study the capability of AADIS has been extended to simulate the spread of the vector-borne disease bluetongue. The objective of this study was to model the spatial distribution of *Culicoides brevitarsis,* the main competent vector for bluetongue virus in Australia.

Materials and methods: We used a raster approach to adapt Kelso and Milne's 2014 model to estimate the spread of *C. brevitarsis* across Australia as a function of calendar time. Growth and spread of *C. brevitarsis* within each raster cell was dependent on three factors: average daily temperature, short range diffusion and wind-borne dispersal. Wind-borne dispersal was simulated using the Hybrid Single Particle Lagrangian Integrated Trajectory Model. Partial validation of the model was carried out by comparing *C. brevitarsis* counts at locations throughout Australia, as recorded by the National Arbovirus Monitoring Program (NAMP) with the simulated *C. brevitarsis* counts at the same location.

Results: Our model provided biologically plausible estimates of the spatial distribution of *C. brevitarsis* across Australia as a function of time. While *C. brevitarsis* were not present further south than northern coastal New South Wales during the cooler winter months of the year they re-emerged in more southerly coastal regions of New South Wales as temperatures increased and midges were re-introduced from wind-borne spread.

Conclusion: Our model provides a credible estimate of the distribution of *C. brevitarsis* across Australia in response to temperature and wind. This model provides a basis for simulating the dispersion of *C. brevitarsis*, the main vector of bluetongue virus in Australia.

Key words: Models, Vector-borne disease, *Culicoides brevitarsis*, wind spread

A freedom of disease survey: African horse sickness virus in South Africa's surveillance zone in 2017

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ABSTRACT

Objective: An African horse sickness (AHS) virus (AHSV) outbreak occurred in South Africa's AHS controlled area in autumn 2016. A once off freedom of disease survey was performed to establish the likelihood of ongoing circulation of this virus during the same period the following year. The seasonality of AHS outbreaks, the authorized AHS vaccination period against AHS and the inability to differentiate infected from vaccinated animals on laboratory testing impacts the ability to perform a freedom of disease survey for AHS in the same year as outbreaks in the controlled area.

Materials and methods: During March 2017 a total of 336 randomly selected horses from 51 farms were sampled from the 2016 outbreak population at risk of 1817 horses. A base population level design prevalence of 1% was used to establish the sample frame and 3 within herd and herd level design prevalence scenarios were used in evaluating the outcome of the surveillance sensitivity and probability of freedom.

Results: Depending on the underlying design prevalence, effectively ranging between 0.8% and 6.4%, and the use of informed or uninformed priors the confidence of freedom from this surveillance ranged between 81.9% and 99.9% (uninformed prior) and between 97.9% and 99.9% (informed prior). Based on the results the authors conclude that it is unlikely that the 2016 AHSV was still circulating in the autumn of 2017 in the outbreak containment zone.

Conclusion: The ability to perform freedom of disease surveys, and also to include risk-based surveillance, in the AHS controlled area of South Africa is influenced by the changing underlying population at risk and the high level of vaccination coverage in the horse population, and ongoing census post-outbreak must be undertaken to maintain a representative sampling frame for future surveillance activity.

Key words: Freedom from disease, surveillance, vector-borne

A field investigation of an African horse sickness outbreak in the controlled area of South Africa in 2016

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ABSTRACT

An outbreak of African horse sickness (AHS) caused by AHS virus (AHSV) type 1 occurred within the South African AHS surveillance zone during April and May 2016. The index case was detected by a private veterinarian through passive surveillance. There were 21 cases in total, which is relatively low compared to case totals during prior AHS outbreaks in the same region (and of the same AHS virus type) in 2004, 2011 and 2014. The affected proportion of horses on affected properties was 0.07 (95% CI 0.04, 0.11). Weather conditions were conducive to high midge activity immediately prior to the outbreak but *Culicoides* midge numbers decreased rapidly with the advent of winter. Surveillance to detect AHSV in midges was performed on one infected property. *C. imicola* was most prevalent (95.5% of total caught) but viral RNA was not detected in these samples. The outbreak was localised, with 18 of the 21 cases occurring within 8 km of the index property and the three remaining cases on two properties within 21 km of the index property, with the direction of spread consistent with a wind-borne dispersion of infected midges. Control measures included implementation of a containment zone with movement restrictions on equids. The outbreak was attributed to a reversion to virulence of a live attenuated vaccine used extensively in South Africa. Outbreaks in the AHS control zones have a major detrimental impact on the direct export of horses from South Africa, notably to the European Union.

Key words: AHS outbreak, arbovirus, control, trade

Modelling temporal dynamics of Culicoides populations on Reunion Island (Indian Ocean) vectors of viruses of veterinary importance

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ABSTRACT

Objective: Reunion Island regularly faces outbreaks of epizootic haemorrhagic disease (EHD) and bluetongue (BT), two viral diseases transmitted by haematophagous midges of the genus *Culicoides* (Diptera: Ceratopogonidae) to animals of economic importance such as cattle, sheep and goats. To date, five species of *Culicoides* are recorded in Reunion Island: *Culicoides bolitinos*, *C. enderleini*, *C. grahamii*, *C. imicola*, and *C. kibatiensis*. Although epizootics and *Culicoides* diversity are already well documented, abundance and seasonality of the five species are not. According to a recent viral screening of local *Culicoides* populations (unpublished data), at least four species are involved in the transmission of each virus. Therefore, characterizing the risk period by modelling the temporal dynamics of the five *Culicoides* species is a key step to better understand BT and EHD epidemiology and improve their control.

Materials and methods: Between 2016 and 2018, 56 biweekly *Culicoides* catches using OVI traps were set up in 11 sites. A hurdle model (*i.e.* a presence/absence model combined with an abundance model) was developed for each species in order to determine climatic and environmental drivers of presence and abundance of *Culicoides*.

Results: Diversity and abundance differ between sites: *C. imicola* is dominant at low altitude and *C. kibatiensis* at high altitude and catch average per site ranges from 9 to 47,142 *Culicoides*. A marked seasonality is observed for the 3 other species. Among 10 determinants, temperature is the only parameter associated significantly with both presence and abundance of each species. Humidity, length of nearby watercourse, rain, land use and vegetation index are the other main parameters driving presence and/or abundance.

Conclusion: This is the first study to model *Culicoides* population dynamics in Reunion Island. In the absence of vaccination and vector control strategies, determining periods of high abundance of *Culicoides* is a crucial first step towards identifying periods at high risk of transmission for both viruses.

Key words: *Culicoides*, temporal dynamics, hurdle model, Reunion Island

Estimating force of infection of Rift Valley fever virus in an endemic area of South Africa using reversible catalytic models

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ABSTRACT

Objectives: Rift Valley fever (RVF) is a mosquito-borne zoonotic disease causing large epidemics amongst ruminant livestock in Africa, but RVF virus (RVFV) can circulate in endemic areas without causing obvious morbidity. This study used cross-sectional age-specific seroprevalence data to estimate past seroconversion and sero-reversion rates in cattle, goats and wildlife in an endemic area, and to compare them with prospectively measured seroconversion rates in the same area.

Materials and methods: Cross-sectional serological surveys using the serum neutralization test were conducted in cattle (n = 606), goats (n = 104) and wildlife (n = 156) in an area with a high current level of RVFV circulation. Reversible catalytic models of the form: Pa = lambda/(lambda+rho)*(1−exp(−(lambda+rho)*a)), where Pa is seroprevalence in animals of age a, lambda is past seroconversion rate and rho is sero-reversion rate per animal-year, were fitted to seroprevalence data. Model estimates were subjectively compared with seroconversion rates calculated from follow-up of the seronegative livestock.

Results: Seroprevalence increased with age in all species, although it was high even in young animals (25% in animals ≤2 years). Model estimates of the number of infections per animal-year were 0.29 (95%CI: 0.08-1.04) for cattle, 0.15 (95% CI: 0.06-0.35) for goats, 0.18 (95% CI: 0.08-0.42) for wildlife and 0.23 (95% CI: 0.14-0.38) for all species combined. For livestock, this was less than half that observed prospectively in the same study area. This could possibly be explained by extremely low rainfall during previous years, followed by relatively normal rainfall during the study period. The combined estimate of rho suggested that average duration of seropositivity was 3.0 years (95% CI: 1.3-6.7).

Conclusion: This study provided evidence of sustained RVFV circulation in an endemic area even during drought conditions. Reversible catalytic models provide a relatively simple way of estimating force of infection using cross-sectional data and may be useful in epidemiological studies of RVF and other diseases.

Key words: Rift Valley fever, vector-borne diseases, force of infection, seroconversion, reversible catalytic model

High seroprevalence and seroconversion rate to Rift Valley fever virus in an endemic area in the absence of outbreaks

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ABSTRACT

Objectives: Rift Valley fever (RVF) is a mosquito-borne zoonotic disease characterized in South Africa by large epidemics amongst ruminant livestock at very long, irregular intervals, mainly in the central interior. However, the presence and patterns of occurrence of the virus in the eastern parts of the country are poorly known. This study aimed to detect circulation of RVF virus (RVFV) in cattle, goats and wildlife in far northern KwaZulu-Natal Province and to estimate rate of seroconversion in livestock.

Materials and methods: Cross-sectional studies were performed in wildlife (nyala and impala; n = 326) and in communally farmed cattle (n = 423) and goats (n = 104), followed by longitudinal follow-up of seronegative livestock (n = 289) on 13 occasions over 18 months, representing 160.3 animal-years at risk. Exposure to RVFV was assessed using the serum neutralization test. Incidence rate of seroconversion was calculated using midpoint-imputed seroconversion dates and was compared using Poisson models. Hazard of seroconversion was plotted over time using the derivative of the kernel-smoothed Nelson-Aalen estimator with randomly-imputed seroconversion dates.

Results: Initial overall seroprevalence was 34.0% (95% CI: 29.5-38.8) in cattle, 31.7% (95% CI: 22.9-41.6) in goats and 35.0% (95% CI: 29.8-40.4) in wildlife, and was high in all age groups. Overall rate of seroconversion in cattle was 59.2 (95% CI: 46.5-75.3) and in goats 41.2 (95% CI: 26.6-63.9) per 100 animal-years, being 3 to 4-fold higher during the first year than the second year and varying significantly between localities within a 10 km radius. Seroconversions were detected throughout the year, with incidence rate peaking during the high rainfall months of December to March.

Conclusion: The high seroprevalence in all age groups and evidence of year-round viral circulation indicate a hyperendemic situation in the study area. This is the first study to directly estimate infection rate of RVFV in livestock in an endemic area and provides the basis for further investigation of mechanisms for virus survival during interepidemic periods.

Key words: Rift Valley fever, vector-borne diseases, zoonoses, seroconversion, incidence rate

Epidemiology and economic impact of Anaplasmosis in southern Illinois beef cattle

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ABSTRACT

Objective: Cattle movement and changes in climate may have had an impact on the geographic distribution and prevalence of bovine anaplasmosis in Illinois. The last serological survey of bovine anaplasmosis in Illinois reported a statewide beef cattle prevalence of 9% in 1989. At that time, southern Illinois was identified as a high prevalence region with a prevalence of 19.6%. The objectives of this study were to provide a current estimate of the prevalence, distribution and economic impact of bovine anaplasmosis in beef cattle from herds in 27 southern Illinois counties and to assess producer awareness of effective prevention and control strategies.

Materials and methods: A random sampling procedure stratified on herd size and location was conducted. Whole blood samples were collected from cattle and a questionnaire was administered to owners of participating herds. A qPCR was used to test samples using primers for Anaplasma marginale 16s ribosomal RNA and msp1a genes. Cases were defined as positive for both 16s ribosomal RNA and msp1a gene.

Results: To date 876 cattle have been tested from 27 herds in 15 counties. The crude anaplasmosis prevalence rate was 54.8%. Approximately 24% of producers reported a history of anaplasmosis. The mean number of cows per herd was 78.85. Average yearly losses of $4,590 (mean of 3.75 cow deaths per year) due to anaplasmosis were reported. Producers with positive herds were more likely to report maintaining an open herd.

Conclusion: Preliminary results indicate that the prevalence of positive cattle in southern Illinois has increased since the previous study and many herds may be impacted by anaplasmosis unbeknownst to their owners. Significant financial losses are reported by producers that are aware of anaplasmosis in their herd. Final results of diagnostic tests for an additional 150 herds and regression models will be presented.

Key words: bovine anaplasmosis, Anaplasma marginale, Prevalence, Economic Impact

Sea lice (*Lepeophtheirus salmonis*) transmission between farmed and wild salmon in Muchalat Inlet, British Columbia

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ABSTRACT

Objective: To evaluate the association between the abundance of sea lice recorded on salmon farms and the infestation levels on wild out-migrating Pacific salmon (*Oncorhynchus spp.*).

Materials and methods: This study included 10 years of sea lice count and management data (2007-2016; aggregated at the sampled month level) from all Atlantic salmon farms (n = 5) and wild Pacific salmon monitoring sites (n = 16) along Muchalat Inlet, British Columbia, Canada. The potential effects of farm-origin sea lice pressure from farms (X) on the prevalence of infestation on Chum salmon (*O. keta*), the dominant species in the study region, (Y) during their outmigration period (March-June) were assessed using mixed-effects logistic and linear regression models. Fixed effect of months and random effect of study years were included in the final models. To define X, sea lice output from each farm was weighted using a Gaussian Kernel density function based on seaway distance.

Results: Our analyses indicated a significant positive association between the sea lice abundance on farms and the probability that wild fish would be infested. However, increased abundance of lice on farms was not significantly associated with the prevalence of infestation observed on Chum salmon.

Conclusion: Our results suggest that Atlantic salmon farms may be an important source for the introduction of sea lice to wild Pacific salmon populations, but that the absence of a dose-response relationship indicates that any estimate of farm impact requires more careful evaluation of causal inference than can typically be found in the extant scientific literature.

Key words: Sea lice, salmon farming, wild Pacific salmon, Canada

Screening for the presence of infectious agents in historical Sockeye salmon (*Oncorhynchus nerka*) samples from British Columbia, Canada (1985-1994)

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ABSTRACT

Objective: To estimate the prevalence of salmonid infectious agents in historical return-migrating Sockeye salmon from mid-1980s to 1990s, before and during aquaculture expansion in British Columbia (BC), Canada and to evaluate the historical patterns in agent distribution and diversity by region.

Materials and methods: A high-throughput microfluidics qPCR platform was applied to detect the presence of 45 infectious agents in frozen liver tissue samples of historically collected adult Sockeye salmon belonging to six regions of BC. We used mixed-effect logistic, linear, and Poisson regression models to evaluate the regional variability () in prevalence, load, and diversity of infectious agents, and hierarchical cluster analysis to identify coexisting agents.

Results: Twenty-three infectious agents (7 bacterial, 2 viral, and 12 parasitic) were detected in 652 samples distributed among six regions. Prevalence ranged from 0.5 to 83.3% and varied significantly by region and between years. Agent diversity in the fish ranged from 0 to12 (median 4) and was significantly higher in fish from regions other than the Transboundary and Central Coast. We also identified significant coexistence among *Ceratonova shasta, Parvicapsula minibicornis,* and *Kudoa thyrsites*, and were most prominent in samples from the Thompson region. We also detected infectious agents that have been described only recently in BC salmon (Pacific salmon parvovirus, *Ca. Branchiomonas cysticola,* and *Parvicapsula pseudobranchicola*).

Conclusion: Some infectious agents detected in our study are known endemic (*Flavobacterium psychrophilum,* infectious hematopoetic necrosis virus, and *P. minibicornis*) in Sockeye salmon in BC. Detection of others such as *Kudoa thyrsites* and *Piscirikettsia salmonis,* both known to be endemic now, and some other recently described agents suggests these agents were likely present historically prior to the expansion of the aquaculture industry. This study serves as a historical baseline inventory of infectious agents' profiles in Sockeye salmon stocks in BC.

Key words: Sockeye salmon, historical, Fluidigm BioMark™ PCR, infectious agents, British Columbia

Use of regulatory surveillance data for industry sanitary improvement: A case study of Chilean salmonid data and salmon rickettsial septicaemia risk factors

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ABSTRACT

Objective: The aim of this study was to identify risk factors for salmon rickettsial septicaemia (SRS) to enhance SRS management.

Materials and methods: The Chilean National Fisheries Service (SERNAPESCA) collects regulatory data from salmon producers on endemic diseases such as SRS, a major disease of salmon globally. Regulatory data from 2010-2018 were extracted. Environmental data and details of the size of the salmonid population at risk by enterprise and counts of SRS-affected salmonids were integrated using SQL and spatial queries to provide a holistic epidemiological database of ~ 87 000 weekly production records. Biologically plausible *a priori* hypotheses of factors associated with the presence of SRS were developed. Zero inflated mixed negative binomial spatial models were developed to represent each of the hypotheses. The most supported models were selected using information theory. Coefficients of the most supported models and other models generated *post hoc* were examined to quantify associations between risk factors and SRS.

Results: Several important risk factors for SRS were identified. Species of salmonid, co-infection with sea lice, sea vaccination for SRS, infection pressure in a local waterway, site fish density and indicators of smolt quality were key risk factors associated with SRS mortality. Many are modifiable, providing an opportunity to reduce the incidence of SRS in Chilean farmed salmon. Accumulating cumulative degree days were strongly negatively associated with the likelihood that a site would remain un-infected in the zero-inflated part of the model. Coho and rainbow trout were less likely to be infected by SRS (excess of zero's), but once infected rainbow trout experienced high mortality rates compared with Atlantic salmon.

Conclusion: These results indicate that regulatory data maybe inexpensively used a second time to advance the industry wide management of severe production and trade limiting diseases, thereby enhancing the sanitary status of a national industry.

Key words: Salmonid, SRS, Risk factors, Chile, regulatory surveillance data

Risk factor analysis for improving post-harvest survival in Australian southern rock lobster holding facilities

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ABSTRACT

Objective: Southern rock lobster (SRL, *Jasus edwardsii*) is the highest value fishery export commodity (average AUD 84.5/kg) from Australia with an approximate total value of AUD 255 million. Between landing and export, SRL are held in specialised holding tanks for varying time periods. During the 2015-16 fishing season a higher variation in survival rate was reported by some holding facilities when compared to previous fishing seasons. A multidisciplinary investigation was undertaken to identify possible causes and favouring factors. The presentation reports the findings of a retrospective study of facility-level risk factors that may contribute to or mitigate survival in SRL.

Materials and methods: A custom questionnaire was built and trialled to collect qualitative and quantitative information on facility's infrastructure and capacity (10 questions), water systems (16 questions), SRL stock and health management (12 questions). SRL holding licence holders across South Australia, Victoria and Tasmania were recruited via e-mail and/or telephone. Onsite visits and interviews of consenting facilities, with active holding operations, were conducted. As the industry consists of a few tens of facilities, an advanced multifactorial analysis could not be conducted. Therefore, facilities were first categorised based on a multivariate analysis and clustering of their responses in questionnaire. Then the association between facility profiles and sub-optimal survival was explored using simple logistic regression models.

Results: Out of the 83 license holders on record, 63 were holding SRL stocks and 52 (83%) consented to participate. Sub-optimal survival was reported in 22 (42%) facilities. Some facility and management profiles were more at risk of having lower survival during the 2015-16 season. The detail of these profiles will be presented.

Conclusion: This facility-level investigation identified SRL holding practices at risk of lower SRL survival. The results will guide the industry to improve their infrastructure and management to control and optimise SRL post-harvest survival.

Key words: Southern rock lobster, risk factor analysis, questionnaire, holding facility

Is 'too late' always too late? The case study of a retrospective investigation in ranched southern bluefin tuna (*Thunnus maccoyii*) mortality outbreak

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ABSTRACT

Objective: The ranching of Southern Bluefin tuna (SBT, *Thunnus maccoyii*) in South Australia started less than 30 years ago to increase the value of a quota restricted fisheries. It relies on the rapid growth of wild caught stocks over a 3-6 month period. The industry produces up to 9,000 tonnes per season for an approximate value of AUD 130 million. In 2017, individual companies experienced unexplained mortality with report of corneal lesions. At the end of the ranching season, a retrospective study was undertaken to investigate the outbreak.

Materials and methods: Accessible data included daily mortalities from all companies (n=10) as well as the presence of corneal lesions (CL) on dead SBT for half of the companies. A case-control study was designed to investigate the association between CL and mortality and between CL and body condition at harvest. The presence of CL (exposure) was measured on all of the dead SBT (cases) and on a fraction of harvested SBT (controls) from three volunteering companies that experienced an outbreak and for which detailed mortality dive records were accessible.

Results: Industrywide, 1.65% of ranched SBT died during 2017. Mortality peaked at the start of the season in March before to decrease monotonically. Mortality was highly clustered within 4 companies (2.7-5.1% cumulative mortality) and most cages within these companies were affected. After adjusting for cage and farm clustering, CL was highly associated with mortality ($P<0.001$), and if a SBT with CL survived until harvest, its body size and condition index would be significantly lower than the cage average ($P<0.001$).

Conclusions: The economic impact of CL was estimated by stochastic modelling at AUD 501.5 per affected fish and AUD 63,803 per affected cage. Although the aetiology of CL remains unknown, the retrospective investigation of mortality can provide valuable clues about the cause and impact of an outbreak in aquaculture.

Key words: case-control study, Southern Bluefin tuna, corneal lesion

The use of a refined Fish Health Assessment Index to evaluate the effect of contaminants of emerging concern on fish health in northeastern Minnesota, USA

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ABSTRACT

Objective: Water is arguably the most essential natural resource in the world; yet, freshwater ecosystems are threatened by many human activities. Contaminants of emerging concern (CECs), such as pharmaceuticals and personal care products, are increasingly detected in the environment, but the distribution of such contaminants in northeastern Minnesota is currently unknown. Consequently, we aimed to evaluate the health of subsistence fish species harvested by an indigenous community, at sites with detected CECs and different anthropogenic impact, using a refined Fish Health Assessment Index (rFHI) and ectoparasite prevalence.

Materials and methods: We collected 545 fish from 17 sites – categorized as developed, undeveloped, and wastewater effluent according to a multi-criteria selection process – in the Lake Superior watershed. The rFHI contains numerical scores from 10 fish health variables that were summed to provide a total score for each fish examined. A higher score may be associated with lower health. We identified ectoparasites by examining gill and skin wet-mount preparations via microscopy.

Results: For Lake Superior, fish captured at wastewater effluent sites (rFHI mean = 91.19) had higher scores than fish at undeveloped sites (rFHI mean = 59.04), whereas fish at inland sites did not follow a consistent pattern. Overall, Lake Superior fish (rFHI mean = 72.57) had higher rFHI scores than fish at inland sites (rFHI mean = 42.78). Liver, fat, and internal parasitism scores contributed most to the total rFHI score. There were fewer ectoparasites in fish from Lake Superior sites than inland sites, which could be related to capture method or to the conditions in Lake Superior.

Conclusion: Given the observed differences in rFHI scores and parasite prevalence between inland and Lake Superior sites, a unique set of rFHI and parasite metrics need to be employed for different sites. Metrics from this study will be further evaluated in association with CEC levels across these human-impacted sites.

Key words: ecotoxicology; aquatic ecosystem; health; parasites; subsistence fish

Monitoring quality of young stock rearing in dairy herds: a data-based scoring method

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ABSTRACT

Objective: A young stock rearing quality system (KalfOK) based on routinely collected data was developed, aiming to provide an objective and standardised means to evaluate and monitor young stock rearing in Dutch dairy herds.

Materials and methods: In total, 201 dairy farmers participated and twelve key indicators were defined that were related to calving, successful rearing, antimicrobial use and herd health. For each key indicator, the value was calculated per herd and quarter of the year between January 2014 and April 2017. Benchmark values were determined to compare herd specific results with and for selection of threshold values. Each of the key indicators were graded when the value scored above the threshold. Combining the grades resulted in the herd specific KalfOK-score, which could vary between 0 and 100 points. Additionally, 100 participating dairy herds were visited and the quality of young stock rearing was scored by a trained veterinarian. The herd specific KalfOK-score was compared to the results of the health checks and the validity of KalfOK to distinguish herds with an excellent or insufficient quality of young stock rearing was assessed.

Results: The average KalfOK-score was 77 points (25th percentile = 71 points, 75th percentile = 85 points). The combination of the sensitivity (88%, 95% CI: 47-100%) and specificity (67%, 95% CI: 54-78%) of KalfOK to correctly classify herds with an excellent quality of young stock rearing was highest at the cut-off value of 80 points. Detection of dairy herds with an insufficient quality of young stock rearing was best at a cut-off value of 70 points (sensitivity 86%; 95% CI: 42-100%, specificity 77%: 95% CI: 66-86%).

Conclusion: KalfOK is implemented on national level as a voluntary program since 1 January 2018. At this moment already 9,800 dairy farmers participate (60% of all farmers) and participation levels are still increasing. KalfOK illustrates how routinely collected data can be transferred into herd specific information in support of animal health and welfare. Given the increasing availability of automatically assembled data, the development of similar monitoring tools seems feasible.
Key words: dairy calves, young stock rearing, management, data-based

Report on the use of antibiotic dry cow therapy (DCT) in Finnish dairy herds

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ABSTRACT

Objectives: The objective of this study was to survey the current use of antimicrobial dry cow therapy (DCT) in Finnish dairy herds by using an online questionnaire.

Materials and methods: The questionnaire was designed using close-ended questions, and it was accessible to all dairy farmers of the Finnish dairy herd recording system. In total, 715 dairy producers across the country, representative of the Finnish dairy industry, participated in the survey.

Results: Selective DCT was the most common approach when drying off cows (78% farms, 558/715). Of the selective DCT farms, 36.5% reported to use also internal teat sealant (ITS) alone or in combination with DCT. Most farmers (71.5%, 398/557) using selective DCT reported treating only up to one-fourth of their cows at dry-off. Blanket DCT was applied in 13.3% (95/715) of farms, and within these farms 35.8% also applied ITS. Blanket DCT was most commonly used in larger herds and in farms with automatic milking system (AMS). Of the responding farms, 8.7% (62/715) did not apply DCT at all, and of those only 5% used ITS. Microbiological testing of milk samples at dry-off was the preferred method to select cows for DCT. Milk was microbiologically examined at dry-off in 81.9 and 64.2% of farms using selective and blanket DCT, respectively. The percentage of farms examining milk samples was high in all milking systems, pipeline milking (68.6%), AMS (73.4%), and palor (79.3%).

Conclusion: Use of antibiotic DCT in Finland is limited and it is most often administered selectively. Most of farmers tested milk samples bacteriologically at dry-off to select cows receiving antibiotic treatment.

Key words: Dry cow therapy, internal teat sealant, selective dry cow therapy, bacteriological analyses

Estimation of the cost of different severity levels of lameness in dairy cows: A dynamic programming approach

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ABSTRACT

Objective: Lameness is a common, costly problem in the dairy industry, worldwide. Our objective was to estimate the cost of different lameness severity levels in dairy cows as a function of milk production, lameness risk, conception probability, mortality, and treatment cost.

Materials and methods: A veterinarian and hoof trimmers assigned lameness scores (sound (n=759), moderate (n=92), severe (n=91)) to cows in a Pennsylvania (USA) dairy from June 2015 to August 2017. Scores' effects on milk production in these cows were estimated using generalized linear mixed models. Parameters for lameness risk, conception probability, mortality, and treatment cost associated with lameness severity were obtained through literature review. All parameters were input to a dynamic programming economic model to obtain costs of lameness severity levels and management recommendations based on individual cow characteristics.

Results: The optimal profit per cow (average across all cow characteristics) per year under assumed expenses and revenues was $426.05 when lameness incidence was assumed to be 0% (ideal situation) in the herd. Profit per cow per year decreased to $396.18, with an assumed total lameness incidence of 19.1% (7.1% moderate and 12.0% severe cases). The model recommended that 94.9% of lameness cases be treated under the scenario assuming both moderate and severe lameness in the herd. Cost per case was $156.39 in an average herd with 19.1% lameness incidence. When only severe cases were assumed, total cost was $177.55: $84.75 (47.7%) due to milk loss, $31.61 (17.8%) to fertility loss, and $61.19 (34.5%) to treatment costs.

Conclusion: Our results derived from monthly human-assessed lesion scores. They could be compared to results from an automated lameness detection system ("FitGait") based on daily locomotion measurements, which our team is currently developing. Once this is available, we will customize our model to estimate the economic gains due to earlier lameness detection. The USDA provided funding for this project.

Key words: dairy cows, lameness, severity scores, economic modeling

Myocardial infarction in beef and buffalo calves during Foot and Mouth Disease outbreak in Nakhon Phanom province, Thailand, Dec 2016 – Jan 2017

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ABSTRACT

Objective: Foot and mouth disease (FMD) is an endemic disease in Thailand. It is seldom to find calf death among cattle and buffalo affected herd. On 4th January 2017, Nakhon Phanom Provincial Livestock office was notified of the calf's death among the suspected FMD beef herd in one village. An investigation was conducted to verify the diagnosis and found out probable risk factors.

Materials and methods: A case control study was held in the affected villages. We interviewed the farmers, face to face, regarding animal herd management, signs/symptoms and sick animal management. Tissue lesion of sick animals and internal organs of dead animal were collected and submitted to Veterinary Research and Development Center for laboratory diagnosis. Risk factors were identified using logistic regression analysis.

Results: There were 112 (25.1%) out of 447 animals, in 36 cases and 42 control farms, defined as suspected FMD animals. The mortality rate was 3.6% (16/447). The median age of the dead calves was 1.8 months (3 day-4 months). Nine calves carcasses were dissected. All carcasses found myocardial infarction. FMD was confirmed by PCR in 8 carcasses. FMD serotype A with the r-value of 0.25 was revealed in ELISA typing. Sharing pasture sources herd was more likely to being sick 7 times more than non-sharing herd (AOR=7.1 95%CI=1.6-32.9). The other risk factor was exposed to animal movement paths (AOR=7.3 95%CI=1.4-39.0). The FMD vaccination coverage at least 80% seem to be a protective factor (AOR= 0.1 95%CI=0.01-0.3).

Conclusion: This FMD outbreak was documented the death of cattle and buffalo calves that never reported before in Nakhon Phanom. FMD viral variation was concerned. Quarantine the calves apart from sick animal and infected herd, withdraws sharing pastured during the outbreak were recommended. FMD vaccination coverage of 80% should be practiced and promoted as one of a protection measure.

Key words: FMD, cattle, buffalo, tiger heart

Streptococcus agalactiae mastitis: an indication of sequence type-specific effect on milk production in Norwegian dairy cows

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ABSTRACT

Objective: Our aim was to estimate milk production loss associated with *Streptococcus agalactiae* mastitis and to assess differences between frequently occurring sequence-types of *S. agalactiae* in Norwegian dairy herds.

Material and methods: A cohort study was performed utilizing the Norwegian Dairy Herd Recording System database. Herds in which *S. agalactiae* had been detected in individual animals (by bacteriological culture or qPCR) between 2012 and 2015 were included. Multi locus sequence typing (ST) was performed on *S. agalactiae* isolates from 86 herds. Monthly test-day milk yield records for the entire period were accessed for comparison of milk yield between *S. agalactiae*-postive and remaining cows, within each herd. Effects of *S. agalactiae* mastitis and sequence type on test-day milk yield were evaluated using a multilevel linear regression model controlling for clustering by herd and cow. Estimates were adjusted for parity, days in milk, season of calving, and selected health events. A second model was fitted to a subset of herds in which the ST1 and ST103 had been found, to compare their effect on production.

Results: The study population consisted of 150 herds, located throughout Norway. The dataset included 15.757 cows, 30.850 lactations and 204.126 test-day milk yield records. In 11.451 of the lactations, at least one diagnostic sample (BC or qPCR) had been taken. Of these, 1.519 *S. agalactiae* positive lactations were detected. Overall, *S. agalactiae* positive cows produced approximately 1.5 kg/day more than the remaining cows two months pre-diagnosis. Their milk production declined until one month post-diagnosis and stabilized at approximately 1.0 kg/day lower than the remaining cows. ST 103 was associated with milk loss for the duration of the lactation, whereas ST1 had a shorter effect.

Conclusion: Milk production loss associated with *S. agalaciae* ST103 was more severe than the loss associated with *S. agalaciae* ST1.

Key words: *S. agalactiae*, sequence type, milk loss

The prevalence of Fasciola hepatica in irrigated dairy regions of Victoria, Australia

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ABSTRACT

Objectives: *Fasciola hepatica* is a widespread problem in south-eastern Australia due to its relatively high annual rainfall and a mild climate suitable for the main intermediate host, *Austropeplea tomentosa*. A Victorian study carried out in the 1970's identified a strong correlation between the prevalence of fascioliasis and the grazing of irrigated pastures. The aim of this study was to estimate the prevalence of *F. hepatica* in dairy cattle that graze irrigated pastures in Victoria.

Materials and methods: This was a cross-sectional study of cows in dairy herds in six irrigation districts of Victoria. Sampling was carried out using a stratified, two-stage cluster design. Faecal samples were collected from 20 cows in 83 herds and individual cow fluke burdens were estimated using the coproantigen ELISA (cELISA) (BIO K 201/2). A Bayesian approach was used to estimate the true individual-animal prevalence of fascioliasis. True individual animal prevalence estimates were then adjusted to account for the stratified, two-stage cluster sampling design.

Results: *F. hepatica* prevalence ranged from 13% (95% CI [credible interval] 5% to 21%) in the Loddon Valley Irrigation Area to 68% (95% CI 55% to 84%) in the Macalister Irrigation District. Across all of the study districts *F. hepatica* prevalence was 38% (95% CI 28% to 48%).

Conclusion: Our results show that the individual animal prevalence of fascioliasis in irrigated dairy areas of Victoria was relatively high, similar to the 42% reported by Watt in 1977. *F. hepatica* prevalence varied by irrigation area with more than 50% of animals infected in two of the six study districts. Future work will investigate the epidemiology of *F. hepatica* in irrigation areas that had a low prevalence and to use this information to better define fluke control measures in all of the study regions.

Key words: Fascioliasis, dairy cattle, cross-sectional study, cluster sampling, Bayesian statistics

Can precision dairy monitoring technologies (PDMT) be used for early detection of changes in metritis status in dairy cattle during post-partum?

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ABSTRACT

Objectives: To characterize different cow behaviors measured with precision dairy monitoring technologies (PDMT) and to estimate their association with changes in metritis score throughout post-partum.

Materials and methods: 21 dairy cows that did not experienced any disease postpartum other than metritis were retrospectively selected from a dataset with 140 cows. Information per cow included daily cow behaviors (steps, visits to feedbunk, rumination time, eating time, activity) measured with PDMTs up to 21 days postpartum, and their metritis scores (1 to 3), assigned after inspection of uterine discharge on days 3, 5, 7, 9, 11, 14, 17, 19, and 21, with metritis being score 2 or higher. K-means cluster analysis (k = 2) on the behavior variables during the 3 days prior to a change in score, followed by Chi-Square test for the association between clusters and score change was conducted using open-source software Python.

Results: 116 valid measurements of metritis scores were used for the analysis. With separate cluster analysis per behavior variable, there was a significant association between activity, number of steps, and feedbunk visits during the 2 days prior to a change in metritis score was determined.

Conclusion: K-means clustering is a valid method to determine different patterns in dairy cow behaviors up to 2 days prior to a change in metritis status. Cluster analysis provides real-time measurements compared with traditional methods of disease diagnosis. Therefore, this approach can be considered for data preprocessing prior to more complex prediction models used in syndromic surveillance for early detection of diseases through PDMT. Similar analyses will be explored using other behavior variables for their association with other syndromes, such as fatty liver or immunosuppression in dairy cattle.

Key words: syndromic surveillance, cluster analysis, dairy cattle, real-time monitoring, risk-based approaches

Prevalence of *Mycobacterium avium* subsp. *paratuberculosis* infections in Canadian dairy herds

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ABSTRACT

Objectives: Johne's disease (JD) is a progressive, chronic infection and inflammation of the small intestines of ruminants caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP). Accurately estimating the prevalence of MAP infections is an important part of controlling the spread of infections, and monitoring the effectiveness of control programs. Due to the number of varying diagnostic methods that are used across Canada, prevalence estimates between regions and programs cannot be compared. The aim of the current study was to estimate the herd-level prevalence of MAP infection in the Western Canada, Ontario, Quebec, and the Atlantic Provinces, using the same diagnostic method across Canada.

Materials and methods: In all 10 provinces (4 regions), 2 environmental samples were collected from the lactating cattle area and manure storage on 362 dairy farms and cultured for the detection of MAP. An additional sample was collected from the breeding age heifers (BAH). Diagnostic sensitivity (Se) and specificity (Sp) were calculated for the ability to detect MAP-positive farms using only 2 environmental samples based on previous research, resulting in a Se and Sp of 0.40 and 0.99, respectively. There was no difference in the Se and Sp test characteristics when including BAH samples. These test characteristics were applied to the environmental culture results from the 362 participating farms in the 4 regions to estimate true prevalence.

Results: True prevalence was 66% of farms in Western Canada, 54% in Ontario, 24% in Québec, and 47% in the Atlantic Provinces. Herds housed in tie-stalls had lower prevalence than free-stall housed herds, and herds with 101-150 and >151 cows had higher prevalence than herds with ≤ 100 cows.

Conclusion: This is the first time MAP prevalence has been determined using a single detection method, laboratory, and within a single year across Canada, allowing for the direct comparisons of prevalence among different regions, housing types, and herd sizes within the country.

Key words: Johne's disease, prevalence, environmental sampling, culture, Canada

Relationships between type of hoof lesion and behavioural signs of lameness in Holstein cows housed in tie-stall facilities

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ABSTRACT

Objective(s): Hoof lesion type and severity may or may not influence a cow to change their gait. In tie-stall facilities gait scoring can be difficult to perform, alternatively stall lameness scoring (SLS) can be used to identify lameness through observation of changes in weight bearing and foot positioning of tethered cows. The objective of this study was to examine relationships between SLS and hoof lesions.

Materials and methods: SLS assessments were completed by one observer looking for the following four behaviours: shifting weight, resting one foot, standing on the edge of the stall and uneven weight bearing when moved side to side. Hoof trimming records were collected from two hoof trimmers trained and assessed for agreement using lesion identification quizzes *kappa* (>0.9). Relationships between the SLS observations and the hoof trimming records were explored using logistic regression.

Results: Of the 557 cows assessed, from seven tie-stall herds, a behavioral change (e.g. regularly shifting weight) was identified in 25% and a hind limb lesion was present in 19%. Common lesions identified in these cows were digital dermatitis (DD), sole ulcer (SU) and sole hemorrhage (SH). Cows with a lesion had higher odds of resting one foot [odds ratio (OR) = 4.66; *p*<0.001] and bearing weight unevenly when moving side to side (OR = 2.49; *p*<0.01) than those without lesions. Cows with SU had higher odds of resting one limb (OR = 8.72; *p*<0.001) and bearing weight unevenly (OR = 2.77; *p*<0.05) than cows without SU. Cows with SH had a higher odds of shifting their weight (OR = 4.27; *p*<0.01) than those without SH and cows with DD had higher odds of bearing weight unevenly (OR = 3.65; *p*<0.01) than those without DD.

Conclusions: SLS can help identify cows with hoof lesions which may lead to earlier intervention and reduce duration of clinical lameness in tie-stall cows.

Key words: Dairy, tie-stall, lameness, hoof lesion

Animal and management factors associated with weight gain in dairy calves/heifers on smallholder dairy farms in Kenya

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ABSTRACT

Objectives: Our objective was to describe a random sample of youngstock and to determine factors associated with weight gain in dairy calves and heifers in smallholder dairy farms (SDF) in Kenya.

Materials and Methods: A census of 321 calves and heifers, sampled from 200 randomly selected SDF in Naari, Kenya, formed the study population. Youngstock management was recorded using a questionnaire. Biodata were obtained through subsequent physical examination and heart girth measurement. Descriptive statistical analyses were conducted, and mixed model regression was used to identify factors associated with the natural log transformation of average daily weight gain (ADG).

Results: Median and mean ADG *(and s.d.)* of the youngstock were 360 and 443 (±375) g day^{-1}, respectively. In the final model, ADG was highest in pre-weaned calves, lower in post-weaned calves, and lowest in heifers. Supplementing with quality hay during the dry season at least weekly was a herd-level variable significantly associated with increased ADG. Supplementing with concentrates was correlated with hay feeding. There was a significant interaction between breed and historical disease on ADG; disease was associated with decreased ADG in *Bos taurus* breeds, especially in Guernseys, while ADG in *Bos indicus* breeds was not negatively affected by disease. There was also a significant interaction between education levels of the husband and wife on the farm; when the man's education was low (having less than or equal to primary school), ADG was highest when the woman had not completed primary school, but was lower when the woman had completed primary, secondary or tertiary education, possibly because such women worked off farm more often.

Conclusion: With the observed suboptimal growth, supplementation of diets (with hay and/or concentrates) is recommended in calves and heifers, especially in the dry season.

Key words: smallholder dairy farms, calves, heifers, average daily weight gain, Kenya

Compliance to a recommended claw trimming routine in Swedish dairy herds

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ABSTRACT

Objective: Healthy claws are a prerequisite for a sustainable dairy production. Several claw problems are endemic in Swedish herds, which is negative both from an animal welfare and economic perspective. In most herds all cows are trimmed at the same occasion once or twice yearly. However, to prevent and detect claw problems at an early stage the recommendation is to trim each individual cow around dry off and about 2-3 months after calving. The objective of this study was to investigate the compliance to this claw trimming strategy.

Materials and methods: Data were retrieved from the Swedish Official Milk Recording Scheme (SOMRS) for the period 1 January 2011 to 31 January 2015. Of the 2557 herds enrolled in the SOMRS, 969 herds also had claw trimming information during this period. In total, the study comprised 318,045 calvings from 969 herds. If a cow was examined and/or trimmed 122 to 30 days before calving and 0 to 122 days after calving the recommended trimming strategy for that calving was considered fulfilled.

Results: In 20% of the calvings, cows were trimmed according to the recommended trimming strategy. There was a larger proportion of cows that were trimmed in the recommended time frame after calving (n=169,366; 53%) than before calving (n= 122,956; 39%). The within herd proportion for cows trimmed according to the recommended trimming routine ranged from 0 to 76% (Q1=5%, Q2=14% and Q3=25%).

Conclusion: The compliance to the recommended claw trimming routine was low. One explanation is that this trimming strategy is difficult to apply in small herds as it requires a sufficient number of cows for the regular visits of a claw trimmer. There is great potential to improve the compliance in herds with over 200 cows. The next step is to identify how incidence and severity of claw problems are affected by trimming strategies.

Key words: Claw trimming, dairy cows, preventive herd heath management, hoof trimming

Field study to investigate the impact of dairy cow space allowance on health in GB dairy farms

J. Thompson*, J. Huxley, C. Hudson, J. Kaler, M. Green

ABSTRACT

Objectives: 1) Investigate current housing practices being undertaken across GB dairy farms; 2) Define space allowances in a random sample of GB dairy herds; and 3) Evaluate the impact of living space on cow health and welfare

Materials and methods: Seventy farms were selected at random from a subset of 750 dairy farms, representative of the British dairy sector. Fifty three farms agreed to participate (response rate = 76%). Data were collected using a face to face questionnaire to obtain farmer opinions on loafing space and from measurements taken from buildings used to house dry and lactating adult dairy cows. Measurements were made using a laser (Leica Disto D510) to quantify all areas including lying areas, passageways and other living spaces. Farm details were recorded, such as housing period, geographical location and breed. Access to health and welfare records was also gained. Multivariable analyses comprised conventional linear models in the R statistical platform.

Results: Substantial variability was identified in space allowances between farms. Total area available per cow ranged 7.25m^2 between farms at maximum stocking densities. The median area was 8.1m^2 (IQR: 7.3 - 9.2m^2). When space was calculated without cubicle bedding areas a range of 6.6m^2 per cow was found (median: 5.4m^2; IQR: 4.4 - 6.4m^2). Associations between space allowance and herd level health and welfare scores will be presented.

Conclusion: Living space requirements for dairy cows and its significance has not been rigorously evaluated. This study has highlighted variability of space allocations for housed dairy cows and its impact on health and wellbeing. Long term experimental studies are needed to precisely assess how living space influences production, health, welfare and behaviour.

Key words: Dairy, loafing, space, housing, health

The effect of infection with bovine corona virus on dairy milk shipped per cow per day

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ABSTRACT

Objective: Infections with bovine coronavirus (BoCV) are endemic to the cattle populations in most countries, causing respiratory and/or enteric disease. In affected dairy cattle herds, milk production has been reported to be affected significantly. The aim of the present study was to estimate the loss of milk after BoCV infection.

Materials and Methods: Milk shipment data and herd seroprevalence of BoCV in 93 Swedish dairy herds (54 organic and 39 conventional) were studied. Information on seroprevalence was retrieved from 3 testing periods (fall 2011, spring 2012 and spring 2013). At each test occasion four primiparous cows were sampled as an indicator of a recent infection in the herd and for each testing period, the herd was classified as being negative (0 or 1 test-positive cows) or positive (2-4 cows test-positive). When primiparous and homebred cows are sampled, the serostatus will give an accurate description of the recent BoCV history of the herd. A random effect linear regression model was used to evaluate the effect of BoCV on milk shipped per cow per day. A set of variables were forced in to the model as fixed effects: organic vs conventional, herd size, year (4 levels), season (sine/cosine function), region (3 levels) and breed (4 levels) while herd was treated as a random effect.

Results: Herds with new infections and herds staying positive were found to have reduced production (P <0.001). The model indicated that new infections reduced production by approximately 1 kg per day over a period of 120 days, and for herds being classified as being positive the loss was estimated to 0.6 kg per day over an average period of 185 days.

Conclusion: The results indicate that infections with BoCV has a significant effect on milk production and we believe that preventive measures to avoid infection are important.

Evaluating the effects of neonatal immunity and other animal-level and herd-level risk factors on liver abscess incidence in Holstein steers raised on feedlots in California

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ABSTRACT

Objectives: Holstein steers account for approximately 20% of all beef cattle produced in the U.S. Recently, liver abscess prevalence in Holstein steers has increased to 30-40% on some feedlots. The primary objective of this study was to determine whether neonatal immunity is associated with liver abscess development in Holstein steers at feedlots. A secondary objective was to determine at what age and days on feed, they develop liver abscesses.

Materials and methods: This prospective cohort study was carried out over 16 months. To eliminate the confounding effect of calf source, study calves were enrolled upon arrival at one calf-ranch in California in their first week of life and allotted to the unexposed cohort if their serum immunoglobulin G (IgG) level was > 1000 mg/dL and to the exposed cohort if IgG was £ 1000 mg/dL using radial immunodiffusion assay (RID). At 4 months of age, study calves were shipped to three feedlots in southern California. Transabdominal ultrasonography was used at baseline and every 3-4 months until slaughter to evaluate for liver abscess development along with serum liver enzyme parameters. Multi-level logistic regression and survival analysis were used to determine the association between animal and herd-level risk factors from the calf ranch and feedlot on liver abscess incidence.

Results: A total of 310 Holstein steers were enrolled with 140 in the exposed cohort, and 170 in the unexposed cohort. No liver abscesses were found at baseline. Exposure status, feed formulation, temperature, treatment records, bunk management, and feedlot were evaluated as fixed and random effects in the model. Liver abscess incidence increased with increasing days-on-feed.

Conclusion: Concern regarding Holstein steer liver abscesses is leading some producers and packing plants to process only beef breed cattle. Results of this study highlight important risk factors that may be modified to reduce liver abscess incidence.

Key words: Liver abscess, calf-fed Holsteins, feedlots, neonatal immunity, liver enzymes

Postpartum Subacute Ruminal Acidosis (SARA) and Subclinical Ketosis (SCK) in dairy cattle: frequency and effects on postpartum anestrus incidence risk

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ABSTRACT

Objective: The study objectives were to determine: the frequency of postpartum Subacute Ruminal Acidosis (SARA) and Subclinical Ketosis (SCK) in dairy cows from Nariño, Colombia; and the effects of these diseases on postpartum anestrus.

Materials and methods: A cohort study was conducted in a random sample of 149 dairy cows from 29 herds from the Nariño dairy region in 2016. Ruminal liquor and blood samples were taken once at seven days in milk (DIM). Case definitions were: 1) "SARA: healthy cows with ruminal pH <5.6"; and 2) "SCK: healthy cows with 10-30 mg/dl of blood Beta-Hydroxy-Butyrate". Anestrus was determined as the absence of a follicle and corpus luteum during the first 60 DIM, after ultrasound assessments at 30, 40 and 60 DIM. Farm-level nutritional management was determined through a questionnaire. Unconditional (P≤ 0.1) and multivariable (P ≤0.05) mixed logistic regression models, with herd as a random effect, were used to determine associations between predictors of interest (SARA and/or SCK) and anestrus.

Results: Results showed SARA and SCK frequencies were 23% and 46%, respectively, with 5.2% of cows having both. Incidence risks of anestrus were 42%, 64% and 78% for all, SARA and SCK cows, respectively. The final model showed a reduction of 1.9 in log-odds of anestrus if a transition diet was used in the herd (P<0.01), compared to no transition diet. Second-parity cows showed a reduction of 1.5 in log- odds of anestrus, compared with first-parity cows (P<0.05). In an interaction variable, having both SARA and SCK increased the log-odds of anestrus by 4.2 (P<0.001), compared to having neither, while individually, SARA and SCK increased the log-odds of anestrus by 3.6 (P<0.001) and 3.8 (P<0.001), respectively, compared to having neither

Conclusion: In conclusion, parity, postpartum SARA and SCK, and poor nutritional management during the transition period of the herds were associated with postpartum anestrus

Key words: Reproductive efficiency, nutrition, dairy cattle, tropical

The epidemiology of seasonal fluctuations in colostrum yield in Jersey cattle

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ABSTRACT

Objectives: Some dairy herds have reported colostrum production ranging from a low volume to no colostrum produced by cows during fall and winter. The purpose of this study was to characterize the syndrome and identify potential risk factors for low colostrum yield.

Materials and methods: A 2,500-cow Jersey dairy farm was enrolled in a year-long prospective cohort study to evaluate possible effects of photoperiod, temperature, and cow factors on colostrum production. Dairy personnel were trained to collect, weigh, and evaluate colostrum quality. Information on parity, previous lactation length, previous 305ME milk production, and dry period length were collected through the farm's dairy management software. Weather and photoperiod data were also collected.

Results: Over 2,900 cows were enrolled, 38% primiparous, 25% second lactation, and 37% third or greater lactation. Average colostrum yield was 6.6 kg per cow in June 2016, 2.5 kg in December, and 4.8 kg in May 2017. Multiparous cows had a larger decline in colostrum production between June and December (6.6 kg to 1.3 kg) compared to primiparous animals (6.5 to 4.2 kg). Average weekly colostrum production decreased by 0.22 kg for multiparous cows and 0.08 kg for primiparous cows. A logistic regression model for >1 lactation cows found dry period length, calf sex, singleton or twin, age at freshening, month of calving and previous lactation length significantly associated with low colostrum yield (< 2.7 kg at first milking). A cross-correlation function analysis between the time series for colostrum yield and photoperiod revealed a high correlation at the time of calving and one month prior particularly for multiparous cows. A pedigree analysis showed that extreme colostrum yield (low vs high) followed some sire lines.

Conclusion: Photoperiod was the most important risk for low colostrum production. Low colostrum production in this herd also appears to have a genetic component.

Impact of OS supplementation on preweaned dairy calf growth

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ABSTRACT

Objective: Evaluate the impact of oligosaccharide (OS) supplementation on dairy calf growth and health.

Materials and methods: A randomized clinical trial was conducted on 3 dairy farms selected as a convenience sample, raised their own heifer replacements, housed at least 200 preweaned dairy calves. Calves were enrolled at each farm and randomly assigned to one of six treatment groups: mannanoligosaccharide MOS (14 days), galactooligosaccharide GOS (14 days), MOS (7 days), GOS (7 days), Lactose (14 days), and unsupplemented. All calves received one or two feedings of colostrum. On the first day of milk feeding and continuing through 14 days of age, each calf received 5g of supplement added to a bottle containing whole milk and fed twice per day. Calves were weighed at enrollment and weaning. All calves were evaluated twice daily for 21 days for appetite and attitude. The primary study outcome was average daily gain (ADG).

Results: Three hundred and fifty four calves were enrolled in the study. Calves within each study group were similar weight and passive transfer status. Calf mortality across the study was 3% and ranged from 1-5%. The primary monitored health outcome was appetite. Calves were scored at each feeding for finishing the milk meal. Appetite categories were based on proportion of feedings completed: 1.00 (completing all meals), 0.81-0.99, and <0.80. ADG was modeled as a function of supplement group, farm, appetite category for days 1-10 and days 11-21, and the interaction of supplement with appetite. There was a strong negative impact on ADG from not completing milk meals during the follow up period but much of this loss was mitigated in those calves receiving the GOS and Lactose supplements.

Conclusion: GOS and Lactose supplemented milk were effective at decreasing the impact of poor appetite and associated disease events on ADG.

Key words: Calf health, oligosaccharides, clinical trial

Welfare-Adjusted Life Years (WALY): A novel metric of animal welfare that combines the impacts of impaired welfare and abbreviated lifespan

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ABSTRACT

Objectives: Adapting the Disability-Adjusted Life Years, the paper introduces a novel metric, the Welfare-Adjusted Life Year (WALY), allowing the estimation of total disease impact by considering both welfare compromise and premature death.

Materials and methods: The WALY is the sum of a) the years lived with impaired welfare (YLIWs) and b) the years of life lost (YLLs) due to the same disease. The YLIWs are the product of the average duration and the probability of each welfare impediment, reflecting the actual condition that compromises animal welfare, and impaired welfare weights (IWWs), representing the degree of impaired welfare. The YLLs are the expected lifespan at the time of premature death. To demonstrate the concept, we estimated WALYs for 10 common canine diseases. A survey of veterinarians (n=61) was conducted to elicit IWWs for 35 welfare impediments. Paired comparison was the primary method to elicit weights, whereas visual analogue scale and time trade-off approaches rescaled these weights onto the desired scale, from 0 (the optimal welfare) to 1 (the worst welfare). WALYs for the 10 diseases were then estimated using the IWWs and published epidemiological data.

Results: Welfare impediment "amputation: one limb" and "respiratory distress" had the lowest and highest impaired welfare weights at 0.117 and 0.857, rescaled with the time trade-off results. Among the 10 diseases, thoracolumbar intervertebral disc disease and atopic dermatitis had the smallest and greatest adverse impact on dogs with WALYs at 2.83 (95% uncertainty interval [UI]: 1.54 - 3.94) and 9.73 (95% UI: 7.17 - 11.8), respectively, rescaled with the time trade-off results.

Conclusion: The WALY metric was developed and demonstrated in the current study. Future potential applications of the WALY metric are extensive and may include prioritisation of disorders for control and quantification of population welfare. The WALY may be extended to production animals.

Key words: Welfare-Adjusted Life Year, WALY, disability-adjusted life year, animal welfare, companion animals

Raw chicken consumption, campylobacter infection and acute polyradiculoneuritis in dogs

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ABSTRACT

Objectives: Acute polyradiculoneuritis (APN), also known as 'Coonhound paralysis', is an immune-mediated peripheral nerve disorder in dogs similar to Guillain-Barré syndrome (GBS) in humans. Infection with Campylobacter is a major triggering factor in GBS in humans. We undertook a case-control study to investigate the association between Campylobacter infection in dogs and APN and to identify potential risk factors associated with APN including consumption of raw chicken meat.

Materials and methods: Data on potential explanatory variables and clinical specimens were collected from 27 'case' dogs and 47 'control' dogs. Faecal samples were collected from each enrolled animal to perform direct culture, DNA extraction and polymerase chain reaction for detection of *Campylobacter spp*. Data were obtained from the medical records and owner questionnaires in both groups. Statistical analysis involved estimation of odds ratios (OR) and their 95% confidence intervals (CI) for each putative risk factor and multivariable exact logistic regression.

Results: In cases in which the faecal sample was collected within 7 days from onset of clinical signs, APN cases were 9.4 times more likely to be positive for *Campylobacter spp*. compared to control dogs (OR = 9.4; 95% CI: 2.28, 48.4; P<0.001). In addition, a statistically significant association was detected between dogs affected by APN and the consumption of raw chicken (96% of APN cases; 26% of control dogs; OR = 70.7; 95% CI 9.67, 3193; P<0.001).

Conclusion: Raw chicken in the diet clearly increases the risk of developing acute polyradiculoneuritis in dogs, which potentially is mediated by infection with *Campylobacter spp*. Based on the findings reported here, veterinarians should not recommend feeding raw chicken to dogs.

Key words: Acute polyradiculoneuritis, coonhound paralysis, raw chicken, campylobacter

An estimate of the number of dogs in US shelters and their fate

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ABSTRACT

Objectives: Estimates of the number of dogs in animal shelters across the United States are empirical. The objectives of this study were to quantify the number of dogs that entered shelters in 2015 and better understand their fate.

Materials and methods: An initial list of 10,890 animal shelter and rescue organizations, from online sources, was refined to include only animal shelters with physical locations and having dogs available for adoption by the public. The final sampling frame of shelters included 3,064 organizations. A telephone-based survey of each shelter on the list was conducted by Mississippi State University's Social Science Research Center. A total of 413 shelters (13.5%) completed the survey. A capture-mark-recapture method was used to estimate the total number of shelters in the United States. Marked shelters were from the original frame, captured shelters were shelters identified from reviewed lists from 5 states, and recaptured shelters were those shelters common to both lists.

Results: We estimated there are 7,076 (95% CI 6,399-7,890) shelters in the US that adopt out dogs, and in 2015: 5,532,904 dogs entered these shelters, 2,628,112 dogs (47%) were adopted, and 776,970 dogs (14%) euthanized. The characteristics of shelters associated with dog outcomes were size of the shelter, funding source, region the country and source of animals.

Conclusion: Compared to previously reported statistics, the proportion of dogs adopted from shelters is higher than previously estimated and the proportion of dogs euthanized is lower.

Key words: Dog, shelter, census, survey

Progression of surgical efficiency, incision length and complication rate in senior veterinary students enrolled in a 2 week spay/neuter surgical elective

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ABSTRACT

Objectives: Veterinary schools continually seek new ways to provide students with opportunities for education, as well as ways to track the progress of their students. The purpose of this study was to evaluate 4th year veterinary student progression in surgical efficiency, incision length and complication rate during a series of routine canine spays performed over a 2 week elective.

Materials and methods: Data from surgical records were collected from a 2 week senior elective surgical rotation. Data included the signalment of the animal, name of the student (surgeon), surgical start time, finish time, surgical incision length and complications encountered during surgery. The association between number of surgeries conducted by a student and surgical time or incision length was tested using linear regression in a generalized linear mixed model with a correlation structure defining clustering by student. The association between number of surgeries conducted by a student and the occurrence of serious hemorrhage or a dropped ovarian pedicle was tested using logistic regression in a generalized linear mixed model with a correlation structure defining clustering by student. A p-value of ≤ 0.05 was considered significant.

Results: Records were evaluated from 1137 canine ovariohysterectomy surgeries conducted by 90 student surgeons. The mean number of canine spays performed by each student was 9.8, (range of 1 to 46). Surgical time was recorded on 1132 records. The mean surgical time was 43.9 minutes (range of 4 to 153). A decrease of 0.61 minutes was observed for each consecutive surgery (p= <.0001). The incision length was recorded in 1068 of the records. The mean incision length was 2.8 cm (range of 1 -11).Incision length decreased by 0.2 mm (p=0.0014) with each consecutive surgery. No significant difference was found in the occurrence of hemorrhage or dropped pedicles.

Conclusion: Students showed significant decrease in surgical time and incision length with each surgery.

Key words: Efficiency, students, surgery

Reproducibility of the mark-resight method for estimating abundance in free roaming dogs

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ABSTRACT

Objective: Dog abundance estimates are an important part of the strategic planning of dog population interventions targeted at free-roaming dogs and the mark-resight method is one technique used for this. The marked percentage of dog is an integral data point for both vaccination coverage and population abundance measures and the aim of this study was to assess the variation of the marked percentage across repeated surveys.

Materials and Methods: A total of 90 areas in Goa, India, were surveyed on two occasions. Dogs were paint-marked during net capture alongside a vaccination campaign for rabies by the Mission Rabies charity. The number of dogs counted in the survey as well as the percentage of marked dogs were the two main outcomes recorded. The absolute differences between the first and second survey were analysed with linear models to evaluate the effect of differences in surveyor, day, time of day and weather, on the variation between surveys. The survey outcomes were further evaluated using linear mixed-effect models.

Results: The mean absolute difference in marked percentage between surveys was 16.7% (SD 12.9%). Increasing variation of the marked percentage between surveys was associated in the linear model with using different surveyors compared to the same surveyor (8.3%, 95%CI 0.4-16.2), and the variation was 3.5% (1.1-5.9%) higher for every 1mm difference in rainfall. From the mixed models, 5.2% (1.4-8.9%) more marked dogs were likely to be seen in the second survey compared to the first survey. There was a tendency for fewer dogs to be counted in a survey in the afternoon compared to the morning (9 dogs, 95%CI 2.3-15.3).

Conclusion: There was a fair amount of variability in the marked percentage between repeated surveys but regular staff training, to ensure equal effort and quality of survey techniques, could help to standardise the survey outcomes.

Key words: Dogs, mark-resight, population abundance, vaccination coverage, free-roaming

A comparative study of enumeration techniques for Free-roaming dogs in rural Baramati, District Pune, India

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ABSTRACT

Objective: The unvaccinated free-roaming dogs (FRD) amidst human settlements are major contributors to the high incidence of rabies in countries where the disease is endemic, such as India. Estimating FRD population size is crucial to the planning and evaluation of interventions, such as mass immunisation, against rabies. Enumeration techniques for FRD are resource intensive and can vary from simple direct counts to statistically complex capture-recapture techniques primarily developed for ecological studies.

Materials and methods: We compared eight enumeration techniques (direct count, Lincoln–Petersen's index, Chapman's correction estimate, Beck's method, Schumacher-Eschmeyer method, Regression method, Huggin's closed capture models and Application SuperDuplicates on-line tool) using data collected from rural Baramati town in Western India, to recommend a technique which yields a reasonably accurate count to use for effective vaccination coverage against rabies with minimal resource inputs.

Results: A total of 263 unique dogs were sighted at least once over 6 observation occasions with no new dogs sighted on the 7th occasion. The methods that do not account for individual heterogeneity yielded population estimates in the range of 248-270, which potentially underestimate the real FRD population size. The highest estimates were obtained with the Huggin's M_h-Jackknife (437±33), Huggin's M_{th}-Chao (391±26), Huggin's M_h-Chao (385±30), models and Application "SuperDuplicates" tool (392±20). When the sampling effort was reduced to only two surveys, the Application SuperDuplicates online tool gave the estimate of 349±36, which is 74% of the estimated highest population of FRD in Shirsuphal village.

Conclusions: This method is recommended as a reliable tool for estimating the FRD population size.

Bias analyses for observational studies: Non-specific protective effect of rabies vaccine on all-cause mortality in dogs

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ABSTRACT

Objective: Non-specific effects (NSE) of vaccines are defined as effects on individual health beyond those due to an effect on the specific target agent. A number of studies have investigated NSEs in a small number of human vaccines. Results were sometimes divergent and final interpretation difficult. For ethical reasons, these studies are mostly observational and subject to bias. Analysis of information and survival biases lead to estimates of NSEs for some human vaccines that were closer to the null value. Recently, an observational study in dogs reported a beneficial NSE from rabies vaccine. As bias analyses are rarely done in veterinary epidemiology, the present study aims to investigate their impact on the results of the dog study.

Materials and methods: Data were collected as part of a population surveillance system of owned, largely free-roaming dogs in a low-income community in South Africa. Data on dog demographic were collected every approximately six months from 2012 to 2015. All data (sex, age, vaccination status and demographic events including birth, death and migration) were reported by owners. For each age group (puppies 0-3 months, juvenile 4-11 months and adult 12 months and older), a piecewise exponential survival model using the Poisson link was fitted with generalized estimating equation. Sex, number of dogs in the house and residence were included in the model. Two bias analyses were performed: 1) Information bias: Probabilistic sensitivity analyses with 1,000 combinations of sensitivity and specificity of owner recall of vaccination following trapezoidal distributions and differential misclassification were performed; 2) Survival bias: Landmark analysis approach was run.

Results: Mortality rate ratio of rabies vaccine was of 0.44 for puppies, 0.56 for juvenile and 0.83 for adult. All bias analyses indicated a change in these rate ratios, supporting the need for bias analyses in observational studies of NSE of vaccines in owned animal populations.

Key words: Rabies vaccine, information bias, survival bias, non-specific effect, dog

Ewe lameness: prevalence and risk factors in 162 English sheep flocks in 2015

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ABSTRACT

Objective: In England, the geometric mean flock prevalence of lameness in sheep fell from 5.4% in 2004 to 3.4% in 2013. The reduction was associated with changes in management of lameness. The Farm Animal Welfare Committee, a national advisory body to Government, set a target of <2% flock prevalence of lameness by 2021. The aim of the 2015 study was to investigate the prevalence of lameness in a subset of the 2013 flocks and identify risk factors associated with lameness.

Materials and methods: A total of 162 English sheep farmers completed a questionnaire on prevalence and management of lameness in their flock. A multivariable quasi-Poisson regression model was used to identify managements associated with the prevalence of lameness in ewes. The population attributable fractions (PAF) were then calculated.

Results: The geometric mean prevalence of lameness in ewes in 2015 was 4.2% which was significantly higher than in 2013. Managements associated with a higher prevalence of lameness were routine foot trimming such that [3]5% of sheep bled and mixing the sheep with other flocks. Managements associated with decreased prevalence of lameness were treating lame sheep within three days of onset and annual vaccination with Footvax for >5 years. This model explained 65.3% of the prevalence of lameness; the PAF of each risk factor ranged from 2.4 – 34.7%. The percentage of farmers treating lame sheep within three days and routine foot trimming had decreased since 2013.

Conclusions: The prevalence of lameness in ewes increased between 2013 and 2015. If farmers treated all lame sheep within three days and stopped routine foot trimming the prevalence of lameness in ewes in England is predicted to fall to 3.0%. Further reductions could be achieved if farmers committed to a long-term footrot vaccination programme for >5 years and did not mix their sheep with other flocks.

Key words: England, Ovine lameness, Prevalence, Population attributable fraction, Risk factors

Bacterial causes of small ruminant abortion: A systematic review and meta-analysis

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ABSTRACT

Objective: Abortion in sheep and goat is an important cause of wastage impacting productivity and welfare of flocks and thus jeopardizing livelihoods of livestock producers worldwide. Bacterial agents are the most common infectious cause of abortion in small ruminant. The aim of this study was to conduct a comprehensive literature search and meta-analysis of reports which identify bacterial agents from abortion cases of small ruminants.

Materials and methods: Electronic literature search was performed through PubMed and Google Scholar databases to accessed studies published between 2000 and 2017.

Results: Forty-five articles from 27 countries (20 Europe, 14 Asia, 6 Africa, 3 South America and 2 North America) fulfilled the inclusion criteria, resulting in compiled data from 33,066 tests conducted on samples from aborted small ruminants (21,899 Europe, 6,928 Asia, 1,658 Africa, 1,920 North America and 661 South America). A total of 17,398, 7,410 and 3,439 samples were tested for *C. burnetii, C. abortus* and *Brucella spp.*, respectively and the remaining 4,819 samples were tested for *Leptospira spp.*, *Campylobacter spp* and *Listeria spp*. A random-effect model was fitted to derive pooled prevalence estimates for each pathogen and to assess association with covariates (species, world region and sample type). Separate analysis was conducted for each pathogen. The most common identified cause was *C. abortus* with an estimated pooled prevalence of 26.56% (95% CI: 21.24-32.21) among the 7,410 samples tested for *C. abortus*. As expected a high degree of heterogeneity was observed across studies.

Conclusion: In conclusion, abortion in small ruminants is caused by multiple bacterial agents. There are surprisingly few published research studies that report actual causes of abortion and well-designed studies to evaluate the relative importance of bacterial and other infectious causes of abortion in small ruminants are needed.

Key words: Abortion, bacterial agents, goat, meta-analysis, sheep

Can farmers' observations help us determine prevalence? Quantifying ewe mortality based on imperfect data

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ABSTRACT

Objectives: Farmers who observe their animals regularly are a rich potential source of surveillance information. The objective of this study was to use regular reports of farmers' observations to quantify ewe mortality on sheep farms in southern Australia. While some ewe deaths are inevitable on sheep farms, the number of ewes dying and the seasonal pattern of mortality are rarely determined.

Materials and methods: From 2014 to 2016, 31 sheep farmers in Victoria, Australia were asked to provide monthly syndromic summaries of their disease observations, including all cases of mortality in adult ewes. Timing of deaths was categorised as 'peri-parturient' (2 months pre- to 3 months post-lambing) or 'non-parturient' (remaining months of the year).

Results: Ewe deaths were reported in 230 of 579 reports, describing 2048 individual deaths, with a median of 4 deaths per positive monthly report. Farmers' descriptions of cause of death were evenly distributed between peri-parturient and non-parturient causes. In a subset of 29 farm-years with sufficiently consistent responses, overall median farm-level cumulative mortality rate as reported by the farmers was 2.0 deaths/1000 ewes/month. The incidence rate ratio of mortality in the peri-parturient period was 2.8 (95% CI 2.0 to 4.1) compared to the remaining seven months of the year. This quantifies the increased risk of death in ewes around lambing time. Overall ewe mortality could therefore be reduced through strategies targeted to improving peri-parturient ewe survival.

Conclusion: This study demonstrates the potential use of farmers' observations as a surveillance data source, while acknowledging the potential biases arising from non-diagnostic data. Further investigation of how and why farmers respond to ewe deaths without veterinary support is needed, to determine the best farm management strategies to reduce mortality.

Key words: Syndromic surveillance, ewe mortality, sheep, farmer reporting, farmers

Transmission patterns of *Peste des Petits Ruminants* in the Karamoja region of Uganda

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ABSTRACT

Objectives: The strategy for the global eradication of *peste des petits ruminants* (PPR) relies on epidemiological targeting of control interventions to populations critical for the maintenance of virus transmission. The objective of this research was the development of a working hypothesis regarding the patterns of PPR virus circulation in Karamoja across potential host populations on the landscape that can be tested in subsequent operational research.

Materials and methods: The available information on the history of outbreaks and serological data were synthesized with results of field-based participatory assessments with livestock owners and focus group discussions with kraal leaders, community animal health workers, and field veterinarians. In the field-based assessments, clinical descriptions, terms consistent with PPR, and reports of outbreaks were assembled. In focus groups, participatory mapping exercises and timelines were used to assemble the history of PPR in the region.

Results: Two systems of PPR circulation were identified that spanned the border with Kenya. In the northern system, critical transmission points were identified as the adjacent sub-counties of Loyoro and Nakepelimoru in Kotido and Kaabong Districts, respectively, where the Turkana and Karamojong share grazing. In the southern system, the Pokot community spanned the border and the sub-counties and of Loroo and Karita in Amudat District played pivotal roles in repeated waves of disease.

Conclusion: Patterns of disease will be investigated on the Kenya side of the border to develop a more complete picture of the endemic system. Serosurveillance and analysis of herd immunity levels will be implemented to validate the reported patterns of disease. Control and surveillance will be closely coordinated across border in one unified strategy. To interrupt transmission, vaccination interventions will prioritize the sub-counties identified as critical points in the transmission pattern.

Sheep health, welfare and value chain improvement in South Australia

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ABSTRACT

Objective: The South Australian (SA) sheep industry aims to improve the value of sheep farming with a joint project between the Sheep Industry Fund, Thomas Foods International, JBS, PIRSA Biosecurity SA and the University of Adelaide by optimising current decision support systems. The objective of this presentation is to introduce and illustrate the project with a case example.

Materials and methods: The project is co-funded by MLA and AHA and relies on the Enhanced Abattoir Surveillance programme collecting the prevalence for 21 endemic conditions as observed by meat inspectors at two major abattoirs since 2007. These disease records will be aligned with carcase traits and geographical and weather data to identify potential risk factors and to estimate the economic impacts of these conditions. Automated feedback to farmers through an online dashboard will include bench marking and extension resources on how to manage the conditions of concern. It is expected that the abattoir feedback will optimise the flock health and management in the sheep chain. One endemic condition is cat-borne sarcocystosis, which causes losses due to trimming of lesions and condemnation. We investigated the geographic distribution of sarcocystosis in sheep across SA and explored ecosystem characteristics that may facilitate the occurrence of this disease from 4,242 sheep properties for the period 2007-2017. Associations were tested using a Poisson point process model.

Results: Sarcocystosis was highly clustered in the Kangaroo Island region and positively associated with increased rainfall and soil clay content across South Australia. However, the location itself explained sarcocystosis intensity better than any other environmental factors. We hypothesise that location predominately acts as a proxy for cat density across SA.

Conclusion: These findings support the implementation of a targeted cat management program on Kangaroo Island which likely will lead to increased sheep health and welfare, less trimming losses and an increase in sheep production and value.

Key words: Sheep, value chain, abattoir data, sarcocystis

The association between Coxiella burnetii shedding at the time of parturition in dairy goats and daily milk yields produced during the subsequent lactation

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ABSTRACT

Introduction: This was a panel study of the prevalence of *Coxiella burnetii* in goats in a Q-fever endemic dairy enterprise in Victoria, Australia. Our objectives were: i) to determine the prevalence of does shedding *C. burnetii* at the time of parturition; ii) to select a subset of does identified as *C. burnetii* positive and to resample them at their subsequent kidding event to determine the proportion that were persistent shedders; and iii) to quantify the association between *C. burnetii* qPCR status at the time of kidding and daily milk yields produced during the subsequent lactation.

Materials and methods: Vaginal swabs ($n = 490$) were collected from does on three herds and analysed using qPCR targeting *COM1* and *IS1111*. Does were classified as qPCR-negative ($n = 417$), qPCR-positive low ($n = 59$) and qPCR-positive high ($n = 14$) based on the estimated number of genome equivalents (GE) from the qPCR *COM1* analyses. A mixed effects regression model was developed to compare daily milk yields among the three *C. burnetii* qPCR *COM1* status groups.

Results: Across the three study herds there were 15 (95% CI: 12, 18) *COM1* qPCR-positive does per 100 does at risk. The number of GE in positive qPCR *COM1* samples was highly skewed, with a small number of animals shedding extremely large quantities of *C. burnetii* (super-shedders). Persistent shedding was detected when using the more sensitive *IS1111* qPCR in 8 (20%; 95% CI: 10% to 35%) out of 40 does resampled. Super-shedders produced 0.53 (95% CI: 0.08 to 0.98) liters less per day compared to qPCR negative does ($p = 0.02$).

Conclusion: Q-fever control strategies for dairy goat herds should aim at identifying and removing super-shedder does before they kid to reduce disease transmission. An additional benefit of this strategy is the removal of low producer does.

Key words: Coxiella burnetii, Q fever, dairy goats, disease dynamics, production losses, Australia

Footrot in sheep: What's n-ewe in the *Dichelobacter nodosus* community?

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ABSTRACT

Objective: Footrot, caused by *Dichelobacter nodosus*, accounts for 70% of foot lesions in sheep in the UK. There are two clinical presentations: interdigital dermatitis (ID) and severe footrot (SFR) where hoof horn separates from the underlying tissue. Neither *D. nodosus* load in relation to the severity within ID and SFR, nor the effects of footrot treatments on *D. nodosus* load, have been investigated.

Materials and methods: A previous study used cultivation of *D. nodosus* from a limited number of samples, however, *D. nodosus* is notoriously difficult to culture. *D. nodosus* load was investigated using molecular techniques, on the feet of 99 ewes from one farm previously analysed predominantly by culture, then compared with disease severity and treatment. Both culture- and molecular-based results were analysed. Each ewe was assigned one of two treatments; foot trimming plus topical antibiotics (FTA) or parenteral plus topical antibiotics (PTA). The interdigital skin was swabbed, and ID and SFR severity recorded, on at least 16 occasions over 10 months. Two feet of 25 of the ewes were analysed (~950 swabs) and *D. nodosus* load quantified using qPCR.

Results: Of these, only 5% of samples were positive for *D. nodosus* by cultivation, whereas 68% were positive by qPCR. As ID score increased *D. nodosus* load increased. *D. nodosus* load decreased one week after treatment with either FTA or PTA, but not with parenteral antibiotics alone (administered for a separate health reason). This indicates that topical antibiotics reduced *D. nodosus* load on feet. Mean *D. nodosus* load was higher in samples where an isolate was cultured than that of all *D. nodosus* positive samples (p<0.01).

Conclusions: This implies that culturing is not suitable for accurately detecting *D. nodosus* presence on feet, while topical antibiotics are important in reducing *D. nodosus* load on feet, with a reduction in load being associated with less severe disease.

Key words: Footrot, *Dichelobacter nodosus* load, culture, molecular analysis, treatment

Impact of vaccination, lameness control and biosecurity practices on the productivity of 649 British sheep flocks

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ABSTRACT

Objective: Sheep farming in the United Kingdom has traditionally been performed under extensive grazing conditions, with poor record keeping and low veterinary involvement. Currently there is still little published data on the most prevalent husbandry practices and their relationship with flock health and productivity. This study aimed at estimating the relative impact of husbandry practices on commercial sheep flocks productivity, using the number of prime lambs sold per ewe as a proxy for flock productivity.

Materials and methods: During 2016 summer, a survey on husbandry practices, flock characteristics, and number of prime lambs sold /month (outcome of interest) was undertaken with commercial sheep farmers supplying lamb meat to a British food retailer. Descriptive statistics were calculated, followed by multivariable linear regression modelling, using husbandry practices as predictors of productivity. Interaction and confounding effects were tested.

Results: The final sample was composed of 649 farms with a median flock size of 500 ewes (IQR 269-900), located in Wales (n=395), England (n=186) and Scotland (n=68). Health practices significantly associated with number of prime lambs sold per ewe in multivariable analysis ($p \leq 0.05$) were: vaccinating ewes against abortion and clostridial disease (regression coefficient (r.c.) = 0.12, 95% C.I. [0.001 – 0.24]), anthelmintic treatment of ewes during a quarantine period with derquantel+abamectin or monepantel (r.c. = 0.08, 95% C.I. [0.02 – 0.15]), treating lame ewes with individual antibiotic treatment (recommended best practice) (r.c. = 0.07, 95% C.I. [0.01 – 0.15]), and weighing lambs between birth and weaning (r.c. = 0.11, 95% C.I [0.06 – 0.17]). Use of terminal sire breeds was also associated with higher flock productivity.

Conclusion: This is the first study providing a quantitative estimation of the relative impact of key flock health practices on productivity. Evidence on association between greater flock productivity and biosecurity and disease control actions could enhance adoption of good husbandry practices in sheep flocks.

Small ruminants' health and production indicators for migratory Kuchi serviced by Veterinary Field Units in central Afghanistan

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ABSTRACT

Objective: The Dutch Committee for Afghanistan (DCA) is an NGO working to create a sustainable network of privatised Veterinary Field Units (VFUs) in Afghanistan. Through paravets, these VFUs provide high quality animal healthcare services and training to livestock owners. We quantified the effect of these livestock services provided on health and production indicators in small ruminants by comparing data of migratory Kuchi who were serviced under a livestock project in central Afghanistan with migratory Kuchi who had not been serviced by paravets.

Material and methods: A survey on health and production indicators such as mortality, weight at sale, net annual income per head of livestock, was conducted in September 2017. A total of 168 migratory Kuchi (male and female) from nine provinces were interviewed, 114 beneficiaries and 54 non-beneficiaries of the paravet services. Regression analyses were used to quantify the difference in the non-beneficiary group compared with the beneficiary group.

Results: Preliminary results indicated that the incidence rate ratios of mortality in non-beneficiary's flocks were 3.1 (95%CI: 2.1-4.2) and 2.5 (95%CI: 1.7-3.6) compared with beneficiaries for young stock and adult stock, respectively. Weight at time of sales were 5.8 and 3.5 kg less in non-beneficiary's flocks compared with beneficiaries for young and adult stock, respectively. Additional indicators are currently being analyzed.

Conclusion: We demonstrated a significant improvement of health and production parameters in livestock owned by migratory Kuchi and serviced by DCA-trained paravets, emphasizing the importance of a sustainable system of private veterinary service delivery in Afghanistan.

Key words: Afghanistan, Paravets, Veterinary Field Units, Livestock projects, Comparative analysis

Causal web of ovine breech flystrike in Australia

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ABSTRACT

Objective: Ovine breech flystrike (cutaneous and subcutaneous infection with strike fly larvae, particularly *Lucilia cuprina*) is an important production and welfare concern for sheep production in Australia. The identification and application of methods to minimise the occurrence this disease is important for the future of the Australian wool industry. This project aimed to produce a preliminary causal web of ovine breech flystrike in Australia, to identify knowledge gaps in causality and inform associated research strategy.

Materials and methods: A literature review, and a workshop involving experts in parasitology, entomology, molecular biology, animal production and genetics, were undertaken. These activities generated comprehensive lists of host, agent, environmental and management factors that are known to, or are considered likely to, contribute positively or negatively to development of ovine breech flystrike. Putative interrelationships between these factors were identified by the same means. A preliminary causal web of ovine breech flystrike was constructed using these factors and putative interrelationships.

Results: The preliminary causal web is complex, and highlights areas of uncertainty in the causal chains. It indicates many known or biologically plausible interrelationships between putative risk factors in causing ovine breech flystrike in Australia. This includes effect modification, which is relevant to the practical application of breech flystrike risk factor data, and the potential for confounding, of relevance to future research focussed on clarifying the causal nature of many putative risk factors.

Conclusions: Further research addressing causality, considering the uncertainty and potential interrelationships between variables highlighted by this preliminary causal web, will aid in identification and prioritisation of intervention strategies to yield the greatest benefit in reducing flystrike incidence across different farming conditions in Australia. Expanded causal data would also inform further predictive modelling studies, such as those exploring breeding strategies favouring sheep resistant to breech flystrike.

Untangling the respiratory disease complex in small ruminants in Ethiopia

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ABSTRACT

Objectives: Respiratory diseases are a major constraint to small ruminant production in Ethiopia with various pathogens involved. Participatory epidemiological studies on disease priorities in 23 villages showed that across production systems livestock keepers prioritised respiratory diseases. Pasteurellosis was suspected as a key disease, but in most cases diseases were not identified and described as pneumonia and coughing. Descriptions of clinical cases in some areas were consistent with Peste des Petits Ruminants (PPR) or Contagious Caprine Pleuropneumonia (CCPP). Past surveys on pasteurellosis have shown high seroprevalence with cross-reaction observed for different serotypes. This study aimed to further investigate occurrence of different pathogens involved in the respiratory disease complex in the communities enrolled in the participatory research.

Materials and methods: In total 2110 serum samples (1547 sheep, 563 goats) were collected in 432 households. In addition, tissue samples were collected from clinically suspicious animals. Vaccination history, clinical signs observed, data on husbandry and health management, and production data were collected at household level.

Results: Sero-prevalence for PPR was 71.4% and 20.8% in vaccinated and unvaccinated animals, respectively. In two regions, Amhara and Oromia, the PPR sero-prevalence in vaccinated animals was above 80%, indicating sufficient vaccination coverage, whereas in Tigray it was only 58.9%. Much less vaccination had been done for CCPP, and in lowland areas that had vaccination, sero-prevalence was 52.9%. In unvaccinated areas, seroprevalence was 1.3%. Household level data on covariates was used to identify risk factors for PPR and CCPP by fitting multivariate regression models. Three out of 55 samples collected from diseases animals tested positive for *Pasteurella* spp. in culture assays.

Conclusion: Our results provide evidence of ongoing PPR circulation in lowlands and highlands, but the participatory research indicates that livestock keepers struggle to identify the disease. To further understand the relative importance of different pathogens and the role of co-infection, a longitudinal survey is indicated.

Key words: Small ruminant, PPR, CCPP, pasteurellosis, Ethiopia

Epidemiology and economic impact of goat pox on small holder small ruminants farmers in Kanam local government area, north central Nigeria

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ABSTRACT

Objective: This study is a response to report of goat pox (GTP) outbreak by Sheep and goat farmers from Kanam local government area (LGA) of Plateau State, Nigeria. GTP is an important disease of sheep and goats in many part of the world, causing significant economic losses.

Materials and methods: The participatory rural appraisal techniques (group discussion) and participatory active disease follow-ups (transect work, iterative probing, triangulation and sample collection) were employed to investigate GTP outbreaks in Kanam LGA. This is to understand the epidemiology of the disease and to estimate its financial impact on the goat farmers.

Results: All the respondents are familiar with goat pox and have had cases of goat pox in the flocks, but only approximately 33% of them seek for veterinary services and try to manage the disease. Morbidity and mortality rates are estimated to be 47% and 33%, with mortality rate higher in the young than adults. Based on the perspectives of the respondents, the annual cost of treating goat pox amongst them ranges approximately between 538 – 1,307USD; the annual loss due to mortality amounts to 2,730USD and the annual financial loss is estimated as 6,455USD.

Conclusions: This study reiterates that PRA is an indispensable tool in identifying and understanding the grass root problems facing farmers, making it a useful tool for sustainable disease control, rural development and food security. The implication of the prevailing husbandry and farm management practices amongst the respondents on the incidence and severity of goat pox disease in the LGA were discussed with the farmers.

Key words: Epidemiology, economic impact, goat pox, Kanam LGA, north central Nigeria

Dynamic of antimicrobial resistance in diseased horses in France since 2012

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ABSTRACT

Objective: Horses are considered as one of the potential reservoirs of antimicrobial resistance (AMR) determinants that could be transferrable to human. The aim of our study was to describe the AMR pattern of the major bacterial pathogens isolated from diseased horses in France.

Materials and methods: Data collected between 2012 and 2016 by the French national surveillance network of AMR referred to as RESAPATH were analysed. Proportions of mono and multidrug resistance to antibiotics of relevance in veterinary and human medicine were calculated and compared over the whole period by major equine diseases. Resistance trends were investigated using non-linear analysis (generalized additive models).

Results: A total of 12,695 antibiograms were analysed. *Streptococcus spp.*, *E. coli*, *Pseudomonas spp.*, *Staphylococcus aureus, Pantoae spp.* and *Klebsiella spp.* were the five most frequently isolated microorganisms. *S. aureus* and *Pseudomonas spp.* showed the highest resistance proportions to gentamicin (22.1% and 26.9% respectively). *Klebsiella spp.* (15.5%) and *E. coli* (26.2%) had the highest resistance level to trimethoprim-sulfamethoxazole. Third-generation cephalosporins resistance proportions were below 10% for all *Enterobacteriaceae*. *S. aureus* isolates showed the highest proportions of multidrug resistance (22.5%), which is concerning considering their zoonotic potential. *S. aureus* isolates presented higher levels of resistance when they were collected from reproductive diseases than from respiratory or skin diseases. During the period, AMR trends decreased in *Pseudomonas spp.* isolates for enrofloxacine and gentamicin, but were all stationary for *S. aureus*. For streptococci and *E. coli,* resistance trends to trimethoprim-sulfamethoxazole increased over the period.

Conclusion: These findings are essential to estimate the magnitude of the potential threat to public health and to design efficient control strategies. Additionally, they provide useful information to guide initial empirical treatment of major horse diseases and to foster a prudent use of antibiotics.

Key words: antimicrobial resistance, horse, time-series, multidrug resistance, RESAPATH

Meta-analysis of risk factors for catastrophic musculoskeletal injury in racehorses

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ABSTRACT

Objective: To conduct a meta-analysis of risk factors for fatal or catastrophic musculoskeletal injury (CMI) in racehorses that provides a consolidated resource for assessing findings from new studies with those historically, and to identify gaps in reporting of epidemiological studies.

Materials and methods: We conducted a systematic search of the relevant literature published from 1990 to 2017. Peer-reviewed articles were eligible for inclusion if they reported the incidence of CMI in Thoroughbred flat races and/or risk factors for CMI. We identified a total of 424 articles; 21 were included in a quantitative synthesis of incidence rates and 65 in a synthesis of risk factors. Our meta-analyses were restricted to factors that were statistically significant in at least two studies. Pooled effect sizes were estimated using a random-effects approach under the DerSimonian-Laird model.

Results: The pooled incidence rate of CMI was 1.17 (95% CI 0.90, 1.44) per 1000 race starts. More than 250 factors have been investigated in epidemiological studies for associations with CMI. Factors found to have good evidence of increasing risk of CMI are horse-level factors such as older horse age and age at first start, male sex (particularly entires), and factors indicating the horse's quality such as higher race class or lower claiming price; race-level factors such as firmer track conditions on turf and wetter conditions on dirt, longer race distance, and a greater number of starters; and factors related to exercise history or management including more time since previous start, greater number of starts during career and in the last year, longer career length, and issues identified at pre-race examination, previous injury, and recent administration of medication or injections. Studies investigating recent cumulative distance of high-speed exercise were conflicting and suggestive of at least two mechanisms of injury related to: (1) the accumulation of bone damage, and (2) poor adaptation of bone.

Conclusion: Studies of racehorse injury or fatality in various countries have identified common, but in some cases conflicting, risk factors. Future studies should evaluate success of interventions and mechanisms for injury.

Key words: Meta-analysis, racehorse injury, musculoskeletal, risk factors, epidemiology

The French surveillance network of equine mortality causes: a new way of monitoring the horse industry

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ABSTRACT

Objective: The French surveillance network of equine mortality causes (Resumeq) was created in 2015 for the qualitative surveillance of equine mortality through the centralization of autopsy data in a national database and their overall epidemiological analysis. Its objectives are the qualification of the causes of equine mortality, the monitoring of their evolution over time and space and the early detection of emerging diseases.

Materials and methods: Resumeq is an event-based surveillance system that involves a diversity of actors and structures. An institutional organization has been defined that includes a steering body, a scientific and technical support committee and a coordination unit. Different specific tools have been developed such as standardized autopsy protocols, thesaurus for the anatomo-pathological terms and the causes of equine death and an interactive web application for the visualization of data analysis results by the network contributors.

Results: The 4 French veterinary schools, in addition to 16 veterinary laboratories and 9 veterinary clinics already contribute to the production and centralization of standardized data. To date, around 1000 cases of equine autopsy, mainly located in the West part of France, have been collated and the geographical coverage is gradually improving. Data analysis allows the ranking of the main causes of death and the identification of particularly threatening causes of death at a local, regional or national level.

Conclusions: These first results demonstrate the feasibility and interest of this surveillance at a national level. Moreover, in the future, this surveillance could take an international dimension if several countries decided to jointly value their autopsy data.

Key words: Surveillance, mortality, equines, autopsy, resumeq

Incidence rate and clinical signs of owner-reported laminitis in a cohort of horses and ponies in Great Britain

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ABSTRACT

Objectives: To estimate the incidence of, and describe clinical signs associated with, owner-reported active laminitis in horses/ponies, using both owner-recognised and/or veterinary-diagnosed episodes.

Materials and methods: Data were prospectively collected from a cohort of horse/pony owners in Great Britain between August 2014 and December 2016. The overall, and stratified, incidence of owner-reported laminitis was estimated for first incident and repeat episodes reported during the study period via a previously validated laminitis reporting form. Owner-reported clinical signs present in these episodes were recorded.

Results: A total of 1,070 horses/ponies contributed 1,066 horse-years at risk (HYAR), with 97 reported to have at least one active laminitis episode while enrolled. Nineteen horses/ponies had repeat episodes, resulting in a total of 123 active laminitis episodes reported, of which 50.4% (95% Confidence Interval [CI] 41.6-59.2%; n=62) were veterinary-diagnosed. Of the horses/ponies with owner-reported laminitis, 75.3% (CI 66.7-83.8%; n=73) had a laminitis history. The overall incidence of owner-reported active laminitis, using only first incident episodes, was 9.6 episodes (CI 7.8-11.7)/100 HYAR. The overall incidence, accounting for repeat episodes, was 11.5 episodes (CI 9.7-13.8)/100 HYAR. Episodes were reported across seasons with the combined monthly incidence being highest in May and lowest in March. Incidence was highest in Connemara and New Forest and lowest in Thoroughbred and Cob breed categories. The most prevalent owner-reported clinical signs (≥70%) were difficulty turning and a short/stilted or lame walk. Laminitis was reported in all limbs, with bilateral forelimb lameness being most common (62.9%, CI 54.1-71.7%).

Conclusion: Laminitis remains a considerable year-round welfare issue affecting all breeds. Frequency estimates utilising owner-reported data are more representative of actual disease burden, compared to using veterinary-diagnosed episodes only. Owner-reported prevalence of clinical signs was in keeping with previous veterinary-reported estimates.

Key words: Laminitis, epidemiology, equine, incidence, cohort study

A prospective web-based cohort study to identify factors associated with owner-reported laminitis development in horses and ponies in Great Britain

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ABSTRACT

Objectives: To confirm and quantify associations between previously identified risk/protective factors and laminitis, as well as identifying novel risk/protective factors using a prospective cohort-based approach.

Materials and methods: Self-selected horse/pony owners in Great Britain enrolled in a web-based epidemiological study by completing a baseline health and management questionnaire and submitting regular follow-ups. Data on owner-recognised and/or veterinary-diagnosed episodes of active laminitis occurring during the study period (August 2014 – December 2016) were collected using a validated laminitis reporting form. Risk/protective factors were identified using multivariable Cox regression modelling with variables retained in the final model if the likelihood ratio test $P \leq 0.05$.

Results: From 1,801 horses/ponies with baseline data, 59.4% (n=1,070) had subsequent follow-ups and contributed 1,066 horse-years at risk. The median number of submissions per horse/pony was four (Interquartile Range 2-8). Owners reported 123 active laminitis episodes in 97 horses/ponies during the study period. Seventeen risk/protective factors were identified. Factors associated with significantly higher rates of laminitis, and also identified in a previous case-control study, were weight gain, a prior history of laminitis (particularly non-veterinary-diagnosed episodes) and soreness after shoeing/trimming. Some of the potentially modifiable risk factors identified included trimming/shoeing frequency >8 weeks, morning-only access to grass, partial use of grazing muzzles and feeding of ryegrass forage. Horses/ponies with longer laminitis recovery periods, those treated with benzimidazole-containing wormers, steroidal or non-steroidal anti-inflammatories and animals with lameness due to soft-tissue injury represented high risk groups.

Conclusion: Although recruitment and retention of owners to this cohort study was challenging, the collected data demonstrated significant temporal relationships between a number of horse- and management-level factors and laminitis. Study findings can be used to identify potential interventions and important risk groups for which these interventions would be of particular importance.

Key words: Laminitis, epidemiology, equine, risk factors, cohort study

Epidemiology of multi-drug resistant ESBL-producing *E. coli* isolated from horses at five equine hospitals in the UK

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ABSTRACT

Objectives: To determine prevalence and risk factors for extended-spectrum β-lactamase (ESBL) producing faecal *E. coli* in horses at five UK equine hospitals.

Materials and Methods: Study design was prospective multicentre cohort study. Five equine hospitals were sampled for three weeks: faecal samples and data were collected daily from inpatients and 15-20 areas of the hospital environment sampled weekly. Samples were inoculated onto Harlequin agar±cefotaxime and incubated overnight to select for ESBL-producing *E. coli*. Antibiotic susceptibility was performed against clinically relevant antimicrobials; ESBL-producers were confirmed by double-disc diffusion tests followed by screening with PCR assays for relevant ESBL genes.

Results: 746 faecal samples were collected from 216 horses. ESBL-producing and MDR (multi-drug resistance to ³3 antimicrobial classes) *E. coli* were detected in 43.6% and 57.7% of samples respectively, with significant variation in carriage between hospitals (Table 1). The overall prevalence of ESBL-producing *E. coli* increased during hospitalisation (22% <1day to 92% <10days). ESBL-producing *E. coli* were isolated from 22.6% (n=60) environmental samples (n=266, range across hospitals 3.7-64.6%). Group 1 bla_{CTX-M} genes responsible for ESBL-phenotype were detected in 92.3% of ESBL-producers. Ongoing analysis using multilevel regression modelling will identify risk factors associated with carriage.

Conclusion: This study demonstrated high prevalence of ESBL-producing and MDR *E. coli* from faeces of hospitalised horses and their environment; however, there was significant variation between hospitals. Prevalence of carriage of ESBL-producing and MDR *E. coli* increased during hospitalisation. Strategies aimed at identifying and limiting risk factors associated with carriage are important to reduce antimicrobial resistance in hospitalised patients.

Key words: extended-spectrum β-lactamase, *Escherichia coli*, antimicrobial resistance, horse, hospitalisation

Combined use of two national equine databases in order to get a better knowledge of equine mortality and other demographic issues in France

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ABSTRACT

Objective: Imperfect knowledge of the equine population at regional, national or international levels is a limiting factor for epidemiological studies and equine health surveillance. In France, two complementary databases centralize national equine population data: the French equine census database SIRE, managed by the French Horse and Riding Institute, collects individual equine data while information on dead equines are centralized in the Fallen Stock Data Interchange database (FSDI) managed by the French Ministry of Agriculture. The objective of our study was to evaluate whether the combined use of the FSDI and SIRE databases can provide relevant estimates on equine mortality and a better knowledge of equine demography.

Materials and methods: Annual mortality ratios were calculated for the French equine population and survival analyses performed. Spatial and temporal variations in equine mortality were described.

Results: The mean annual mortality ratio for the French equine population was estimated at 3.17% Survival rates differed according to breeds with the highest median age at death for ponies. The spatial distribution of deaths varied according to breeds and age categories. The weekly description of mortality highlighted marked seasonality of deaths.

Conclusions: The joint analyses of the two databases are very promising in terms of knowledge of equine mortality and its monitoring in time and space. This study also underscored the possibility of reciprocal corrections of the databases resulting in an improvement of the demographic data quality of each database. However, a better traceability between the two bases is desirable in order to enable their comprehensive interoperability and synergistic use.

Key words: Horse, database, epidemiology, mortality, surveillance

Equine owners and rendering companies: A complex relationship that can help to improve equine traceability

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ABSTRACT

Objective: Following the death of an equine, French owners have to return, directly or through rendering companies, the passport to the French horse and riding institute (IFCE), which manages the French equine census database (SIRE), in order to ensure traceability. Indeed, this allows the passport destruction and avoids any fraudulent use of the latter. Besides, the SIRE database can be updated allowing the size of the live equine population to be actualized. However, the equine death is often a painful moment during which the traceability is not perceived as a priority and passports are not always returned. Our objectives were, firstly, to record the attitudes and perceptions of equine owners towards the rendering companies and secondly, to highlight the drawbacks of the passport transmission by owners to IFCE or renderers.

Materials and methods: A web-based survey was performed with Sphinx® software and sent to owners who reported a death between April 2017 and April 2018 and whose mail address was known by IFCE (n=5,000).

Results: The response rate was 17%. 7% of animals were not identified at the time of death. 85% of owners were satisfied by the service provided by renderers even if around 10% pointed out difficulties to join them and a long pick-up delay. Regarding the traceability, 66% of respondents provided the passport to the renderer and 8% a photocopy. Only 2% preferred to send the passport to IFCE themselves. The three main reasons stated by the owners to keep the passport were sentimental reasons (13%), not being aware of the regulation (4%) and not being available the day of pick-up (1%).

Conclusion: These results suggest that renderers are key players in equine traceability and information campaigns towards owners deserve to be carried out to acquaint them with their obligations.

Key words: Horses, traceability, owners, rendering companies, passport

Survey of equine evisceration following castration considering method, position, and breed

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ABSTRACT

Objectives: The objective of this study was to estimate the odds ratio (OR) of evisceration after castration considering breed, method, and position as risk factors.

Materials and Methods: Online surveys of members of the American Association of Equine Practitioners (AAEP) general discussion group and the Equine Clinicians Network (ECN) was conducted in May 2017 concerning post-castration evisceration. For each participant, questions included number of horses castrated in the last 10 years, horse breed, castration method (emasculation, twisting, ligature), posture during castration (standing, recumbent), and how many of those castrated did eviscerate. Breeds selection in the survey were taken from the USDA top 9 USA breed registries plus 'Draft' and 'Other breeds'. Three different logistic regression models were fitted to compute the OR with breed, castration method, and posture while castrating as risk factors for evisceration. Open-source statistical software R was used for all statistical analysis. A confidence level of 0.05 was used for all analyses.

Results: 144 responses were collected. Eviscerations represented 0.20% of 41,664 castrations. Standardbreds, Saddlebreds and Other breeds have higher odds of evisceration when compared to all the other breeds (OR: 3.15, 3.31, 2.9; p-value: <0.001, 0.042, <0.001, respectively). Horses castrated while standing had lower odds of evisceration than those recumbent (OR: 0.35; p-value: 0.015). Horses castrated by twisting the cord are at higher odds of evisceration than those castrated with emasculator (OR: 2.09; p-value: 0.027).

Conclusion: In agreement with results reported in other studies, evisceration is a rare but serious complication. Castration with emasculator while standing should be preferred, however, other risk factors and their interactions should be studied such as recovery from anesthesia, infection, and operator safety.

Key words: Castration, evisceration, horses, risk factors

Infectious respiratory disease in a standardbred training facility: incidence, clinical signs, and risk factors for infection

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ABSTRACT

Objective: Infectious respiratory disease is a common morbidity of young racehorses. Infections can lead to compromised welfare, and economic loss. Identification of risk factors for infection through clinical signs monitoring and collection of demographic data can aid in development of prevention and control strategies. Study objectives were to describe the transmission and clinical course of infectious respiratory disease in standardbred racehorses in a multi-barn training facility. In addition, to determine the relationship between demographic variables and probability of clinical disease.

Materials and methods: The study population included standardbred racehorses (age 1-5 yrs) housed at a multi-barn training facility in southern Ontario (n = 103). Clinical signs were monitored daily over a 41-day period in fall 2017. Descriptive statistics, such as incidence, prevalence and attack rate were calculated for the observed period. Associations between demographic variables (age, sex, and gait) and disease were investigated using multivariable logistic regression.

Results: Respiratory disease cases were characterized by mucopurulent discharge (100%), intermittent cough (37.7%), and ocular discharge (62.3%). Fever (> 38.5 %) and inappetence were rarely reported (15.2 & 3.8% respectively). Total, and yearling-specific attack rates were 52.5% and 87.9%. Cumulative incidence was 0.027 new cases / horse day. Daily incidence was 0 - 0.135 new cases/ day (median = 0.02, IQR = 0-0.024). Daily prevalence was 2.27 – 29.54% (13.64, 10.91-15.51). A negative association (OR = 0.011) between increasing age and respiratory disease was significant (p = <0.001) in the regression model.

Conclusion: Yearling horses were at increased risk of infectious respiratory disease as demonstrated by the high yearling-specific attack rate, and the negative association between age and infection. Disease control strategies, such as vaccination programs and isolation of new horses arriving from auction, should be targeted at young animals entering training facilities.

Key words: Equine, infectious disease, respiratory

Use of proximity loggers to establish contact patterns in a multi-barn standardbred training facility

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ABSTRACT

Objective: Race horses may be at increased risk of exposure to infectious disease due to training stress, the potentially high contact rate between horses, and the open population structure in a training facility. The quantification of contact patterns in standardbred training facilities has not been previously reported. These data are needed to inform and refine equine infectious disease models and hence aid in the development of effective disease control strategies. The objective was to quantify contact patterns within a multi-barn Standardbred training facility using radio-frequency identification loggers.

Materials and methods: The 7-day study took place at a multi-barn standardbred training facility in southwestern Ontario, Fall 2017. Proximity loggers were secured to halters (n= 79), different premise locations (i.e. paddocks, racetrack), and worn by staff during work hours. When a logger (node) came within 2 metres of another logger, the time, individual logger IDs, and duration of contact were recorded. These data were used to describe contact network metrics and identify highly connected nodes. Clusters were identified through modularity-based analysis.

Results: The network density was 0.22. The unweighted mean degree was 33.3 contacts per node (1- 134). Eigenvector centrality for each node ranged from 0–0.55 (mean=0.018). Mean betweenness score was 250.8 (0–1422.9). Modularity analysis revealed 12 network clusters with a modularity score of 0.8. Nodes in the network came in contact with a mean of 33.3 other nodes, with a wide variation of between 1 and 134. Senior staff, active racehorses, and yearlings stabled in the main barn had the highest centrality scores. Node clusters indicate that mixing patterns were heterogeneous and incorporation of contact patterns into equine infectious disease models may result in more robust estimates of disease transmission and effectiveness of control strategies.

Key words: Equine, infectious disease, contact network

Uncovering contact patterns and network dynamics of equine movements and association with *Burkholderia mallei* outbreaks

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ABSTRACT

Objectives: This is the first epidemiological study describing the spread of Glanders disease in horse populations in Brazil. We approach the spatial and temporal characteristics for the movement of animals to reconstruct the monthly network within municipalities, farms and to investigate trade communities clustering.

Materials and methods: Data of equine movements from 2014 to 2016 in Rio Grande do Sul, Brazil, were summarized. The complete network was described and temporal trends were explored in two hierarchical levels, for properties and municipalities to establish regional areas of high internal trade and to investigate communities clustering. To access temporal variations for both level municipalities and farm location, a time-aggregate windows of 30 by 30 days was assumed for the Social Network Analysis. We track farms and, implementing the "k test" to find casual paths between *Burkholderia mallei* outbreaks.

Results: We established causal paths associations between *B. mallei* outbreaks through the network. We described the patterns of equine trade and established high internal trade zones. We uncover contact patterns and its association with *B. mallei* outbreaks describing dynamics of trade between farms and municipalities, providing a useful knowledge base to inform and design efficient control strategies for Glanders disease based on contact network.

Conclusion: Our approach allowed us to capture and established a direct relationship between outbreak farms to track and predict the occurrence of Glanders disease in RS state. The use of network analysis provides good measures to describe the entire network behavior, due to temporal fluctuations in the trading activities, our modeling exercise suggests the necessity to focus on structural changes over time, to offer the opportunity for applying empirical knowledge to infectious disease communication, surveillance and, prevention.

Key words: Social network analysis, equine trade, glanders, disease spread, epidemiology

Utilising opportunistic primary care data for equine disease surveillance in New Zealand

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ABSTRACT

Objective: The New Zealand equine sector contributes significant cultural and economic benefit to the economy via the racing and recreational sectors. Despite this, there is a paucity of accessible real time health data on the equine population. To bridge this gap a national industry owned system (VetIntel) is currently being developed to systematically collect primary care data from equine veterinary clinics to inform the equine disease surveillance network

Materials and methods: Following the approach pioneered by VetCompass in the UK, a pilot study was successfully conducted in 2015/2016 to field test the system IT infrastructure. The New Zealand system allows veterinarians to enter standardised codes for diagnosis and presentation reason for each case, which are then automatically extracted from the practice management system alongside other relevant data fields and uploaded into a dedicated central database. Additional equine practices have since been added to the network and an interactive dashboard under development allows easy access to the data for a variety of stakeholders.

Results: Work is underway to to translate granular diagnostic codes into meaningful indicators for population health to support disease management and preparedness.

Conclusion: The high value of primary care data for companion animal health research has already been demonstrated and has equal relevance to other sectors including equine. How this passively collected data will support surveillance and preparedness activities remains to be observed.

Key words: Population health, data, equine, diagnostic codes, surveillance

Estimating the potential distribution of the infectious pathogen *Pythium insidiosum* between two Latin American countries

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ABSTRACT

Objectives: *Pythium insidiosum* is a widespread pathogen that causes pythiosis, a disease with severe health consequences in horses and humans worldwide. Latin America hosts one of the largest, but scattered, horse herds, making it critical to identify areas at high risk of pythiosis transmission to help guide surveillance in areas with high horse density. We utilized ecological niche modeling and epidemiological data to reconstruct the ecological conditions for pathogen circulation to identify areas with potential risk of pythiosis in Brazil and Uruguay.

Materials and methods: We surveyed 338 horse farm locations in southern Brazil and reconstructed the landscape conditions where the disease is endemic based on high-resolution satellite imagery, *P. insidiosum* serology, and correlative algorithms.

Results: The final model was projected to the entire Brazil-Uruguay border region to predict areas at risk of disease transmission. We detected 66 seropositive farms and transmission risk in areas with low vegetation and low temperatures. There was a significant difference between seropositive and seronegative locations, mainly during the summer, suggesting that *P. insidiosum* circulates in specific landscape conditions. Areas that were unsuitable for *P. insidiosum* circulation were clustered in the central, northeastern, and northwestern regions of the study area.

Conclusion: Our findings suggest that *P. insidiosum* is a generalist pathogen that has the potential to circulate across broad areas in Uruguay and Rio Grande do Soul in Brazil. The risk maps generated may help stakeholders with disease prevention, as well as highlight pythiosis as a potential transboundary disease with economic and public health importance.

Key words: Disease mapping, spatial epidemiology, ecological niche modeling, equine, pythiosis

Human disease from *Chlamydia psittaci* associated with equine foetal membranes and critically ill neonates: an example of a One Health approach to an emerging risk in a climate of poor diagnostic capacity and minimal funding

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ABSTRACT

Objectives: Psittacosis is a severe systemic infectious disease in humans caused by *Chlamydia psittaci*. While birds are traditionally considered to be the source of *C.psittaci*, a cluster of five cases of severe respiratory illness that occurred in individuals exposed to equine foetal membranes in Australia signalled the potential for a novel route of infection. The objective of this work was to identify the significance of this putative route of transmission for human disease.

Materials and methods: A coordinated One Health approach, involving stakeholders in each sector, was used to explore the potential risk that equine products of abortion may pose to human health. A cross-disciplinary expert advisory group led the work, which consisted of a retrospective cohort study in veterinary workers exposed to foetal membranes, an enhanced surveillance system tracing human contacts of equine chlamydiosis cases, and a pilot risk factor study of stud farms in a premier breeding region in Australia. This work was conducted within the context of limited numbers of cases, diagnostic capacity and external funding.

Results: A strong association was made between direct contact with equine foetal membranes and illness (OR = 11.77) in the retrospective cohort study, confirming the membranes as a source. The enhanced surveillance system was successful in increasing awareness, but despite numerous equine events, did not identify any laboratory-confirmed human cases within the region studied. However, heightened surveillance identified another human cluster in another region associated with exposure to a clinically unwell equine neonate where psittacosis was PCR confirmed. Some management practices were identified to be positively associated with farm likelihood of equine cases: frequent manure removal, increased frequency of feed trough cleaning and bird sightings at feed sheds.

Conclusion: Equine foetal membranes and critically unwell neonates represent an emerging threat for transmission of *C.psittaci* to humans.

Key words: Equine, zoonosis, One Health

Attitudes and risk perception of Australian horse owners towards flying foxes in relation to Hendra virus

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ABSTRACT

Objective: Hendra virus (HeV) is a zoonotic paramyxovirus that has threatened both equine and human health in Australia. It sporadically spills over from flying foxes (*Pteropus* spp.) to horses then on to humans causing neurological and respiratory disease with high mortality in horses (75%) and humans (57%). While outbreaks significantly impact the equine industry, they also propagate fear and misinformation amongst horse owners about flying foxes. This study investigated knowledge and risk perception of horse owners towards flying foxes as reservoirs of HeV to identify common attitudes, knowledge gaps and misconceptions.

Materials and methods: Data derived from a two-year, online longitudinal survey of horse owners in Australia. Questionnaires comprised horse owner demographics, property management and mitigation measures, HeV risk awareness and knowledge, and attitudes towards flying foxes and their management. Responses were stacked and generalized linear mixed modelling was used to evaluate association of demographic, management and behavioral variables with perception of flying foxes as a significant threat to human and equine health. Respondent ID was included as a random effect to adjust for multiple observations for some respondents over time.

Results: Attitudes towards flying foxes and their management differed among the participants. Descriptive analyses revealed that 59% of all observations (N=1335) listed flying foxes as a health threat. The majority (69%) acknowledged the important role flying foxes play in the environment, yet 37% supported their culling if roosting in areas where there are horses. Horse owners who saw flying foxes or believed that a HeV case was likely to occur in their area were more likely to perceive flying foxes as a threat.

Conclusion: These findings reflect an increasing human-wildlife conflict in urban and peri-urban areas due to anthropogenic changes. They facilitate a better understanding of horse owner perspectives and help to inform effective communication strategies.

Key words: Hendra virus; horse owners; bats; risk perception; longitudinal survey

Risk factors for race-day fatality in flat racing Thoroughbreds in Great Britain (2000 to 2013)

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ABSTRACT

Objective: A key focus of the racing industry is to reduce the number of race-day events where horses are euthanised due to catastrophic injury or die suddenly. The objective of this study was therefore to determine risk factors for race-day fatalities in Thoroughbred racehorses.

Materials and methods: Using a cohort of all horses participating in flat racing in Great Britain between 2000 and 2013, horse-, race- and course-level data were collected and combined with all race-day fatalities, recorded by racecourse veterinarians in a central database. Associations between exposure variables and fatality were assessed using logistic regression analyses for (1) all starts in the dataset and (2) starts made on turf surfaces only.

Results: There were 806,764 starts in total, of which 548,571 were on turf surfaces. A total of 610 fatalities were recorded; 377 (61.8%) on turf. In both regression models, increased firmness of the going, increasing racing distance, increasing average horse performance, and first year of racing increased the odds of fatality. Generally, the odds of fatality also increased with increasing horse age, whereas increasing number of previous starts reduced fatality odds. Horses wearing eye covering (e.g. blinkers, visors) for the first time were at an increased odds of fatality. In the 'all starts' model, horses racing in an auction race were at an increased odds of fatality compared with horses not racing in this race type. In the turf starts model, horses racing in Group 1 races were at an increased odds of fatality compared with horses not racing in this race type.

Conclusion: Identification of novel risk factors including wearing eye cover and race type will help to inform strategies to further reduce the rate of fatality in flat racing horses, enhancing horse and jockey welfare and safety.

Key words: Risk factors, fatality, logistic regression, race-day injury, racehorse, Thoroughbred

From scientific evidence to horse welfare: Understanding barriers and drivers to implementation of optimal horse-care practices

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ABSTRACT

Objective: Laminitis is a debilitating foot disease that often requires prolonged treatment and can result in euthanasia. A number of studies estimate the prevalence in the UK to be between 1.5 and 34%. Several husbandry-related risk factors have been identified, but it is unknown whether or how research evidence translates into changes in horse care and improved welfare. The aims of this mixed methods study are to investigate horse carers' awareness of evidence-based best practices for reducing the risk of laminitis and to identify barriers and drivers affecting the implementation of research-based recommendations. Thus, using laminitis as an exemplar for other important equine welfare issues, we will determine whether and how scientific evidence influences horse care.

Materials and methods: In phase one of the study, UK horse carers (horse owners, equine yard owners and managers who make some primary decisions regarding the day-to-day care of horses) are being recruited to complete an online questionnaire. The questionnaire captures demographic information about the participant, their horses or yard, information-seeking behaviours, views on equine-focussed scientific research, knowledge of laminitis risk-reducing husbandry practices and whether or not they are implemented. Questionnaire findings will be used to inform the design of the second phase of the study: a qualitative, interview-based investigation of horse carers' barriers to and drivers for acceptance of research evidence and implementation of best practices. The ultimate aim is to improve horse welfare through optimised communication between researchers and horse carers.

Results: Results of preliminary analyses of questionnaire data will be presented.

Key words: Equine, owners, decision-making, research translation, laminitis

Describing horse owners' knowledge, awareness and perceptions of exotic diseases

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ABSTRACT

Objectives: The international nature of the horse industry poses challenges for exotic disease prevention. Horse owners play a critical role in exotic disease prevention and control. However, little is known about their knowledge, awareness, and perceptions of exotic diseases. The objectives of this study are to (1) describe horse owners' knowledge and awareness of exotic diseases; and (2) identify factors that influence horse owners' perceptions of exotic disease risk.

Materials and methods: A cross-sectional study of non-racing horse owners in the United Kingdom (UK) is currently underway. Horse owners were invited to complete an online questionnaire consisting of 45 questions relating to: (1) owner demographics, (2) premises demographics, (3) previous experiences of equine infectious disease (endemic and/or exotic), (4) knowledge of exotic diseases, (5) dimensions of perceived exotic disease risk, and (6) preferred information sources.

Results: The results of this study aim to identify gaps in horse owners' knowledge and awareness of exotic diseases. In addition, the results will describe the dimensions of horse owners' perceived risk of an exotic disease outbreak in the UK. The study results will be discussed further at the conference.

Conclusion: Understanding horse owners' knowledge, awareness, and perceptions of exotic diseases is a fundamental step in identifying barriers to exotic disease prevention and recognition. The results of this study will provide greater insight into the risk of an exotic disease incursion into the UK. Lastly, the results will inform the design of further, qualitative investigations of equine disease control.

Key words: Disease prevention and control, equine, exotic disease, perceptions

Veterinarian and horse owner contact and horse health information delivery in Australia

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ABSTRACT

Objective: Hendra virus is an emerging bat-borne virus endemic in Australia that can be transmitted from horses to humans and has a high fatality rate. Recent controversy surrounding the Hendra virus vaccine has potentially strained the veterinarian-horse owner relationship. This study aimed to characterise the veterinarian-horse owner relationship in general and also in the context of Hendra virus.

Materials and methods: A total of 1,449 Australian horse owners were recruited via emails, social media and word-of-mouth for a series of five surveys that were administered online at six-monthly intervals over a two-year period to capture baseline knowledge, attitudes and practices of horse owners regarding Hendra virus and any changes over time. In the current study, descriptive analyses were performed to understand the use of veterinarians as a Hendra virus information source. Ordinal logistic regression analyses were conducted to determine factors associated with the frequency of horse owner contact with a veterinarian.

Results: This study found relative increases over the study period in the proportion of horse owners who had used veterinarians as an information source (from 10.3% to 19.1%) and who found veterinarians to be a useful information source. Owning more horses, being older, having a primary 'duty of care' for other people (adjusted OR = 1.79, 95% CI: 1.25-2.58) and deriving the main income from horse-related activity (OR = 1.90, 95% CI: 1.00-3.58) were factors associated with more frequent veterinary contact. Results also suggest that hypothetical information delivery systems such as smart phone apps, You Tube documentaries and webinars may be considered as Hendra virus information sources and require further investigation for horse health communication.

Conclusion: The findings of this study may be helpful in optimising strategies for horse health information delivery.

Key words: Hendra virus, communication, horses, Paramyxoviridae, OneHealth.

Seroprevalence of avian influenza (H9N2) in broiler chicken flocks in Iran

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ABSTRACT

Objective: Iran is considered as the largest poultry producer in the Middle East. Avian influenza virus (AIV) as one of the most important pathogens in poultry is threatening this industry. A cross sectional study was designed to investigate the seroprevalence of AIV H9N2 subtype in broiler chickens of Iran.

Materials and methods: During 2014-2017, along with influenza surveillance program in December and October, high capacity slaughterhouses receiving chickens from various provinces in Tehran, Qom, East Azerbaijan, Isfahan, Fars and Razavi Khorasan provinces were selected for blood sampling. Samples were taken from farms with no history of AIV H9N2 subtype vaccination. Serum samples were subjected to haemagglutination inhibition test using H9N2 antigen.

Results: During 4 years, 747 blood samples were collected from 74 epidemiologic units in 13 provinces. 57 epidemiological units (77%) and 445 blood samples (59.57%) were found positive. Mean antibody titer was 4.54 ± 2.95. Mean titer of antibody of chickens was significantly lower in 2014 compared to 2015 ($P<0.01$), but there was no significance difference between 2014 with 2016 and 2017($P>0.05$).

Conclusion: The results revealed that H9N2 virus is circulating widely in broiler chicken farms of Iran. In favorable condition, the virus is able to cause clinical infection and high mortality in flocks. Biosecurity measures are the main procedures to prevent challenges with virus and decrease economic losses.

Key words: Avian influenza, broiler, hemagglutination inhibition, Iran

The transmission dynamics of *Campylobacter* among broilers in semi-commercial farms

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ABSTRACT

Objective: *Campylobacter* is the leading cause of foodborne bacterial gastroenteritis in humans worldwide, often associated with the consumption of poultry meat. In Jordan, the majority of broiler chicken production occurs in semi-commercial farms, where poor housing conditions and low bio-security are likely to promote *Campylobacter* colonization. In this study, we estimated the rate of transmission of *Campylobacter* among broiler chickens within a semi-commercial farm, the day when the flock first became infected with *Campylobacter,* and the within-flock final prevalence (WFP) at clearance.

Materials and methods: These parameters, never explored before in Jordan and in semi- commercial broiler farms in low and middle-income countries, were estimated by fitting a transmission dynamics model in a Bayesian framework to longitudinal prevalence data collected from a semi-commercial broiler farm.

Results: *C. jejuni* colonization is most likely to have occurred during the first eight days of the production cycle, followed by a transmission rate value of 0.13 new infections caused by one colonized bird/day (95% CI 0.11;0.17), and a WFP at clearance of 34% (95% CI 0.24;0.47). Our results differ from published studies conducted in intensive poultry production systems in high income countries, and could be explained by the different environmental conditions in which the flock was raised, the strain of *C. jejuni* colonizing the flock, or the broilers' intestinal microbiota.

Conclusion: Here, we provide the most likely estimates and credible intervals of epidemiological parameters driving the dynamics of *C. jejuni* infection in broiler production systems commonly found in low and middle-income countries.

Key words: Bayesian analysis, *Campylobacter*, Jordan, poultry

A value chain approach to enhance avian influenza A (H7N9) detection in Myanmar informal trade areas

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ABSTRACT

Objective: Avian influenza viruses (AIV) continue to threaten public health and the poultry industry in Asia. An unusual increase in influenza A (H7N9) human cases and in its geographical distribution within China occurred during the 5th epidemic wave (October 2016 to September 2017). This represented a significant shift in the risk of H7N9 spread within the region. In response, the Food and Agriculture Organization of the United Nations (FAO) supported activities that enhance the capacity to detect early any AIV incursion. This research documents the FAO Myanmar AIV surveillance, its design process, methods employed and main challenges to implement the surveillance effectively.

Materials and methods: A participatory approach was adopted to collect key information on the China-Myanmar cross-border poultry value chain. A multi-disciplinary team analyzed the value chain information in combination with previous virological and serological surveillance laboratory results. Higher risk townships were mapped. A tool was developed to estimate the surveillance programme cost.

Results: Higher-risk townships were identified, where the likelihood of detecting any AI incursion from China should be maximized in targeted AIV surveillance. A budget was developed with an estimated cost per sample collected of USD 4.80. Challenges to implement the programme were identified, such as the inaccessibility to certain townships due to insecurity and the transport constraints between sampling sites and laboratory. Whilst, no H7N9 virus has been found to date, positive H7 serological samples were detected in early 2017.

Conclusion: The Myanmar avian influenza surveillance programme review followed a multi-disciplinary approach to target high-risk areas. Serological results are evidence of past infection in live poultry illegally traded between China and Myanmar. While virological surveillance results suggest that A (H7N9) is not present in the country, lack of access in certain Townships bordering China impedes detection of AIV incursions in Myanmar.

Poultry trading networks in Bangladesh: implications for control and surveillance of avian influenza

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ABSTRACT

Objectives: Avian influenza viruses (AIVs) (including H5N1) are endemic in Bangladesh. Live bird markets (LBMs) play a major role in AIV circulation and persistence, and in Bangladesh more than 90% of poultry are marketed through them. This study aimed at assessing the potential for poultry trading practices and networks to promote maintenance and spread of AIVs, to identify suitable targets for control and surveillance measures.

Materials and methods: Data on trading practices (numbers, origins, destinations, types of poultry traded, and hygiene practices) was collected from 2000 poultry traders in a cross-sectional and a longitudinal survey conducted in LBMs of Dhaka and Chittagong, the two largest cities of Bangladesh.

Results: Consumers in the study area bought, on average, 2 million poultry/week at LBMs; 77% were commercially raised chickens, and 14% were local poultry types (desi) and ducks. Farming systems, production areas, value chains and trading networks supplying the cities' LBMs varied according to poultry type. Commercially raised chickens were mainly sold to consumers in their production district, whereas ducks and desis travelled longer distances and their value chains involved twice as many intermediaries. Consequently, the time spent by the latter poultry types along the value chain was increased, and so was the potential for viral amplification. Value chains that started off independently (97% of middlemen traded exclusively one poultry type) intermingled at LBM level, where 65% of market traders sold several poultry types, to form a highly interconnected overall network.

Conclusion: Trading patterns identified here enabled interactions between different farming systems and distant poultry populations, and mixing, amplification and persistence of their viruses. Implementation of control measures in a selection of LBMs would reduce the network's connectedness, thus reducing AIV spread. Preventing interactions between poultry from different geographical origins and types at LBM level would reduce the risk of viral recombination.

Key words: Avian influenza, Bangladesh, poultry value chain, poultry trading networks

Prevalence and distribution of gastrointestinal helminths, and associated risk factors in small-scale chicken farms in the Mekong Delta of Vietnam

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ABSTRACT

Objectives: In the Mekong Delta region of Vietnam, small-scale chicken farms that operate with low standards of hygiene and biosecurity are common. These conditions facilitate pathogen transmission, including gastrointestinal helminth infections, but currently there are no data on these infections in the region. The objectives of this study were: (1) to determine the species, prevalence and burden of gastrointestinal helminths in 'normal' and diseased chicken flocks; (2) to investigate the association between husbandry practices, use of anti-helminthic drugs and disease on the prevalence and levels of helminth infections.

Materials and methods: Randomly selected farms raising meat chickens in Dong Thap province (Mekong Delta of Vietnam) were visited. One representative chicken was selected at the end of production visit to conduct a full dissection of the gastrointestinal tract. In addition, flocks with chickens with respiratory or severe disease were also investigated. The gastrointestinal tract of chickens was systematically dissected using a sieve and a binocular microscope. All visible helminths were dissected and placed into dedicated Falcon tubes, counted, and identified based on their morphology.

Results: A total of 120 'normal' and 90 sick chickens were dissected. Overall, 54.3% chickens contained visible helminths (39.0% contained nematodes only, 1.0% cestodes only, and 14.3% both types of parasite). Anti-helminthic drugs had been used on 32.5% 'normal' flocks. Helminth counts were not different between chickens from flocks that used and did not used anti-helminthic drugs. Full helminth species identification and epidemiological analyses will be presented at ISVEE 15.

Conclusion: Levels of parasitic infection were high in small-scale poultry flocks in the area. The data supports lack of efficacy of current anti-helminthic use practices. We recommend upgrading alternative control measures to control helminth infections in small-scale chicken flocks.

Key words: Gastrointestinal helminths, small-scale chicken farms, risk factors

Pen trial to evaluate effects of necrotic enteritis disease prevention antibiotics on antimicrobial resistance in broiler litter

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ABSTRACT

Objective: Antibiotics and ionophores are used in broiler production to prevent necrotic enteritis (NE) and coccidiosis, respectively, but little is known about resistance selection following the administration of these compounds. The objective of this pen trial was to quantify the effect that these administrations have on the microbiome in the litter over time as well as on the quantity of antibiotic resistance genes in the broiler environment.

Materials and methods: The study consisted of 5 pens per antibiotic treatment group with 60 day-old chicks placed per pen. For this presentation, data from four of the treatment groups will be discussed: 1) No narasin, no antibiotic; 2) narasin (70 g/ton), no antibiotic, 3) narasin (70 g/ton), oxytetracycline (100 g/ton); 4) narasin (70 g/ton), oxytetracycline (400 g/ton). Birds were fed antibiotics and ionophore from days 1 through 28, and birds were sacrificed at day 35. Following a 7-day downtime, birds were again placed in the pens and assigned the same treatments. A total of 3 flocks were followed per pen. Tetracycline concentrations in the litter were assessed with mass spectrometry. DNA was extracted from the litter of every pen weekly. Microbiomes were assessed by sequencing the 16S rRNA gene. 47 antibiotic resistance gene quantities were assessed with a quantitative PCR microfluidic device.

Results: In the pens that used oxytetracycline, there was an accumulation of antibiotic in the litter over the flock cycle, and because the litter was reused, there was carryover of tetracycline in the litter in the high dose pens. There were no significant differences in gene quantities among the groups, although there were differences in microbial community structure. Resistance gene quantities and microbiomes did change over time as each flocked aged. Administration of antibiotics for prevention of NE in broiler chickens might not play a significant role in augmenting antibiotic resistance within the broiler litter.

Key words: Antibiotic resistance, microbiome, broiler chicken, litter

Phylogenetic group and serotype of *E. coli* isolates as important risk factors affecting intensity of colibacillosis in broilers

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ABSTRACT

Objectives: i) To determine the phylogenetic group, serotype and carriage of Class 1 integrons among *E. coli* isolates from colibacillosis outbreaks and ii) to ascertain their association along with other parameters with vital disease measures of colibacillosis.

Materials and methods: The data collected for 106 flocks affected with colibacillosis was analyzed for apparent morbidity, apparent mortality and case fatality rate (CFR). Phylogenetic group and carriage of Class 1 integrons was determined by polymerase chain reaction (PCR). Modified Chi squared test for clustered data was used with some modifications to ascertain the association between different risk factors and vital measures of disease. All other statistical analyses were carried out using STATA™.

Results: O2 serogroup comprising of 12 (37.5%) isolates was the most prevalent serogroup in the present study. 85 (80.19%) isolates belong to phylogenetic group B2. Mean apparent morbidity, mortality and case fatality rate (CFR) was 3.77%, 2.32% and 0.61, respectively. There was significant difference in no. of outbreaks reported in different age groups ($p<0.0001$). Also, there was significant association between phylogenetic group and age of outbreak ($p=0.024$). Comparatively, no significant association was observed between age of outbreaks and serotypes ($p=0.980$). There was significant association between various disease measures and *E. coli* isolates affiliated to various phylogenetic groups and serotypes. All the measures were highest in outbreaks due to isolates of phylogenetic group B2 (apparent morbidity-4.07%, $p=0.0026$, apparent mortality-2.52%, $p=0.0003$ and CFR-0.62, $p=0.0003$). Maximum apparent morbidity of 6.49%, apparent mortality of 2.52% and CFR of 0.74 was observed for serotype O20. However, the measures were not significantly affected by the presence of integrons in the *E. coli* ($p=0.9983$ for apparent morbidity, $p=0.9768$ for apparent mortality and $p=0.8176$ for CFR).

Conclusion: Phylogenetic group and serotype of *E. coli* isolates are important risk factors affecting intensity of colibacillosis in broilers.

Key words: Colibacillosis, Class 1 integron, *E.coli*, phylogenetic group, serotype

Avian influenza A (H5N1) outbreaks in different poultry farm types in Egypt: the effect of vaccination, closing status and farm size

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ABSTRACT

Objectives: The winter of 2014/2015 was particularly worrying in Egypt as it marks the emergence of a new cluster of HPAI A (H5N1) virus leading an important number of AI outbreaks in poultry farms and sporadic human cases. The aims of the study was to analyse surveillance data based on observation of sudden and high mortality or of a drop of egg production in duck and chicken production and to estimate from this data the risk of HPAI A (H5N1) presence at the farm level in a large part of the Nile Delta.

Materials and methods: The samples were collected from 2014 to 2015 in five governorates located on the Western-side of Nile delta, on the Mediterranean coast of Egypt. In order to test the effect of a list of independent variables on the probability of presence of HPAI A (H5N1) virus at farm level (n = 1110 farms) such as the type of poultry production system, the vaccination status, the closed vs. open status of the farm and the farm size, a binomial generalized linear model was formulated.

Results: The HPAI A (H5N1) virus was detected in nearly every villages visited. The probability of HPAI A (H5N1) presence was depended of some biosecurity characteristic of farms and it was notably found that the vaccination status, the absence of windows/openings in farm and the number of birds per cycle of production were protective factors, whereas the presence of duck farms in the village was a risk factor of farm infection.

Conclusion: Results demonstrate the key role of biosecurity to manage HPAI A (H5N1) virus circulation and should give incentive to the provision of additional capacity for poultry farm biosecurity in Egypt.

Key words: Avian Influenza A (H5N1), Egypt, poultry farms, risk or protective factors, biosecurity

Towards real-time surveillance of broiler health and welfare: data mining of meat inspection records

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ABSTRACT

Slaughterhouse condemnation of broiler meat results from identification of highly polymorphic symptoms in broiler carcasses. Previous studies have demonstrated that factors associated with conditions leading to condemnation might have complex linkages between them, while it is not known how the comorbidities combine. Here, we analysed meat inspection data on 23 health and welfare-related morbidities for 14,045 batch-level records from a large UK-based broiler producer using k-means and correlation-based hierarchical cluster analyses, and the Apriori algorithm-based association rules mining (ARM). A combination of methods was used to identify homogeneous subgroups in broiler health and welfare conditions, while establishing the change of these patterns over time; therefore evaluated application of the data mining methods for surveillance of broiler health and welfare over classical statistical methods using Meat Inspection records.

Multimorbidity was prevalent in nearly all studied broiler batches, with only 5% of batches diagnosed with a single condition. This was reflected in a high level of overlapping between clusters estimated using k-means analysis in nine analysed months. In contrast to this, a very distinct outlier cluster was identified in May 2016 of batches of similar condemnation profile in which high number of carcasses were condemned for dermatitis, hepatitis, farm other, and joint lesions. These conditions were also clustered together using correlation-based hierarchical clustering on the same data, with the two methods complementing each other results and discovering potential intervention points. Additionally, potentially infection-related conditions, such as pericarditis, perihepatitis, peritonitis, and abnormal colour were found to cluster in the same month identifying a formation of a syndromic indicator.

High number of association rules have passed the specified thresholds in May 2016, 47 in total, revealing strong associations with high lift and confidence between most prevalent conditions ascites, abnormal colour, and cellulitis and less frequent conditions like partial liver rejects, perihepatitis, hard breast, and tumours. Abnormal colour, perihepatitis, tumours and ascites had the highest comorbidity conditional probability score in all analysed months.

Combined results from three data mining methods established the overtime co-occurrence of conditions commonly associated with shared biological systems implicated common underlying causes, suggesting opportunities for interventions which target multiple conditions.

A cluster of consistent with general inflammatory syndrome in broiler population was identified, indicating potential use of hierarchical cluster analysis for syndromic surveillance. Using novel application of ARM to meat inspection data we were able to obtain even more detailed information on association between condemnation conditions. Taken together, results of data mining methods are likely to have useful application for surveillance of multimorbidity with generated information to be used for design of effective interventions to improve health and productivity of broiler populations.

Characterization of commercial and non-commercial poultry systems in Purbalingga, Java, Indonesia

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ABSTRACT

Objective: The aims of this study were to describe the features of the poultry production system in a typical poultry-dense district of Java, Indonesia. A secondary objective was to predict the location and number of poultry enterprises within villages using spatial models based on environmental and poultry enterprise data.

Materials and methods: Trained enumerators visited households (HH), commercial farms, live bird markets, collector yards and nomadic duck flocks between March and May 2016. Data gathered included flock structure, biosecurity, and marketing practices, connections between poultry units within and outside the study district, as well as environmental features surrounding each unit. Additional environmental data for the study district such as rainfall, land cover, elevation, roads and water bodies were gathered from official Indonesian government websites or departments.

Results: A total of 14 360 households, 204 Commercial farms, 129 Collector yards, and 18 live bird markets were visited. The overall poultry density across the district was 19 birds per square kilometer whilst for commercial and backyard flocks this was 17 and 2 respectively. The median number of poultry was 3 (0 - 70000). Of the households visited, 60% (95% CI: 59% - 61%) of HH owned poultry. There was no evidence of spatial clustering in location of poultry-positive households. We found positive associations between poultry presence and a number of environmental factors.

Conclusion: These results provide valuable information for risk assessment and avian disease control across Indonesia.

Key words: Poultry, spatial analyses, social network analyses, risk factor

Prevalence and risk factors of avian influenza H9N2 among backyard birds in Iran

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ABSTRACT

Objective: Avian Influenza H9N2 subtype causes a contagious and zoonotic viral disease. It causes significant losses in poultry in many countries throughout Asia, the Middle East and North Africa. This cross-sectional study was conducted with the aim to investigate the prevalence and the risk factors of H9N2 AI among backyard birds in villages of Iran during October and November 2015.

Materials and methods: Five hundred fifty nine villages were included in the study and 15500 unvaccinated birds including 12976 chicken, 1768 duck, 630 turkey, 19 pigeon and 107 other birds species were selected for blood samples. Then, Serum samples were examined with the HI test. The birds that had serological titer ≥ 4 (log2) and villages that had at least one seropositive bird were considered positive. The Association between sero-positivity of villages and independent variable were tested using chi square test.

Results: out of 559 villages, 526 (94.1%, CI 95%; 91.8%-95.9%) were seropositive for the infection. Among 15500 birds, 7468 (48.1%, CI 95%; 48.6%-50.1%) birds were seropositive the infection. The sero-prevalence according to species was 54% among chickens, 17.5 % among duck, 18.7% among turkey, 84.2% among pigeon and 12.1% among other species. The sero-prevalence in mild climate area is less than that in mountains area ($P<0.05$). The sero-prevalence in villages with distance less than 1 km to dam was higher than that in other villages ($P<0.05$).

Conclusion: H9N2 AI has high prevalence among backyard birds of Iran. Therefore, preventive measures such as biosecurity measures and monitoring should be applied to reduce the prevalence.

Key words: Influenza, H9N2, Iran, backyard birds

Transitions of prevention and control measures of HPAI virus in Thailand

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ABSTRACT

Highly pathogenic avian influenza continues to pose an animal and public health risk in the countries in East and South-East Asia. However, in Thailand, which experienced H5N1 epidemics in 2004-2008, the disease has been successfully reduced and controlled. The recurrence of HPAI worldwide in various poultry industry systems in the last decade asks for more research effort on the effect of monitoring and control options, specific for the situation of each poultry system. The outbreaks in Asia showed that the increased risks of HPAI infection in commercial poultry flocks are consistent with other studies conducted in connection with outbreaks of HPAI in several countries. As a result, implemented measures that aimed to reduce the role of commercial farms in the spread of infection, such as the drive to bring aspects of the supply chain 'in house', may help to explain the subsequent success in controlling HPAI in Thailand. We also found that periods of active surveillance substantially improved the rate of outbreak detection.

Understanding interactions between animals and humans is critical in preventing outbreaks of avian influenza. Poultry production have changed from small-scale methods to industrial-scale operations. Since the epidemic of highly pathogenic avian influenza A (H5N1) virus, poultry production has been transformed in several affected countries in Asia including Thailand. There is substantial evidence of pathogen movement between and among these industrial facilities, release to the external environment, and exposure to farm workers, which challenges the assumption that modern poultry production is more biosecure and biocontained as compared with backyard or small holder operations in preventing introduction and release of pathogens. Optimal control options are of more vital importance for HPAI than for various other infectious animal diseases, because of the zoonotic potential of HPAI. Knowledge gained from the outbreaks, control measures taken in several countries in Asia, and epidemiological analysis provide insight information of past epidemics which can be used for improving control measures and preventing the future epidemic.

Key words: HPAI, Avian influenza, control measures, biosecurity, Thailand

B. Epidemiologic principles and methods

Effect of sample handling on the detection of PRRSV in oral fluids by real-time quantitative reverse transcription polymerase chain reaction (qRT-PCR)

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ABSTRACT

Objective: This study evaluated the effect of specific handling procedures on the detection of porcine reproductive and respiratory syndrome virus (PRRSV) in oral fluid by real-time quantitative reverse transcription polymerase chain reaction (qRT-PCR).

Materials and methods: The experiment was conducted using a composite sample of PRRSV-positive oral fluid modified-live PRRSV vaccinated pigs. Five pre-extraction sample-handling steps and all combinations thereof were evaluated: [1] thaw temperature (4°C vs 25°C); [2] sample diluent (1:2 dilution with nuclease-free water vs Trizol®); [3a] sonication of the sample (yes vs no); [3b] temperature (4°C vs 25°C) at which Step 3a was conducted; and [4] temperature at which the sample was maintained after Step 3b and until RNA extraction was initiated (4°C vs 25°C). All combinations of the five sample handling steps, were tested in a completely-randomized factorial design with 4 replicates and one negative control for each treatment. The entire experiment was repeated on 5 separate days to produce a total of 800 PRRSV qRT-PCR results. Binary (positive/negative) data were analyzed by logistic regression and quantitative results (Cts) were analyzed using a generalized linear model.

Results: Among the factors evaluated, only [Step 1] had a significant effect on the detection of PRRSV RNA, i.e., samples thawed at 4°C had a higher rate of positivity (94% vs 80%, $p < 0.0001$) and lower Ct values (36.2 vs 37.5, $p < 0.0001$).

Conclusion: The possibility of false-negative PCRs resulting from routine sample handling procedures within the diagnostic laboratory is a matter of concern and mandates the development of protocols that optimize the preservation of nucleic acids in oral fluids and other specimen types. This study determined that thaw temperature as a significant effect on RNA degradation.

Key words: Porcine reproductive and respiratory syndrome virus, quantitative reverse transcription polymerase chain reaction, oral fluid

Detection of porcine epidemic diarrhea virus (PEDV) antibodies in meat juice specimens using PEDV enzyme-linked immunosorbent assay (ELISA)

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ABSTRACT

Objective: This study evaluated the diagnostic performance of an ELISA designed to detect antibodies against porcine epidemic diarrhea virus (PEDV) in individual meat juice specimens.

Materials and methods: Serum and *longissimus dorsi* muscle were collected from 50 PEDV naïve and 88 PEDV-infected pigs at 14 days post-inoculation. PEDV-naïve and inoculated pigs were necropsied separately to avoid cross-contamination of samples. All serum samples were randomized and tested for antibody using a PEDV ELISA offered on a routine basis at the Iowa State University-Veterinary Diagnostic Laboratory. Meat juice samples were tested using the same protocol, with some modifications, i.e., meat juice samples were diluted 1:50 and conjugate concentrations were 1/40,000 and 1/10,000 for IgG and IgA, respectively. The association between PEDV antibodies levels in serum and meat juice specimens detected by each serological assay was analyzed using a mixed-effects repeated measures model. The diagnostic performance (diagnostic sensitivity and specificity) of each serological method was evaluated using the exact Binomial formula.

Results: Figure 1 summarizes the PEDV ELISA (IgG S/P, IgA S/P) test results of serum and meat juice from known status PEDV-naïve and PEDV-inoculated pigs. The cumulative diagnostic performance estimates (IgG, IgA ELISAs) for meat juice were varied among selected cut-offs.

Conclusion: ELISAs for the detection of PEDV antibody in meat juice provided excellent diagnostic performance and suggest that meat juice, e.g., from samples collected at slaughter, could be used in routine surveillance.

Key words: Porcine epidemic diarrhea virus, meat juice, enzyme-linked immunosorbent assay

Oral fluid specimens can be clarified ("cleaned up") without affecting porcine epidemic diarrhea virus (PEDV) isotype-specific (IgG, IgA) ELISA responses

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ABSTRACT

Objective: The objective of this study was to reduce the suspended particulate matter in oral fluid specimens using chemical clarification without adversely affecting the detection of PEDV.

Materials and methods: Aliquots of PED oral fluid samples collected under experimental conditions (Study One) and under field conditions (Study Two) underwent one of 3 chemical treatments (A, B, C) and were then tested by IgG and IgA whole virus PEDV ELISAs. Treatments were evaluated in terms of 1) effect on the diagnostic performance of PEDV IgG and IgA ELISAs and 2) the stability of PEDV-specific IgG and IgA in samples held at 4°C over the course of 7 days, i.e., the residual effect of treatment. In Study One, oral fluid samples from pigs inoculated with PEDV were collected on day post inoculation (DPI) -3, 0, 5, 10, 15, 20, 25, 30, 35, and 42. In Study Two, oral fluid samples were collected on DPIs -4, 0, 3, 7, 10, 14, 17, 21, 24, 28, 31, 35, 38, and 42. Each oral fluid sample was split into 4 aliquots and treated with one of 3 chemical treatments. The 4th aliquot served as an untreated control. Treatments consisted of adding the oral fluid sample to a 5 ml tube containing the lyophilized chemical treatment, vortexing briefly, then centrifuging for 3 minutes. All samples were tested by PEDV IgG and IgA ELISAs immediately following treatment (day post treatment (DPT) 0). Thereafter, treated and control oral fluid samples were stored at 4°C and tested again on DPT 2, 4, and 6 to evaluate the residual effect of the treatment. Serum samples were tested by PEDV IgG and IgA ELISAs on day 0, then held at 4°C and tested again on 2, 4, and 6 to be compared with oral fluid antibody responses.

Results: Treatments were easily administered, i.e., the lyophilized chemicals were easily resuspended in oral fluid samples and the clarifying effect was immediate. Statistical analysis (nonparametric ANOVA) of oral fluid IgA and IgG S/Ps found that neither treatment nor time affected the ELISA S/P results ($p > 0.05$). That is, pairwise comparisons of DPT 2, 4, and 6 results to DPT 0 IgA and IgG S/Ps detected no significant differences ($p > 0.05$).

Conclusion: The results indicated that chemical treatment removed particulates from oral fluids without affecting test performance. Given the low cost and ease of use, this approach could be used either in the field or in veterinary diagnostic laboratories to improve the characteristics of oral fluids tested for PEDV antibody.

Key words: Porcine epidemic diarrhea virus, clarification, oral fluid, chitosan

Evaluation of three serological tests for diagnosis of bovine brucellosis in Pakistan using Bayesian latent class analysis

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ABSTRACT

Objective: This study aimed to address concerns about varied test accuracy for diagnosing bovine brucellosis in the field by estimating the sensitivity (Se) and specificity (Sp) of three commonly used serological tests in naturally-infected smallholder farms in Pakistan.

Materials and methods: Between February and June 2015, a cross-sectional study was conducted in five districts of Punjab and two districts of Sindh. Sera from cattle (n = 441) and buffalo (n = 621) were diagnosed using the Rose Bengal test (RBT), indirect ELISA (I-ELISA) and competitive ELISA (C-ELISA). A Bayesian latent class analysis was used to estimate the Se and Sp of these in the absence of a gold standard test. The model was fitted under the assumption of conditional independence between the three tests and also conditional dependence. In addition, the model was also fitted with three different prior information of beta distributions to incorporate the prior information from the published literature.

Results: The test with the highest Se was the C-ELISA, with a range from 76.1 to 81.2%. The RBT was found to have the highest Sp (99.1 to 99.4%) of the tests. The results of present study identified discrepancies in Se of these tests with the published literature, especially for RBT which is usually thought of as a very highly sensitive test. Results echo anecdotal reports and show that RBT has lower Se and higher Sp when used in the field conditions of the current study. Therefore, we raise issues regarding the reliability of using RBT as a screening test in such conditions, as its use may result in false negative results.

Conclusion: Consequently, we recommended that none of the evaluated tests should be performed in isolation in smallholder scenarios, with the use of RBT and C-ELISA in parallel combination producing optimum Se and Sp for field condition in Pakistan.

Key words: Brucellosis, latent class analysis, serological test, Pakistan

Validation of a field-friendly capsule-staining technique for detecting *Bacillus anthracis* in animal samples

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ABSTRACT

Objective: *Bacillus anthracis* is a spore forming bacterium causing anthrax, a serious disease in animals and humans that affects the livelihoods of underprivileged and livestock-dependent communities, especially in Africa and Asia. Disease detection is an essential component of surveillance strategies, and should therefore be practical in areas where the burden of the disease is highest. Rapid and inexpensive detection of *B. anthracis* can be achieved using M'Fadyean stain microscopy, including situations where infrastructure for culture or molecular diagnostics such as polymerase chain reaction (PCR) is not in place. However, the original M'Fadyean technique using polychrome methylene blue (PMB) has limitations such as the commercial unavailability of quality controlled PMB and the requirement for prolonged oxidation. We aimed to test the performance of azure B, a potential alternative stain that overcomes these limitations.

Materials and Methods: The performance of azure B, PMB and two commonly used staining techniques – Giemsa and Rapi-Diff – was compared to PCR. Blood smear samples (n=102) from animals suspected to have died of anthrax were collected from the Ngorongoro Division of northern Tanzania between 2016 and 2017. The smear samples were stained using the above techniques and examined at X1000 magnification. Quantitative PCR was carried out on DNA extracted from smear scrapings. Point estimates and 95% confidence intervals for the test sensitivities and specificities were obtained using latent class analysis.

Results: The performance of azure B (sensitivity: 94% (85-100%), specificity: 98% (92-100%)) based on its capsule-staining ability was comparable to that of PMB (sensitivity: 94% (85-100%), specificity: 98% (91-100%)). However, the sensitivity of Giemsa (sensitivity: 39% (10-96%), specificity: 97% (89-100%)) and Rapi-Diff (sensitivity: 40% (11-95%), specificity: 98% (89-100%)) was uncertain.

Conclusions: Azure B is a reliable replacement for PMB for the rapid detection of *B. anthracis* by microscopy, making it particularly valuable in resource-limited settings.

Key words: Anthrax, surveillance, diagnosis, azure B, microscopy

Diagnostic performance of direct and indirect methods for assessing failure of transfer of passive immunity in dairy calves using latent class analysis

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ABSTRACT

Objective: Accurate diagnosis of failure of transfer of passive immunity (FTPI) in newborn calves is an essential component of dairy farm management plan. Several methods (direct and indirect) are available for diagnosis of FTPI in dairy calves. However, the indirect methods offer an advantage over the direct methods in not requiring an experienced veterinarian, rapid, cost efficient and can be performed under field-setting. The objective of this study was to estimate the diagnostic performance of radial immunodiffusion (RID) assay, transmission infrared (TIR) spectroscopy and digital Brix refractometer for diagnosis of FTPI in dairy calves using latent class models at four cut-offs values of digital Brix refractometer.

Materials and methods: Holstein calves (n = 691) from 40 commercial dairy farms in the four Atlantic Canada provinces were blood-sampled and tested for detection of FTPI.

Results: Results showed that the number of calves with FTPI was 253 (36.6%) by RID, 194 (28.1%) by TIR and 204 (29.5%) by Brix refractometer at cut-off value of 8.2%. Estimates of SeRID was higher than SeTIR and SeBrix, at all Brix refractometer cut-offs, but with increase of Brix refractometer cut-off from 8.2 to 8.5%, SeRID and SeTIR were decreased from 96% and 79% to 93% and 75%, respectively. SpRID and SpTIR were always higher than SpBrix at all tested cut-offs and were above 92%, and 96%, respectively. By increasing the cut-off of Brix refractometer from 8.2 to 8.5%, SeBrix estimate has remarkably increased from 79% to 95%, respectively. Whilst, SpBrix was decreased from 95% at cut-off 8.2% to 84% at cut-off 8.5%. In conclusion, RID showed the best Se and Sp at all the tested cut-offs of digital Brix refractometer. However, the higher the cut-off, the more comparable sensitivities of RID and digital Brix refractometer. SpRID and SpTIR were always higher than SpBrix at all tested cut-offs.

Conclusion: Test estimates of RID, TIR spectroscopy and digital Brix refractometer were the best at cut-off 8.2% comparing to other cut-offs.

Sensitivity and specificity of clinical diagnoses for HPAI and ND in chickens in West and Central Java

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ABSTRACT

Clinical case definitions are important tools for detecting disease, particularly in resource limited settings. This study used virus isolation and typing to measure the accuracy of clinical diagnoses for sudden death, HPAI-compatible disease, and VVND-compatible disease in chickens on Java, Indonesia. Using frequentist calculations, the diagnosis of sudden death was found to have a sensitivity of 76.4+5.9%, specificity of 41.8+9.8%, and positive predictive value of 72.7+6.0%. The diagnosis of HPAI-compatible disease was found to have a sensitivity of 71.2+7.3%, specificity of 62.3+7.7%, and positive predictive value of 64.6+7.4%. When considering the sensitivity and specificity of the diagnosis of HPAI-compatible disease as series diagnoses, the sensitivity and specificity was found to be 54.4+8.1% and 78.0+6.6%, respectively. Determining the accuracy of the VVND-compatible disease diagnosis was not possible, because an appropriate 'gold standard' test that differentiated VVND from other forms of ND was not available. These results are comparable to other studies. Elbers et al. (2005) found the Se and Sp for a H7N7 case definition in commercial and backyard chickens in The Netherlands was 99% and 23%, and 100% and 26%, respectively. Verdugo et al. (2016) found a Se and Sp of 40% and 92%, respectively, for a combined H5N1 case definition with clinical exam used by community animal health officers in Egyptian backyard chickens. Robyn et al. found 89% Se and 96% Sp for a participatory disease surveillance and response case definition. These results indicate a potential tradeoff between sensitivity and specificity for case definitions. Therefore, they should be designed with the surveillance objective in mind. This includes an emphasis on sensitivity when aiming to rapidly detect the highest number of potential new cases, and specificity when a more cautious approach is necessary to avoiding the unnecessary slaughter of unaffected animals.

Key words: Highly Pathogenic Avian Influenza, backyard poultry, diagnostic accuracy, case definition, Indonesia

Validation of an indirect immunoperoxidase test for rabies virus in domestic and wildlife species in South Africa

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ABSTRACT

Objective: The objective of this study was to estimate the diagnostic sensitivity (Se) and specificity (Sp) of a rabies indirect chromogen-immunohistochemistry test (IC-IHC) relative to the rabies direct fluorescent antibody test (FAT).

Materials and methods: The IC-IHC test was performed on CNS tissues obtained from routine submissions to the two accredited FAT rabies laboratories in South Africa during the period from 2013 - 2017. Specimens from both domestic and wild animal species were included in the study. Ninety-nine FAT positive and 100 FAT negative specimens were evaluated by IC-IHC. The effects of autolysis, extended time in formalin and freezing on IC-IHC Se and Sp were also estimated.

Results: The IC-IHC test results were compared to those of the gold standard to determine its sensitivity (Se) and specificity (Sp). The overall Se and Sp for the rabies IC-IHC test was 98 % (95 % confidence interval (CI): 93 % - 100 %) and 99 % (95 % CI: 95 % - 100 %) respectively. The test worked optimally in all wildlife species, the only discrepancies were seen in specimens from 3 dogs. It was determined that autolysis and formalin fixation does not affect the test results.

Conclusions: The IC-IHC test was accurate and compared well with the FAT. The test has the added benefit of working on formalin fixed tissues and since formalin inactivates the virus, the safety of field and laboratory staff and couriers is assured. Also, if the sample examined with the IC-IHC is negative, there is the added benefit that histopathologic examination of the brain tissue is possible in attempt to diagnoses other neurological diseases.

Key words: Rabies, immunohistochemistry, validation, sensitivity, specificity

Sensitivity and specificity of fecal culture in liquid medium to detect paratuberculosis infections in Québec dairy herds, using a hierarchical Bayesian latent class model

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ABSTRACT

Objectives: Our objectives were to estimate the sensitivity and specificity of the individual fecal culture (IFC) in liquid medium for the detection of *Mycobacterium avium* subsp. *paratuberculosis* (MAP) infections in dairy cows, and to estimate the within herd paratuberculosis prevalence in Québec dairy herds.

Materials and methods: A dataset including 1386 cows from 21 Québec dairy herds already participating in other research studies was retrospectively analyzed. Fecal and blood samples have been collected from all adult cows in the herd during the previous studies and were analyzed for MAP culture (using the Para TB culture liquid medium and the BACTEC 960 system) and serum-ELISA. A hierarchical Bayesian latent class model assuming conditional independence between the tests was built. Non-informative priors for IFC accuracy and paratuberculosis prevalence were used. Informative priors obtained from the literature were used for serum-ELISA accuracy. The WinBUGS statistical freeware was used to obtain posterior inferences (median and 95% credibility intervals; CI) for each parameter.

Results: Covariance among infected animals suggests that both tests were not conditionally independent regarding the true MAP infection status of cows. Assuming conditional dependence between the tests, the sensitivity and specificity estimates for IFC were 34.4% (20.3-66.1) and 99.5% (98.6-100), respectively. The probability of IFC sensitivity being ≥ 50% was 0.11 (Monte Carlo (MC) error=0.004). Sensitivity and specificity for serum-ELISA were 27.3% (18.1-38.3) and 97.4% (96.6-98.0). In our sample, median paratuberculosis within herd prevalence was estimated to be 0.4% (0-3.3).

Conclusion: Sensitivity of IFC was higher than sensitivity of serum-ELISA both in the conditionally dependent and independent models. The conditional dependence between IFC and serum-ELISA may be due to the low sensitivity of both tests. One limitation of this study was the very low within herd prevalence of the participant herds.

A novel method to perform antigenic vaccine matching for foot-and-mouth disease in absence of the homologous virus

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ABSTRACT

Objective: Foot-and-mouth-disease (FMD) is a highly contagious transboundary animal disease that affects cloven-hoofed animals. Vaccination is one of the most important approaches for FMD control but the FMD virus used to produce the vaccine must share antigenic characteristics with potential outbreak strains for vaccination to be effective. The objective of this study was to develop a new vaccine matching technique that does not require live homologous vaccine virus in the laboratory performing vaccine matching.

Materials and methods: As a proof of concept, we assessed the vaccine match of 40 FMD field viruses isolated from southern Africa during the last 25 years. A diverse group of 20 Southern African Territories (SAT) 1 and 20 SAT2 isolates collected from 1990-2015 were selected for this study. Virus neutralization tests (VNT) were performed following the method described in the OIE Manual (2012). Two sets of pooled sera were used for each serotype; vaccinated bovine sera (4 to 16 weeks post-vaccination) and convalescent bovine sera collected 3 weeks post experimental challenge. Novel r_1-values were calculated for the vaccine titre compared to a standardized positive control.

Results: There was a strong positive correlation between the Novel r_1-value and the validation method (Spearman's rho = 0.84, p< 0.01 for SAT1 viruses; Spearman's rho = 0.90, p< 0.01). In addition, there was good agreement between the novel and validation methods for both serotypes based on a r_1-value cut-off of 0.3, which is assumed to represent a good vaccine-match (kappa = 0.70; 95% CI, 0.47-0.95). The prevalence-adjusted and bias-adjusted kappa (PABAK) estimated the agreement between the two methods to be 0.67 and 0.84 for SAT1 and SAT2, respectively.

The new method provided a feasible, rapid, repeatable and reliable vaccine matching approach that will contribute to control of FMD in southern Africa.

Key words: FMD, vaccination, vaccine matching, SAT1, SAT2, VNT

Using pig movement network as a support tool for the development of risk-based surveillance strategies of swine pathogens: application to hepatitis E virus

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ABSTRACT

Objectives: Animal movements between farms are a major route of pathogen spread in the pig production sector. This study aims at coupling network analysis with epidemiological data in order (i) to evaluate the impact of animal movements on pathogen prevalence in farms and (ii) to assess the risk for local areas to be exposed to diseases because of their inter-area movements. Our methodology was applied to hepatitis E virus (HEV), an emerging and worrying foodborne zoonotic agent that is highly prevalent in pig farms.

Materials and methods: First, pig movement network and results of a nation-wide seroprevalence study were modelled and analysed. Then, the link between network centrality measures of farms and their HEV seroprevalence level was explored using a generalized linear model.

Results: Farms' in-degree and ingoing closeness were found statistically associated with high HEV within-herd seroprevalence (p<0.05). Finally, the risk for each French department to be exposed to HEV through in-going movements was estimated by combining the distribution of HEV seroprevalence in source departments with the number of movements coming from those source departments. Mapping the risk of exposure at department level highlighted differences between geographical patterns of HEV prevalence and risk exposure due to incoming movements, suggesting that surveillance should not only focus on highly prevalent areas but also on those having at-risk movements from infected areas.

Conclusions: Pairing network analysis with epidemiological data has evidenced that HEV management and surveillance in pig production sector should take animal movements into account. More generally, the methods we have proposed prove that movement-based parameters can support risk-based selection of farms for surveillance programmes or the implementation of differentiated surveillance strategies depending on the area movement characteristics. Hence, risk-based epidemiological approaches benefiting from network analysis should be fostered.

Key words: Animal movement network, pig, hepatitis E virus, seroprevalence, risk-based surveillance

Social network analysis of free-roaming dog populations in the Torres Strait, Australia, to inform disease spread modelling

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ABSTRACT

Objective: Characterise the social structure of free-roaming dog populations in island communities in the Torres Strait (TS), Australia, to inform disease spread modelling.

Material and methods: Dogs in Kubin, Saibai and Warraber communities in the TS were collared with GPS units that recorded locations at 15s intervals for up to 1 week. Social networks were constructed for each dog population; association between dogs (nodes) was defined as spatio-temporal proximity (5m and 30s). Edges were weighted according to the duration of spatio-temporal association between pairs of dogs. Network statistics were calculated for each population and the robustness of networks to the duration of association between dog pairs was assessed in terms of efficiency (index of average node connectivity), degree distribution and fragmentation (number of components).

Results: Datasets were obtained from 24 (62%), 23 (53%) and 21 (51%) of the dogs in Kubin, Saibai and Warraber, respectively. Networks had 'small-world' structures, with characteristic clustering and low average shortest-path length. Individuals in each network were highly connected in terms of degree distribution and global and local efficiency. Network structures were significantly different between communities. The Kubin network was least robust and fragmented when edges of short duration were removed (14 components with minimum edge-weight of 2 hours). The Warraber network was relatively robust with 7 components at minimum edge-weight of 2 hours as well as high local efficiency within components.

Conclusion: Consistent with 'smallworldness', disease that requires a short duration of contact for transmission is likely to spread rapidly in all three networks in this study. In contrast, fragmentation of networks once edges of short duration are removed is likely to limit the spread of disease that requires a longer duration of direct contact. The results of this study will inform disease control strategies in free-roaming dog populations.

Key words: Social network analysis, dog, disease spread

Dynamic network measures reveal the impact of cattle markets and alpine summering on the risk for epidemic outbreaks in the Swiss cattle population

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ABSTRACT

Objective: Livestock herds are interconnected with each other via an intricate network of transports of animals which represents a potential substrate for the spread of epidemic diseases. We analyzed four years (2012-2015) of daily bovine transports to assess the risk of disease transmission and identify times and locations where monitoring would be most effective. Specifically, we investigated how the seasonal dynamics of transport networks, driven by the alpine summering and traditional cattle markets, affect the risk of epidemic outbreaks.

Material and methods: We considered on one hand monthly static networks, and on the another hand, temporal networks. The proportion of holdings from which at least or more 100 other holdings can be reached within 30 days time window, was calculated at regular time intervals in the four years' time series.

Results: We found strong and consistent seasonal variation in several structural network measures as well as in measures for outbreak risk. Analysis of the consequences of excluding markets, dealers and alpine pastures from the network shows that markets contribute much more to the overall outbreak risk than alpine summering. Static descriptors of monthly transport networks were poor predictors of outbreak risk emanating from individual holdings; a dynamic measure, which takes the temporal structure of the network into account, gave better risk estimates. A stochastic simulation suggests that targeted surveillance based on this dynamic network allows a higher detection rate and smaller outbreak size at detection than compared to other sampling schemes.

Conclusion: Dynamic measures based on time-stamped data—the outgoing contact chain—can give better risk estimates and could help to improve surveillance schemes. Using this measure we find evidence that even in a country with intense summering practice, markets continue being the prime risk factor for the spread of contagious diseases.

Key words: Cattle networks, alpine pastures, surveillance, contact chain

A description of the U.S. livestock industry: spatial and network analysis of Interstate Certificates of Veterinary Inspection animal movements from April 2015 to March 2016

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ABSTRACT

Objective: Patterns of livestock movements in the U.S. are complex across different farm types due to the dynamic flow of animals within the country. An understanding of this network is needed to minimize the impact of unexpected events such as epidemics of highly infectious diseases.

Materials and methods: Social Network Analysis (SNA) was used to describe the contact structure derived from farm-to-farm livestock movements throughout the contiguous U.S. from April 1, 2015 to March 31, 2016. Five network types are described: a) beef, b) dairy, c) porcine, d) small ruminants, and e) overall network. Livestock movement data were sourced from Interstate Certificates of Veterinary Inspection while county-level farm location data were from the National Agricultural Statistics Service.

Results: In the described networks, nodes are represented by counties and links by movements/shipments between nodes; the networks were weighted based on the number of shipments. For the analyses, movement data were aggregated at the county level. The overall network consisted of 3057 nodes and 91,350 directed links. None of the observed networks were cohesive as evidenced by only the beef network showing the presence of 1 giant weak component with 2,918 nodes. All networks were characterized by low reciprocity (>0.12) indicating that return movements are not common in the livestock industry. The median in- and out-degree in the overall network were 16 and 27, respectively. Counties with high in-degree were most commonly found in the Great Plains and counties with high out-degree were distributed within the Great Plains and West. Colorado, Nebraska, Kansas, and Oklahoma had counties with high betweenness in the overall network.

Conclusion: Our study helps to identify important counties linking other parts of the network. Removal of these links during an epidemic might mitigate disease transmission and consequences. Moreover, this work highlights the need for a more efficient national livestock traceability system.

Key words: U.S. livestock industry, interstate certificate of veterinary inspection, social network analysis, livestock traceability

Integration of SQl, R and shiny to analyze interactively animal trade network

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ABSTRACT

Objective: The objective of this project was to develop an interactive tool application to analyze in an easy way the animal trade network information.

Materials and methods: To do our tool we used "SQl" program to store and organize the data, "R" program to analyzes, and "Shiny", an R' package which create an interactive interface. In our tool there are needed two databases to work. The first is the animal movement dataset, which has information about source, destination, date and number of transported animals. The second is an attribute dataset, which has individual information of the properties. Furthermore, the tool can include another variable to the attribute dataset, like social network parameters. Our tool offer to the user the follow issues: (1) an interactive map, where the user can manipulate the information inside it in accordance with the attribute and animal movement datasets, (2) a video with the spatial and temporal patters of the animal movements, (3) a picture of the animal trade patterns with the accumulated information between two periods, and (4) descriptive graphs about the attribute dataset. To validate the successful of the tool application, we used the data of the bovine movements between 2014 and 2015 and the properties census from Espírito Santo State, Brazil.

Results: The tool generated results as previously planned, developing graphics, maps and videos. Regarding the tool validation it was possible identify the trade intensity between properties and the regions of the State, such as their spatial- temporal patterns.

Conclusion: The developed tool application works fast, is easy to be used and does not require deep knowledge regard the applied programs. Therefore, it can be useful by researchers and people who work in epidemiological surveillance.

Key words: Surveillance, interactive tool, animal movements, bovine, free software

Spatial risk and transmission of bovine tuberculosis in Espírito Santo, Brazil

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ABSTRACT

Objective: Brazil is an endemic Country for Bovine Tuberculosis (BTb). However, the prevalence of this disease is different for each State. Espírito Santo (ES) is the second State with highest BTb prevalence. Thus, there is needed to improve the surveillance measures currently used by the government in order to reach an effective control of this disease. The objective of this study was evaluate the spatial distribution of the infected farms with Bovine tuberculosis and the potential spread of the disease in the bovine and bubaline trade network in Espírito Santo, Brazil.

Materials and methods: The study was developed in base of information generated and shared by the Animal Health Service of the State of Espírito Santo (Instituto de Defesa Agropecuária e Florestal do Espírito Santo-IDAF/ES). These data was originated from registers of both animal transit between 2014 and 2015 and farms identified as positive to BTb. The BTb transmission between infected farms was evaluated using K statistic, and the spatial analyze was evaluated using kernel density with relative risk surfaces.

Results: There was no evidence that the distribution of BTb in ES was the result of the transmission by the trade network (p<0,05) and there was no areas identified with higher risk for BTb within the State. One possible reason for our results can be that the farms sampled were no enough to detect the transmission or risk spatial patterns in ES. Thus, the use of more complete data, such as the information from surveillance in slaughter houses can improve the quality of futures analysis.

Conclusion: The methodologies used here can help to indentify how is the spread of one disease given a set of infected farms in a trade network, and where are the regions of the study area with higher risk.

Key words: Kernel, k statistic, surveillance

Time to consider livestock movement as a temporal network: temporal network analysis of Australian sheep movement data

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ABSTRACT

Objectives: In social network analysis of livestock movement data, the connections (edges) in the network are explicitly temporal; an animal movement connecting two farms links them only at a single time point, which is important for the temporal aspect of infectious disease transmission. Standard static network measures cannot account sufficiently for network temporality. In this paper, we review and demonstrate analytical methods that incorporate the temporality of network edges, which offer new insights into network data available in many countries worldwide.

Materials and methods: Temporal network measures are demonstrated using sheep movement data from Victoria, Australia in 2015, aiming to identify high-risk farms for targeted surveillance. Farm values for the temporally explicit incoming and outgoing contact chain values are compared to static network measures such as betweenness. We also compare network 'small world' and 'slow world' properties, illustrating how accounting for temporality can reduce the perceived connectedness of the network, and therefore its potential for rapid infectious disease spread.

Results In the Victorian sheep movement network, farm betweenness showed strong correlation with farm incoming contact chain (Spearman's rho 0.68, p < 0.001) and very weak correlation with farm outgoing contact chain (Spearman's rho 0.16, p < 0.001). Despite correlation, the subset of farms with betweenness values in the top 1% of the state only captured 12% (17/141) of farms with top 1% incoming contact chain values, demonstrating that influential farms in the network may not be identified using static measures alone.

Conclusion: Temporal network measures can improve network analyses to better reflect the true disease transmission risks associated with livestock movement. By reviewing and demonstrating temporal network measures, we aim to encourage uptake and continuing development of temporal approaches to livestock movement network analysis.

Key words: Social network analysis, temporal analysis, livestock movement, sheep

Cattle dung trader: a potential hidden actor for the spread of FMD virus between beef and dairy cattle farms in Northern Thailand

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ABSTRACT

Objective: To investigate the role of dung trader in the propagation of FMD virus between beef and dairy cattle farms.

Materials and methods: A structured questionnaire was employed to identify sequences of farms routinely visited by each trader. A total of 392 participants living in Mae-on district, Chiang Mai province were interviewed including 76 beef, 277 dairy cattle farmers and 39 dung traders. A one-mode network was constructed. A node denotes farms or traders and a tie represents the farm connection by common trader. Network metrics were measured. The percentage of trader movement was calculated with the direction of positive to negative farms to illustrate the likelihood of FMD spread.

Results: The dung trade network possessed 389 nodes and 397 ties. Focusing on the dung traders, degree, betweenness centralities and k-core were 3 (IQR: 2-14), 0.0 (IQR: 0.0-1.1) and 2 (IQR:1-2) respectively. Our results found that one dung trader contacted the maximum number of cattle farms to 70 dairy and 2 beef farms. Based on our data, we identified four risky dung trade direction including the movement from FMD positive to negative beef farm (PB-NB), positive to negative dairy farm (PD-ND), positive beef farm to negative dairy farm (PB-ND) and positive dairy farm to negative beef farm (PD-NB). The percentages of these four contact patterns were 2.13 % (PB-NB), 33.85% (PD-ND), 3.36 % (PB-ND), and 5.38 % (PD-NB), respectively.

Conclusions: Dung cattle trading pattern should be profoundly explored as it was preliminarily revealed in this study as a possible FMD disseminating route. A related risk based surveillance maybe set up by veterinary authorities.

Key words: Cattle dung trader, Foot and Mouth Disease, hidden actor, Network centrality values

Improving disease contact tracing using individual animal data

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ABSTRACT

Objective: Trading of livestock generates a dynamic network of connections between agricultural holdings. The characteristics of these connections can be very important in the event of a disease outbreak. Contact tracing is a widely used technique for uncovering relevant aspects of the movement network in the context of a specific disease outbreak. Typically, moves are identified, both forwards and backwards from the index holding during a pertinent time window. In practice, sequences made up of multiple moves may be apparent during the time window. However, the risk associated with such a sequence can depend on the identities of the individual animals involved e.g. whether any individual animal went through the entire sequence of moves or not. Given that data on individual animal moves may be available, we explore methods for taking into account individual animal identities when tracing contacts.

Materials and methods: We developed algorithms for contact tracing that make use of data from both batches and individual animals. We developed techniques to account for uncertainty in individual animal identities within batches. Specifically, we construct possible movement histories for a given animal and then weight the possibilities according to how consistent they are with the available batch data. The algorithms were applied to realistic scenarios based on Scottish sheep movement data. For this application we assume that our knowledge of batch movements is complete, while partial knowledge of individual movements is provided by the scanning of EID tags at markets and abattoirs.

Results/conclusion: Simulations suggest that use of individual animal data can lead to more efficient contact tracing, even when only partial knowledge of individual animal data is available. Potential applications could include prioritising potential contacts during the early stages of a disease outbreak and improved techniques for declaring areas as "disease risk free".

Key words: Contact tracing, individual animal, uncertainty

Analysis of temporal contact networks in feedlot cattle and implications for disease transmission model assumptions

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ABSTRACT

Objective: Temporal contact network analysis provides a method for characterization of complex social structures; however, use in animal systems has primarily relied on the static descriptive approach to describing networks. The aim of this study was to use dynamic contact network analysis to characterize networks metrics and inform the construction of network-based disease transmission models.

Materials and methods: A Real-Time Location System was used to continuously record movements for 70 feedlot steers from May 23rd, to July 10th, 2017 (49 days). Overall, daily, and segmented 6-hour networks were constructed by defining a direct contact when a pair of steers were within a 0.66m distance threshold within any given 10sec interval.

Results: The overall network consisted of 70 vertices and 2415 undirected links. The average weighted degree (i.e. number of contacts per steer) for the overall observation period was 1089 (477 to 2708). The 49 daily networks had an average weighted density of 0.99 (0.60 to 1.00. When aggregated into 6-hourly periods: morning (6:00-11:00), afternoon (12:00-17:00), evening (18:00-24:00), and night (0:00-5:00), average network density was 0.79 (0.11 to 0.99). The average densities observed for night versus morning hours were 0.53 and 0.94, respectively. The importance of individuals in the network based on centrality measures such as degree, betweenness, and closeness was examined for each 6-hour period.

Conclusion: Due to the high density seen in the 49 daily networks, variation in the contact structure patterns made throughout the day were masked. When compared to the overall and daily networks, the 6-hour aggregated networks displayed more heterogeneity. The observed averaged network densities in the night periods versus the morning periods were different, implying that time of day impacted the observed network. No individual was identified as a consistent hub over all periods. The explicit network increases the understanding of heterogeneous contact structure within a pen of steers and appropriate incorporation into disease transmission models.

Key words: Network, feedlot, cattle, contact, temporal

Reconstruction of the cattle movement network in New Zealand: exploring the underlying drivers of cattle trade

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ABSTRACT

Objective: Understanding the drivers of cattle movements between farms is crucial for modelling realistic infectious disease transmission through the cattle industry especially in situations where the movement records are incomplete or where the prediction of future movements is of interest. Using historical data of the cattle movements in New Zealand, we analysed the underlying drivers of cattle trade to reconstruct the network.

Materials and methods: Only farm-to-farm trade of female cattle during 2013-2016 was extracted from national cattle movement data. We first developed a multivariable logistic regression model to generate probabilities for whether a movement was likely to between any two farms in the network based on factors such as Euclidean distance, time of year, previous trade (i.e. fidelity), or whether farms were located in the same bovine tuberculosis control area. We then created a network re-wiring algorithm where pairs of farms that sent and received cattle in any given week are connected using the following different scenarios; 1) with the closest distance, 2) with weighted random selection based on the distance, and 3) with weighted random selection based on the predicted probability of the logistic regression.

Results: According to the regression models, distance between farms explained the largest variability in the cattle trade with smaller contribution from fidelity. The network rewired according to the closest distance showed the most clustered trading pattern than observed whereas the networks rewired with weighted random selection tended to overestimate the movement distances.

Conclusion: Although cattle trade appears to be highly driven by distance and fidelity, other unmeasured variables such as sharing the same livestock trader, looking to purchase to cattle with specific characteristics, or mitigating biosecurity risks are important to consider in developing more realistic models.

Key words: Network reconstruction, network rewiring, cattle movement network, cattle trade

Livestock trade network: the potential for disease transmission and implications for risk-based surveillance on the island of Mayotte

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ABSTRACT

Objective The island of Mayotte is an EU outermost region, located in the Indian Ocean. This study aimed at identifying the network characteristics of livestock movements in Mayotte and assessing their potential implications for risk-based surveillance.

Materials and methods: Data on livestock movements (2007-2014) were presented as a network of administrative communes connected by livestock movements and characterised by social network analysis. Second, we developed a mathematical model to assess the time from the introduction of an exotic livestock disease into the island to the infection of individual communes by stochastic simulations. Finally, to assess the validity of the inferences from our analyses, we compared the network analysis results to Rift Valley fever (RVF) seroprevalence data (2008-2014).

Results: The majority of livestock movements occurred between communes in the central region and from communes in the central to those in the outer region, with centrality measures being higher in communes in the central than those in the outer region (Figure 1). Communes in the central region were more likely to be infected earlier than those in the outer region when the spread of a pathogen was simulated on the network. Finally, during the RVF epidemic (2008-2010), seroprevalence was higher in communes in the central than those in the outer region, further supporting our results.

Conclusion Communes in the central region would play a major role in the spread of infectious diseases via livestock movements, which needs to be considered in the design of risk-based surveillance systems in Mayotte.

Key words: Social network analysis, mathematical modelling, livestock movement network, risk-based surveillance, epidemic
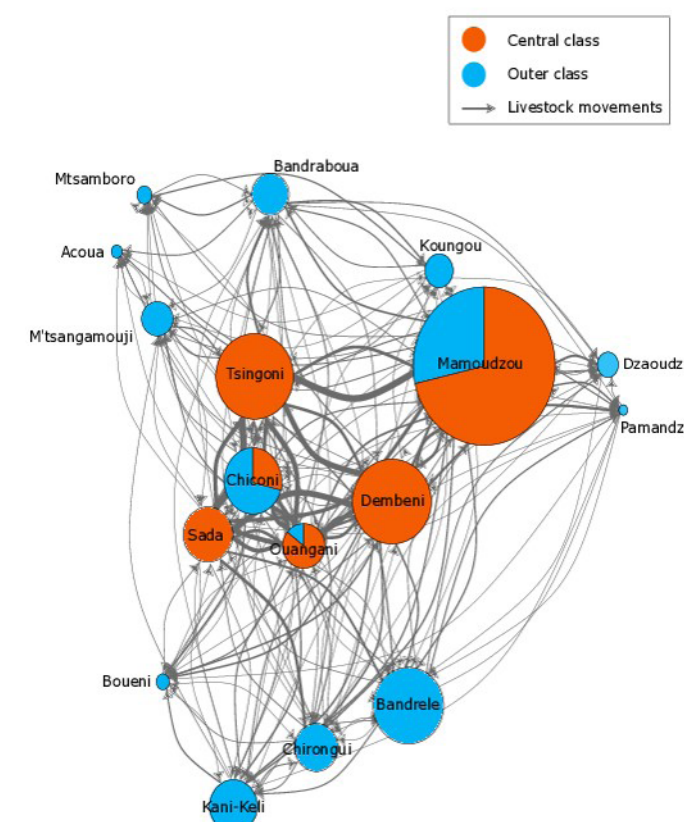
Figure 1. Livestock movement network in Mayotte from 2007 to 2014. Nodes and edges correspond to the 17 communes and livestock movements between them. The nodes are located according to their geographical coordinates, with their size being proportional to their livestock population size in 2010. The arrow and width of the edges are the direction and the total number of livestock movements between communes. Nodes were expressed as pie charts, showing the proportion of communes' structurally equivalent class over the study years.

Understanding how disease information diffuses through farmer social networks

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ABSTRACT

Objectives: Managing health risks in livestock populations first requires farmers to be aware that a problem exists and then to be sufficiently motivated by the potential impacts of the disease to implement appropriate control measures. In recent years, social media sites such as Facebook and Twitter have provided a novel means for disseminating information about animal health risks through farming communities, but there has been little work to understand how messages spread and whether the messages can help promote farmer behavioural change. In this analysis, we explore this social contagion phenomenon in the context of four different events that occurred within New Zealand that had animal health implications: (1) the *Mycoplasma bovis* outbreak of 2017/2018 (epidemic disease), (2) the launch of a national bovine viral diarrhoea virus (BVD) campaign in 2018 (endemic disease), , (3) the magnitude 7.8 Kaikoura earthquake in 2016 (localised geophysical risk), and (4) the widespread droughts in 2017/2018 (weather risk).

Materials and methods: Data were extracted from publicly available messages on Facebook and Twitter following the event dates and analysed to describe changes in the number of postings, sentiments in relation to the event, and indications of possible behavioural actions. The data were also used to reconstruct the farmer social media networks to identify whether there are any individuals or organizations that are acting as information hubs.

Result: The preliminary findings from this investigation highlight the important role of social media as a communication tool to improve animal health risk management.

Key words: Information diffusion, social networks, farmer behaviour, risks, social contagion

Impact of African Swine Fever occurrence on international swine meat trade - 2012 to 2016

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ABSTRACT

Objective: As international trade is significant with respect to commercialization of animal products, the present retrospective, descriptive and ecological study aims at characterizing the world's pork trade Network and the occurrence of African Swine Fever, by considering the years of 2012 to 2016.

Materials and methods: The trade information obtained from TradeMap (Internation Trade Center) was evaluated and cross-checked with African Swine Fever data obtained from the World Organization for Animal Health (OIE). The softwares Stata 12.0 (College Station, TX: StataCorp LP) and Pajek 1.24 (Pajek, 2009) were used for analysis and network design.

Results: During the study period, 228 countries were involved in the export and/or import of pork products (fresh, chilled or frozen). It was possible to characterize the pork trade network in the world, from 2012 to 2016, and to identify the African Swine Fever health status of the main exporting countries. About 53,849,513 tons of products were exported in the 5 years observed.

Conclusion: In the sum of the period, there were 26 occurrences of countries that were exporters and positive for the disease. However, occurrences of exporting and disease-negative countries were more frequent, with a sum of 527 occurrences.

Key words: Network analysis, epidemiology, African Swine Fever

Spatial & temporal patterns of the swine trade in Argentina from 2011 to 2016 using graph theory and network analysis

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ABSTRACT

Objectives: The aim of this study is to evaluate the spatio-temporal characteristics of swine movement network in Argentina from 2011 to 2016.

Materials and methods: Network analysis, graph theory methodologies, and graphic representation were used. First we created a directed network for each year, plotting farms and markets as nodes and individual movements as edges. We then calculated measures of degree centrality, closeness, and betweenness per year, to identify and locate farms and markets of interest in regards to both the potential introduction and distribution of diseases. We next identified communities of strongly interconnected farms and markets using Infomap and Walktrap algorithms. We also looked at impact of markets by looking at networks that involved only market related trades, or removing key markets to see how they impact the network.

Results: The network consists of approximately 19,000 nodes (19.5% of the country's farms) and 135,500 movements. On average there were 1,883 movements per month over a mean distance of 143km (89 miles). The mean number of pigs transported in each movement was 44, with an increasing trend over the years. The main destination and source provinces were Buenos Aires (39,122 incoming and 40,878 exiting movements), Córdoba (37,457 and 44,274) and Santa Fe (30,869 and 26,523). Though these provinces represent 36.7% of farms, they concentrated 79.3% of incoming and 82.2% of outgoing movements during that period. The departments generating the largest number of movements were Carmen Areco, Caseros, General López, Marcos Juárez and Río Cuarto, which were involved in 20% of all movements whilst only containing 3% of farms. Though few markets were involved in few trades overall, they held central positions in the network.

Conlusion: The results of this work will be useful for Decision Makers to improve risk-based surveillance and better target control measures for both endemic and emerging swine diseases in the country.

Key words: Space-time networks, swine diseases, risk-based surveillance, pig movements, South America

Social network analysis for determining cattle and poultry movement pattern in Lampung, West Java and Central Java provinces in Indonesia

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ABSTRACT

Objective: Livestock movement is considered as one of the main factors for the spread of infectious diseases in livestock populations. Little information is available about livestock movement networks in Indonesia. Social network analysis (SNA) was used to determine poultry and cattle movement patterns.

Materials and methods: The data for the poultry and cattle movement were retrieved from Indonesia's national animal health information system (iSIKHNAS) database and the unit of interest for analysis was district. The analysis involved measuring centrality parameter, measuring cohesion and identifying the network topology monthly for 12 months.

Results: In total, 2,837 poultry and 1,372 cattle movements were recorded, this movement involved 10,033,941 poultry and 11,654 cattle. The median distance of movement was 1,118 km and 190 km for poultry and cattle, respectively. Network structure of combined poultry and cattle network revealed that districts with a high out-degree tend to have a high betweenness and are concentrated in Central Java Province, while districts with high in-degree are located in major cities (Jakarta, Bandung and Semarang).

Conclusion: Both networks were characterized by a scale free network, which was intercepted by small world properties one month prior to Idul Fitri for the poultry network and during Idul Adha for the cattle network. It is recommended that during an outbreak situation, the authorities should be focused implement control measures and surveillance on highly connected districts.

Key words: Social network analysis, poultry, cattle, Indonesia

Livestock movement in northern Tanzania: exploiting routinely collected data to infer networks for infectious disease transmission and control

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ABSTRACT

Objectives: Infectious zoonotic diseases are a significant burden on human and livestock health in northern Tanzania, causing febrile illness in people, often misdiagnosed and mistreated, and impairing livestock productivity. Movements of livestock provide a route for pathogen transmission thus an opportunity for control. Effective control requires detailed knowledge of livestock movements, currently lacking in Tanzania and this study endeavours to fill this knowledge gap.

Materials and methods: All available livestock movement permits (n»59,000) from 2009/2011/2013/2015 in Arusha, Manyara, and Kilimanjaro regions were collected and 612 surveys with livestock buyers and sellers in 22 markets in the study regions were conducted to complement the permit data. We created directed weighted networks of cattle and small ruminant movements between all 398 administrative wards in the study regions. A gravity model was used to identify predictors of livestock movements and infer movement networks while accounting for subsampling and non-random missingness. The model-generated dynamic monthly networks will be used for social network analysis to identify key network properties for pathogen transmission and simulate the effects of pathogen introduction and different interventions.

Results: Cattle journeys (mean 116km) were longer than small ruminants (mean 88km), with similar seasonal trends. Inter-ward distance (49% of explained variance; P<0.001), destination human population size (30%; P<0.001), and the presence of a secondary market at origin and/or destination (23%; P<0.001) were strong predictors of cattle movement. Distance (64%; P<0.001) and destination human population size (14%; P=0.004) were strong predictors of small ruminant movement. Network analysis with disease and intervention simulations will be complete for presentation in November.

Conclusion: We demonstrate the feasibility of using routinely collected data to infer livestock movement networks in developing country settings. The inferred networks will underpin models of disease dynamics that allow us to address a range of questions around livestock movements and zoonotic disease transmission.

Social network analysis of live poultry movements in the province of Kerman, southeast of Iran

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ABSTRACT

Objective: Movements of animals are one of the most important ways of transmission of infectious animal diseases within and between regions. Social Network Analysis (SNA) was used to describe the contact patterns of the poultry network and to identify the most important premises for potential disease introduction into the region. This study is the first characterization of a network of live poultry movements in Iran which may be to increase the efficacy of the detection of possible secondary outbreaks in case a poultry disease is introduced into the region.

Materials and methods: A cross sectional survey was carried out from October to December 2017 in 10 poultry slaughterhouses in Kerman. The information provided by Iran veterinary organization was the live poultry movement records related to poultry slaughterhouses in Kerman, specifically, the day of movement, the location of origin and destination were provided. SNA was used to describe the connectivity pattern within the network. To evaluate whether the degree centrality of both Slaughterhouses and sources varied with time we used Generalized Estimating Equations models.These analyses were carried out in UCINET 6.135 and Stata14.

Result: During October to December 2017, a total of 10 slaughterhouses were investigated, resulting in a total record of 3994 movements. Most movements were recorded in the Sirjan (n=1335; 33.4%), Kerman (n=1184; 30%), Rafsanjan (n=697; 17.4%), Bardsir (n=422; 10.5%) Zarand (n=315; 7.8%) and Bam (n=41; 0.01%) respectively. Regarding the 26 poultry sources identified in this period of time,13(50%) were located in within of province of Kerman. Our results also show that the mean degree centrality was not significantly different between the months of October to December.

Conclusion: The results of this study may be useful to design control programmes of poultry diseases and detection of secondary outbreaks in future epidemics. Also will help to reduce the Major economic and sanitary impact of poultry diseases.

Key words: Social network analysis, live poultry movements, poultry slaughterhouses, Kerman

Social-butterflies at the wildlife-livestock interface: disease-relevant variation in individual animal sociality

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ABSTRACT

Objective: Disease spillovers at the wildlife-livestock interface pose serious threats to the agricultural and recreation industries. Disease dynamics are influenced in part by the social behavior of individual animals. Individuals within the same population may exhibit different social behaviors, both in the number of individuals or species they associate with, and the intensity of those associations. We model association networks between domestic cattle and free-ranging elk (*Cervus elaphus*) and test for differences in individual animals' sociality.

Materials and methods: Using network theory, we develop three types of association models: 1) elk–elk, 2) elk–cattle, and 3) a global network containing associations among all elk and all cattle. We quantify these networks using GPS location data from collared elk and cattle at the Starkey Experimental Forest and Range in Oregon, USA. The dataset contains 1,492,564 elk and 497,674 cattle location estimates (2007-2013). An "association" is any spatial intersection of the error ellipses surrounding two animals' synchronous point location estimates.

Results: Our dataset contains 491,735 elk–elk and 1304 elk–cattle associations. Of the 319 collared elk, 208 associated with at least one other elk, while 194 elk associated with at least one cow. Statistics indicate that elk are more social with other elk than with cattle, but the most social (within species) elk are also most likely to associate with cattle. All elk that associated with cattle also associated with elk. Yet 40% of elk that had at least one association with another elk never had an association with cattle.

Conclusion: At the Starkey Forest site, elk most willing to associate with cattle are also more social with other elk. These more-social individuals, both with their own and other species, could complicate control of wildlife-livestock diseases in the event of an incursion.

Key words: Cattle, elk, edge-weight diversity, network analysis, Starkey

Spatial clustering of staphylococcal infections and antimicrobial resistance among dogs presented at a veterinary teaching hospital in South Africa

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ABSTRACT

Objective: The objective of this study was to investigate spatial patterns of staphylococcal infections and antimicrobial resistance patterns of *Staphylococcus* spp. clinical isolates from dogs from Gauteng province in South Africa.

Materials and methods: Records of 1,497 dog clinical samples from Gauteng province processed at a Veterinary Teaching Hospital (VTH) laboratory for microbiological diagnosis during the time period 2007-2012 were included in the study. Spatial empirical Bayesian smoothing, using first-order queen's spatial weights, was used to investigate spatial distribution of staphylococcal infections, antimicrobial resistance (AMR) and multidrug resistance (MDR) of *Staphylococcus* spp. isolates. Global Moran's I was used to assess for evidence of global spatial clustering while spatial scan statistics were used to identify local clusters of staphylococcal infections, AMR and MDR at the municipality and town spatial scales.

Results: Significant global spatial clusters of staphylococcal infections were identified at municipality (Moran's I=0.342, p=0.006) and town (Moran's I=0.398, p=0.001) spatial scales. However, global clusters of AMR (Moran's I=0.356, p=0.003) and MDR (Moran's I=0.303, p=0.007) were only identified at the town spatial scale. Local clusters of staphylococcal infections were identified at the municipality (RR=1.71, p=0.003) and town (RR = 1.65, p = 0.039) spatial scales.

Conclusion: Results show that there is evidence of spatial clustering of staphylococcal infections, AMR and MDR among dogs from Gauteng Province that are presented at the VTH. However, no specific drivers of the observed clusters were identified. Future studies will need to identify local factors responsible for the identified clusters so to guide targeted control efforts and mitigate development of antimicrobial resistance.

Key words: Staphylococus, antimicrobial resistance, multidrug resistance, South Africa, dogs, Moran's I, clustering, clusters

Estimating contact rates from utilisation distributions of dogs: The influence of roaming patterns

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ABSTRACT

Objective: To estimate contact rates of free-roaming domestic dogs with heterogeneous roaming patterns in the Northern Peninsular Area (NPA), Australia.

Methods: GPS datasets were used of 21 dogs whose roaming patterns had been categorised ('stay-at-home', 'roamer' or 'explorer') based on utilisation distributions (UDs). For all dog pairs, individual dog UDs were placed at 10m increments (10-600m) and in a random direction (0-360°). At each increment, the Probability Home Range (PHR) index was calculated, to estimate the probability of finding Dog A in Dog B's 95% home range and *vice versa*. The contact probability was estimated by multiplying these two values. All pairs of dogs were simulated to produce distance kernels for each combination of roaming categories, which describe contact probabilities between individual pairs of dogs depending on the distance between their homes. The median (95% range) probabilities were calculated for each 10m increment. A logistic curve was fitted to estimate the probability of contact at every 1m.

Results: Six different distance kernels were produced based on the combinations of roaming categories. Kernels which included explorer dogs showed the most variation in contact probability, especially at short distances. However, the median contact probability reached zero at longer distances compared to the kernels without an explorer dog (420m, 350m and 260m for kernels with an explorer dog and 260m, 200m and 140m for kernels without an explorer dog).

Conclusion: Explorer dog contacts have a lower probability of occurring at shorter distances compared to roamer and stay-at-home dogs because explorer dogs visit different areas more frequently. However, explorers are likely to contact more dogs because their larger UD allows for contact at longer distances. The effect of these kernels will be tested by their incorporation into a rabies-spread model to realistically simulate a potential outbreak.

Key words: Contacts, roaming pattern, free-roaming dogs, disease modelling

A discussion on synchronized fallowing to control salmon lice populations in aquaculture based on empirical evidence

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ABSTRACT

Objective: Employing coordinated control measures is a common strategy to control infectious diseases, aiming for reduced treatment frequency or complete eradication of diseases. Everything from synchronized efforts to control head lice in kindergartens to stamping out livestock are thoroughly tested and successful examples of this approach. In salmon aquaculture, coordinated operations include discrete generations of fish and "all-in-all-out" in farms, with a fallowing period between generations. The system has later been extrapolated to the use of synchronized treatments and even fallowing in areas holding several farms. The effect on sporadic diseases like Infectious Salmon Anaemia is well proven. There are indications of positive effects from coordinated treatments of salmon lice, but there is little evidence regarding effects of synchronized fallowing.

Materials and methods/Results: We use real life data from Norwegian aquaculture to model the spread of salmon lice, and we show that salmon populations held in surrounding areas maintain a substantial infestation pressure of salmon lice copepoidtes in fallowed areas. The data does not provide a reliable control group, and our results do not give definitive answers to whether salmon lice numbers are lower in areas that practice synchronized fallowing.

Conclusion: We argue however, that there is a fundamental difference between fallowing an area to limit the spread of sporadic infectious diseases, and fallowing to mitigate an endemic problem. The expectation in a sporadic disease outbreak is that the surrounding areas are not infected, leaving low probability for reinfection. Endemic pathogens may proliferate in surrounding areas, thus generating an increased infestation pressure with time in a coordination area, due to increase in host biomass towards the end of fish generations and harvesting. Re-infestation therefore becomes unavoidable.

Spatial analysis of human echinococcosis in Kyrgyzstan

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ABSTRACT

Objective: Human echinococcosis is a parasitic zoonosis caused by the ingestion of infective eggs produced by tapeworms of the genus *Echinococcus*. The life cycle of the parasite involves several intermediate and definitive host species and specific ecosystems supporting the presence of the infective eggs in the environment. Given that human echinococcosis is a serious public health concern in Kyrgyzstan, we sought hotspots in the geographic distribution of the disease to identify regions where potential risk factors should be further investigated.

Materials and methods: We collected all hospital records of the surgical cases of the two most important forms of echinococcosis — the cystic (CE) and alveolar echinococcosis (AE) — in Kyrgyzstan in 2014-2016. CE and AE cases were mapped according to the address of the patients, and standardized incidence rates were computed at the district level. The rates were tested for significant ($p<.05$) global and local spatial autocorrelation through the Moran's I statistics and the Local Indicators of Spatial Association (LISA).

Results: Our preliminary results show remarkable geographic variations in the distribution of CE and AE, spanning between 1.2 and 43.9 cases per 100,000 inhabitants and 0 and 84.9 cases per 100,000 inhabitants, respectively. Through spatial analysis, we uncovered weak but significant global spatial autocorrelation for the standardized incidence rates of CE and AE. Furthermore, the LISA identified significant hotspots of CE and AE in the South-West of the country, specifically in three districts of the Osh region, and also in other two districts in Osh and Batken regions for CE.

Conclusion: We detected significant hotspots of AE and CE in the South-West of Kyrgyzstan. Further spatial analyses of potential risk factors need to be performed to better understand the geographic variations of the disease risk and to target control measures in the country.

Key words: Human echinococcosis, alveolar echinococcosis, cystic echinococcosis, risk mapping, spatial modelling

Risk factors for bovine rabies in Rio de Janeiro state, Brazil, 2010-2016

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ABSTRACT

Objective: The temporal and spatial epidemiological distribution of bovine rabies and risk factors for bovine rabies in Rio de Janeiro for the period 2010-2016 are described.

Materials and methods: Counts of the number of confirmed bovine rabies cases and estimates of the number of bat roosts per square kilometer in Rio de Janeiro municipalities for 2010-2016 were provided by the State Secretariat of Agriculture and Livestock and Agricultural Research Enterprise. A Bayesian, zero-inflated Poisson model, including spatially structured and unstructured random effect terms was developed to quantify the association between the density of cattle and density of bat roosts on the risk of bovine rabies.

Results: For 2010-2016 the incidence rate of bovine rabies ranged from 0.81 (95% CI 0.52 to 1.22) cases per 100,000 cattle-years at risk in 2015 to 3.00 (95% CI 2.35 to 3.79) cases per 100,000 cattle-years at risk in 2011. After adjusting for unobserved spatially structured and unstructured heterogeneity in the data, one unit increases in the number of cattle per square kilometer increased the municipality bovine rabies risk by a factor of 6.82 (95% credible interval [CI] 1.33 to 86). Unit increases in the number of bat roosts per square kilometer decreased bovine rabies risk by a factor of 0.98 (95% CI 0.51 to 1.47).

Conclusion: The incidence rate of bovine rabies in Rio de Janeiro state decreased markedly since 2011. We identified a relatively strong association between cattle density and bovine rabies risk, supportive of the hypothesis that there is a greater likelihood of infection, detection of clinical signs and subsequent reporting of cases to animal health authorities in areas where the number of cattle per unit area is high. Municipalities where there were no rabies cases were detected should be targeted for surveillance.

Spatial analysis of canine visceral Leishmaniasis in Panorama city, São Paulo, Brazil

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ABSTRACT

Objective: Visceral leishmaniasis (VL) is a zoonosis of great importance, having worldwide distribution and complex epidemiology, being dogs its main reservoir. This study aimed to characterize the distribution of canine VL and relate it to spatial features in Panorama, an endemic city of São Paulo State, Brazil.

Materials and methods: Using data collected in a serological survey between August 2012 and January 2013, 986 dogs were classified as positive and negative for VL. A spatial analysis was conducted comprising from data visualization to the elaboration of a relative risk (RR) map, undergoing global (K function) and local cluster analysis (spatial scan). To evaluate a possible relation between clusters and vegetation, the Normalized Difference Vegetation Index was calculated.

Results: The prevalence of canine VL was 20.3%. Spatial visualization showed that positive and negative animals were distributed throughout the study area. Intensity map of positives showed two sites of possible clusters compared to intensity map of negatives. One cluster was detected in a central region of Panorama, with a RR of 2.63 (p=0,01). The spatial variation of the RR in the study area was mapped and the same region was identified as a significant high risk area (p<0.05). No differences were observed in the vegetation pattern comparing the cluster internal and external areas.

Conclusions: The prevalence data, the cluster location and the RR map provide subsidies for the efforts of the city epidemiological surveillance department towards high risk areas, saving resources and improving control of VL in Panorama.

Key words: Cluster analysis, dogs, *Leishmania spp*, NDVI, Spatial variation of relative risk

Spatial autocorrelation in a non-linear disease risk environment

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ABSTRACT

Objective: The dissemination of fish diseases in aquaculture regions often involves water-borne transmission. In near-coastal environments the use of Euclidean distances to study spatial disease risks is counter-intuitive as it does not account for the presence of land masses nor the complexity of coastlines, such as in Chile. The objective of this study was to assess spatial autocorrelation between Salmonid Rickettsial Septicaemia (SRS) outbreaks in Chilean aquaculture farms based on non-linear distances.

Materials and methods: Longitudinal data on the occurrence of SRS in salmonid farms were obtained for the time period 2011 – 2018 from the Chile national veterinary services. Seaway distances, or the shortest routes between two points via water, were calculated for each pair of farms in the dataset using both a custom-built routing algorithm and an existing open-source grid-based algorithm. Then, an existing spatial variogram function was adapted to use seaway distances rather than Euclidean distances to study spatial auto-correlation of SRS occurrence.

Results: Spatial variograms based on Euclidean distances suggested that some spatial influence exists over long distances (up to 200 km). However, they displayed high variance, high anisotropy and suggest substantial discontinuity, indicating very limited spatial correlation between SRS occurrence in neighbouring sites. The spatial influence identified at long distances was likely due to regional factors rather than local scale effects. Although difficult to visualise, using the shortest seaway distance between all sites overcame the implausibility of waterborne disease spreading over significant land masses and thus provides a reasonable pathway to assessing the risk of disease spread between 'neighbouring' farms. Last, we compared the results and computational costs of both routing algorithms.

Conclusion: This approach, based on open-source tools, demonstrates an improved method to account for spatial heterogeneity when using spatial epidemiological tools to reflect biologically plausible disease transmission risk.

Key words: Spatial autocorrelation, disease risk, seaway distances, aquaculture

Using climate data to create prediction models for brucellosis prevalence in Pakistan

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ABSTRACT

Objective: Mapping disease burden across a large geographic area is problematic in terms of the need for extensive on-the-ground field surveillance. However, new freely-available global fine-scale geographic and climate data may be able to assist in this process. This has particular potential for disease mapping in developing countries where local disease information is often lacking but nonetheless there is a need for this to inform authorities to assist in monitoring and resource allocation.

Materials and methods: In this study, herd-level prevalence of bovine brucellosis has been mapped over Pakistan. A previous study obtained seroprevalence data on brucellosis status of farms across seven districts in Pakistan (five in Punjab, two in Sindh), and at each farm, geographic coordinates were recorded. Fine-scale climate (precipitation, minimum and maximum temperature, relative humidity) as well as digital elevation data were downloaded from publically-available sources at the coordinates recorded from the study. These were then used to form a predictive model of brucellosis prevalence, by means of developing a generalised additive model. In addition, the climate and elevation data were downloaded on a fine 0.5 x 0.5 decimal degree (DD) grid over the entire country. Using the model, predictions were the obtained for each 0.5 x 0.5 DD pixel and mapped; all analyses undertaken using R.

Results: The mapping revealed a relatively high prevalence in Punjab and low prevalence in Sindh, which aligns with our previous findings. However, it also suggested a high prevalence in Balochistan and low prevalence in Khyber Pakhtunkhwa and the Federally Administered Tribal Areas.

Conclusion: As no studies on bovine brucellosis have been conducted in these regions, this provides potentially useful information for livestock authorities, although 'on-the-ground' validation of these findings needs to be undertaken. This approach has potential application in many other areas of disease mapping.

Key words: Brucellosis, climate, Pakistan, statistical models, disease mapping

Correcting observer-dependent detection bias in citizen science data when modelling abundance

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ABSTRACT

Objective: To correct detection bias in citizen science data to estimate wildlife population abundance.

Materials and methods: We compiled koala sighting locations reported by members of the public in 2012 in South-East Queensland, Australia, and used environmental and ecological covariates to model koala abundance. Inhomogeneous Poisson process model were fitted by lasso regularisation. Best lasso penalty was selected by cross validation while the best spatial resolution for the model was identified by testing maximum likelihood at varying spatial resolutions. Three models were fitted: firstly, abundance was modelled as a log linear function on a set of covariates which represented environmental conditions required for koala occurrences; a second model was then fitted using additional environmental conditions and distances to roads from where koalas were most likely sighted, but interactions were not allowed between environmental and distance covariates; and finally the predictions were obtained to correct spatial bias which affect probability of detection by setting the distance covariates to their minimum value level everywhere in the study region.

Results: Maximum likelihood unchanged from 0.5 - 1 then decreased beyond 1 square km spatial resolution. Adding distance covariates to the environmental only model improved intensity in new areas. Bias correction further improved intensity estimates in low accessibility areas where koalas were known to occur but not correctly predicted from the other two models.

Conclusion: Using Poisson process models, we show that distance to roads was identified as a suitable covariate to correct the spatial bias in koala sighting data collected by members of the public

Key words: Inhomogeneous Poisson processes, bias, abundance

Comparison of spatiotemporal patterns of historic animal anthrax outbreaks in Minnesota and Kazakhstan

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ABSTRACT

Objective: The epidemiological triad recognizes the effect that the interaction between host, pathogen, and environment has on the resulting disease pattern in a population. Yet the influences of each triad component may dramatically vary for different conditions. For example, recurrence of Anthrax in endemic areas is believed to be correlated with environmental characteristics, suggesting that comparable epidemiological patterns should be evidenced in regions with similar environmental conditions, despite differences in the demographic, socio-economic, and historical backgrounds. The objective here was to compare the spatiotemporal patterns of historic animal Anthrax records from two endemic sites that are located at a similar latitude but have been subjected to different demographic and socio-economic conditions. The spatiotemporal directionality test and scan statistics were used to compare between the sites.

Materials and methods: The spatiotemporal directionality test and scan statistics were used to compare between the sites. Reported animal Anthrax cases in Minnesota, USA (n=255 cases between 1912-2005) and Kazakhstan (n=3,997 cases between 1933-2014) were analyzed.

Results: Epidemic curves indicated sporadic Anthrax outbreaks in Minnesota, whereas a long-term epidemic was detected in Kazakhstan. A comparable seasonality of the animal Anthrax cases was observed at both sites with a peak in August. The maximum time-span between cases at the same location were 55 and 60 years apart for Minnesota and Kazakhstan respectively. The spatiotemporal directionality test pointed a northeastern directionality for long-term trends in Minnesota, whereas a southwestern directionality was observed in Kazakhstan. The spatiotemporal permutation model of the scan statistic detected 15 clusters in northwestern Minnesota of which seven were overlapping, indicating recurrent locations. Seventeen clusters were detected in the periphery of Kazakhstan with eight of them overlapping.

Conclusions: Results support the hypothesis that despite the limited commonalities, spatiotemporal epidemiological patterns for Anthrax in both locations, are defined mainly by the different demographics, disease control strategies, and historical contexts of the settings.

Key words: animal Anthrax, cluster analysis, site comparison, spatiotemporal directionality

Identification of high risk areas for avian influenza outbreaks in California using disease distribution models

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ABSTRACT

Objective: The coexistence of different types of poultry operations such as free range and backyard flocks, large commercial indoor farms and live bird markets, as well as the presence of many areas where wild and domestic birds co-exist, make California susceptible to avian influenza outbreaks. The 2014-2015 highly pathogenic Avian Influenza (HPAI) outbreaks affecting California and other states in the United States have underscored the need for solutions to protect the US poultry industry against this devastating disease.

Materials and methods: We applied disease distribution models to predict where Avian influenza is likely to occur and the risk for HPAI outbreaks is highest. We used observations on the presence of Low Pathogenic Avian influenza virus (LPAI) in waterfowl or water samples at 355 locations throughout the state and environmental variables relevant to the disease epidemiology. We used two algorithms, Random Forest and MaxEnt, and two data-sets Presence-Background and Presence-Absence data.

Results: The models performed well (AUCc > 0.7 for testing data), particularly those using Presence-Background data (AUCc > 0.85). Spatial predictions were similar between algorithms, but there were large differences between the predictions with Presence-Absence and Presence-Background data. Overall, predictors that contributed most to the models included land cover, distance to coast, and broiler farm density. Models successfully identified several counties as high-to-intermediate risk out of the 8 counties with observed outbreaks during the 2014-2015 HPAI epizootics.

Conclusion: This study provides further insights into the spatial epidemiology of AI in California, and the high spatial resolution maps may be useful to guide risk-based surveillance and outreach efforts.

Key words:HPAI, LPAI, spatial epidemiology, risk map, ecological niche model

Modeling the spatiotemporal dynamics of foot-and-mouth disease in during mass vaccination programs India

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ABSTRACT

Objective: Foot-and-mouth disease virus (FMDV) causes a disease that affects domestic livestock and numerous wildlife species. In the past two decades, many of the most widespread and important viral lineages have emerged from the south Asia region, especially India. Therefore, understanding the FMD situation in India is critical for both India's and global progress towards reducing the impact of the disease. The first phase of India's FMD control program (FMD-CP1) commenced in 2003 and was implemented in 54 districts of 10 states. Mass vaccination of all cattle and buffalo was carried out twice a year with the locally produced trivalent vaccine. Our objective herein was to assess epidemiological outcomes of FMD-CP (2003-2010) based on data collected by the Directorate on Foot and Mouth Disease.

Materials and methods: For each of 20 rounds of vaccination, serum antibody titers of randomly selected cattle and buffalo were measured pre- and post-vaccination from the districts involved in FMD-CP1, with a total of 997,893 animals tested. Antibody status was determined by the Liquid Phase Blocking Elisa (LPBE).

Results: We describe temporal trends in the percent of the population in each district that were inferred to be protected from FMD pre and post-vaccination. We also show that the number of outbreaks per year, controlling for population size, was lower in districts participating in the control program compared to those that were not. We apply Bayesian space-time models to further assess the impact of vaccination and other factors, such as road networks, land cover, proximity to international borders, on the dynamics of FMD in the country.

Conclusion: India expanded their control program to include the 167 remaining districts of the country, with the goal of creating FMD-free zones. Spatial and temporal analysis of the dynamics of FMD in vaccinated districts is essential for meeting this goal.

Key words: Foot and Mouth Disease, India, vaccination program, Spatial and temporal analysis

Spatial epidemiology of cystic echinococcosis in Aysén region, Chile

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ABSTRACT

Objective: Cystic echinococcosis (CE) is a parasitic zoonosis, produced by larval stage of *Echinococcus granulosus*. This parasite has a worldwide distribution and in Chile is considered the most important zoonosis, especially in regions where rising livestock is predominant and the life cycle occurs among dogs and intermediate hosts, such as cattle and sheep. This study was carried out in Aysén Region, and we aimed to determine the spatial epidemiology of CE in bovine and ovine herds slaughtered in the region between 2015 and 2016.

Materials and methods: Clustering of CE at herd levels was carried out applying the Moran Global Index test and LISA test in ArcGIS 10.1 and also by ScanTest in SaTScan 9.4.4 using the Poisson distribution model. We also made a spatial interpolation with DMAP IV to estimate areas with higher risk of disease exposure.

Results: Overall, 4,830 cattle farms and 42,573 animals were analyzed. Of these farms, we obtained coordinates of 1,078 of which 70% were positive to CE. In addition, 348 sheep farms and 42,800 animals were analyzed. Of these farms, 296 were georeferenced of which 68% were positive to CE. We observed that globally the CE prevalence of both cattle and sheep herds were not clustered. However, when LISA test was carried out we found 14 cattle and 23 sheep farms with high prevalence showing high clustering. Using ScanTest, we also detected 6 and 11 clusters in cattle and sheep farms, respectively.

Conclusion: These results indicate that there is a high rate of infection by *E. granulosus* in livestock across the whole region. Despite this, there are some areas that have more infection than expected by chance, which are mostly small farms presenting conditions that would facilitate the maintenance of infection, such as dogs feeding with offal, among others.

Mediation Analysis Concepts: To control for or not to control for? That is the question

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ABSTRACT

Objective: The objective of this work is to review three possible sources of bias in mediation analysis: 1) mediator-outcome confounding (M-Y); 2) exposure-mediator interaction (Ex-M Int); and 3) mediator-outcome confounding affected by exposure (M-Y Ex) using epidemiological tools.

Materials and methods: A case study of the effect of reproductive diseases in dairy cattle on the probability of conception was used. A causal diagram was built and then any mediating (intervening) variables was removed from the diagram to estimate the total effect. Then, the total, direct and indirect effects were estimated using a counterfactual framework using the mediation command available in Stata and R.

Results: Several commands are available for mediation analysis. In Stata, for instance, *"medeff"* and *"G-formula"* are being used for this type of analysis. In R, the package *"medflex"* has similar capabilities. The commands *"medeff"* and *"medflex"* can address the M-Y and Ex-M Int biases. However, G-formula can handle all three types of biases. The major differences between *"medeff"* and *"medflex"* is that the later can fit models for continuous, binary and count data for both the outcome and the mediator. However, *"medeff"* can only use continuous and binary data for the mediator. Estimates of total, direct and indirect effects were obtained for each type of bias.

Conclusion: This presentation provided an overview of the current methods used for mediation analysis using pre-defined commands available in the two most common statistical packages used in epidemiology. It highlights the importance of building a causal diagram for making causal inferences and the importance of understanding sources of biases present when conducting a mediation analysis.

Key words: Causal diagram, mediation analysis, intervevning variable, biases

Mediation Analysis: a case-study

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ABSTRACT

Objective: The current study was undertaken to disentangle the relationships among water temperature (*temp*), the estimated lice exposure (*ele*) pressure arising from aquaculture sites, and attached lice counts (*lc*) on wild sea trout based on the following causal diagram. Data consisted of counts of attached lice on 424 sea trout over a 5 year period (2012-2016).
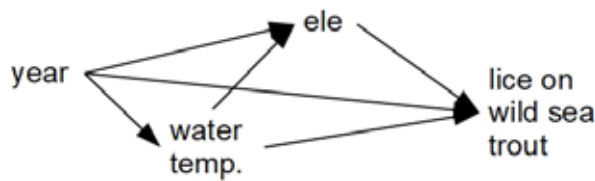
Materials and methods: A combination of negative binomial models and a mediation analysis which took into account an interaction between *temp* and *ele* was carried out to determine the direct effects of *ele* and the direct and indirect effects of *temp* and *year* on *lc*.

Results: The effects of *ele* and *temp* interacted, with strong positive effects of *ele* evident at warm water temperatures. Approximately 80% of the total effect of *temp* was mediated through *ele*. Year was treated as a set of 4 indicator variables with 2013 as the baseline. Overall, more of the annual variation was mediated through *ele* then *temp*. However, there was also a direct effects indicating that some of the variation in lice counts was attributable to other differences among years.

Conclusion: Lice from aquaculture sites did contribute to the observed burden of lice on wild sea trout. Mediation analysis was useful in sorting out the roles of water temperature and the estimated sea lice exposure.

Key words: Mediation analysis, direct and indirect effects, sea lice, aquaculture

Machine learning tools for understanding mastitis epidemiology

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ABSTRACT

Objective: As automated milking systems (AMS) continue become more widely adopted in the dairy industry, the need for accurate, early automated disease detection becomes greater. Chemical sensors integrated into AMS are used to detect milk characteristics and identify possible cases of mastitis. Previous studies have developed predictive models for mastitis with varying degrees of success using subsets of these characteristics, while ignoring behavioral and other animal characteristics. To integrate all measurements from AMS to develop accurate mastitis detection models using state-of-the-art machine learning algorithms while identifying characteristics or behaviours that indicate health changes preceding clinical mastitis.

Materials and methods: Detailed disease recording for individual animals were collected from 9 commercial AMS dairy herds in Ontario, Canada, and two research herds from Alberta and Saskatchewan. Animal and herd-level features that are not directly measured were generated using AMS measurements: incorporating refusals to determine the number of attempted visits, latency to exit milker, daily temperature, and number of cows per robot on the given day. Animal-level features may indicate behavioural changes that are difficult to detect manually, while dynamic or user-supplied herd-level features may affect behavior independently of health. Before prediction, data from visits on a single day were reduced to a single observation as only the day of diagnosis is known. Information loss from compression was determined by comparing heuristics with dimensionality reduction using neural network-based encoders or convolution.

Results: Autoencoders are readily incorporated into deep neural networks but resulted in greater loss of information and decreased interpretability whereas convolution and summarizing heuristics generated more noise while obscuring finer temporal details.

Conclusions: These compression methods will be incorporated into predictive models to identify which characteristic changes impact prediction accuracy as well as compare changes in accuracy depending on the compression method. Detailed results will be presented at the conference.

Key words: mastitis, automated milking systems, disease prediction, machine learning, neural networks

Full Model Selection with Regression Trees

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ABSTRACT

Objective: Current limitations of full model selection (FMS) methods have slowed their incorporation into the field of applied epidemiology; therefore, data preprocessing options and model algorithms are still commonly selected empirically. Here we present the use of regression trees as an innovative method for FMS that does not only result in a robust final model for prediction but also illustrates the significant decision criteria and the most appropriate order for making these decisions. The process includes building a model for every combination of options available for comparison. Then, the iterated cross-validation performances of these models are passed through a regression tree resulting in the selection of a final model. Unlike current methods, FMS by regression tree is easy to implement, does not have internal parameters to select, and is straightforward to interpret.

Materials and methods: A milk Fourier transform infrared spectroscopy dataset with 1034 observations from 381 dairy cows was used to build a prediction model for blood non-esterified fatty acids >= 0.7 mmol/L. Seven decisions criteria were compared: milk data subset, inclusion of cow information, standardization, feature extraction, no-information wavenumber removal, removal of highly correlated predictors, and algorithm.

Results: The decision criteria had 4, 2, 3, 2, 2, 2, and 11 options, respectively. A total of 660 models were built with 10-fold, 10 repeat cross-validation. A regression tree with Bonferroni correction for multiple comparisons was then used to estimate the models' balance accuracies. The decision criteria were included as independent variables. The final model was selected after three statistically significant (p-value < 0.05) decision nodes representing two decision criteria (milk data subset and algorithm).

Conclusion: Applied epidemiology will benefit from systematic FMS using regression trees as an alternative to empirical selection of data preprocessing options and model algorithms, since these decisions and the order in which these decisions are made can significantly affect model performance.

Key words: Full model selection, regression tree, preprocessing, prediction model, Fourier-transform infrared spectra

Estimation of market- and bird-level Newcastle disease (ND) prevalence from a complex sampling design

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ABSTRACT

Objective This study aimed to estimate market- and bird-level ND prevalence in live bird markets in Dhaka and Chittagong cities, Bangladesh, from pooled samples collected using a stratified three-stage cluster sampling design.

Materials and methods: From February to March 2016, swabs were collected from different market and poultry types. Markets, shops and birds constituted the primary, secondary and tertiary sampling units, respectively. The swabs collected from the same shop and poultry type were pooled by five and tested for ND virus using rRT-PCR. A Bayesian hierarchical logistic regression model was developed, using market and poultry types as market- and bird-level fixed effects, respectively, and a market-specific random effect. All unknown parameters were specified by weakly informed priors. The model was run via a Markov-chain-Monte-Carlo simulation using JAGS software.

Results: Results In total, 477 pools were collected from 2384 birds from 40 markets. Table 1 shows the market- and bird-level prevalence estimated from the model. Nearly all surveyed markets were estimated to be infected with ND virus. At the bird level, ND was more prevalent in mixed than retail markets, and in industrial broiler and indigenous chickens than waterfowl and crossbred chickens. Convergence was achieved for all parameters, and a posterior predictive check showed that the model predicted the observed pool-level prevalence well (Bayesian P-values, Table 1).

Conclusion Our model provided robust estimates of market- and bird-level ND prevalence from pooled sample by accounting for stratification and cluster sampling, showing its usefulness when inferring prevalence based on data from complex survey designs.

Key words: Newcastle disease prevalence, poultry, live bird market, Bayesian approach, pooled sample

Table 1. Market- and bird-level Newcastle disease prevalence estimated from Bayesian hierarchical logistic regression model

Market-level risk factor[1]	No. of markets	Observed market-level prevalence[2]	Estimated market-level prevalence[3]	
Retail	20	85.0	95.6 (79.1-100.0)	
Mixed	20	90.0	96.0 (80.9-100.0)	

Bird-level risk factor	No. of pools	Observed pool-level prevalence	Estimated bird-level prevalence[3,4]	Bayesian P-value[5]
Retail				
Broiler	96	18.8	3.2 (0.7-10.1)	0.233
Desi[6]	61	18.0	3.3 (0.7-10.4)	0.429
Sonali[7]	62	4.8	1.7 (0.3-5.9)	0.285
Waterfowl	20	0	1.4 (0.4-5.7)	0.334
Mixed				
Broiler	57	22.8	5.7 (1.1-17.7)	0.418
Desi[6]	66	27.3	5.8 (1.1-18.2)	0.468
Sonali[7]	60	20.0	3.0 (0.5-10.6)	0.286
Waterfowl	55	12.7	2.5 (0.4-10.0)	0.400

[1] Markets only with retailers were classified as retail, and those with wholesalers were classified as mixed.
[2] The prevalence of markets that had at least one positive pool
[3] Median and 95% highest density intervals are reported.
[4] Bird-level prevalence in infected markets
[5] Proportion of the predicted pool-level prevalence that were equal to or more extreme than the observed pool-level prevalence
[6] Indigenous chicken breed
[7] Crossbred of the Rhode Island Red cocks and Fayoumi hens

A general method for performing sample size calculations with non-standard hypothesis tests: an example application to the faecal egg count reduction test

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ABSTRACT

Objectives: Sample size calculations are essential to study design, but their application to non-conventional hypothesis tests, such as those used in non-inferiority testing, is an area of active research. We illustrate a general method for sample size calculations based on Monte Carlo approximation, using a novel test applied to faecal egg count reduction test data with two null hypotheses.

Materials and Methods: Observed treatment and control egg count data were evaluated against two null hypotheses: (A) the observed efficacy is equal to the expected efficacy, and (B) the observed efficacy is below a given equivalence margin of the expected efficacy. A hybrid Bayesian/frequentist statistical method was developed to implement these two tests, defining the expected sum of treatment data as a negative binomial distribution with parameters defined by the control data. The combination of these two tests yield four typologies: *reduced*: only hypothesis (A) is rejected; *inconclusive*: neither hypothesis is rejected; *marginal*: both hypotheses are rejected; *adequate*: only hypothesis (B) is rejected. Sample size calculations were implemented using a method based on Monte Carlo approximation.

Results: The expected frequencies of the four typologies can be calculated for any arbitrary sample size and parameter value set within a total computation time of a few seconds. This method also allows the properties of the statistical tests to be evaluated, revealing that the notional type 1 error rate is accurate for both individual hypothesis tests (A) and (B). The software developed has been made publicly available via http://www.fecrt.com

Conclusions: Monte Carlo approximation is a powerful and flexible tool that allows sample size calculations to be performed for any combination of computationally simple statistical hypothesis tests. There is considerable potential for this method to be applied to other problems within epidemiology.

Key words: Sample size calculations, Monte Carlo approximation, hypothesis testing, study design, FECRT

Data cleaning; is it time to stop sweeping it under the carpet? Novel methods for epidemiological studies

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ABSTRACT

Objectives: Epidemiological datasets are often heterogeneous and require cleaning prior to analysis to prevent losses in research validity, quality and statistical power. Our aim was to develop novel, reproducible, automated data cleaning workflows for several variables including sex, age, colour, weight, height, date of illness incidences and others for a large, internet-based questionnaire database (the Dogslife project).

Materials and methods: We developed our data cleaning workflows in R software and the code is openly available. We used rule-based approaches, non-linear mixed-effects mathematical models and text analysis to identify common errors, such as duplicate entries, typing, decimal point, unit, menu/option, intentional, website-generated and measurement errors. Individuals were permitted to differ from the population by making use of repeated measurements and alternative data sources. The methods avoid the modification of unusual but biologically plausible values, prioritise data repair over removal and explicitly report the decision making process behind why a particular data entry is modified or deleted.

Results: We successfully developed cleaning workflows for several variables that were fully automated in R software. We validated our cleaning algorithm for growth variables (weight and height) on two other independent data sources from studies with fundamentally different designs and found that it could be reproducibly applied as an effective data cleaning method. We also compared our method to uncleaned data and six different cleaning methods and found that our algorithm out-performed these with greater accuracy and fewer unnecessary data deletions.

Conclusion: There is an increasing demand for data cleaning methodologies to be thoroughly reported so that they can be reproduced, tested and adapted by the wider research community. Our methods have broad applicability to longitudinal and cross-sectional growth data and we propose that they could be adapted for use in other breeds, species and fields.

Key words: Data, cleaning, errors, methods, Open-Source

Impact of imperfect disease detectability on identification of epidemiological risk factors

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ABSTRACT

Objectives: Risk factors are key epidemiological concepts that are used to explain disease distributions. Identifying disease risk factors is generally done by comparing the characteristics of diseased and non-diseased populations. However, imperfect disease detectability generates disease observations that do not necessarily represent accurately the true disease situation. In this study, we aimed at scrutinizing the impact of imperfect sensitivity on the outcomes of logistic and zero-inflated Poisson (ZIP) models.

Materials and methods: We first used a probabilistic framework to simulate both the disease distribution in herds and imperfect detectability of the infected animals in these herds and compared the effectiveness of logistic and ZIP models for correctly identifying disease risk factors.

Results: The study showed that, under the logistic model, true herd-level risk factors are generally correctly identified (low chance of type II error) but their associated odds-ratio are heavily underestimated as soon as the sensitivity of the detection is imperfect. Moreover, if the detectability of infected animals is heterogeneous between herds, the variables associated with the detection heterogeneity are likely to be incorrectly identified as risk factors. This probability of type I error increases with increasing heterogeneity of the detectability and decreasing sensitivity. If disease count data is available (e.g. number of infected animals in herds), they should not be reduced to a presence/absence dataset at the herd level (e.g. presence or not of at least one infected animal) but rather modelled directly using zero-inflated count models which are shown to be much less sensitive to imperfect detectability issues.

Conclusion: We strongly recommend that efforts should be made to account for imperfect disease detectability when modelling disease risk, or at the very least to discuss its potential impact on model outcomes.

Key words: Risk factors, logistic model, bias, surveillance, sensitivity

A piecewise linear mixed model to assess the effect of Hendra virus vaccination on horse racing performance

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ABSTRACT

Objective: Concern about a potential effect on horse performance can be a reason for non-adoption of the horse vaccine against zoonotic and fatal Hendra virus in Australia. This retrospective pre-post exposure study aimed to evaluate the effect of Equivac® HeV Hendra virus vaccine on thoroughbred racing performance.

Materials and methods: Thoroughbreds with at least one start at one of six major race tracks in south-eastern Queensland, Australia, between 1 July 2012 and 31 December 2016 and with starts in the three-month periods before and after Hendra virus vaccinations were identified. Piecewise linear mixed models compared the trends in 'Timeform' performance rating before and after Hendra virus vaccinations. The piecewise model allowed separate slopes to be fitted to the observations representing the periods before and after vaccination. The approach was suitable for the unbalanced (horses having different numbers of race starts), non-uniform (race starts at different timepoints) and non-equidistant (unequally spaced race starts) data, thereby improving efficiency. The mixed model also addressed the autocorrelation of the repeated measures data. Horses acted as their own controls to optimally address horse-level confounding factors and the short comparison periods aimed to address time-varying confounding of performance.

Results: Analysis of data from 4,208 race starts by 755 horses revealed no significant difference in performance in the three months before versus three months after initial Hendra vaccination (p = 0.32). Further analysis for 7,844 race starts by 928 horses failed to identify any significant change in performance trends before versus after the second and subsequent vaccinations (p = 0.16) or any evidence of a cumulative effect for the number of vaccines received (p = 0.22).

Conclusions: No evidence of an effect of vaccination on racing performance was found. The findings allow owners, trainers, industry regulators and animal health authorities to make informed decisions about vaccination.

Key words: Piecewise linear mixed model, Hendra virus, vaccination, thoroughbreds, racing performance, Timeform rating

Modelling recurrent circulation of Rift valley fever virus in northern Senegal

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ABSTRACT

Objective: Rift Valley fever (RVF) is a mosquito-borne zoonosis, endemic in Northern Senegal. The last outbreak occurred in 2013-2014. Aedes vexans arabiensis and Culex poicilipes are the two main vectors. Recurrent circulation may be explained either by regular viral introduction by nomadic herds or vertical transmission of the virus in Aedes eggs that can survive dry season and re-merge being infected. Both mechanisms may be involved.

Materials and methods: To explore the mechanisms that drive this endemicity, a published hydrologic model (Soti et al, 2010) was first used to simulate pond surface variations of Younofere region, our pilot area. Temperature, humidity and pond surfaces were then used to parameterize a published generic model of mosquito abundance for both Aedes and Culex populations (Cailly et al, 2017). Mosquito trapping data (2014, 2015) were used to validate model outputs. The daily predicted mosquito abundance was used as input in a transmission model, ie SIR model for hosts, and SEI for vectors. Resident and nomadic ruminant population size, dynamic and movement data were obtained from available census, and semi- structured questionnaire survey. All data were collected in the same pilot area. Serological data collected in 2016 from resident small ruminants living in this area were used to calibrate the model. The model was used to analyze mechanisms that could explain the recurrent circulation of RVFV in the pilot area from 2012 to 2016, years for which serological data are available. The vector/host ratio was estimated by likelihood maximization for 4 introduction scenarios: no introduction, early introduction (during the Aedes abundance peak), late introduction (during the Culex peak), or both, for each year between 2012 and 2015.

Results: Results suggest 2 successive viral introductions in 2014 and 2015, either from the North (early introduction) or from the South (late introduction), consistent with serological and recorded outbreak data.

The impact of environment on vector-borne diseases; the case of Rift Valley fever

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ABSTRACT

Objective: An important goal in managing vector-borne diseases (VBD) is to identify the climatic and environmental conditions underlying persistence of the vector populations and pathogen.

Materials and methods: We focused on Rift Valley fever virus (RVFV), a mosquito-borne zoonotic pathogen, which causes major epidemics in Africa and is expanding to other regions. The complex ecology of RVFV depends on, among other factors, water-body dynamics (influencing mosquito oviposition, development of other aquatic stages) and on ambient temperature (influencing mortality and development rates of mosquitoes, extrinsic incubation period of the pathogen). We formulated an eco-epidemiological, mechanistic model, driven by the seasonal dynamics of temperature and water-bodies. The model is applied in a realistic setting by using data on temperature and water-bodies from Kenya. Floquet analysis was used to investigate the stability of the seasonal system.

Results: We identified the range of seasonally varying temperatures and water-bodies leading either to mosquito population and/or RVFV extinction (non-persistent regimens) or to persistent mosquito populations and endemicity of RVFV infection (persistent regimens). Instabilities arise when the range of the environmental variables overlaps with the threshold of persistence. The model captures the intermittent nature of RVFV, explained as low level circulation under the threshold of detection, with intermittent emergence, sometimes after long periods of apparent absence.

Conclusions: Detecting the environmental limits of VBD is crucial to assess the likelihood that a new infection becomes endemic in different parts of the globe, e.g. due to climate change. It is also critical for effective control. For a system supporting stable oscillation in mosquito abundance, temporary control measures will likely fail, as the system returns to the original configuration once control measures stop. For special ranges of temperature and water-body dynamics the system is no longer stable and small perturbations can change outcomes, challenging the predictive power of statistical/mathematical models.

Key words: Vector-borne diseases, zoonosis, cross-species transmission, stability analysis, Floquet analysis, viral haemorrhagic fever

Bluetongue disease dynamics and control in France: from emergence to re-emergence

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ABSTRACT

Objectives: The bluetongue largest epizootic ever recorded in Europe was due to serotype 8 (BTV-8), which spread from 2006 to 2010. In France, it affected over 45,000 herds. Vaccination allowed France to regain a *disease-free* status in 2012, but infected herds have been reported again from September 2015. We developed a dynamical model of BTV spread in France between 2006 and 2017 to disentangle the relative importance of vectors and hosts movements in disease spread.

Material and methods: The model represented BTV transmission between small-sized spatial units based on administrative boundaries, each containing hosts and vector populations. Within-unit BTV dynamics was represented by a compartmental model and between-units transmission occurred through three distinct networks built from: *(i)* spatial proximity (physical network) and livestock movements between *(ii)* pastures of the same herd (pasture network), or *(iii)* between different herds (trade network). Control measures were accounted for. The model was parameterized based on cattle and sheep census and trade data, land register and meteorological data. We estimated model parameters by approximate Bayesian computation, using incidence (clinical cases) and serological prevalence data.

Results: A topological analysis revealed small-world properties of the pasture network, and scale-free properties of the trade network. BTV transmission simulated through each network produced contrasted spatial and temporal spread patterns. Parameter estimation highlighted the relative contribution of vector and host movements through the physical, pasture and trade networks, and provided a retrospective assessment of the control measures implemented.

Conclusion: By allowing a better understanding of BTV spread, this model may provide scientific support to decision makers and help them design efficient control and surveillance measures. This framework could be extended to other vector-borne diseases of farm animals.

Key words: Bluetongue, France, cattle, vector-borne, transmission dynamic modelling

Designing a stochastic individual-based multi-pathogen model to understand hepatitis E virus (HEV) dynamics in a farrow-to-finish pig farm

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ABSTRACT

Objectives: Hepatitis E virus is a zoonotic pathogen for which pigs have been recognised as the major reservoir in industrialised countries. High variability of HEV infection dynamics has been described in pig farms and may be related to the influence of other pathogens, particularly viruses modulating pig immune system. The aim of this study was to understand the conditions for HEV spread and persistence in farrow-to-finish herds in which pigs may be co-infected with an intercurrent pathogen using an individual-based modelling approach.

Material and methods: A stochastic individual-based model was developed to represent the population dynamics of a farrow-to-finish pig herd, accounting for breeding and growing pigs. To analyse the role of herd structure on within-herd HEV spread and persistence, this population dynamics was coupled with a multi-pathogen model combining two epidemiological models: the first one represented the dynamics of an immunosuppressive virus (e.g. PRRSV) in a simplified way (SIRS), whereas the second one was designed as a MSEIRS model of HEV, accounting for the partial passive immunity protection in piglets. On an individual and daily basis, epidemiological parameters of the HEV model were modified according to the pig's status as regard the immunosuppressive virus. Parameters were derived from experimental and field data. The minimal conditions for virus spread and persistence between batches were evaluated by simulations.

Results: Co-infection with an immunosuppressive pathogen was found to favor HEV spread and persistence and to increase the prevalence of contaminated livers at slaughter. Herd structure, driven by the batch-rearing system, and lack of biosecurity measures were also evidenced as a pivotal factor facilitating HEV spread.

Conclusions: Our model, coupling the dynamics of interacting pathogens, allowed gaining insight on within-herd HEV dynamics. Controlling intercurrent pathogens and enhancing farming practices would be major levers to mitigate the HEV-related risk for public health.

Key words: Multi-pathogen model, hepatitis E virus, intercurrent pathogen, public health

Bovine brucellosis within-herd modeling to simulate infection dynamics and evaluate different control strategies

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ABSTRACT

Objectives: Bovine brucellosis (bB) is an important zoonosis that causes serious economic losses. Although it can be controlled/eradicated by applying different strategies, choosing the most convenient one is not easy because of the many involved factors. The objective of this work was to develop a simulation model able to predict the transmission of bB within a cattle herd and to analyze scenarios in order to evaluate the efficiency of different control strategies.

Material and methods: A stochastic, individual-based model, with state transitions on a daily basis was built to simulate bB within a cattle herd. It was developed using MS Visual Basic with MS Access as the interface to define parameters and analyze outputs. The stochastic process is based on Monte Carlo simulations. The model simulates the structure and dynamics of a cattle herd and the *Brucella abortus* transmission among animals. The effect of vaccination, management practices and testing and culling strategies were also represented.
Different scenarios were simulated:
I) Population: production system (beef *vs* daily), type of mating (seasonal *vs* no seasonal).
II) Disease: high *vs* low prevalence.
III) Vaccination: strain19 *vs* RB51 applied with different schemes.
IV) Management practice: heifers isolated from general herd *vs* no isolation of heifers.
V) Testing and culling: applied at different times.

Results: Annual number of new infections, abortions, infectious deliveries and newborn infected calves were compared among different initial scenarios. The model also provided the number of simulations in which eradication was achieved and the time until eradication. For each of the simulated scenarios the strategies that allowed eradiation earlier and/or at a lower cost was identified. Some results were compared with data from herds that eradicated the disease in order to validate the model.

Conclusion: The results produced by the model were highly compatible with reality, according to experts' opinion.

Using sociological data in scenario tree modelling: the example of the evaluation of the French bovine tuberculosis surveillance system

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ABSTRACT

Objective: Scenario tree modelling is a quantitative evaluation method for assessing the sensitivity, the specificity and the cost of surveillance components, integrating epidemiologic and economic factors. Despite their importance, sociological factors, as the choice to report a suspicion, are rarely integrated in this method because of the difficulties for their collection and their implementation in quantitative models. That is why we developed, through the example of the evaluation of the French bovine tuberculosis (bTB) surveillance system, an approach to integrate sociological factors in quantitative scenario tree modelling.

Materials and methods: A working group of the National School of Veterinary Services (ENSV) ran a qualitative sociological study based on semi-structured interviews about the realization of intradermal cervical tuberculin test (ICT) and the attitude of veterinarians towards non-negative results. Based on these qualitative results, we identified typologies of practices and decision models and conceived two quantitative on-line surveys intended to French rural veterinarians, about skin tests and the cattle restraint methods in farms and their impact on the realisation of the ICT, respectively.

Results: Thanks to these surveys, we estimated quantitatively the part of each practice and decision model and their impact on the effectiveness of the surveillance component. Then, we integrated them in our scenario trees as detection category nodes. We thus obtained an estimation of sensitivity, specificity and cost of French bTB surveillance system in farms, for each geographical area characterized by its farm type, the bTB prevalence and consequently the experience and training of the veterinarians towards the surveillance of bTB.

Conclusion: This method illustrates how sociological data, originally collected in a qualitative form, can be used in a quantitative evaluation method in order to model at best the field conditions and thus obtain a more realistic cost-effectiveness ratio. The result of this study allowed identifying some of the obstacles to bTB eradication in France.

Key words: Sociological evaluation, scenario tree model, surveillance, bovine tuberculosis, France.

Reconstructing foot-and-mouth disease outbreaks: a methods comparison of transmission network models

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ABSTRACT

Objectives: A number of transmission network models are available that combine genomic and epidemiological data to reconstruct the network of 'who infected whom' in outbreaks. For such models to reliably inform decision-making in foot-and-mouth-disease (FMD) outbreaks they must be transparently validated, robust and be capable of producing accurate predictions within short timeframes based on the types of data actually available early in outbreaks. We undertook a formal comparison of the performance of nine transmission network models.

Materials and methods: The Australian Animal Disease Spread (AADIS) hybrid model was used to simulate a set of FMD outbreaks in a previously free country using the baseline configuration. Phylogenies nested in the simulated transmission network and genomic samples from animals on infected premises were simulated using VirusTreeSimulator and SeqGen. Based on a review of the published literature, nine transmission network models were selected. The accuracy of inference of each approach was benchmarked by estimating the proportion of infected premises whose true source was correctly identified across model runs. For methods that estimated other parameters, such as mutation rates and timing of infection, estimates and coverage were compared to the true values.

Results: Lau's systematic Bayesian integration framework was found to be the most accurate for inferring the transmission network and timing of exposures, correctly identifying the source of 75% of the infected premises (with 92% accuracy for sources with model support >80%). The Structured Coalescent Transmission Tree Inference and Lau's model both provided highly accurate inference of molecular clock rates.

Conclusion: This formal comparison points to which models might be reliably used to reconstruct similar future outbreaks, identifies the key limitations of popular models and how to interpret their outputs to inform control.

Key words: Transmission network, reconstructing outbreaks, foot-and-mouth disease, genomic data

Control of swine Influenza A virus endemic persistence in farrow-to-finish herds: insights from a stochastic metapopulation model

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ABSTRACT

Objectives: Swine Influenza is known to persist in an enzootic form in farrow-to-finish farms with recurrent occurrence in successive batches at a similar age. The specific population dynamics of farrow-to-finish pig farms, the immune status of the animals at the infection time and the co-circulation of distinct subtypes and their reassortants have been evidenced as factors favouring swIAV persistence within herds. The aim of this study was to evaluate the efficacy of control strategies related to herd management and/or different vaccination schemes using a modelling approach.

Material and methods: An event-driven stochastic metapopulation model has been developed to represent the co-circulation of two distinct swIAVs within a typical farrow-to-finish pig herd comprising two subpopulations: breeding sows and growing pigs. Model parameters were estimated in specific experiments. Model outputs were compared to field data to assess the model validity. Different control strategies were evaluated including vaccination schemes (batch to batch or mass vaccination of the sow herd and vaccination of growing pigs) alone or in association with the export of piglet batches at weaning.

Results: The introduction of one infected gilt in service room led to endemic swIAV within-herd persistence as observed in the field. Although some vaccination schemes (batch-to-batch vaccination) had a beneficial effect by reducing swIAVs persistence in breeding sows, no vaccination strategies achieved swIAVs fade-out at the herd level. The export of consecutive piglets batches at weaning, whatever the vaccination scheme, was found as the most efficient measure facilitating swIAV infection fade-out (HR=13.7[8.0–23.4]).

Conclusions: Vaccination showed limited efficacy in controlling swIAV within-herd persistence alone. Introducing gaps in the growing pig population and preventing virus transfer between the breeding and the growing part of the herd through increased internal biosecurity are key factors for swIAV control.

Key words: Swine Influenza A viruses (swIAV), transmission dynamics, persistence, control strategies

A network-based simulation model to predict the probability and impact of a rabies incursion in the Torres Strait, Australia

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ABSTRACT

Objective: Determine the probability and impact of a canine rabies incursion from Papua New Guinea (PNG) to the Torres Strait (TS), Australia.

Materials and methods: The TS comprises a group of islands between PNG and mainland Australia. Telemetry data from dog populations on selected islands were obtained using GPS collars. Movement data about people and dogs between PNG and TS islands were obtained from Indigenous residents using semi-structured interviews and participatory methods. A stochastic, individual-based rabies spread simulation model was implemented; rabies infection in dogs followed an SEI_1I_2R process and humans could be infected following a bite from a rabid dog. An incursion was simulated following entry of a latently rabies-infected dog to a probabilistically selected island (based on movement data of PNG residents to the TS). Sobol sensitivity analysis was used to determine the most influential input parameters.

Results: Predicted annual median probability of entry of a rabies-infected dog to the TS was 0.084 (95% range 0.002-0.314). The predicted median duration of outbreaks was 57 days (95% range 5-537) and the median number of rabies infected dogs was 1 (95% range 1-227). Human cases occurred in 35% of simulated incursions (median 0 humans infected; 95% range 0-14). Median time to onset of symptoms in the first infected human was 89 days. The most influential parameter was the prevalence of rabies in dogs in PNG.

Conclusion: Although the predicted probability of an incursion and duration and number of rabies-infected dogs was low, the subsequent impact of infection of a human in over one third of simulations was high. Effective control of an outbreak in PNG is likely to protect the TS but would be difficult to achieve given logistic and resource constraints in PNG. Therefore, pre-emptive vaccination of dogs in the TS should be considered.

Key words: Rabies, dogs, disease spread, simulation model

A model of foot-and-mouth disease transmission, detection, and intervention strategies within a U.S. beef feedlot

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ABSTRACT

Mathematical modeling is a tool to simulate epidemics of infectious diseases such as foot and mouth disease (FMD) in disease-free areas. Most published models focus on farm-to-farm FMD transmission and represent the farm as a single unit. We developed a model of FMD transmission dynamics in a typical U.S. beef feedlot. It is a stochastic susceptible-latent-infectious-recovered model nested in a meta-population of home pens and hospital pens in the feedlot. Within-pen and between-pen transmission are explicitly modeled. The model estimates time to detection depending on surveillance sensitivity, and evaluates outbreak progression depending on post-detection interventions. A feedlot of 24,000 cattle distributed in 120 pens with 200 head per pen, and 2 hospital pens was modeled. Active observational surveillance by feedlot employees and detection threshold of 3% prevalence of clinical FMD cattle in the index pen were assumed. Four post-detection intervention scenarios were modeled - S1: no intervention; S2: stopping hospital-pen cattle mixing on day of detection; S3: S2 and culling cattle in pens surrounding the index pen; S4: S2 and culling cattle in home-pens that received animals from the hospital within 7 days prior to detection. Detection occurred at a median of 8 days post FMD introduction. Model simulations showed that under S1 the outbreak took 75-90 days to fade-out and all pens were infected by a median of 47 days post FMD introduction. Daily incidence decreased under S2 and S3 but the outbreak continued. The outbreak was controlled under S4 but this required culling ~50% of the feedlot population. Targeted culling may be challenging to implement due to the labor requirements and animal welfare complications, and its efficacy is dependent on the time to detection and the daily ability to depopulate the infected and at-risk pens. Slowing the outbreak may allow time to effectively implement a vaccination strategy.

Key words: Foot-and-mouth disease, Mathematical modeling, Meta-population, Intervention strategies, Beef feedlot.

A simplified model of bluetongue risk in Europe

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ABSTRACT

Objective: To develop a model of bluetongue risk to understand how risks vary spatially and temporally across Europe. This is applied retrospectively to understand the recent historical patterns of bluetongue epidemics.

Materials and methods: Some of the parameters required to estimate the basic reproductive ratio of bluetongue are uncertain, so our simplified model describes the number of *Culicoides* that must become infected on a given day for (on average) one further animal to become infected. Parameters for the extrinsic incubation rate, vector mortality rate and vector feeding rate are taken from published literature and informed by temperatures derived from the ENSEMBLES climate models for 2000 – 2016. This model is fit to ENSEMBLES 0.25 degree grid cells for each day between February and November for these years. We analysed the overall annual risk, number of days at risk and the timing of the peak in risk for Europe and for specific sites within Europe.

Results: We demonstrate that the area with potential for transmission generally covers France, Italy, the Iberian Peninsula, Germany, the Low Countries and England, with 100-200 at-risk days. The extent of at risk period in Scotland and Scandinavia varies year-by-year, with up to 50 days at risk of transmission. The peak in transmission typically occurs in mid-July across most of Europe, except in Southern Europe where there can be a bi-modal pattern to risk with a period of low risk in mid-summer when temperatures are above optimal for transmission. Conclusion: The bimodal nature of transmission potential could explain the late season transmission in France in recent years. Furthermore, as the second peak in transmission potential occurs after the main part of the season in northern parts of Europe this may explain how the epidemic has largely remained contained in France.
Key words: Bluetongue, basic reproductive ratio, climate change, *Culicoides*

Combining genetic and epidemiological data to unveil bovine tuberculosis spread pathways

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ABSTRACT

Recently, epidemiological investigations have been helped by the increased availability of Whole-genome-sequencing (WGS) techniques. This is able to detect single-nucleotide polymorphisms (SNPs) in pathogens genome, to track their evolution through time. This was already possible for fast evolving pathogens (e.g. RNA viruses) but not slow spreading infections.

Although previous studies demonstrated the utility of WGS in understanding the broader patterns of Mycobacterium bovis (the causative agent of bovine tuberculosis, bTB) transmission in cattle or wildlife, using it for forensic investigations presents new challenges. In fact, the slow rate of spread increases the number of potential infectious contacts, and the infection of an individual could have happened years before the detection.

Here, we developed new analytical methods using Kolmogorov forward equations (KFEs) to combine WGS data, obtained from infected individuals, with epidemiological knowledge and the underlying network of contacts. We defined the system's status as the combination of the considered individuals' bTB compartment status (Susceptible-Exposed-Test positive-Infectious), including the number of SNPs in the sampled bacteria strain genome. From that, we could exactly compute the relative probability of competing transmission pathways, underpinning the relation between important parameters, such the substitution rate, and the temporal contact patterns. We demonstrate the utility of this approach by applying it to a bTB infected populations, to help identify the more likely infection patterns.

Key words: Transmission pathway, Kolmogorov forward equations, bovine tuberculosis, contact network, contact tracing

Novel approach for sensitivity analysis for epidemiological models combining Sobol indices and polynomial chaos expansion

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ABSTRACT

Objective: Global sensitivity analysis (GSA) on epidemiologic model outputs is used to identify critical parameters. For models with high inherent stochasticity, interactions and skewed model outputs, GSA is not trivial. To overcome this challenge, we propose an estimation of Sobol indices using polynomial chaos expansions (PCE) – a method borrowed from engineering for epidemiological models - and apply it to a canine rabies transmission model.

Materials and methods: We estimated PCE-based SIs of an agent-based, spatially explicit, stochastic dog rabies simulation model developed for a dog population in Northern Australia. A combination of vaccination, culling of exposed dogs and dog movement restrictions was included as intervention strategy. We sampled 1000 sets of varying values for the 32 input parameters and iterated 20 repetitions of model simulations for each set. The SIs of the model's parameters for the mean and variance of the outbreak duration and size of the 20 repetitions were estimated. While SIs for the mean of the output inform on the sensitivity of the average expected outbreaks, SIs for the variance are instead informative about the sensitivity of the internal stochasticity to the input parameters.

Results: The outbreak durations' average was most sensitive on the outbreak detection period and levels of vaccination, culling and dog movement restrictions, while for the outbreak sizes' average it was the detection period. The SIs to assess influence of stochasticity on output were of limited value due to wide confidence intervals. Using more repetitions per parameter set will allow exploration of more suitable statistics.

Conclusion: The estimation of SI using PCE is novel for epidemiological modeling. It greatly reduces the number of simulations required for SI estimation, allowing the exploration of complex scenarios with combinations of interventions in the highly stochastic models required to describe epidemiologic processes.

Key words: stochasticity, sensitivity analysis, agent-based modelling

The effects of different romaing patterns and their contact rates on the spread of canine-rabies in Northern Australia

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ABSTRACT

Objective: Evaluate the effects of different contact kernels estimated from different roaming patterns on rabies spread using a simulation model.

Materials and methods: Contact kernels based on dog roaming patterns (stay-at-home, roamer and explorer) were incorporated into a rabies simulation model of potential rabies spread in dogs in the Northern Peninsula Area (NPA), Australia. These kernels describe the contact probability between dogs at certain distances apart. Six model scenarios were developed based on the pairwise combination of kernels. The dog population within each model was assumed to behave according to the model's kernel. For example, all dogs were explorers in the explorer–explorer scenario and evenly distributed between explorer and roamer for the explorer–roamer model. Each scenario was simulated 100 times, assuming no outbreak control. Summary statistics (number of rabid dogs, outbreak duration) were used to identify differences between the six scenarios.

Results: The six kernels produced different outbreak statistics, and highlighted an indirect relationship between outbreak duration and number of rabid dogs. The explorer–explorer scenario had the lowest median outbreak duration (269 days, range 34–385) and the highest number of rabid dogs (417 dogs, range 1–424). Conversely, the stay-at-home–stay-at-home scenario had the highest median outbreak duration (412 days, range 31–794) and the lowest median number of rabid dogs (331 dogs, range 1–380).

Conclusion: The roaming pattern of the dog population affects the type of rabies outbreak predicted. The large roaming ranges and consequently, the greater number of contacts of explorers, caused more explosive outbreaks compared to slow-moving epidemics of the stay-at-home dogs who had smaller roaming ranges. This is likely to impact outbreak detection e.g. explosive outbreaks being more easily detected compared to slow moving outbreaks. Eradication and control programs could subsequently be impacted by differing detection times.

Key words: Contacts, roaming pattern, rabies, modelling, free-roaming dogs

The effect of co-morbidity on disease control decisions: a stochastic modeling approach

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ABSTRACT

Objectives: Some infectious diseases are known to increase the risk of other diseases, resulting in co-morbidity effects. For instance, we have found that paratuberculosis increases the rate of clinical mastitis (CM). To date, decision model estimates of the cost-efficacy of paratuberculosis controls have been ambiguous. In addition, none have accounted for the effect of paratuberculosis on susceptibility to other diseases. We hypothesized that including co-morbidity effects of paratuberculosis on the rate of CM would change the results of a decision model determining best controls.

Materials and methods: A stochastic model of a 1000 cow dairy farm for paratuberculosis control through decreased milk production, early culling, and poor reproductive performance, has been well-studied. The benefit of control programs, however, has been debated. A recent stochastic compartmental model for paratuberculosis transmission in US dairy herds was modified to predict herd net present value (NPV was adapted to include CM and the co-morbidity effect between CM and paratuberculosis. Stochastic dominance for 5-year farm net present value was estimated across a broad range of control programs by multiple methods (first- and second-order dominance, pairwise comparisons, mean-risk dominance, and quantile maximization) with and without CM.

Results: The set of dominant control methods for paratuberculosis changed with endemic prevalence, dominance estimation method, and whether CM was included in the model.

Discussion: Many factors play a role in on-farm disease control decisions, and models should reflect those factors. We find that co-morbidity with CM may change the cost-efficacy of paratuberculosis control, although many control programs will provide roughly equivalent results. Further research should focus on methods for inclusion of multiple diseases within on-farm decision models, including expansion to individual-based models.

Key words: Paratuberculosis, economics, modeling, mastitis, disease control

Changing geographic patterns and risk factors for avian influenza A (H7N9) infections in humans, China

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ABSTRACT

Objectives: The 5th epidemic wave in 2016-2017 of human infections with avian influenza A (H7N9) virus in China demonstrated a geographical range expansion and caused more human cases than any previous waves. Earlier studies investigating the 5th wave showed significantly more human cases in peri-urban and rural settings, but did not identify other factors that may help explain a surge in incidence. Using spatial models, we investigated the effect of anthropogenic, poultry and wetland predictor variables and of market closure measures on the incidence of H7N9 human cases.

Materials and methods: We analyzed all confirmed H7N9 human cases during February 19, 2013–August 9, 2017. Poisson boosted regression tree (BRT) models and generalized linear models were built to explain the daily incidence rate of H7N9 human cases as a function of a set of anthropogenic (live poultry markets density, human population density), poultry (poultry density, chicken to duck ratio) and water bird habitat (distance to water, proportion of water in the county) predictor variables.

Results: We observed an important recent shift, with poultry predictor variables becoming more important than anthropogenic predictor variables over time, particularly during the fourth and fifth epidemic waves. This supports the hypothesis of an increase in H7N9 transmission in the poultry reservoir, which could have been paired with the higher pathogenicity in poultry reported in recent molecular studies. Our results also showed that although measures such as live-poultry market closure measures appear to be effective in reducing the daily incidence rates of H7N9 human cases, this effect was mostly local.

Conclusion: Measures allowing for the prevention of H7N9 circulation along the poultry production and value-chain networks should be intensified alongside market closure measures in order to prevent further range expansion, and minimise the risk of human infection with H7N9 virus.

Key words: Avian influenza A (H7N9), human cases, live-poultry market closure measures, Poisson boosted regression tree, daily incidence rate

Using directed acyclic graphs (DAGs) for hypothesis generation and *a priori* model building: An investigation of risk factors for SRS and lice in Chilean salmonids

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ABSTRACT

Objectives: Information-theoretic methods work on the assumption that the researcher has already carefully formed the study objectives and developed a set of science-based *a priori* candidate models to represent study hypotheses. Careful thinking about plausible hypotheses cannot be underestimated, particularly when the study objective is to infer key biological and ecological processes that generate the data. Here we use a case study to highlight how directed acyclic graphs (DAGs) can be used to generate hypotheses and candidate models in a structured, transparent, and justifiable way.

Materials and methods: A study designed to describe risk factors for mortality attributable to Salmon Rickettsial Septicaemia (SRS) and sea lice infestation used regulatory data managed by the Chilean National Fisheries Service (SERNAPESCA) for the period 2011-2017. DAGs were constructed using a browser-based model builder, DAGitty. The principles of constructing DAGs combined with *a priori* knowledge were used to arrange causal explanatory factors in biologically plausible pathways leading to outcome variables. Based on the arrangement of variables in the DAG, hypotheses to describe the potential causal pathways between explanatory, outcome and confounding variables were generated and used to construct a set of candidate models for testing in a multivariable analysis. The most supported models were selected using information theory. Coefficients of the most supported models and other models generated *post hoc* were examined to understand which factors modulated the outcomes.

Results: Twenty-seven hypotheses were generated to explain SRS mortality and twelve for lice infestation. In each case, one of the *a priori* models were supported by the data. Post-hoc modelling provided support for the significant associations identified through these main models.

Conclusion: This case study shows that DAGs are an easy and useful method to aid the development of carefully considered and transparent study hypotheses; harmonising well with information theoretic approaches.

Key words: Causality, confounding, hypotheses, risk factors, aquaculture

Inferring the spatial spread of highly pathogenic avian influenza H5N2 clade 2.3.4.4 during the 2015 epidemics in Iowa

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ABSTRACT

In 2015, outbreaks of H5N2 clade 2.3.4.4 highly pathogenic avian influenza (HPAI) were detected in 21 states of the United States of America. The outbreak in the Midwestern state of Iowa was one of the largest. Over a 10-week period a total of 77 poultry farms were detected as infected and depopulated, costing a combined USD1.6 billion to Iowa's tax payers and poultry industry. This study was to infer disease transmission dynamics and detection and estimate the number of incursions unrelated to local spread.

Materials and methods: Here we use a continuous time semi-Markov processes, using data-augmentation Markov Chain Monte Carlo techniques within a Bayesian framework to analyse this outbreak dataset.

Results show transmission of H5N2 is strongly dependent on the spatial location of farms with relatively high rate of infection (>1.76 per 1000 infectious premises per day) for farms within 10km of infected farms. Compared to literature, this estimated distance-based transmission rate between farms was relatively high, despite a median of only 4.62 days (95% Cr. I. 2.19 - 8.41) to detect clinical signs. Together, these results imply that over the entire course of the outbreak the probability of infection is approximately 0.986, 0.078, 0.027, 0.008 for farms at 0km, 1km, 3km, 10km from an infected farm, respectively. Mapping farms for which the reproduction number is greater than 1 highlighted that epidemics could have been generated from an incursion occurring in half of the farms in Iowa, and these high-risk farms are mostly concentrated in 2 areas.

Conclusion: Although we cannot identify the routes by which disease was introduced, our results nevertheless suggest that multiple incursions occurred during the outbreak in Iowa. This work provides an improved understanding of how this H5N2 HPAI virus spread in Iowa, which can strengthen planning for surveillance and response activities.

Key words: Transmission kernel, outbreak investigation, between-farm distance, HPAI

What are drivers that influence backyard and commercial farmers to implement avian influenza control in Bangladesh?

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ABSTRACT

Objective: To identify drivers influencing farmer's beliefs and practices to implement avian influenza (AI) control in Bangladesh.

Materials and methods: Two cross-sectional studies were conducted in two south-east districts of Bangladesh. Using a Health Belief Model framework, (1) 144 backyard chicken farmers were interviewed in February-April 2016, and (2) 106 commercial broiler and 113 layer chicken farmers in February-April 2017, about their beliefs and attitudes towards AI control.

Results: Using Structural Equation Modelling, it appeared that farmer's perceptions on the benefits of improved biosecurity (e.g. less AI outbreaks, less zoonotic AI risk) increased the likelihood of both commercial layer (p<0.01) and broiler chicken farmers (p<0.01) to implement preventive actions, and seek information about AI (e.g. attending meetings on AI control). However, backyard farmers' perceptions on benefits of AI control did not influence any of their actions to control AI. Nevertheless, perceived barriers, such as wearing protective clothing being not conducive for working on farms, refrained both backyard (p<0.0001) and broiler farmers (p<0.0001) to implement AI control; however these barriers were not important for layer farmers. Furthermore, farmer's perceptions on the susceptibility of chickens (e.g. increased risk of infection if farm equipment is not regularly cleaned) increased the chance of broiler farmers (p=0.05) to implement preventive measures, but it did not influence layer and backyard farmers.

Conclusions: Our results indicate that farmers of different chicken production systems have different perceptions on AI control; thus while barriers to implement control measures were important for broiler and backyard farmers, benefits of control measures were only important for commercial farmers. Outcomes of this research can be used to adjust and improve current AI prevention and control policies.

Key words: Avian influenza, farmers, health belief model, drivers, Bangladesh

Mitigating the risk of highly pathogenic avian influenza in the Vietnamese nomadic free-grazing duck system

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ABSTRACT

Objectives: The presence of free-grazing ducks has consistently been shown to be one of the most important risk factors associated with highly pathogenic avian influenza (HPAI) outbreaks. Here, we aimed at characterising the mechanisms driving HPAI H5N1 virus transmission between nomadic free-grazing duck flocks and assess the effectiveness of different scenarios of prevention and control strategies.

Materials and methods: To meet the study objectives, we developed a stochastic risk model of HPAI H5N1 transmission between nomadic FGD flocks in Vietnam that could estimate the basic reproduction number (R0) and the relative contribution of the different transmission routes involved. The transmission routes considered were defined by provincial and district veterinary officers. The model was calibrated using parameter distributions retrieved either from the literature of from structured discussions with the main actors involved in the production of nomadic free-grazing ducks in Vietnam (farmers, transporters and rice field owners).

Results: The R0 was estimated at 0.81 (95% CI: 0.40-1.82), suggesting that the FGD production system is unlikely to be able to sustain HPAI H5N1 circulation on its own. Said differently, the model predicted that there is still a 30% chance that R0 is above 1. The two main transmission routes involved direct transmission in the field when grazing and indirect transmission in the boats when being transported from one grazing place to another. Being 95% confident that R0 < 1 would require 70% of FGD flocks to be vaccinated and fully protected, or boats to be effectively cleaned and disinfected every other day.

Conclusion: In a context of limited budgets allocated to the surveillance and control of HPAI in Vietnam, priority should be given to the development of a certification scheme for "clean transporters" who commit to disinfect their transport vehicle on a regular basis.

Assessment of within-herd transmission of pathogenic Leptospira by a structured-Age Multi Host model

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ABSTRACT

Objective: Leptospirosis is a neglected zoonosis that occurs in tropical, subtropical and temperate regions, with a higher frequency in warm-climate countries. It has a complex transmission that includes several strains and serovars involving multiple maintenance and incidental hosts, including humans. To assess the effects of different conditions on within-herd transmission of pathogenic *Leptospira* among cattle, dogs, rodents and humans in dairy operations in Southern Chile.

Materials and methods: An age-structured multi-host model was developed in AnyLogic (V. 8.2.3) using a set of 51 differential equations represented in five modules. The age-structure and transmission model was assigned to each module according to the main epidemiological characteristics of the disease for each host population. The model included direct, indirect, sexual and environmental transmission pathways and it accounts for within and between-hosts transmission. For environmental transmission, the model included several parameters to simulate the survival of the bacteria in the environment. Several conditions were evaluated like herd size and vaccination of some species like cattle and pets on overall transmission. The disease dynamic was simulated for a time horizon of 25 years.

Results: The results showed that the introduction of an index case either in cattle, rodents or pets resulted in both within- and between-hosts outbreaks for different farm sizes. However, vaccination of pet and cattle populations resulted in protective effect for that populations but does not affect significantly infection dynamics in rodent population.

Conclusion: The main conclusions are: a) Infection dynamics differs by herd size b) Vaccination of cattle and pets seems to delay and decrease risk of outbreak within species but not affect transmission on rodents and therefore maintain bacteria circulating.

Key words: Leptospira, modelling, multiple-host

Evaluating the impact of zoning in Norwegian aquaculture on sea lice populations at salmon production sites

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ABSTRACT

Objective: Recent aquaculture research focuses on quantitative assessments of spatial allocation of production and disease control policies on the resulting host-pathogen infection dynamics. As a template for such assessments, we conducted a study to quantify the impact of aquaculture zoning currently implemented in Hordaland County (HC), Norway, on the sea lice population at salmon production sites.

Materials and methods: HC aquaculture is currently organized in seven zones, within which the sites coordinate their fallow periods and stocking times. A scenario mimicking the abandonment of such coordination was constructed by randomly reallocating retrospective production records from all sites across the entire region. Post intervention, novel simulated values for sea lice infestation were generated from a complex partly stage-structured time series model for transmission of sea lice within and between salmon aquaculture sites in Norway. Sea lice (chemotherapeutant, mechanical or other with instant effect) treatments were introduced in accordance with legislative regulations. Multiple scenarios were run for four years following the hypothesized intervention, and results were aggregated to one production cycle per site and per zone.

Results: Numbers of treatments per production cycle and average sea lice abundances of adult female and mobile lice differed between scenarios both at the individual site level and in the patterns observed across all sites within each zone. The most pronounced differences were temporal (i.e., within production cycles), whereas overall summaries of treatment use across zones were similar between scenarios.

Conclusion: Individual site differences between scenarios reflected their sensitivity to changes in area management. Zoning practices did not appear associated with overall reductions in sea lice loads, but induced spatio-temporal patterns in sea lice abundances that in practice might facilitate control of the parasite. Simulation studies provide useful information about the impact of interventions in complex systems when the scenarios studied capture relevant features of real-world situations post intervention.

Key words: Sea lice abundance, simulation, time series, spatial transmission

Comparison of transmission characteristics of a US non–InDel and a French InDel strain of porcine epidemic diarrhea virus (PEDV)

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ABSTRACT

Objectives: Two types of porcine epidemic diarrhea viruses (PEDV), called the InDel and the non-InDel strains with different virulence features, have spread throughout the world. In 2014, a PED outbreak involving an InDel strain occurred in a French pig farm. This study aimed at comparing, under experimental conditions, the transmission characteristics of two strains isolated in 2014 from PED-affected piglets: a non-InDel highly pathogenic strain from the USA and the French InDel strain.

Material and methods: The study was carried out in Anses Biosafety level-3 facilities. Four rooms were used, each housing 10 piglets (2 pens of 5 pigs, 40 cm apart). In each room, one pig from one of the two pens was inoculated orally with a PEDV inoculum of one of the two strains (2 repetitions per strain). The inoculated piglet was in direct contact with 4 other piglets and in indirect contact with 5 other piglets in the adjacent pen. The viral genome was quantified in feces and in air samples by RT-PCR. Transmission parameters were estimated by mathematical modelling of the transmission dynamics.

Results: All infected pigs showed severe diarrhea with the non-InDel strain while only the inoculated and direct contact pigs showed clinical signs in the InDel strain group. The estimated transmission rate by direct contact was twice as high for the non-InDel strain (=2.96 [1.33-5.23] compared to the InDel strain (=1.36[0.6-5.6]). Furthermore, the airborne spread of the non-InDel strain by indirect contact was estimated to 0.5[0.1-1.3] whereas the InDel strain was not transmitted to the pigs in the neighboring pen.

Conclusion: The non-InDel strain could spread to direct and indirect contact pigs with a faster and more efficient transmission than the InDel strain. These characteristics should be considered to implement adapted control strategies to reduce the disease spread in a pig population.

Key words: Porcine Epidemic Diarrhea virus, Transmission

Big models for big data - exploiting the network of cattle movements in Great Britain to understand a complex multi-host pathogen system

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ABSTRACT

Objectives: Livestock movements in Great Britain represent an exceptionally well-described dynamic network, and are an invaluable tool for investigating the role of networks in the transmission of disease. One of the great challenges to exploiting such densely described data is maintaining computational tractability while retaining sufficient model sophistication to address relevant infectious disease problems. This is particularly difficult for multi-host pathogens where often one or more transmission mode is poorly described. Here, we used individual-based cattle data at the national level, together with detailed testing outcomes, to fit the epidemic of bovine Tuberculosis in British cattle and badgers at the national level.

Material and methods: A simulation model of bovine Tuberculosis transmission was developed to directly exploit the explicit record of individual level, premises-to-premises cattle movements recorded in Great Britain, augmented by independently imputed badger population densities. Using Sequential Monte Carlo Approximate Bayesian Computation (SMC-ABC) inference methods, this model was fitted to the available cattle testing data.

Results: A modelling formulation directly-based on a previous result (Brooks-Pollock et al. 2014) which was fit to the Bovine Tuberculosis epidemic in the period from 1997 to 2007, generated qualitatively poor outcomes when fitted over the period from 2008 to 2014. Modifying the model structure to increase the probability of disease persistence in the environment was shown to improve this fit.

Conclusion: Our outputs support a hypothesis that the balance of the processes driving this epidemic has changed over the course of the last two decades, with implications for the spread of endemic disease areas at a national scale and therefore its control.

Improving herd-level bovine tuberculosis breakdown predictions in GB cattle by applying machine learning methods

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ABSTRACT

Objective: Bovine tuberculosis (bTB) is one of the biggest challenges of the GB cattle industry at the moment with control costs estimated as £100 million in 2011/2012. Despite the control program, an increasing number of cases are observed every year. The low sensitivity of the primary diagnostic test for bTB – a single intra-dermal comparative cervical tuberculin (SICCT) test - is estimated as 50%-60% and presents a major limitation to the detection of infected herds. The disease spread is driven by cattle movements between farms, therefore, predicting breakdowns at herd-level in advance associated with animal movement restrictions is crucial for an effective disease control program.

Materials and methods: Here a data-driven modelling approach is proposed as a means to improve our ability of predicting breakdowns based on the SICCT test results. A Neural Network and a Random Forest are trained with data collected between 2012 and 2014 as a part of the bTB control programme and evaluated using data from 2015. The whole dataset consists of 600,000 herd-level SICCT test results and it is extended with data related to infection risk e.g. previous bTB breakdowns, size of herds, holding locations and animal movements between farms. Training and evaluation of the models are also conducted using dataset divided into subsets by region. Techniques addressing dataset imbalance caused by different prevalence of bTB in various regions are discussed.

Results: Overall, our algorithm performed better than the current interpretation of the SICCT test, leading not only to improved sensitivity (64%, increase of 4%), but also specificity (92%, increase of 2%) of breakdown predictions. The predictive performance may vary in regions of different bTB prevalence (Scotland and North England vs West England).

Conclusion: This study is a first step towards developing better control activities against bovine tuberculosis and it promotes a better-informed decision making.

Epidemiological study to understand the perception and practice of local livestock farmers on Foot and Mouth Disease and Newcastle disease (ND) vaccination by using adapted Health Belief Modelling Approach

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ABSTRACT

Objective: Livestock rearing is an important income source for farmers in Myanmar, but FMD and ND disease are the major threatening risk in livestock trade and marketing in the CDZ of Myanmar. This study was conducted in the Central Dry Zone of Myanmar to identify the vaccination practice of farmers by using Health belief framework.

Materials and methods: A total of 613 small-scale farmers owning cattle, small ruminants and/or village chicken were interviewed. We conducted descriptive analysis and F statistics to compare the perception of farmers across different livestock species and we also develop the path analysis modelling approach to estimate the causal relationship.

Results: Majority of livestock farmers (>70%) reported that they were aware of the risk and impact of FMD and ND and were willing to vaccinate their livestock (>60%). While information about FMD and ND vaccinations for cattle was widely accessed through local veterinary authorities (73.7%), the majority of small ruminant (43.6%) and village chicken farmers (58.4%) were not able to access this information. The significant effect of the availability of information about vaccination, the limited accessibility to vaccination, perceived impact of the disease and village size on willingness of farmers to their animal vaccinated was observed across all the livestock species (p<0.05).

Conclusion: Our study highlights that the development of strategies for improving public awareness and the accessibility of resources for vaccination will help to raise practicing vaccination for disease control in the CDZ of Myanmar.

Key words: Foot and Mouth Disease (FMD), Newcastle Disease (ND), small-scale livestock farmers, vaccination practice, Health belief framework

How to release Cyprinid herpesvirus 3 (CyHV-3) to control invasive common carp (*Cyprinus carpio*) in southeast Australia – a Big Data integration approach

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ABSTRACT

Objective: Common carp are a serious invasive species problem in the waterways of south-eastern Australia, and to enable a reduction in their population, a viral biocontrol agent, CyHV-3, has undergone extensive specificity testing to show that it will not affect non-target species. With this confirmed, the challenge has moved to developing a "release strategy", i.e. where and when to release the virus so as achieve maximum impact.

Materials and methods: We used an infectious disease SIR-type model, coupled with river flow, water temperature, habitat suitability and a life stage demographic model, to determine scenarios in which the virus will have maximum impact. Scenarios explored include the effect on the knockdown in carp population of releasing the virus in different seasons, at aggregation points and during different flow conditions. To integrate the models and run the ~900 scenarios, we used a Big Data approach, storing and managing all the data through a database management system, handling all the model processing with R and Python scripts.

Result: Somewhat surprisingly, we show that in many of the scenarios, the release of the virus will not have any substantial knockdown effect on the carp population. However, we argue that this is in fact beneficial in the development of a release strategy, as it will enable the targeted release of the virus with the certainty that only under very defined conditions will it be effective, with the implication that "clean-up" operations can predicted and therefore carefully planned.

Conclusion: To date, there has never been an attempt to develop a release strategy for vertebrate biocontrol agent based on epidemiological modelling, and thus if successful, our use of this technology will provide an innovative example of how it can assist in the planning for the control of an invasive species.

Key words: Infectious disease modelling, invasive species, common carp, vertebrate biocontrol

Identification of high-risk areas of CSF in Peru using a network-based disease spread model

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ABSTRACT

Objective: Classical swine fever (CSF) is a viral disease of swine typically associated with severe impact in affected countries. In 2010, Peru initiated an intensive vaccination and surveillance program to advance towards the control and eradication of CSF in the country. Since then, CSF incidence has decreased substantially, although there are still areas that report recurrent CSF outbreaks in the country.

Materials and methods: In this study, we simulated disease spread over a stochastic dynamic SIR network-based model, based on an observed, real-data network of live pig movements in Peru in 2011. Epidemic curves, prevalence of infection across the studied time, and a choropleth map highlighting disease risk at the district level are shown.
Results: Our model simulated 320 CSF outbreaks in 2011, overestimating the observed value of 34 outbreaks. Of all districts with available data on trade, only eight reported a CSF outbreak in 2011. These results could indicate problems with underreporting or data coverage.

Conclusion: Identified districts at higher risk of CSF could be the target of control and surveillance tools, such as vaccination and biosecurity reinforcement. Results of this study could be useful to improve the cost-effectiveness of the CSF control program in Peru which ultimately should contribute to the sustainability of the swine industry in the country.

Key words: classical swine fever, network, simulation model, Peru

Simulation-based decision support tool for planning control strategies of Classical Swine Fever in Japan

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ABSTRACT

Objectives: Epidemiological modeling is becoming a decision support tool for planning disease control strategies. To prepare for the future outbreaks, we developed CSF transmission simulator (Japan simulation model of infectious animal diseases CSF, JSMIN-CSF) which can easily be operated by the national and regional government officials.

Materials and methods: This simulator employs a stochastic spatially explicit individual-based model to generate between-farm transmission. Transmission process was modelled by the movements of pig/people/vehicles and local spread. The transmission by the movements depends on frequency, distance, and probability of disease transmission. Local spread was modeled by a transmission kernel depending on the inter-farm distance. User-friendly GUI enables to set input-parameters regarding farm status and control measures and to obtain model outputs with maps and graphs. Using this simulator, CSF transmission was simulated in three different areas: high-, medium-, and low-density area (HDA, MDA, LDA). Then, the effectiveness of the different control strategies were examined. Each scenario was simulated for 180 days for 100 iterations.

Results: With a strategy of culling infected farms within 24 hours, the outbreaks were contained within 47 (22-61) and 17 (1-52) days in LDA and MDA, respectively. Meanwhile, the outbreak was not contained in 30% of iterations in HAD. In HDA, the outbreaks were successfully contained within 15 (4-129) days by the 10km vaccination on 7 days after the first detection was added. Even though the vaccination strategy seemed favorable in HDA for the disease containment, the number of farms to be culled was greater (273, 194-287) compared to that without vaccination (122, 66-170) when the vaccine-to-kill rule was applied.

Conclusion: This simulator could provide useful information for decision makers to make CSF emergency plans suitable for regional conditions.

Key words: Classical swine fever, disease modelling, control measure, simulator, Japan

Detection of BVD herd management changes using model-based clustering of BVD antibody dynamics

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ABSTRACT

Objectives: Determining the Bovine Viral Diarrhoea (BVD) status of cattle herds is a challenge for any control and eradication programme. The changing dynamics of BVD antibody patterns over time make it difficult for herds to maintain a stable BVD status over any period. These dynamics are often influenced by antibody responses to exposure. We explore alternative approaches of classifying herds based on longitudinal patterns of BVD antibody as this is more likely to reflect the dynamics of management changes thus yielding more useful information about farm status.

Materials and methods: Data were collected from 15,500 adult cows between 2007 and 2010 from thirty-nine (11 dairy and 28 beef) farms located in Scotland and Northern England. Serum samples were collected annually from each cow and BVD antibody titres were measured using a commercially available ELISA test kit. Given differences in farm exposure and control measures, mean longitudinal antibody levels and shapes may differ between farms. We used multivariate Gaussian mixture modelling methods to cluster farms in two ways: using their antibody longitudinal shape and their magnitude.

Results: Different cluster memberships were obtained for magnitude and shape clustering, depicting farm groups with similar longitudinal antibody levels and shapes. Strong concordance was found between the two clustering approaches. Both approaches isolated groups of farms likely to require quite different BVD control interventions.

Conclusion: Antibody magnitude gives an indication of exposure intensity. Shape indicates the direction of change and other complex nonlinear patterns influenced by the frequency of directional changes over time. Such approaches can help assess changes due to impact of control or management measures over time plus detect high risk farms (defined by their antibody longitudinal patterns) for targeted control measures thereby saving resources.

Key words: Longitudinal, cluster, BVD antibody, magnitude, shape

Molecular epidemiology, associated risk factors, and phylogenetic analysis of anaplasmosis in camel population of Punjab Pakistan

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ABSTRACT

Objective: Camel Anaplasmosis is caused by members of family Anaplasmatacae, tick transmitted, obligate intracellular bacteria. The etiological bacteria are transmitted by ixodid tick species. The species have multi host range distribution, which make them very important to be detected and controlled as early as possible. This study was aimed to investigate the molecular prevalence, associated risk factors of camel anaplasmosis along with its effects on various hematological parameters.

Materials and methods: This study revealed an overall 13.33% prevalence in camels. The positive samples were confirmed for *Anaplasma* (*A.*) through sequencing. The BLAST queries confirmed very high homology of our isolates with Chinese, Iranian, Philippines and South African isolates of Anaplasmatacae (Accession no's; KX765882, KP062964, KY242456, LC007100 and U54806).

Results: The phylogenetic analysis found the 03 study isolates clustered with each other and this cluster closely resembled Chinese isolate of *A. phagocytophilum* (KY242456), *A. marginale* (KU586048), and Mongolian isolates of *A. ovis* (LC194134). Two of the isolates resembled Iranian isolate of *Candidatus Anaplasma camelii* (KX765882), while one isolate resembled with Chinese isolates of *A. Platys* (KX987336) and Croatian isolates of *A. Platys* (KY114935). The key risk factors odds ratio (OR>1) identified for occurrence of camel anaplasmosis on the basis of univariable and multivariable analyses were sex and age of animal, housing type, tick infestation, previous tick history, and tick control status, cracks in walls, rearing system and other species in surrounding, respectively. The hematological parameters like lymphocytes, monocytes, granulocytes and platelets count were significantly increased ($p<0.05$) in diseased camels than healthy.

Conclusion: This is the first molecular evidence of anaplasmosis in camel population of Pakistan. The disease needs to be monitored continuously as the causative agents have multi host distribution. The animals should be properly attended in diseased condition as neutropenia, lymphopenia and thrombocytopenia can aggravate the condition by making the animal prone to secondary infections.

Key words: Camel anaplasmosis, Anaplasmatacae, phylogenetic analysis, risk factors, hematological parameters

Molecular Epidemiology of a novel re-assorted epidemic strain of equine influenza virus in Pakistan in 2015-16

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ABSTRACT

Objective: Widespread epidemic of equine influenza (EI) occurred in nonvaccinated equine population across multiple districts in Khyber Pakhtunkhwa Province of Pakistan during 2015-2016. An epidemiological surveillance study was conducted from Oct 2015 to April 2016 to investigate the outbreak.

Materials and methods: EI virus strains were isolated in embryonated eggs from suspected equines swab samples and were subjected to genome sequencing using M13 tagged segment specific primers. Phylogenetic analyses of the nucleotide sequences were concluded using Geneious. Haemagglutinin (HA), Neuraminidase (NA), Matrix (M) and nucleoprotein (NP) genes nucleotide and amino acid sequences of the isolated viruses were aligned with those of OIE recommended, FC-1, FC-2, and contemporary isolates of influenza A viruses from other species.

Results: HA and NA genes amino acid sequences were very similar to Tennessee/14 and Malaysia/15 of FC-1 and clustered with the contemporary isolates recently reported in the USA. Phylogenetic analysis showed that these viruses were mostly identical (with 99.6% and 97.4% nucleotide homology) to and were reassortants containing chicken/Pakistan/14 (H7N3) and Canine/Beijing/10 (H3N2) like M and NP genes. Genetic analysis indicated that A/equine/Pakistan/16 viruses were most probably the result of several re-assorts between the cocirculating avian and equine viruses and were genetically unlike the other equine viruses due to the presence of H7N3 or H3N2 like M and NP genes.

Conclusion: Management such as mixed farming system by keeping equine, canine and backyard poultry together in confined premises were found as the greater risk factors responsible for the re-assortments.

Key words: Equine, influenza, molecular and epidemiology

Rabies virus degenerates neuronal cytoskeleton by down-regulating gene expression of GTPases and synapse related protein

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ABSTRACT

Objectives: Rabies virus (RABV) is a neurotropic pathogen that produces severe encephalitis and terrifying neurological symptoms in humans and animals. The pathological mechanism of RABV is poorly understood, but the current studies show that the RABV preferably causes neuronal dysfunction instead of cell death or necrosis. Proteins involved in synapse and postsynaptic density are integral sub-cellular components that maintain neuronal cell shape in multiple aspects. For example, p21-activated kinases (PAKs) regulate the phosphorylation of cofilin in neuronal cytoskeleton; Rac1 is a G signaling protein belonging to Rho family of GTPases and controls orientation of cytoskeleton and growth of neuronal cell; cell division control protein 42 homolog (Cdc42) also regulates cell cycle and related signaling events.

Materials and methods: Western blotting, immunohistochemistry and real time PCR were carried out to determine the interaction of street and fixed strains of RABV with associated mediators and binding partners of cofilin mediated pathway.

Results: RABV inhibits the gene expression of PAK, phosphorylated cofilin and total cofilin that ultimately interferes with interacting partners such as Cdc42 and Rac1. These changes perhaps cause depolymerization of filamentous actin in neuronal cytoskeleton of hippocampus. Moreover, the street RABV infection also hampers the binding of GTP Rac1 and Cdc42 with PAKs. Street RABV also causes significant reduction in the content of active Rac1 (GTP binding form), while total Rac1 contents remain unchanged after 1 hour of infection. It can also inhibit the transformation of inactive Rac1 to active Rac1 without affecting the expression of total Rac1

Conclusion: RABV may alter the structural and physiological architecture of dendritic spine as well as postsynaptic density by reducing the amounts of specific proteins involved in maintaining the shape of neuronal cytoskeleton

Key words: Rabies virus, GTPases, cytoskeleton, cofilin, down-regulation

Social network analysis in the genomic era: untangling the complex relationship between host population contact structure and disease transmission dynamics

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ABSTRACT

Objectives: This study aimed to integrate whole-genome-based phylogeny with data from social network analysis (SNA) to identify the relative contribution of different transmission pathways to the spread of an antibiotic-resistant lineage of the foodborne pathogen *Campylobacter jejuni* Sequence Type (ST) 6964 and identify strategies for improved food-production biosecurity.

Materials and methods: This study used whole-genome sequencing (WGS) data from 167 *C. jejuni* isolates, originating from the emergence of a new antimicrobial resistant strain in New Zealand's commercial poultry sector, to estimate phylogenetic ancestries using maximum-likelihood methods. Questionnaire data was collected concerning the movement of (1) live birds, (2) feed, (3) waste and litter, (4) personnel and, (5) poultry products. Responses were used to differentiate contacts patterns between each contact network, calculate pairwise Euclidean and road network distances, and build network models to identify hierarchical community structures. Tanglegrams were used to make visual comparisons before using multiple statistical approaches including permutational analysis of variance (PERMANOVA) and quadratic assignment procedures (QAP) to correlate the genetic relatedness of isolates with pairwise geographical and contact network distance matrices.

Results: Preliminary findings provide additional evidence for intra-company transmission whilst also identifying further spread between poultry enterprises located within the same geographical region but belonging to different parent companies. These findings alongside the ongoing burden of human campylobacteriosis cases linked to the consumption of poultry products, highlights a clear gap in biosecurity and a strong need to identify cost-effective strategies for reducing disease transmission along the entire poultry supply chain.

Conclusion: Future work aims to identify which of these contact networks were facilitating this local spread, focusing on using the reconstructed evolutionary history alongside SNA to gain insight into where this resistant lineage had come from, the extent to which it had spread and how to prevent further transmission.

Key words: Whole genome sequencing, phylodynamics, social network analysis, biosecurity, *Campylobacter jejuni*

Optimizing strategies for sampling pathogens in contact networks to make phylodynamic inferences

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ABSTRACT

Objective: As the cost of sequencing pathogen genomes has continued to decrease, there have been a growing number of research studies using phylodynamics to make inferences about the epidemiology of important livestock pathogens. Many studies to date have used pathogen isolates from convenience samples and there is currently limited understanding of how the selected farms and timing of sampling may introduce bias into the phylodynamic inferences. In this study, we developed an individual-based disease simulation model where (1) a pathogen spreads within herds via contacts and between herds via livestock movements, (2) the pathogens' sequence randomly mutates over time, and (3) infected individuals are sampled and detected based on a pre-defined probability.

Materials and methods: We used foot-and-mouth disease virus (FMDV) as a sample disease. The network of farms and livestock movements occurred based on the real observed dairy cattle movement data in New Zealand between July 2000 and June 2010. The model events (disease transmission, pathogen mutations, and detection of infected animals) were modelled using a modified Gillespie algorithm. Different inclusion criteria of samples were tested including (1) random selection, (2) uniform probability selection based on time and geographical areas (GA), (3) proportional to the number of detected herds in each GA, (4) proportional to the number of herds in each GA, and (5) all isolates. The pathogen isolates were analysed in BEAST v1.8.4 to estimate the time to the most recent common ancestor (TMRCA), which is equivalent to the time to the initial disease introduction (TIDI). The Extended Bayesian Skyline Coalescent model was used as a tree prior and the estimated TMRCA was compared to the true TIDI.

Results: The results showed that using all available samples do not improve phylodynamic inferences and can lead to an erroneous inference. We will discuss the importance of sample inclusion criteria in the molecular era.

Key words: Phylodynamics, bias, sampling, Bayesian Evolutionary Analysis, disease simulation model

Investigating potential cases of vaccine failure against *Erysipelothrix rhusiopathiae* in swine in the UK through comparative genomics

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ABSTRACT

Objective: Recent advances in whole genome sequencing are providing unprecedented opportunities for investigating pathogen evolution and infectious disease dynamics. *Erysipelothrix rhusiopathiae* is a multi-host bacterial pathogen that is re-emerging in swine and poultry productions globally. There are concerns that the bacterial strains used to produce vaccines may be failing to provide protective immunity because of differences in relation to circulating field strains. The objectives of this study were to: 1) assess the genomic diversity of *E. rhusiopathiae* in UK swine within the context of the global population structure of this bacterium; and 2) compare the genomic features of these circulating strains to those of the vaccine strain, with the aim of assessing whether genetic differences could be responsible for *E. rhusiopathiae* vaccine failures in swine in the UK.

Materials and methods: Whole genome sequence data was obtained from 48 isolates from UK swine belonging to serotypes 1 and 2, as well from one of the two serotype 2 bacterin vaccines licensed for swine in the UK.

Results: Extensive genomic diversity was found amongst the sequenced isolates, including strains from Clades 2, 3 and the Intermediate clade. However, the majority of the newly sequenced isolates belonged to Clade 2, along with the vaccine strain. Serotype was not correlated with the genetic relatedness of isolates, suggesting it may not be a useful typing method for predicting cross-protection. Data will be presented on the diversity of SpaA gene sequences and other immunogenic surface proteins, and how this diversity maps onto the population structure.

Conclusion: This study highlights the limitations of commonly used typing schemes for *E. rhusiopathiae*, as well as the need for an improved understanding of the factors that confer protective immunity for this bacterial species.

Key Words: *Erysipelothrix rhusiopathiae*, genomics, swine, vaccines

Understanding the emergence and evolution of *Mycobacterium bovis* in Michigan, USA

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ABSTRACT

Objectives: Bovine tuberculosis (bTB) caused by *Mycobacterium bovis* was recognized to be a problem in Michigan since 1994. Infection has been found in multiple wildlife and livestock populations. Identifying the roles of different species in the transmission of bTB and how it spread across space are challenging and understudied problems, mostly because of the difficulty of observing wildlife. Here, we use an evolutionary context to address these questions in an exceptionally rich dataset via an unusual combination of spatial and temporal information about the wildlife host populations, and dense, high-resolution bacterial sequence data.

Materials and Methods: *M. bovis* isolates were obtained from naturally infected wildlife and livestock. In total 770 isolates (5 elk, 57 furbearers, 496 deer and 212 cattle) were identified. After verification of purity of isolates, DNA was collected and submitted for sequencing using Illumina NexteraXT 2x 250 chemistry and MiSeq instrument technology. Raw sequences were aligned to the reference AF2122 using BWA and SNPs were called using GATK. Phylogenetic tree was created using a neighbor joining tree and evolutionary relationships among *M. bovis* isolates were generated using a Bayesian coalescent Markov Chain Monte Carlo analysis in Beast 2.

Results: Preliminary phylogenetic results show two major distinct clades, consistent with at least two distinct introductions of the disease in the area (Fig. 1). Both clades showed broad host species inclusion, suggesting that inter-species transmission events are involved. Future work will investigate the roles of the different major species in the transmission of the disease and will reconstruct the spatial spread of infection over the landscape.

Conclusion: By providing insights into reservoir status and bacterial migratory patterns, genomic analyses such as these can refine our understanding of fine scale transmission patterns beyond the capabilities of traditional epidemiological methods, helping to target surveillance and control.

Key words: Ovine tuberculosis, whole genome sequencing, interspecies transmission, reservoir

Molecular epidemiology of Newcastle disease, avian infectious bronchitis and Avian Influenza (H9N2) in Iran, 2017: An update and comprehensive data

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ABSTRACT

Objective: Avian Infectious Bronchitis (IB), Newcastle Disease (ND) and Avian Influenza (AI) H9N2 are avian viral diseases with significant economic impacts on the poultry industry in the world including Iran. This study aimed to update molecular epidemiological studies and genotypic characterization of the mentioned viral agents.

Materials and methods: 200 samples were taken from the clinically suspected broiler of the houses located in different regions of Iran. The samples were subjected by specific RT- PCR for NDV (Velogenic), IBV and AI (H9N2) detection and characterized by sequencing the spike glycoprotein gene (IBV), fusion gene (NDV) and hemagglutinin (H9N2).

Results: Of the 200 samples tested, 80%, 30%, and 60% were positive for IBV, NDV and AI (H9N2) respectively. The IBV isolates formed four distinct phylogenetic groups as IS/1494/06 (Var2)-like, 4/91-like, QX-like, Mass-like, and D274. The NDV positive samples belonged to genotype VIId and VIIi, and finally, H9N2 is placed in a new cluster but in G1 lineage. The phylogenetic relationship of the strains concerning different time sequences and geographical regions indicated complexity and diversity.

Conclusion: This study demonstrates a constant evolution of IBV, NDV, and AI (H9N2) in Iran, demonstrating the need for continuous monitoring and development of new vaccines based on indigenous viruses.

Key words: Molecular epidemiology, Iran, newcastle disease, infectious bronchitis, avian influenza, poultry

C. Health policy and capacity building

Application of biosecurity in veal calf farms

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ABSTRACT

Objective: The shift from cure towards prevention in veterinary medicine involves the implementation of biosecurity. A low implementation of biosecurity in Belgian dairy and beef herds is described, but no data on biosecurity in veal farms is available. Therefore, a cross-sectional study to map the current implementation of biosecurity measures in veal farms was performed.

Materials and methods: Forty-eight cattle diseases were listed from a literature review, based on results of Belgian laboratories and a veterinary survey combined with occurrence or risk of emerging in Belgium. A questionnaire was established by listing the diseases' risk factors and biosecurity measures, resulting in 144 questions. Face-to-face interviews with the farmer were conducted on 20 veal farms.

Results: Only 20% of the farmers could give a (partial) definition of biosecurity, though 95% considered biosecurity important. Though veal farms purchase from multiple farms and quarantine is practically impossible, all animals are approximately of the same age and remain in the same stable during the production round. The number of times new animals entered the stable and the age range of the animals varied considerably between farms. Specifically for internal biosecurity, none of the farmers consequently isolated sick animals, only 15% had a hospital pen and only 55% of the farmers cleaned and disinfected the stables after each production round. Although external biosecurity measures were better implemented, there is room for improvement: veterinarians and representatives of integrators only wore farm-specific boots on 40% and 30%, and farm-specific clothes on 30% and 40% of the farms, respectively. Disinfection footbaths are only used in 25% of the farms, though present in all.

Conclusion: This survey provides insights in implementation of biosecurity in the veal sector that can be used to improve the biosecurity level on the farms. The non-implementation of easily implementable biosecurity measures shows that there is still room for improvement.

Key words: Biosecurity, cattle, veal, prevention, questionnaire

Development of a biosecurity evaluation tool for cattle: the Biocheck

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ABSTRACT

Objective: Farm biosecurity includes all measures preventing pathogens from entering (external) and spreading within a herd (internal) and is important in establishing the shift from cure to prevention in veterinary medicine. To assess biosecurity on farm level an objective measurement was needed. Biocheck.UGent is a risk-based weighted biosecurity evaluation tool, was first developed for pigs and poultry and is already used in 50 countries. Recently, the tool was developed for cattle.

Materials and methods: The Biocheck-Cattle was developed in several steps. Firstly, 48 priority diseases were selected from an extensive list of cattle diseases occurring in Europe by reviewing prioritization articles, a veterinary survey and Belgian lab results. Secondly, the risk factors and biosecurity measures associated with selected diseases were listed and translated into questions based on literature review. This questionnaire was used in a survey with 120 veal, dairy and beef farms. With these results and the previous information, questions were selected for the Biocheck-tool. Finally, experts in various fields of veterinary medicine were asked to weight the different biosecurity categories and questions, depending on perceived importance in disease prevention according to the method of Gore, to obtain a risk-based weighted scoring system.

Results: The Biocheck-Cattle contains 3 separate questionnaires that consist of 69 (veal), 104 (beef) and 124 (dairy) questions. The questionnaires contained 5 categories for external biosecurity: purchase/reproduction, transport/carcass removal, feed/water, visitors/employees and vermin control/other animals, and 5 categories for internal biosecurity: health management, calving management (only dairy/beef), calf management, dairy management (only dairy), adult management and working organization. The scoring system provides biosecurity scores per category and subcategory ranging from 0 (absence of any measure) to 100 (perfect biosecurity).

Conclusion: With this tool the implementation of biosecurity on cattle farms can be assessed objectively. This herd-specific evaluation shows how and where biosecurity can be improved and allows for benchmarking of farms.

Key words: Biosecurity, cattle, tool, tisk factors, questionnaire

Exploring management practices and attitudes towards biosecurity of small-scale poultry and pig keepers

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ABSTRACT

Objective: Small-scale pig and poultry keepers have been involved in recent outbreaks of African swine fever and avian influenza across Europe. Most European countries have little knowledge about these types of producers, focusing their surveillance and control efforts instead on large commercial populations. Research was undertaken in Scotland to understand the motivation and attitudes towards biosecurity of small-scale producers, to enable policy makers and industry to better target disease surveillance and control programmes.

Materials and methods: Two surveys were conducted: a postal questionnaire in 2013 to small-scale pig keepers (less than 50 finishing pigs or less than 15 adult pigs) and an online questionnaire in 2016/2017 to small-scale poultry keepers (less than 50 birds). These questionnaires comprised questions such as the location of the enterprise, interest in pigs/poultry, details about the enterprise, husbandry, and health/biosecurity. Descriptive statistics were generated for all of the variables.

Results: A total of 145 pig owners responded to the questionnaire; 135 met our criteria for a small-scale producer. The poultry survey received 277 valid questionnaires; 176 met our criteria. The responses allowed characterisation of management practices of small-scale keepers, particularly regarding aspects important for disease transmission and control such as numbers and types of animals kept, movements, and health management. Uptake of those biosecurity measures mentioned in the surveys was highly variable. From a total of 15 biosecurity options small-scale pig keepers, adopted a median of 7 measures; with equivalent measures implemented by poultry keepers at 15 from a total of 25 options. Such measures were not implemented comprehensively in the majority of cases.

Conclusion: Our research fills knowledge gaps which will allow industry stakeholders and policy makers to adapt their current disease control programmes and contingency plans to the reality of small–scale pig and poultry-keeping enterprises' management, health and biosecurity practices.

Key words: Small-scale keepers, pigs, poultry, biosecurity practices

Less is more: Learnings from a biosecurity expert elicitation exercise

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ABSTRACT

Objective: D-BRiEF, the Dairy Biosecurity Risk Evaluation Framework, aims to systematically identify and assess the greatest biosecurity risks to the New Zealand dairy industry. Expert judgments are routinely applied in biosecurity risk analysis, where information on parameters is commonly sparse. Hence, a cost-effective expert elicitation process needed to be developed to support the risk assessment behind D-BRiEF.

Materials and methods: Expert knowledge elicitation in D-BRiEF is primarily conducted in structured workshops following a modified Delphi protocol. A two-stage process was designed and tested that relied on first results to be collected remotely, followed by a face-to-face workshop. The framework adapts a previously used 4-step question format where expert opinion of a quantity (such as the probability of entry) is expressed as "best estimate" as well as the "lowest" and "highest value" to account for both the variability in the parameter and the uncertainty of the estimate. Estimates are standardised to a confidence standard of 80% based on the confidence the expert had expressed in his/her judgement. Results are then mathematically aggregated to represent the opinion of the expert group as a whole. Two different remote delivery methods (Excel spreadsheet and online survey) were employed and feedback from participants was collected to identify the most suitable approach of delivery.

Results: The two different types of remote delivery varied significantly in their success. While the more sophisticated features of the online survey were rated favourably and allowed for additional functionality some users experienced difficulties; roll-out of the survey via XLS proved simpler for individual users and less error prone. The main problems identified were browser compatibility and lack of user confidence working in an online environment.

Conclusion: Expert elicitation can successfully be delivered utilising a process that supports remote collection of Round 1 estimates via a modified Delphi protocol. Due to its simplicity the spreadsheet format was identified as the preferred process for D-BRiEF.

Key words: Biosecurity, expert elicitation, questionnaire, dairy

Identifying the characteristics of LBMs in the Greater Jakarta Area that reduce the risk of avian influenza transmission

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ABSTRACT

Objective: Approximately one million chickens are consumed in Jakarta each day. A significant proportion of these are transported live into the city from neighbouring provinces. This massive movement of live birds and subsequent sale at live bird markets (LBMs) increases the risk of not only disease movement between farms, but also increases the spread of zoonotic diseases along the value chain. This study aims to evaluate the effect of cleaning and disinfection, and LBM rehabilitation on disease spread and to identify the management factors that affect market hygiene.

Materials and methods: After the implementation of hygiene and biosecurity training, infrastructure support and healthy chicken meat (*ayam ASUH*) public awareness training, each of the 20 selected LBMs in Jakarta had the opportunity to improve management and infrastructure. In April and May 2017 each of these LBMs were assessed by FAO staff using both a hygiene checklist and personal observation to identify what interventions had been implemented and the standard of hygiene achieved.

Results: A scoring system was developed to represent implementation levels within each LBM. Thirteen variables were identified in the survey, which represented different elements of an LBM's hygienic status and its ability to produce a safe and healthy product. Results showed that LBMs having higher rankings tended to separate their slaughter area from their carcass cleaning area; source carcasses from outside the market; separated different types of poultry; implemented cleaning programs; encouraged appropriate staff cleanliness; and safely disposed of dead birds.

Conclusion: To encourage LBM management to implement best practices it is not only important to develop capacity and infrastructure, but also to change the mindset of stakeholders throughout the market chain with regard to hygiene, biosecurity and institutional support. Improved consumer awareness, advocacy and stakeholder coordination meetings, and strengthening LBM management can assist with this.

The (in)efficacy of biosecurity trainings - from trainings to changing practices

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ABSTRACT

Objective: Good biosecurity is considered as an effective measure to prevent animal diseases and has received increasing attention as an option to reduce antimicrobial use in livestock production. However, the traditional approach to promote biosecurity has provided limited impact on changing risky practices in developing countries. The objective of this research is to understand why the usual approach to promote biosecurity at the farm level has shown very limited impact on farming practices and propose a new approach that overcomes the challenges.

Materials and methods: The theoretical economic foundations of biosecurity and the traditional approach to promote it are analysed. Potential explanations for why the traditional approach to promote biosecurity has not succeeded are explored and key challenges are identified using concepts from Behavioural Economics. Finally, the economics of biosecurity are contrasted with the economics of vaccination, and a new approach to promote biosecurity is outlined.

Results: Positive externalities associated with biosecurity improvements make the market equilibrium suboptimal and justifies governmental intervention. The traditional approach to promote biosecurity relies on knowledge sharing, which provides key information to farmers on the expected benefit/cost of improving biosecurity. However, insights from Behavioural Economics unveils a much more complex problem. Scarcity imposes cognitive taxes and contributes to impeded cognitive function, which leads to poor decision making. Farmers' high occupational risk for mental disorders exacerbate the problem by diverging the attention to more urgent tasks. A similar approach to the one used to ensure high vaccination coverage is encouraged.

Conclusion: The economics of biosecurity needs to be understood to develop appropriate policies to promote such good practices. Continuing with training efforts without providing additional incentives for biosecurity improvement will lead to the same poor results. The positive externalities associated with biosecurity provide economic foundations to subsidize biosecurity if the government aims to reach the socially optimal level.

Implementation of biosecurity on equestrian premises in Great Britain

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ABSTRACT

Objective: To describe the implementation of biosecurity practices and facilities available on a cross-section of non-racing British equestrian premises.

Materials and methods: Postal questionnaires were administered to a random sample of horse owners, requesting information on owners' involvement with horses, equestrian premises, biosecurity practices undertaken and facilities available at the premises. Factors associated with implementation of biosecurity were assessed using Pearson's chi-squared tests.

Results: Useable response rate was 65% (n=708/1091). The majority of respondents were leisure owners/riders (59%; n=415/708), with 92% (n=638/696) having >10 years of equine experience. A biosecurity plan was present on 42% of premises (n=248/594); this was positively associated with commercial premises (P<0.001). 52% of premises had dedicated isolation facilities (n=355/679); also associated with commercial premises (P<0.001). Isolation facilities were most commonly estimated to be ≥51 metres (27%) or 0–10 metres (25%) from the nearest stable or field border. 58% of respondents (n=412/706) owned/managed their premises, of which 77% (n=296/387) reported having a protocol in place for new horses, most commonly including a passport check and anthelmintic treatment (both 57%). Most respondents vaccinated for influenza (89%; n=627/705); however professional owner status was associated with lower levels of influenza vaccination (P=0.02). 17% of respondents (n=120/692) kept their horses on premises that were part of an approval scheme. As expected, this was positively associated with the presence of a biosecurity plan, a new horse protocol, a dedicated isolation area and a visitor protocol (all P<0.001). However, membership of an approval scheme was also positively associated with recent disease on the premises (P=0.02).

Conclusion: Facilities and implementation of biosecurity practices vary among equestrian premises. The measures undertaken are associated with specific owner and premises factors, which should be considered when providing appropriate biosecurity advice.

Key words: Equine, biosecurity, facilities, cross-sectional, questionnaire

Attitudes towards equine biosecurity among horse owners in Great Britain

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ABSTRACT

Objective: To investigate factors that act as motivators or barriers for horse owners undertaking biosecurity practices.

Materials and methods: Postal questionnaires were administered to a random sample of British horse owners. Questionnaires requested information on the owners' involvement with horses, their equestrian premises and factors that they currently perceive as motivators and barriers, or would influence a change in biosecurity practices.

Results: Useable response rate was 65% (n=708/1091). Concern for the health and welfare of owners' horses was a strong motivator for undertaking biosecurity practices (67%; n=446/663). 64% of respondents also identified a disease outbreak on the premises as a strong motivator (n=425/660); this was considered the factor most likely to change biosecurity practices (Fig. 1). Relatively few respondents had previously discussed biosecurity with their veterinary surgeon (27%; n=190/515). An inability to implement the veterinary surgeon's advice on their premises was the most common reason for owners not fully acting on advice (60%; n=41/69). However, greater veterinary guidance was generally considered a factor that would change implementation of biosecurity (Fig. 1). 69% (n=427/687) of respondents considered that a lack of facilities on their premises presented some level of barrier to undertaking biosecurity practices.

Conclusion: Different factors vary in the extent to which they influence or impact upon the undertaking of biosecurity practices. Factors that act as strong motivators or barriers for owners should be considered in the future development and provision of biosecurity protocols.

Key words: Equine, biosecurity, attitudes, motivators, barriers

Biocheck.UGent: A risk based tool to quantify the level of biosecurity

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ABSTRACT

Objective: An association between antimicrobial usage (AMU) and selection of antimicrobial resistance (AMR) has been proven in several studies. Antimicrobial stewardship in combination with optimal animal health will be the key to slow down the resistance development. A perceived highly effective and feasible alternative to improve overall animal health and reduce the necessity of AMU is the improvement of the level of biosecurity. Biosecurity is also an important measure in the reduction of introduction and spread of epidemic and endemic diseases. To quantify the level of biosecurity Ghent University developed the online free available risk based tool Biocheck.UGent.

Materials and methods: From this system herds receive a score for their internal, external and overall level of biosecurity and areas for improvement are highlighted. At the moment over 8000 registrations have been collected and the tool has been used in over 50 countries worldwide. The Biocheck.UGent is currently available for poultry and pig production and is being placed online for cattle production.

Results: Large variation between and within herds and countries, as well as room for improvement in the level of biosecurity has been seen in several studies making use of the biosecurity quantification capabilities of Biocheck.UGent. Associations of improved biosecurity levels with reduced AMU and increased production results were published in several publications. Improving the level of biosecurity can be economically beneficial as well, resulting in a net benefit of around 2 euro per finisher per year.

Conclusion: Improvement of the level of biosecurity fits into a holistic approach to tackle the world wide problem of antimicrobial usage and resistance and can help us to reduce the risk of introduction of epidemic diseases.

Key words: Biosecurity, antimicrobial stewardship, alternative, epidemic diseases, prevention

Reducing Antibiotic Use in Layer Farms by Implementing 3-Zone Biosecurity

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ABSTRACT

Objective: Since highly pathogenic avian influenza (HPAI) was detected in Indonesia in 2003, the disease has infected poultry in 32 out of 34 provinces, causing the death of millions of poultry, and disrupting the livelihoods of people depending on poultry keeping. Various efforts have been made to control HPAI in Indonesia, amongst them improving biosecurity in poultry farms to reduce the risk of HPAI at farm level. Implementing simple but effective biosecurity on layer farms using the 3-zone biosecurity approach, dividing the farm into three separate zones - a peripheral dirty zone, a buffer zone and a central production zone is a smart way to protect poultry farms from diseases.

Materials and methods: An on-farm study of 3-zone biosecurity implementation was conducted in Waringin farm in Semarang district, Central Java province. Waringin has two open house layer units, each housing 25,000 birds of multiple ages and with the same management system. One farm implemented 3-zone biosecurity while the other did not. After 18 months of implementation, the biosecure farm had reduced its antibiotic use by 42% leading to a saving of USD 773. Hen day production was also more stable reaching 90% in the biosecure farm compared with 87% in the non-biosecure farm.

Results: The implementation of 3-zone biosecurity in poultry farms is an effective way to protect flocks from diseases and improve profitability. It has become one of the key HPAI control strategies promoted by the Government of Indonesia. Other layer farmers in Indonesia have already adopted the 3-zone biosecurity approach in their farms. 3-zone biosecurity could be promoted as a simple and effective method to reduce disease risk, while also contributing to reduced antibiotic use on small scale commercial poultry farms.

Key words: Farm biosecurity, antibiotic use

The effect on knowledge, attitudes and personality traits on biosecurity compliance in French duck farms following a HPAI crisis

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ABSTRACT

Objective: Highly Pathogenic Avian Influenza (HPAI) H5N8 virus spread across Europe in winter 2016-2017, with an unprecedented epidemic in duck farms located in the Southwest of France. Biosecurity plays a capital role in preventing the introduction and spread of infectious agents – including avian influenza - within and between farms. The actual implementation of biosecurity measures is an issue in all types of animal production. Knowledge gaps have been cited as determinants for poor compliance, but human dimensions such as personality traits and attitudes were also suggested as influencing factors.

Materials and methods: A cross-sectional survey was carried out on a random sample of 150 duck farmers from the Southwest of France, which were visited during winter 2017-2018. Data on biosecurity practices were collected during the farm visit. Information on knowledge, attitude and practices regarding biosecurity issues and avian influenza were collected using a questionnaire. A personality test, developed to assess personality traits in the workplace and previously adapted to biosecurity compliance issues, was used. Regression models were used to evaluate relationships between determinants (knowledge, attitude, personality traits) and the outcome (biosecurity compliance).

Results: This study highlighted important variability in farmers' knowledge and attitude regarding biosecurity and avian influenza. In addition, results demonstrated that personality traits and experience play a major role in biosecurity compliance.

Conclusion: An increase in biosecurity compliance is paramount not only to prevent or reduce the spread of pathogens such as avian influenza, but also as a tool to decrease antimicrobial use and resistance. A better understanding of farmers' drivers of biosecurity compliance is an important step in enabling stakeholders to focus on points critical to the implementation of an on-farm biosecurity plan.

Understanding farmer behaviour: role of personality, emotions, perceptions, rewards and sanctions

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ABSTRACT

Objectives: There has been lot of interest in farmer behaviour over the past decade. Management decisions made on farm directly impact level of disease, productivity and welfare of animals on the farm. There are lot of example in veterinary epidemiology where despite having 'best practice' available for management, there has been barriers to its implementation on the farm. We investigated farmer behaviour in the UK for implementation of biosecurity and management of lameness in sheep using various social science methods and psychosocial theories.

Materials and methods: Analysis was conducted using thematic analysis for qualitative data and latent class, factor analysis, multivariable modelling for quantitative data. This talk presents summary of our key published findings from 5 studies (n = 1300 farmers and n = 200 vets) on how differences in farmer personality, emotions, perceptions of self and including attitudes towards disease management, rewards/sanctions influences decision making by farmers.

Results: The results suggest farmer personality plays a role as farmers that were conscientiousness and understood the importance of active control of lameness had reduced risk of lameness (IRR 0.95). Negative emotions, feelings of hopelessness and lack of knowledge about transmission was significantly associated with not adopting best practice. Farmer perceptions around the concept of farming (e.g. 'good farmer') and frames how they view disease perception (e.g. 'what isn't broke does not need fixing') seem to influence how farmers approached disease prevention. Interestingly farmers preferred to sanction negative outcomes rather than reward positive outcomes. This suggests that feeling that losses appear larger than gains and farmers believe that sanctions result in greater behaviour change.

Conclusion: All these studies provide us insight into the complexity of farmer decision making and various factors influencing it. Incorporating this understanding to influence change in behaviour is key to increasing uptake of new information.

Landscape and vegetation data on different scales and the number of wild boar abundance

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ABSTRACT

Objective: The objective of the current study was to determine if landscape factors determine the number of wild boar in the hunting bag.

Material and methods: Landscape parameters like vegetation and altitude were taken from the Digital Landscape Model of Germany (ATKIS). In Germany and other countries, hunting bag statistics are available on different scales, starting at hunting ground level, but often aggregated up to district level. For each of the different scales, landscape classes were correlated with the hunting bag. Significant correlations were investigated in a multivariable model.

Results: Over the whole of Germany, the correlation between landscape data and wild boar abundance (hunting bag) resulted in a moderate correlation. Especially the percentage of forest present in each spatial unit showed a good correlation with the number of wild boar reported. However, if smaller scales were used, the correlation was more limited.

Conclusion: Landscape data only offer limited power for predicting wild boar abundance, especially on smaller scales. It is difficult to use such models for risk assessments in relation to wild boar diseases.

Key words: African swine fever, wild boar, hunting bag, vegetation

Sero - epidemiological survey for acute Q fever antibodies and risk factors among patients with febrile condition in two hospitals in Busia County

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ABSTRACT

Objective: This study aimed at estimating the prevalence of acute Q fever among patient presenting with clinical signs consistent with acute Q fever as well as understand the risk factors for acquiring the disease.

Materials and methods: A cross-sectional survey was carried out in Busia County hospital and Kenya Medical Research Institute (KEMRI) Allupe. Seven hundred and three (703) patients presenting with febrile illness were recruited and a blood sample collected, serum was extracted and stored. An in-depth individual interview was administered seeking to understand the presenting clinical signs as well as possible exposures factors relating to Q fever epidemiology. Later the samples were thawed and tested for Ig M and Ig G phase II antibodies. Regression modelling was employed to obtain the association between the seropositivity and the exposure factors.

Results: The overall antibodies seroprevalence was 3.7 % (95% CI 2.3 - 5.6). Having cattle born in the compound; aOR 2.46 (95% CI: 1.07-5.64) and having goats and sheep born in the compound aOR 3.03 (95% CI: 1.10 - 8.41) were found to be associated with Q fever in the multivariable regression.

Conclusion: These results indicate that Q fever may be endemic with a low prevalence in the region suggesting that Q fever contribution to the burden of febrile illness in the regions may be insignificant. We recommend raising awareness among clinicians, and farmers about the disease and Q fever clinical picture as well emphasizing to farmers and animal health workers the need to handle birthing and, or aborting animals with increased care.

Key words: Q fever, sero-epidemiology, risk factors

A pilot study of the prevalence of Q fever in cattle, sheep and goats in Victoria, Australia

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ABSTRACT

Objective: To estimate the individual animal-level, herd-prevalence and within-herd-prevalence of *Coxiella burnetii* infection among cattle, sheep and goats in Victoria, Australia.

Materials and methods: This survey was carried out from February 2016 to May 2017 in Victoria, Australia. Over 1500 blood samples were collected using a two-stage sampling process from farms and abattoirs. Sera were screened using a commercial Q fever ELISA kit for ruminants. True prevalence and intra-class correlation coefficient for each species was estimated using a Bayesian approach to account for known test imperfections. Post-hoc sample size estimates were calculated based on survey results to inform future study planning.

	Animal-level prevalence (95% CI)	Herd-level prevalence (95% CI)	Within-herd-level prevalence (95% CI)	Intra-class correlation coefficient (95% CI)	Post-hoc sample size
Cattle (Goulburn Valley)	0% (0, 0%)	0% (0, 0%)	-	-	-
Cattle (Gippsland)	0.4% (0, 3.4%)	0% (0, 3.4%)	12.2% (2.2, 31.8%)	0.02 (0.01, 0.24)	550
Sheep	2.1% (0, 3.7%)	1.5% (0, 3.0%)	14.7% (3.0, 29.6%)	0.12 (0.06, 0.41)	2310
Goats	1.6% (0, 2.8%)	0% (0, 2.5%)	19.1% (3.7, 43.3%)	0.10 (0.02, 0.46)	2110

Results:

Conclusion: Q fever is endemic in Victoria at very low levels, and may even be non-endemic in some of the studied areas. Although prevalence was low at the animal and herd level, animal-level prevalence within affected farms could be as high as 30%. This indicates that the prevalence of exposure to *Coxiella burnetii* was geographically uneven, being highly clustered in a small number of farms. To confirm the very low rate or absence of exposure, further surveys that include large numbers of farms and animals are required.

Key words: Q fever, *Coxiella burnetii*, prevalence, ruminants

Why are humans sentinels for canine-rabies incursions?

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ABSTRACT

Objective: to determine the timeliness and sensitivity of thresholds for detection of rabies incursions in dogs to inform surveillance strategies.

Materials and methods: A rabies spread simulation model was implemented in which human infection follows a bite from an infectious dog. Parameters were derived from peer-reviewed literature and empirical data collected from free-roaming dog populations in northern Australia. Tested detection thresholds included: dog deaths (≥ 5 dead dogs/week above the background death rate), the first case of furious rabies in a dog, and the first human bitten by a rabies-infectious dog (assumption: the dog was observed for signs of rabies following the bite). The median time to the first human case of rabies (onset of symptoms) was used as a reference threshold. Time lags accounted for reporting and investigation. Detection thresholds were tested over 30,000 iterations of the model.

Results: Human cases occurred following simulated incursions in 23% of iterations and median time to onset of symptoms was 89 days. All detection thresholds occurred in >90% of simulated incursions in which a human case occurred. The most timely detection threshold was the first dog with furious rabies (median 21 days; median 5 dogs infected). Detection thresholds of an increase in dog deaths or a human bitten by a rabies-infectious dog were less timely (median 49 days and 56 days, respectively).

Conclusion: Although these results indicate that surveillance for a canine-rabies incursion could be sensitive in outbreaks which result in a human case, the median days to thresholds were short given the realities of observation, reporting and investigation. This provides insight into why humans continue to be sentinels for canine-rabies incursions (for example, Bali, Indonesia, 2007, and Sarawak, Malaysia, 2017). Improving detection of dogs with furious rabies (for example, increased awareness to improve recognition and reporting) is most likely to prevent human deaths.

Key words: Rabies, detection threshold, surveillance

Close to real-time conversion of basic space time data into valuable information using open-source technologies: the South African HPAI outbreak as an example

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ABSTRACT

Outbreaks of disease, such as the highly pathogenic (HPAI H5N8) outbreak that occurred in South Africa in 2017/2018, result in significant stress to both the industries affected and the control authorities. This becomes exacerbated when outbreaks are spread over a large area with different reporting and control structures, resulting in delays in broad overview outbreak reporting and analysis. Open-source software is computer software that has freely available source code which can be utilised to improve collaboration between developers. Within the scientific community at large statistical software such as R has become the core of data manipulation and visualisation, and can be utilised in the real-time analysis of data. Open-source software is not limited to statistical analysis and, of relevance to this example, there is database (PostgreSQL), geographic information systems (GIS) (PostGIS and qGIS/qGIS sever) and web-development platforms (RMarkdown/Shiny server) that are also freely available. Cloud computing provides a platform for the dissemination of information in resource-constrained environments where server acquisition and maintenance functions are not sustainable and require significant upskilling of employees. While cloud computing is not free it does allow for short interval subscriptions in a very controlled and secure environment.

For OIE (World Organisation for Animal Health) diseases of exceptional epidemiological events, there are temporal and spatial data publically available for unique outbreaks within each event. Using these data, temporal and spatial analysis can be automated in near real time and, using open source software, can be visualised and reported online. This process has been followed for the HPAI outbreak in South Africa, with a web interface output used by the poultry industry with specific focus on categorised epidemic curves by location and affected species demographics as well as spatial incidence of outbreaks and spatial spread over time.

Key words: Open source, web interface, spatial, temporal, epidemiologic analysis

Improving animal healthcare decision-making in Ethiopian paraprofessionals using a smartphone application

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ABSTRACT

Objective: First-line Ethiopian animal healthcare is predominantly delivered by paraprofessionals with limited training compared to a six-year veterinary degree, yet they still treat the same complex pathologies in multiple species. Often geographically-isolated, they work in a public system with limited resources and few opportunities for professional support and development. Initiatives to improve animal health are frequently disease or species-specific. There is an opportunity to strengthen the animal healthcare system systemically.

Materials and methods: A smartphone application assisting clinical decision-making and effective treatment selection is being developed and trialled in Ethiopia. This is multi-species and context-specific, allowing for local etymological differences and disease presentations. Experts from within Ethiopian government, universities and NGOs participate in workshops that identify and characterise 15-20 common diseases for a given animal species. Outcomes are encoded within the app. Veterinary paraprofessionals in multiple geographical regions across Ethiopia will be supported in using the app and information gathered on its applicability and use.

Results: The app will be part of an ongoing Brooke-run paraprofessional mentoring project that uses a standardised work-based assessment framework to support and monitor clinical decision-making, concentrating on working equids but applicable to all species. The app will support in-person training as a "mentor in your pocket" for a broad range of animal diseases.

Conclusion: As the contribution of working equids is increasingly recognised worldwide, it is appropriate to include them in livestock disease interventions. Brooke works with over 4000 veterinary paraprofessionals globally; the ultimate aim is to develop context-specific versions of the app for those working worldwide in isolated and resource-poor settings. One integrated multi-species app is more user-friendly and useful, and ultimately will reach more animals. Future uses include: improving animal disease surveillance and reporting, delivering in-situ training, providing information on capacity-building needs, and collecting data on responsible antimicrobial use.

Key words: MHealth, smartphone, app, livestock, diagnosis, clinical diagnosis, clinical competency, animal health practitioners, mobile technology, working equids

What factors influence the adoption of technology for improved recording in sheep flocks? The importance of farmers' attitudes

ABSTRACT

Objectives: Strategies for stimulating sheep flock productivity and enhancing disease surveillance include the promotion of precision farming tools, such Electronic Identification devices (EID). EID tools facilitate flock data recording, but anecdotal evidence suggests its uptake in the United Kingdom has been limited. This study aimed at exploring drivers of EID adoption, by investigating uptake rate and farmers' opinions about this technology, associations between farmer characteristics and EID adoption, and the relationship between EID usage and flock lameness levels.

Materials and methods: Two thousand commercial English and Welsh sheep farmers were posted a questionnaire on flock husbandry practices and opinions about EID, and 439 (22%) replied. Exploratory factor analysis and multivariable logistic regression modelling were used to explore farmer beliefs and practices significantly associated ($p \leq 0.05$) with EID technology adoption.

Results: Three factors representing farmer's beliefs were identified – practicality, usefulness, and external pressure and negative feelings – and all were significantly associated with adoption/intention to adopt EID technology. Adopters were significantly more likely than non-adopters to perceive EID as practical (Odds Ratio = 1.18, 95% CI: 1.02 – 1.36) and useful (O.R. = 1.22, 95% CI: 1.10 – 1.35), but technology cost was considered important by both groups. In contrast, adopters were less likely than non-adopters to consider that 'government pressurise farmers to adopt technology' (O.R = 0.73, 95% CI: 0.61 – 0.87). Farmers already using other technologies (O.R = 3.69, 95% CI: 1.36 – 10.13) or intending to intensify their flock production (O.R = 5.10, 95% CI: 1.94 – 13.83) were significantly more likely to be EID adopters. Additionally, flocks managed with EID in the previous year had significantly lower flock lameness levels ($\chi2 = 10.91$, $p = 0.005$).

Conclusion: This study provides a framework for EID adoption which could be utilized for other precision farming technologies. Enhancing familiarity with technology is likely to enhance trust in use and subsequent adoption, but technology must be practical and cost-effective.

Why smallholder pig value chain actors are not willing to report disease outbreak or comply to animal movement restrictions: case of African swine fever in Uganda?

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ABSTRACT

Objective: Poor or absence of disease reporting and compliance with animal movement restrictions has been the biggest challenge to African swine fever disease management in Uganda. Key reasons of why smallholder pig value chain actors do not comply with disease control regulations has not been documented.

Materials and methods: In order to get more insight into value chain actor' decision making, we undertook a household survey involving 960 pig farmers, 81 pig traders/butchers and 36 para-veterinarians operating in Masaka and Lira, two major pig producing districts.

Results: Main reasons for farmers not reporting were: lack of knowledge about disease's symptoms (19%) and fear of losing pig buyers (18%). The later was more pronounced in Masaka compared to Lira (p=0.000); whereas there was no difference in lack of capacities and knowledge to report between men and women (p=0.25). For traders and butchers fear of losing market opportunities (51%) was the main reason. For para-veterinarians, lack of knowledge about the disease's symptoms was evident (24%). Regarding absence of compliance with animal movement restrictions, the main reasons for farmers were: fear of losing buyers (33%) and lack of knowledge about the disease's symptoms (28%); reasons were more evident in Lira compared to Masaka (p=0.000). The fear of losing pig buyers was more reported by women (p=0.007). For traders/butchers, the main reasons were: fear of interrupting their businesses (43%); and for para-veterinarians: fear of losing clients (pig farmers) if quarantine is imposed (22%) and lack of knowledge about the disease reporting (21%). Other major reasons included: authorities not taking action following an outbreak, leading to lack of trust; social protection amongst farmers and high financial cost associated with reporting.

Conclusion: The study highlighted wide knowledge gaps of smallholder pig value chain actors on disease control measures, and pointed out the importance of economic incentive in order to improve disease control.

Key words: African swine fever, reporting, movement control, Uganda

Epidemiological investigations in animal disease outbreaks: a web-based system for reporting and managing the information collected

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ABSTRACT

Objective: Information systems have been developed during years to help veterinary services in collecting and analysing relevant information for the control, surveillance and eradication of animal diseases. Aim of this paper is to describe the web-based epidemiological investigation tool added to the Italian information system for the notification of animal diseases (SIMAN) for the registration and management of information collected during animal disease outbreak investigations.

Materials and methods: The web-based epidemiological investigation tool is based on several templates, each one specifically designed for specific diseases subject to reporting. This allows a standardized data collection, with acknowledged semantics and internal rules. The Web Services technology (WS) assures the interoperability with the National Animal Identification Registration System (BDN).

Results: The tool manages all the steps of the epidemiological investigation, from outbreak suspicion, to outbreak closures. E-mail alerts are sent to the competent authorities in case of delays in information recordings. Data already stored in other information systems (such as BDN, i.e. animal identification, herd health status, animal movements, etc.) are automatically retrieved through WS. During the first three months of 2018, all outbreaks resulted linked with their epidemiological investigation. Regarding the completeness and consistency of epidemiological investigations, all required fields are filled in due to an automatic check.

Conclusion: The management of outbreaks requires a quick, exhaustive and prompt reaction of the competent authorities. The standardization of information and the completeness of the data reported allow and facilitate the use of the collected information for the analysis of risk factors, thus improving the entire surveillance system.

Key words: Epidemiological investigations, evaluation, management, outbreaks, web-based system

Impacts of climate change on facial eczema spore counts in New Zealand

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ABSTRACT

Objective: Facial eczema (FE) is a disease of grazing ruminants and is caused by the mycotoxin sporidesmin produced by the spores of the fungus *Pithomyces chartarum*. FE has long been a concern for New Zealand (NZ) farmers with highest incidence reported in summer/autumn when conditions are warm and humid. According to NZ climate projections, an extension of the warm and moist conditions required for growth and sporulation of the fungus is likely to occur. The objective of this study was to assess the likely impacts of climate change on the FE spore counts in NZ.

Materials and methods: A systematic literature review was conducted to investigate the association between the presence and severity of FE or spores and key climate variables. Historical spore count data were obtained from pastures in several NZ locations. A model was built to quantify the association between spore counts and local climatic data, and projections were made under different climate scenarios to identify the areas where the spore counts are likely to change.

Results: The systematic review identified 233 and 44 articles that reported studying the link between FE and rainfall/humidity and temperature, respectively. The modelling process showed the importance of obtaining adequate animal health data for this type of purpose and that the use of spore counts may not allow extrapolating the projections to clinical manifestations of FE.

Conclusion: Our findings suggested importance of climate change on the distribution of spore counts in NZ. We also demonstrated the difficulty in using such methods to inform preparedness due to the complexity of the relationship between spore counts and clinical FE. This highlights the need of suitable time-series of animal health data to provide reliable information and thus enhance resilience of farming communities to climate change.

Key words: Facial eczema, climate change, grazing livestock, *Pithomyces chartarum*

Linking supply chain governance, biosecurity and epidemiology in the context of HPAI control in Western Java: A value chain perspective

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ABSTRACT

Objective: The highly pathogenic avian influenza (HPAI) remains endemic in Western Java, Indonesia with continued reports of outbreak. To understand the HPAI epidemic, it is important to map the complex structure of the poultry sector. The governance of the poultry value chain in particular, could play a pivotal role, yet there is limited information on the different chain governance structures and their impacts on HPAI control related to the poultry chain risks of HPAI introduction and transmission.

Materials and methods: This study uses value chain analysis (VCA), focusing on an in-depth assessment of governance structures to establish a theoretical framework to examine biosecurity and the risks of HPAI introduction and transmission in the context of HPAI control in the Western Java poultry chain. During the research, semi-structured interviews were conducted with experts, key value-chain stakeholders, and the economic performance of identified actors was estimated.

Results: Results indicated the co-existence of four different poultry value chains in West Java: the integrator chain, the semi-automated slaughterhouse chain, the controlled slaughter-point chain, and the private slaughter-point chain. The integrator chain was characterized by the highest levels of coordination and a tight, hierarchical governance. In contrast, the other three types of value chains were less coordinated. The perceived risks of HPAI introduction and transmission of the different actors within the four value chains also differed. Implementation of biosecurity, the risks of HPAI introduction and transmission, and HPAI control measures were strongly related to the governance structure of the chain, with interactions between different chains and governance structures. Conclusion: Our findings highlight that a proper understanding of the chain governance structure is vital to improve the effectiveness of HPAI control measures, by making the interventions more specific and fit-for-purpose given the incentive structures present in different chains.

Key words: value chain analysis; HPAI; chain governance; biosecurity; risks of introduction and transmission

Application of exponential random graph models to determine nomadic herders' movements in Senegal

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ABSTRACT

Objective: Understanding human and animal mobility patterns is key to predict local and global disease spread. We aimed to establish the nomad herds' movements network in Senegal.

Materials and methods: We used an Exponential Random Graph models (ERGM) to comprehend the reasons behind their migration. We collected data via a questionnaire on nomad herds movements and the reasons behind their decision to take specific routes or gather in certain areas. We constructed a spatial explicit network with villages and nomad herds' movements being the nodes and connecting edges, respectively.

Results: The final ERGM model showed that node, edge and structural attributes such as presence of cattle in the herd (Odd Ratio = 12), morbidity (Odd Ratio = 3.6) and lack of water (Odd Ratio = 2) were important predictors of nomad herds 'movements.

Conclusions: This study not only provides valuable information to help monitoring the livestock diseases such as Rift Valley Fever in Senegal but also helps implement outreach, education and intervention programs for other emerging and endemic diseases affecting nomadic herds.

Key words: Transhumance, Senegal, Network Analysis, ERGM, risk-based surveillance

Transboundary animal disease control: preparedness and hurdles in Europe

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ABSTRACT

Objective: This work, implemented under the SPARE project, describes current practices among European Member States (MS) that promote rapid, timely and efficient access and sharing of relevant data and information to assess emerging risk and establish adequate risk management strategies.

Materials and methods: The consortium developed a generic spatial model to assess the risk of introduction and spread of transboundary diseases in EU. The obstacles faced to access, use and share the data necessary to parameterize the model were gathered by consortium members and analysed. In addition, a survey was implemented to describe the current practices for risk identification and collaborative risk management among MSs in Europe and to identify gaps and challenges that may delay emergency response.

Results: In regions like Europe, massive efforts have been made over the last decades to collect relevant information in centralised databases, e.g. animal movement data, wildlife and vector abundance data, and other relevant risk factor data such as biosecurity. However the accessibility of such data for integrated risk assessments and therefore its utility for risk management was found to be very limited. This is in stark contrast with the increasingly sophisticated methods available for transboundary disease modelling. Additionally, the need for evidence-based decision making in transboundary disease control is increasing, particularly in relation to emerging or re-emerging diseases. This is particularly relevant to minimise the risk of false negative results (Type II error for interventions). Surveys conducted with risk managers in Europe documented their interest to expand the efforts to exchange information (i.e. on biosecurity) and joint decision making on transboundary hazards.

Conclusion: The project highlighted the need for internationally curated data repositories that are managed by trusted experts within a sustainable framework and accessible to researchers. A range of possible solutions to address identified hurdles will be presented and discussed.

Key words: Metadata, risk-assessment, risk-management

Economic evaluation of the eradication program for bovine viral diarrhea in the Swiss dairy sector

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ABSTRACT

Objective: The mandatory eradication program for Bovine Virus Diarrhoea (BVD) in Switzerland has been ongoing since 2008, and is focused on detection and elimination of persistently infected animals. Detection was initially based on antigen testing of the entire cattle population, followed by antigen testing of all new born calves until 2012. Since then, bulk milk testing (dairy herds) and blood sample serology (beef herds) have been used for the surveillance of disease-free herds. The aim of this study was to conduct an economic evaluation of the BVD eradication program in the Swiss dairy sector.

Materials and methods: The situation before the start of the program (herd-level prevalence: 20%) served as a baseline. Production models for three dairy farm types were used to estimate gross margins as well as net production losses and expenditures caused by BVD. The total economic benefit was estimated as the difference in disease costs between the baseline scenario and the implemented eradication program and was compared to the total eradication costs in a benefit-cost analysis. Data on the disease impact of BVD were obtained empirically in a retrospective epidemiological case-control study in Swiss dairy herds. Other production and economic parameters were based on benchmarking data and published agricultural statistics. The economic model consisted of a stochastic simulation and was conducted for a time period of 14 years (2008-2021).

Results: The estimated annual financial losses in BVD virus infected dairy herds were CHF 85-89 per dairy cow and CHF 1337-2535 for an average farm. The median net present value (NPV) obtained was CHF 44.9 million (90% central range: 13.4m to 69.4m) and the break-even point has been reached in 2015.

Conclusion: Overall, these outcomes demonstrate that the Swiss BVD eradication program results in a net benefit for the dairy sector. These finding are relevant for planning similar BVD control programs in other countries.

Key words: Cost-benefit analysis, gross margin, dairy cattle, control program

Treatment strategies for sheep scab: an economic model of farmer behavior

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ABSTRACT

Objectives: To produce and use a Game Theory model to explore the relative economic costs and benefits of different reactive and prophylactic treatment strategies for sheep scab.

Materials and methods: Data from the literature were used to estimate cost and risk parameters for a deterministic game theory model, which recommends the optimum sheep scab prophylaxis strategy for a farmer in relation to the strategy of their neighbour. Two prophylaxis treatments were included; injection of long-acting macrocyclic lactones (MLs) and organophosphate dipping. As regional costs and risks differ, the model was run separately for upland farms (northern England, Scotland, Wales) and lowland farms (rest of England). One-at-a-time sensitivity analyses were used on the baseline scab risk parameter (intervals of 0.005, range 0-50%), overall prevention cost and the cost of prophylactic treatment product alone (intervals of £0.05, range £0-£2) to identify when the optimum strategy would change.

Results: The average cost of sheep scab per year is £35.12 in an upland flock (range £35.01-£35.36) per ewe and her lambs and £40.84 in a lowland flock (range £40.63- £41.02). Under current costs and risks it is only cost-effective to use prophylaxis in the uplands of Great Britain and only when dipping, regardless of the prophylaxis choices of a neighbour. However, under different costs and risk of scab, it can become cost-effective to use prophylaxis.

Conclusion: Under current costs and risks of sheep scab, treating preventatively is only cost-effective in the uplands of Great Britain and when using an OP dip. However, in areas where scab prevalence is higher than average, preventative treatment could be profitable. In other areas, subsidies and penalties would need to be introduced if eradication of scab is desired.

Key words: Sheep scab, game theory, decision-making, prophylaxis, disease management

Modelling interventions to mitigate production loss due to *Fasciola hepatica* in key UK cattle sectors

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ABSTRACT

Objective: Liver fluke *(Fascioloa hepatica)* is a common, ubiquitous parasite that affects the health and welfare of cattle worldwide. The costs incurred, via production losses and liver condemnations, and their effects on the economics of the British cattle industry are being evaluated. In order to effect change, we need to establish which, of any improved intervention protocols, gives the most acceptable cost:benefit outcome.

Materials and methods: Herd-level stochastic bio-economic models for growing animal, beef suckler herd and dairy enterprises were developed to simulate the major management systems used, in @RISK, with a partial-budget approach. These have now been modified to explore how estimates change under specific intervention scenarios (adopt v. not adopt). The interventions relate to use of licensed flukicide products and the scenarios determine the group(s) of animals treated, the timing and number of treatments.

Results: Preliminary results indicate that the optimal intervention protocol depends on the specific production system being modelled. For example, the most effective intervention approach in terms of cost:benefit depends on calving season in suckler herds and on finishing age in beef production.

Conclusion: We conclude that it should be possible to broadly define the most appropriate protocol for flukicide usage, depending on production system. This information may inform a national-level welfare model to estimate potential savings to the UK cattle sector, if adopted by varying proportions of all UK herds, in each type of production system. At the individual herd-level, the models could be adapted into a decision support tool for individual producers - to help guide their choice of control method for fasciolosis, allowing them to input data specific to their own system and therefore obtain tailored outputs.

Key words: Liver fluke, production impact, bio-economic, intervention, partial budget

Use of a stochastic production frontier approach to examine impact of gastrointestinal nematode management in beef cow-calf herds in Canada

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ABSTRACT

Objectives: Blanket treatment at set times of the year of all cattle for gastrointestinal (GIN) parasites is likely to lead to anthelmintic resistance. Understanding how producers make these decisions would be helpful to change, although there is little information on how that takes place. This research developed a basic spreadsheet tool to allow beef producers to estimate changes in economic impact from use of various anthelmintic options, based on production and market price knowledge.

Materials and methods: A basic stochastic production frontier (SPF) approach was applied for cow-calf herds using data from records in Western Canada. Functional form was based on a standard Cobb-Douglas approach. Data were also collected regarding anthelmintic useage, production demographics, and ecozone. These variables were used to define expected differences from the mean for production. Output was valued using current market prices. Users are able to modify data to fit their system.

Results: A spreadsheet tool to estimate impact from anthelmintic application was developed and tested based on concordance with producer records. Sensitivity analysis yielded a deviation of +/1520% from expected outcomes. Previous use of an SPF approach to cow-calf herd GIN management was not located in the literature. This approach accepts modest deviations from perfectly efficient expectations and allows producers to enter their own production details to estimate economic gains from changing GIN management.

Conclusion: An interactive tool is helpful for discussion with producers regarding options for reducing use of GIN antiparasitics. This will be a valuable contribution to sustainable prudent use of anthelmintics.

Key words: stochastic production frontier; production economics; gastrointestinal nematodes; anthelmintic management; beef cattle.

Smallholder benefits and costs of a FMD control program in Cambodia

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ABSTRACT

Objective: Foot and mouth disease (FMD) has been endemic in Cambodia for many decades. The cost-effectiveness of the FMD vaccination program is poorly understood with decisions often made based on vaccine availability and donor support. This study partnered with 300 farmers in two Cambodian provinces to estimate the on-farm benefits and costs of the FMD vaccination and de-worming program.

Materials and methods: Using Benefit Cost Analysis (BCA), the study evaluated various scenarios that identified the important factors that influence productivity and vaccination program success. These included; number of outbreaks per year; morbidity rate; efficacy of the vaccination program and; farmer sale, sick animal treatment and recovery strategies.

Results: If it could be guaranteed that the vaccination program was effective, it was found that farmers would benefit if there were annual FMD outbreaks with morbidity rates of 30%, or two major outbreaks in a five-year period with morbidity rates of 50%. However, if there was only one outbreak every five years, even at morbidity rates of 75%, smallholders would not benefit from the program. The analysis indicated that it is important for government and donors to ensure a successful program and for smallholders not to sell stock automatically during an outbreak or if they show symptoms of FMD. It is important that smallholders have the resources and knowledge on how to treat and manage their stock and farm during an outbreak.

Conclusion: Successful FMD control in Cambodia requires more than just an effective vaccine. This study indicates that there are many social and economic factors at the smallholder level that will influence the success of a FMD vaccination and de-worming program. In many cases there needs to be other non-farm economic benefits of a vaccination program for it to implemente successfully.

Key words: Foot and mouth disease, smallholder, cattle, benefit cost analysis, Cambodia, vaccination

Assessing the aggregate market costs of restrictions on antimicrobial use in U.S. dairy production

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ABSTRACT

Objective: Antimicrobial use (AMU) in dairy production reduces the impacts of infectious diseases, but a drawback is the selection of resistant bacteria. This situation has led some governments to implement policies limiting AMU. We investigate the impacts of two potential public policies on U.S. dairy farmers and consumers.

Materials and methods: We develop a two-step analysis to estimate the costs of AMU reduction for farmers and consumers, at the farm and the market levels. First, we model a representative U.S. dairy herd of 1000 cows with an average prevalence for the most frequent diseases. We calculate the farm net costs of current AMU practice (Business As Usual scenario), of AMU prohibition (Prohibition scenario), and an increase in antimicrobial prices. Second, we evaluate the consequences of AMU restrictions at the market-level using estimates of aggregate milk demand and supply and shifting the supply curve up by the cost increases of the various scenarios.

Results: We find that all the potential policies restricting AMU would have a mild effect at the market level. In the case of AMU prohibition, the average milk price would rise from $0.423 to $0.425 per liter. In the short run, the total annual losses for producers and consumers would be $152 million. Implementing taxes on AMU would also slightly increase milk price, up to $0.426 in the case of a tax multiplying by five the initial antimicrobial prices. Under the Prohibition scenario, the quantity of milk produced plummets by 356 million kilograms, representing 0.4% of the average U.S. milk production over the period 2012-2016.

Conclusion: Our results suggest that the effects of such policies should be mild on milk price, and mainly borne by the producers. Further investigations are needed to estimate the impacts on secondary markets, such as organic and meat productions, as well as on retailers and the pharmaceutical system.

Key Words: dairy production, antimicrobial use, economics, public policy

Assessing the economics associated with cattle health and production research trial results

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ABSTRACT

Objective: An assessment of an economic outcome is often the primary goal of a field trial in which two or more health/production management strategies are compared. However, a commonly used approach that only considers the economic values for statistically significant research outcomes is not ideal - in part, due to inevitable issues with type 1 and type 2 errors. In other words, when costs and benefits are calculated based on only a subset of results (those statistically significant), then the resulting economic values can be inaccurate. While a comprehensive partial budget-type approach is more aligned with production management decisions, the scientific literature is riddled with examples from research trials where statistics are used prior to economic assessments. The goal of this study is to compare and contrast methods for assessing the costs and benefits associated with cattle health/production trials, and to provide scientific guidance and rationale for future research applications.

Materials and methods: Datasets from two primary research trials (an animal health trial and a production technology trial) will be utilized in this study. Each dataset will be analyzed with two general approaches: one with statistical analysis first, and the economic analysis only on statistically significant results; and the second with the more comprehensive partial budget-type economic evaluation as the primary approach.

Results and Discussion: As companies evaluate new animal health products and technologies, the methods used to evaluate the costs and benefits of these products is critical as economic values that are under- or over-estimated relative to actual production costs/benefits could result in significant losses to producers. The results from this study will be compared and contrasted quantitatively. Additionally, we will outline alternative approaches, extensions, and opportunities to improve the value-based assessment of health and production technologies.

How would eliminating pneumonia in calves prior to weaning affect the net income of the US cow-calf industry?

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ABSTRACT

Objective: To investigate the difference in net income between a US beef cow-calf system either with or without pneumonia in beef calves prior to weaning.

Materials and methods: Cattle market data were used to simulate the annual net income of beef cow-calf industry. Parameter values for simulations were drawn from USDA and peer-reviewed papers, and the initial values of beef cow inventory were based on USDA survey data. A system dynamics model was developed using Vensim®. Several scenarios were designed: 1) the current situation with pneumonia in beef calves prior to weaning; 2) elimination of pneumonia without cost; 2) eliminate pneumonia with an annual cost per cow of US$10 - $50. The simulation results were validated against the actual behavior of the beef cattle cow-calf system.

Results: Beef cow inventory, feeder cattle value, and net income per cow followed the classically described 10-year cattle cycle. The cumulative industry net income changed little by eliminating pneumonia without any cost. With cost to remove pneumonia, the beef cow inventory reduced which increased feeder cattle value, and net income increased with less fluctuation.

Conclusion: Beef cow-calf producers not experiencing calf-hood pneumonia have an economic advantage over producers with pneumonia. Affected producers bear the cost of the disease, but, non-affected producers benefit from higher market prices because of fewer calves in the market. Assuming no change in demand, eliminating pre-weaning pneumonia without cost may benefit previously affected producers, but the additional supply of beef reduces calf market prices for all such that net income to the industry does not change. Costs to eliminate pneumonia decrease number of cows and supply of calves into the market resulting in increased cattle value, which may benefit total net income.

Key words: Bovine respiratory disease, pre-weaned calves, economics, system dynamics model

Economic impact of five control strategies to reduce BLV prevalence in endemic region in Canada

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ABSTRACT

Objective: An economic analysis was used to evaluate the financial consequences of four different control strategies to reduce the within-herd prevalence of BLV infection in Alberta dairy farms (Ca).

Materials and Methods: This economic evaluation examined partial costs and net revenues related to on-farm BLV control programs. A decision tree model was created with TreeAge Pro 2017, and within each control option, a Markov Model with 10 stages was applied to mimic a 10-year course of BLV control on farm. The model was analyzed by using Monte Carlo Simulation. The results were calculated as mean per individual cow in a 146-cow herd, with a 40% within-herd prevalence, for 1) management strategies based on literature for BLV control, 2) partial implementation of management strategies, 3) test and cull or 4) test and segregation of infected animals.

Results: Presence of a BLV infection in the herd causes a signficant economic loss to farm profitability. When comparing to a 'no control' on-farm strategy, it was shown that all four BLV control options were always economically beneficial. However, the net benefits of the different options varied from CAD $82.30 to $131.30 per animal per year, providing producers with economic drivers to select the best control strategy to be implemented on their farm. The duration of implementation was shown to be the strongest driver of the net revenue, followed by milk price.

Conclusion: In a BLV-endemic dairy environment, even implementing some control strategies to reduce within herd prevalence is economically beneficial to dairy producers. This provides economic motivators for control, when eradication through test and cull strategies is not feasible.

Key words: Economics, bovine leukosis, control program, disease prevalence, profitability

A cross sectional study to estimate the dog population and economic impact on the use of mass rabies vaccine in a township located at Nay Pyi Taw Council area of Myanmar

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ABSTRACT

Rabies has been addressed as an important disease in the Law issued by the Government of Myanmar. Due to the annual report of animal and human cases, the Veterinary Department is conducting prevention and control of rabies with the support of OIE STANDZ project. Before and during the STANDZ Rabies pilot campaign, a cross sectional study was conducted to understand the dog population estimates and economic impact on the application of mass vaccination campaign. Multiple cross-sectional studies were done at Lewe Townships of Nay Pyi Taw Council area and questionnaire interviews were (n=200) from randomly selected 20 villages and additional information was taken from participatory approaches (n=415). A year after, additional questionnaire interviews (n=446) were conducted in 18 villages to obtain the cost of post exposure treatment and that of vaccination to the dogs. The overall ratio of dog and human population was 1:6 and estimated dog population was approximately 40,000 heads at the study area and dog population and human population were linearly associated. Finding for the economic impacts were that the cost of rabies vaccine per dog was about 2000 Kyats(~1.53 USD) to 5000 Kyats (~3.84 USD) whereas for the PEP treatment, it costs 7000 Kyats (5.38 USD) to 11000 Kyats (8.46 USD) for additional expenses because PEP treatments which costs 34000 kyats (~28USD) to 48000 Kyats (~39USD) per victim, were subsidized by the government. By referring the estimated dog population of 7 million in Myanmar, the cost for the mass dog vaccination was less than that of PEP treatment. Nevertheless, the vaccination can be recommended as the efficient disease preventive measure and for the development of mass vaccination campaign, selection of targeted high-risk areas based on the report and expert opinion is recommended.

Key words: Rabies, epidemiology, economic impact, population estimate

Estimating the economic impact of lumpy skin disease and sheep and goat pox outbreaks on subsistence farmers in Nigeria

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ABSTRACT

Objective: Lumpy skin disease (LSD), sheeppox and goatpox (SGP) are contagious viral diseases, affecting cattle (LSD), sheep and goats (SGP). The diseases have highly characteristic clinical signs and cause negative impact on meat, wool, cashmere and milk production. Although they can be potentially detrimental for the livelihood of subsistence producers, the economic impact has not been formally evaluated on this group.

This study aims to estimate the economic impact of LSD and SGP among backyard and transhumance farmers in Nigeria.

Materials and methods: A retrospective study was conducted on herds and flocks affected during 2017 in Bauchi, Nigeria. Herds and flocks were diagnosed based on clinical signs by a local veterinarian and information was collected once the outbreak concluded using a standardised questionnaire. Data were collected from 40 farmers (29 backyard and 11 transhumance). The average attack and fatality rate were 25.7% and 11.0% in cattle, 38.9% and 45.9% in sheep; 41.7 and 34.7% in goats respectively.

Results: Almost all farmers (92.5%) treated affected animals with antibiotics, spending on average US$39.7 per farm during an outbreak. Transhumance farmers treated animals longer and spent more (average US$97.6). Slaughtering or selling affected animals at low price were common coping strategies mainly among backyard farmers. On average, farmers sold live cattle for 57.4% less than would have been sold if the animal was healthy, while sheep and goats were sold for 60.5% and 60.0% less respectively. Milk production dropped 61.2% when cows were clinically affected and 37.1% after they recovered. Livestock markets were the most common place to sell affected animals but also to buy replacement animals, suggesting these are hubs for spreading diseases. None of the farmers had been able to replace all affected animals.

Conclusions: LSD and SGP have a long lasting impact on subsistence farmers' livelihoods. Similar impacts can be expected in other low-and-middle income countries.

Key words: Lumpy skin disease, sheep and goat pox, Nigeria, economic impact, subsistence farmers

A Preliminary Economic Analysis to Assess the Benefits of Vaccinating Cattle against Rabies in Selected Rabies High-risk Areas of Bhutan

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ABSTRACT

Objective: Rabies is endemic in the southern parts of Bhutan that share a porous border with India. In the high-risk areas there are 17 dog rabies outbreaks reported annually. Frequent spill-over infection in cattle and other livestock can threaten the livelihood of marginal livestock farmers and is a public health concern. Although very effective dog rabies control programs are implemented in the high-risk areas of Bhutan, currently no preventive vaccination is carried out in cattle. The objective of this study was to assess the economic feasibility of vaccinating cattle in two sub-districts of southern Bhutan.

Materials and methods: We computed benefit-cost ratio (BCR) for four different scenarios: 1) Government of Bhutan paying for vaccine and vaccine delivery; 2) cattle owners paying 50% of the vaccine cost; 3) cattle owners paying the entire cost of rabies vaccine; and 4) cattle owners paying 50% of the vaccine and vaccine delivery cost. The average number of rabies outbreaks in cattle reported in the study areas was four. In this assessment the benefits of vaccinating cattle were computed as the costs saved by government for not needing to respond to four outbreaks in cattle. We made several assumptions based on current costs and procedures outlined in the National Rabies Prevention and Control Plan.

Results: The present value (PV) of benefits accrued after one year was estimated to be Nu 1,196,402.9 (USD 18,693). The cost of vaccinating cattle was estimated to be Nu 563,987 (USD 8,773). The BCR under scenario 1 was estimated to be 2.12 and rose to 2.8 under scenarios 2 and 3. The BCR was 4.27 for scenario 4.

Conclusion: This analysis showed that vaccinating cattle in rabies high-risk areas could be a beneficial option. The BCR depended on the number of rabies outbreaks in cattle and the extent of actions undertaken by the Government to respond to an outbreak

Key words: Rabies, BCR, vaccination, cattle, Bhutan

The cost of livestock-associated methicillin-resistant *Staphylococcus aureus* eradication from Danish pig herds

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ABSTRACT

The occurrence of LA-MRSA in Danish pig herds increased rapidly from 3% positive farms in 2008 to 88% positive farms in 2016. Furthermore, due to an increased incidence of human infections, the spread of livestock-associated methicillin-resistant *Staphylococcus Aureus* (LA-MRSA) from pigs into the human population has been a major public and political issue in Denmark. Similar concerns are also being raised about LA-MRSA in other Western European countries. At a time when the proportion of LA-MRSA-positive pig farms was low, Norway adopted a 'trace and destroy' strategy aimed at keeping LA-MRSA out of the pig population. However, to date, no country with a high LA- MRSA proportion of positive pig farms has chosen to use an eradication strategy. This study analyses the cost and complexities of conducting an LA-MRSA eradication program in a situation where a large proportion of herds are positive, using a gross margin analysis. The total cost of the eradication program was estimated based on the following components: 1) planning, 2) monitoring and testing, 3) cleaning and disinfection, 4) production gains and losses, 5) net loss from breeding exports, and 6) loss of genetic progress, including the costs of a mitigating caesarean section strategy in breeding herds. Costs were related to the depopulation of 1 million sows; gilt supply (as this was an important limiting factor during an eradication program in Denmark), and aggregated losses linked to a temporary halt on breeding progress. Using conservative assumptions, the total eradication costs were estimated at €1.8 billion. The long-term effects of an LA-MRSA eradication program in Danish pig production were uncertain and were therefore not taken into account in the analysis.

The small ruminant market network in Afar Region, Ethiopia; Implications for infectious disease transmission

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ABSTRACT

Objective: In the pastoralist production system of Afar Region, Ethiopia, sheep and goats provide milk and meat for the household, and are regularly sold to purchase cereals and other goods. One development approach to supporting pastoralist system resilience is to promote livestock trade, which also helps to meet urban demand for animal-source protein. However, animal movement through markets increases the risk of disease transmission. This study aimed to describe the small ruminant market network in Afar Region.

Materials and methods: Two cross-sectional surveys were conducted in early and late dry season in 15 livestock markets, using structured interviews with traders, semi-structured and informal interviews, and observation. Thematic analysis was applied to qualitative data, and quantitative data was analysed descriptively and by social network analysis.

Results: Pastoralists sold a few animals every 1-3 weeks, moving animals on foot and returning unsold animals to the flock. Buyers ranged from people buying a few animals for slaughter in nearby towns, and traders transporting animals on foot or by vehicle for slaughter in more distant towns, re-sale in other markets, re-sale for export to the Middle East, or to supply highland export abattoirs. Network analysis showed that there were several components that were connected to markets and towns in the neighbouring Tigray, Amhara and Oromia Regions. There was a giant strongly connected component composed of central markets, towns and villages, which was larger in the early dry season than the late dry season, reflecting the greater volume of trade at that time. The network had small world properties which are considered to promote the occurrence of more rapid and widespread epidemics.

Conclusion: In conclusion, trading practices and the market network contribute to local and long distance disease transmission. The observed network provides information that can be used to understand the likely spread of infectious disease within and outside the region.

Key words: Pastoralism, livestock markets, infectious disease, mixed methods

Assessing financial costs of production diseases to pig farms

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ABSTRACT

Objective: Production diseases usually originate from a complex interaction of pathogens, animal genetics and environment. Although production diseases can have a substantial impact on farm economy, their overall impacts are not very well known. The goal of this study was to assess the costs of production diseases in pigs and to identify the most important production diseases economically.

Materials and methods: A systematic review of studies was first undertaken. Studies published during 1995-2015 were searched in electronic databases. The search resulted in 130 publications for review. Cost estimates were converted to per animal-basis, deflated to year 2014 and converted to euros. Second, stakeholders in five countries were enquired about the validity of received cost estimates and financial significance of various production diseases in pigs.

Results: Respiratory diseases were considered as economically the most important production disease in growers and fatteners. Financial losses due to porcine respiratory disease complex were estimated at about €6.8 per fattening pig produced by an affected herd (range €2 to €19). In sows, reproductive, locomotory and gastrointestinal disorders were the most important production disease categories economically. The costs of the complex syndrome 'Mastitis, Metritis and Agalactia' were estimated to range at least up to €95 per affected sow while the costs of lameness ranged from €145 to €180 per lame sow. Reviewed studies showed great case-by-case variation in the costs, and experts from different countries showed different tendencies in their responses regarding the importance of diseases.

Conclusion: Overall, respiratory, reproductive and gastrointestinal diseases were considered as the most important production diseases economically. The overall costs of production diseases in pigs may range up to €35 per pig.

Key words: FInancial loss, pigs, production diseases

Cost of porcine reproductive and respiratory syndrome virus at individual farm level – An economic disease model

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ABSTRACT

Objective: Porcine reproductive and respiratory syndrome (PRRS) is reported to be among the diseases with the highest economic impact in modern pig production worldwide. The aim of this study was to develop an epidemiological and economic model to determine the costs of PRRS for an individual pig farm.

Materials and methods: In a production model that simulates farm outputs, depending on farm type, farrowing rhythm or length of suckling period, an epidemiological model was integrated. In this, the impact of PRRS infection on health and productivity was estimated. Financial losses were calculated in a gross margin analysis and a partial budget analysis based on the changes in health and production parameters assumed for different PRRS disease severities. Data on the effects of endemic infection on reproductive performance, morbidity and mortality, daily weight gain, feed efficiency and treatment costs were obtained from literature and expert opinion.

Results: Nine different disease scenarios were calculated, in which a farrow-to-finish farm (1000 sows) was slightly, moderately or severely affected by PRRS, based on changes in health and production parameters, and either in breeding, in nursery and fattening or in all three stages together. Annual losses ranged from e.g. a median of 75'724 EUR (90% confidence interval (C.I.): 78'885–122'946), if the farm was slightly affected in nursery and fattening, to a median of 650'090 EUR (90% C.I. 603'585–698'379), if the farm was severely affected in all stages. The model is a valuable decision-support tool for farmers and veterinarians if a farm is proven to be affected by PRRS (confirmed by laboratory diagnosis).

Conclusion: The output can help to understand the need for interventions in case of significant impact on the profitability of their enterprise. The model can support veterinarians in their communication to farmers in cases where costly disease control measures are justified.

Integrating Economics into Field Epidemiology Trainings for Veterinarians: Thailand's experience

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ABSTRACT

Objective: The Regional Field Epidemiology Training Program for Veterinarians (FETPV) was established in Thailand in 2009 to strengthen the technical capacity of Veterinary Services in Asia to prevent and control infectious animal diseases. In order to keep the program updated, a regular and systematic evaluation takes place. This research documents the process and results of incorporating Economics into the Regional FETPV.

Materials and methods: As a result of the Regional FETPV evaluation, the Food and Agriculture Organization (FAO) in collaboration with the Department of Livestock Development, Thailand (DLD) developed a module on Value Chain Analysis and Basic Economic Tools, including case-studies so trainees can put their acquired skills in practice. After piloting the module with DLD staff, adjustments were made and the first trial for FETPV was incorporated in the "Outbreak Investigation Module" in November 2017. In December, FETPV trainees participated in a real outbreak investigation related with acute respiratory symptoms in dairy cattle in Ratchaburi province, during which they collected and analyzed economic data.

Results: The content of the module included: 1) introduction to value chains and animal disease control; 2) value chain data collection; 3) value chain data analysis, and; 4) tools for basic economic assessment. The training was structured by combining theory (2 morning sessions) with applications (2 afternoon sessions) by using the case-studies. During the outbreak investigation, trainees were able to estimate the costs associated with the outbreak, focusing on mortality and milk production losses. Such information can be used to assess the profitability of preventive measures, at the farm or community level.

Conclusion: The economics module developed for the Regional FETPV was successfully implemented. FETPV trainees applied economic methods during an outbreak investigation to produce key information for decision making and resource allocation. Moreover, trainees recognized the usefulness of better understanding the livestock value chains when responding to an outbreak.

Key words: Capacity building, economics, livestock, FETPV, Thailand

Comparative analysis of the financial viability of swine and poultry farms using conventional and tunnel ventilation technology in the Philippines

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ABSTRACT

Objective: There is a growing trend in the use of mechanical ventilation technology in farm operations in the Philippines but no substantive studies have shown empirical evidence on its financial viability. Through investment analysis, this study compared the feasibility of investing tunnel ventilation technology (TVT) for both swine and poultry.

Materials and methods: Relevant data in the analysis was obtained through interview with farm managers complemented with review of available production data and literature, and experts' opinion.

Results: Investment analysis with 20-year projection showed that for swine production, the Internal Rate of Return (IRR) for farm without TVT which is 164%, is higher compared to tunnel ventilated farm (TV farm) at 157%. In contrast, the Net Present Value (NPV) computed at different discount rates showed a higher value for TV farm (PhP 109.29M – PhP 125.98M) than conventional farm (PhP 93.07M – PhP 107.22M). Payback period for both is not significantly different at 1.61 and 1.64 years for conventional and TV farm, respectively. For poultry production, results showed higher values of IRR and NPV, and faster payback period for TV farm at 37%, PhP 30.57M – PhP 37.22M, and 3.66 years, respectively while for conventional at 31%, PhP 7.52M – PhP 9.37M, and 4.18 years, respectively. This can be explained due to a much higher production yield obtaining much higher returns despite the fact of higher investment for TV farm.

Conclusion: These very substantive results obtained through robust analysis can help aspiring farm entrepreneurs with their decision making as to which type of farming to invest in.

Key words: Investment analysis, tunnel ventilation, swine, poultry

Risk assessment for pleuromutilins in pigs – using European Medicine Agency's guidelines

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ABSTRACT

Objective: Treatment guidelines may encourage veterinarians to use effective antimicrobials with low probability of developing resistance of importance for human health. In Denmark, treatment guidelines for use of antibiotics in swine have recently been reviewed officially.

Materials and methods: As part of this, a risk assessment of use of pleuromutilins in pigs was done, inspired by guidelines, developed by European Medicines Agency (EMA).

Results: Livestock-associated methicillin resistant *Staphylococcus aureus* of clonal complex 398 (MRSA CC398) and enterococci were identified as relevant hazards. The probability of development of pleuromutilin resistance was high in MRSA CC398 (medium uncertainty) and low in enterococci (high uncertainty). A relatively small proportion of Danes has an occupational exposure to pigs and foodborne transmission was only considered of relevance for enterococci, resulting in an altogether low exposure risk. The human consequences of infection with pleuromutilin resistant LA-MRSA or enterococci were assessed as low for the public in general, but high for hospitalized and immuno-compromised persons. For MRSA CC398, the total risk was estimated as low (low uncertainty), among other due to the current guidelines on prevention of MRSA in place at Danish hospitals. Moreover, MRSA CC398 has a medium human-human transmission potential. For enterococci, the total risk was estimated as low due to low prevalence of resistance, low probability of spread to humans, low virulence, but no screening of hospitalized patients, high ability of acquiring resistance genes and a limited number of alternative antimicrobials (high uncertainty).

Conclusion: The assessment should be repeated, in particular if pleuromutilin consumption increases substantially, resulting in increased prevalence of mobile, easily transmissible resistance mechanisms. Continuous monitoring of pleuromutilin resistance in selected human pathogens should therefore be considered, including Linezolid resistance, due to a coupled resistance mechanisms. The advantages and disadvantages related to the EMA guidelines will be discussed, based upon the experience gained during the assessment process.

Key words: Antimicrobial resistance, treatment guidelines, risk assessment, pigs, One Health

Rapid risk assessment of exotic animal disease introduction

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ABSTRACT

Objective: To facilitate decisions on risk management for exotic animal disease threats, a rapid risk assessment tool (RRAT) was developed to quickly assess the ever-changing risk of animal disease introduction. The objective of the tool is to prioritize diseases for risk management and to identify high risk trade flows and source countries.

Material and methods: The RRAT has been designed as a relational database with the main databases in the tool describing: the worldwide occurrence of animal diseases, the level of trade for each pathway of introduction, and disease specific parameters to assess the relevance of each pathway. The tool calculates a semi-quantitative risk score for the probability of introduction of each disease, the results of which allow for prioritization. The RRAT has been parameterised to assess the introduction risk for the Netherlands by import of live animals for seven diseases, viz. African swine fever (ASF), Aujeszky's disease, bluetongue (BT), bovine tuberculosis (bTB), equine infectious anaemia (EIA), lumpy skin disease, and peste des petits ruminants.

Results: Preliminary results indicate that bTB currently has the highest risk of being introduced. The risk of all other diseases is far lower with BT ranking second and EIA third. Based on legal trade in live animals only, the introduction risk of ASF was very low, despite its presence in Eastern Europe. However, the rank of this disease might change if other pathways would be included in the tool.

Conclusion: The RRAT is a powerful tool to quickly analyse the introduction risk of a multitude of animal diseases. Inclusion of additional pathways will increase the reliability of results, especially when import of livestock is banned from infected areas.

Key words: Import risk assessment, semi-quantitative risk score, ranking

So many risk organisms, so little time – building a framework for the New Zealand dairy industry to effectively assess biosecurity risks

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ABSTRACT

Objective: Recent incursions of exotic organisms into New Zealand and other countries highlight the importance of the systematic evaluation of different biosecurity hazards. Risk evaluation supports priority setting and resource allocation towards those organisms that pose the highest risk. To provide a structured and transparent basis for biosecurity decision-making in the New Zealand dairy industry the Dairy Biosecurity Risk Evaluation Framework (D-BRiEF) was developed.

Materials and methods: Hazards were identified via structured processes and include not only organisms that are the causative agents of cattle disease but also exotic plant and insect species that can negatively impact on the industry. A probability-impact model was then used to assess included hazards. The model accounts for the probability of entry of the organism, the expected between and within herd prevalence as well as on-farm impacts such as drop in milk production and the reproductive ability of affected animals.

Results: A total of 24 animal disease hazards have been included in the framework to date. Results generated provide a strong proof of concept for D-BRiEF and initial framework outputs have already been utilised during the recent incursion of Mycoplasma bovis into New Zealand. Further to the quantitative results a repository of qualitative impacts has been collated including the organism's ability to affect human health and an assessment of its disease vectors.

Conclusion: The development process has revealed the value of a multidisciplinary ranking exercise for preparedness through providing a standardised and industry-tailored information source on the plethora of biosecurity risk organisms New Zealand is exposed to. Results of the framework are interpreted in terms of priority groups and relative risks posed by different hazards rather than as absolute rankings, to address coming shortcomings of ranking approaches and to provide decision-makers with a multidimensional assessment of each hazard.

Key words: Biosecurity, risk analysis, prioritisation, exotic disease, dairy

Untangling farm management risk factors for bovine viral diarrhoea virus infection using Bayesian network modelling

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ABSTRACT

Objective: Many studies have used standard multivariable regression to explore risk factors for Bovine viral diarrhoea (BVD) infection for planning national disease control programmes. However, risk factors for BVD transmission are generally highly correlated farm management factors and traditional statistical approaches may restrict our understanding of BVD epidemiology. In the current study, we applied a multivariable logistic regression model and Bayesian network (BN) modelling to 1) investigate risk factors for BVD under New Zealand pastoral farming conditions and 2) compare and contrast the inferences that can be made about BVD epidemiology from the two different statistical modelling approaches.

Materials and methods: We used data collected from 304 cattle herds in New Zealand during 2015/2016. Blood samples from 15 heifers from each farm were pooled and analysed with an antibody ELISA test to classify BVD virus exposure status. Farmers were administered a survey which contained questions about 19 farm management risk factors. Based on univariable screening, the multivariable logistic regression model was created by a backward stepwise selection method. For BN modelling, an optimal network structure was identified using a random restart greedy hill-climbing method.

Results: The data showed that 57/116 (49.1%) beef and 95/188 (50.5%) dairy farms were likely to be actively infected with BVD virus. Between-herd nose-to-nose contact was a significant risk factor in multivariable logistic and BN modelling approaches. Moreover, BN showed that the between herd contact was significantly associated with the number of neighbouring farms and the frequency of sharing cattle yards. Different risk factors between beef and dairy farms were also identified using BN modelling.

Conclusion: Compared with other countries, over the fence contact appeared to play a more important role in New Zealand pastoral-based production systems and should be considered when developing a national BVD control programme.

Key words: Bovine viral diarrhoea, Bayesian network analysis (BN), logistic regression, risk factor analysis, farm management, disease transmission

The highs and lows of maintaining risk assessments over time: lessons learnt from 14 years of the BSE-Control risk assessment

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ABSTRACT

Objectives: There are constant pressures to re-evaluate surveillance and control measures during disease eradication to ensure they are fit-for-purpose and proportionate to risk. Quantitative risk assessments (QRAs) can be maintained to inform government decisions on proposed legislative changes. Bovine Spongiform Encephalopathy (BSE) in Europe has had a long eradication phase and therefore the associated QRAs have had an unusually long lifespan for such models, resulting in the opportunity to learn lessons for effective long term maintenance.

Materials and Methods: The BSE-Control risk assessment has been developed and maintained over the last 14 years to investigate the impact of variations in the age and risk stream of cattle being testing and which high risk tissues are removed at an abattoir. Outputs include the number of infected animals detected by surveillance and the amount of infectivity entering the food chain. A lessons learnt review was recently carried out by the analysts tasked with updating and maintaining the QRA.

Results: The QRA has met a number of challenges over the years to remain useful. These have been associated with staff turnover, legacy code issues, version control, system instability, mission creep, over-reliance/confidence in absolute outputs and long-term availability of input data. Advantages include the availability to carry out reactive work quickly and cheaply. It also enabled the complex combinations and changes to surveillance and control measures to be temporally mapped into an eradication timeline. As eradication is in sight, it would have been beneficial to have established the conditions under which the QRA should be retired.

Conclusion: Long term maintenance and updating of QRA's can be daunting but extremely rewarding. Regular communications with the policy customer and risk managers are essential to ensure the outputs remain fit for purpose. The resources required for re-coding and overhaul of complex legacy QRAs should not be underestimated.

Key words: Bovine spongiform encephalopathy, prions, legacy models, risk assessment

A Qualitative Risk Assessment for Re-introduction of Rabies into Rabies-free Areas of Bhutan

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ABSTRACT

Objective: Bhutan has eliminated rabies from its northern and central regions. However, rabies remains endemic in the South and incursions are reported from other parts of Bhutan that share a porous border with the neighboring states of India. Anthropogenic factors such as increasing human settlements along highways, increased animal transportation, and the complex and changing human-pet relationship have increased the likelihood of rabies reintroduction from endemic areas to the rabies-free areas of the country. The objective of this qualitative risk assessment was to estimate the risk of rabies re-introduction and to identify the most effective risk mitigation options.

Materials and methods: The assessment was conducted for three risk pathways under scenarios in which the current risk mitigation measures were in place and in which no risk mitigation measures were in place. They were pet dog pathway, stray dog pathway, and cattle pathway. The likelihood of an event occurring was assigned using available literature. Where gaps in knowledge existed, expert opinion was used.

Results: Under the scenario in which no risk mitigation measures were in place, the risk of rabies reintroduction was estimated to be medium for the stray dog pathway with a low level of uncertainty, low for pet dog pathway with a low level of uncertainty, and very low for the cattle pathway with a medium level of uncertainty. When current risk-mitigation measures were included, the risk of rabies reintroduction was estimated to be very low for the stray dog pathway with a medium level of uncertainty, low for pet dog pathway with a low level of uncertainty, and extremely low for the cattle pathway with a medium level of uncertainty.

Conclusions: The risk of rabies re-introduction through all the pathways was greater than negligible. These findings highlight the importance of maintaining and enhancing current risk mitigation measures to prevent re-introduction of rabies into rabies low-risk areas.

Key words: Qualitative risk assessment, rabies, cattle, incursion, Bhutan

Spatial risk analysis of Avian Influenza in the French West Indies and French Guiana

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ABSTRACT

Objectives: The Caribbean region, at the crossroads of the Americas with multiple trade partnerships in this hemisphere and located along several migratory flyways, is exposed to Highly Pathogenic Avian Influenza (HPAI). After the 2015 HPAI epizootics in the US, the Caribbean Animal Health network (CaribVET) has launched a regional capacity-building plan on HPAI risk assessment and risk mapping to optimize epidemiological surveillance in 12 CARIFORUM countries. Three French Departments (Guadeloupe, Martinique and French Guiana) where poultry production is poorly developed and precarious and with under-staffed veterinary services joined this program. Qualitative risk assessment is required in the French departments to enhance Avian Influenza surveillance system through the development of risk-based surveillance protocols and to protect the local production.

Materials and Methods: An integrated method incorporating qualitative risk analysis, mapping and livestock movements under development by Squarzoni-Diaw *et al.* was used to do a spatial risk assessment of AI virus introduction, establishment and spread at the sub-communal level. The likelihood of introduction was estimated from international wild and domestic bird's movements (legal and illegal). The likelihood of establishment and spread was estimated using risk factors such as poultry density, fighting cock activities, biosecurity measures, and accessibility. Those factors were collected from literature and discussed with local and international experts. Finally, these different risks assessment were combined to produce AI occurrence risk maps.

Results: Several maps were produced for each department with 4 risk levels: very high, high, low or negligible. Discussion about the results were organized with experts and with the Chief Veterinary Officer of each territory.

Conclusion: This study will be completed by June 2018. AI occurrence risk maps could be further used to set up national HPAI emergency plans, risk-based surveillance protocols, or to target awareness campaigns for poultry stakeholders and veterinary services.

Key words: Avian Influenza, risk analysis, GIS, wild birds, trade, animal movements

Understanding the use of antimicrobial susceptibility testing by French veterinarians to better interpret antimicrobial resistance surveillance data

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ABSTRACT

Objective: The aim of this study was to provide a better understanding of veterinarians' motivations and role-players' influence concerning the choice of whether to ask for an antibiogram in the bovine, swine, poultry and equine sectors.

Materials and methods: Semi-structured interviews with veterinarians were conducted in France. Thematic analysis was used to analyse transcripts. In all, we surveyed 66 veterinarians. Recourse to AST varied between animal sectors: it was quasi-systematic in poultry, frequent in swine and rare in both bovine and equine sectors.

Results: The use of AST was multifactorial, 46 factors gathered into 11 categories were identified, among which the epidemiological aspects of the disease, the working habits of professionals, their awareness of AMR and the financial aspect. The factors could act as incentives or disincentives and we identified levers to facilitate the use of AST in veterinary medicine. Some factors were common to the animal sectors, while others were specific to one sector (the seasonality of the use in the bovine sector for instance). The decision making to use this test was influenced by relationships between stakeholders, especially veterinarian-customer and veterinarian-laboratory.

Conclusion: Considering a network to collect AST results as the best tool to monitor AMR, our findings are essential to properly analysis such surveillance data: the specificity of animal sector should be taken into account before making any comparison, by stratifying AST results on species, type of production and diseases at best. Overall, providing a comprehensive understanding of the underpinning incentives and reasons behind the recourse to AST, our results will be useful in guiding representative veterinary bodies and regulatory authorities during their decision-making, communication and regulation choices.

Key words: Antimicrobial susceptibility testing, veterinarian, antimicrobial resistance, surveillance, sociological survey

Surveillance of viral disease with total coverage: Money well spent?

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ABSTRACT

Objective: New legislation on Pancreas disease (PD) in Norway requires that all salmonid fish farms must be tested for Salmonid alphavirus (SAV) every month. Negative and positive findings are reported to the National Reference Laboratory (NRL). The total monthly costs for the industry for this sampling equals around 150 000€, or 1,8 mio € per year. The objective of this study is to find out whether this money is well spent with regards controlling for PD.

Materials and method: Monthly reporting of analysis for SAV is used for determining the prevalence of SAV in broodstock, hatcheries and grow-out farms in areas with different status for SAV (endemic vs. non-endemic). The sample size used in this surveillance (20 fish) is designed to detect a prevalence of minimum 10% in one sampling, but we are developing a model in which we estimate how repeated samplings are used to increase the detection limit. The model will then be used to provide recommendations for revision of the surveillance program.

Result: Approximately 5000 samples from each area (endemic and non-endemic) has been submitted for analysis every month since the surveillance was implemented in September 2017. In the first 6 months of the program, the overall prevalence of SAV was 5,5%, and the prevalence in grow-outs, hatcheries and broodstock were 7,5%, 0,05% and 8,8%, respectively.

Conclusion: Preliminary results suggests that more certainty about the occurrence of SAV could be gained if the surveillance was differentiated between areas and type of production. The final model will be presented at the conference.

Key words: Surveillance; Aquatic epidemiology, Prevalence, Modelling, cost-benefit

Disease monitoring and reporting among Australian beef and sheep producers: A cross-sectional study of levels of responsibility for surveillance

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ABSTRACT

Objective: As part of a project to improve animal health surveillance, a cross-sectional study was undertaken to characterise the vulnerability of Australian livestock producers to emergency animal diseases.

Materials and methods: An online survey was developed using a vulnerability framework and distributed through government and industry groups nationally. This paper explores current levels of trust around animal health monitoring and reporting within the beef and sheep industries. Data were analysed descriptively and logistic regression analysis was used to characterise producers.

Results: A total of 234 beef and 194 sheep producers completed the survey. The majority of beef and sheep producers identified themselves as being responsible for observing their animals (93%) and reporting unusual signs of disease in their animals (92.5%). Self-responsibility was lower for disease detection, with 20% producers identifying others as responsible. No significant differences were observed between beef and sheep producers. Of a total of 915 beef cattle health problems recalled in the last 12 months (average 5 per respondent), 33.9% (average 2 per respondent) were reported to a private or government veterinarian. When asked about actions in the event of unusual signs of disease, 90% of beef and 82% of sheep producers, ranked contacting private veterinarians in their top five activities. The majority of beef and sheep producers reported high levels of trust in private veterinarians (85%), with 65% producers reporting high trust with their government veterinarian.

Conclusion: This study indicates that producers perceive a high level of self-responsibility for observing their animals and reporting diseases. However, their perceived responsibility in detecting diseases is lower. In addition, the level of reporting of animal health problems is low. Findings from this study suggest that producer practices in relation to passive surveillance could be improved and there is potential for enhancing surveillance with more effective producer – veterinarian relationships.

Key words: disease reporting, animal health surveillance, beef and sheep producers, Australia

Antimicrobial usage surveillance of animal health in Indonesia to address antimicrobial resistance

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ABSTRACT

Objective: Antimicrobials have been widely used for treat infections, preventions, and growth promoters. However, these practice resulting the emergence of resistant bacteria and the widespread of AMR strains. The objectives of this study is to create a baseline information of AMU in animal health in Indonesia by using iSIKHNAS.

Materials and Methods: iSIKHNAS antibiotic treatment data from 2014 to 2016 were extracted, animal health officer data and Index of animal drugs 2016 were included in the data. Data analysis was done in two stage, stage one was for all species and stage two was for cattle species only. Data analysis consisted of description of AMU in animal health, syndromes associated with AMU, identifying the actors, and veterinary critically important antibiotics (VCIA) analysis.

Results: There were 125893 treatments for all animal and the total data by year increased from 2014 to 2016 while the monthly antibiotic usage was always increasing from September to December. The higgest number of species treated was found in cattle with 70498 (66%) treatments and 93791 total cattle treated. 90.93% of antibiotic used classified as VCIA, oxytetracyclin was the most common active molecule used in the treatment with 58,73% and tetracycline was the most common antibiotic class used with 60%. Bacterial disease were treated with antibiotic only on 11.36% of treatments and most of antibiotic were used for non bacterial disease. 32.52% of antibiotic treatment were provided by veterinarians and 63.47% by paravets, there were 876 veterinarians and 1710 paravets.

Conclusion: Animal health officer showed good correlation for defining diagnosis from clinical signs, however the problem is factors drug of choice. Important informations found were AMU was commonly used to treat non bacterial disease, problem of actors knowledge and limited number of veterinarian, and most of antibiotic used classified as VCIA.

Key words: Antibiotic, surveillance, iSIKHNAS, animal, Indonesia

Surveillance without intervention: Is there a value?

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ABSTRACT

The purpose of surveillance is to support evidence-based decision-making and – ultimately – to improve public health, animal health, the environment, and/or society as a whole. Surveillance continues to be promoted, but with little consideration of how the generation of data will provide feedback on interventions. This loop is closed when data are collected to check whether a specific intervention achieved the expected change in disease or hazard occurrence. Economic analyses should include both intervention and surveillance costs and benefits. We considered examples where the integration of surveillance in the hazard mitigation process is more or less successfully achieved. Success stories can be found among disease control programmes (e.g. Salmonella in poultry, bovine spongiform encephalopathy). Examples where surveillance currently remains largely detached from intervention include Campylobacter and antimicrobial resistance. Significant resources are needed to quantify the links between surveillance and interventions and is particularly challenging for hazards that are complex by nature. The economic value of surveillance for early detection is particularly hard to quantify as consequences of missed incursions may remain unknown. We lack examples of surveillance systems designed to determine the economic impact of a health issue. We also argue that the current single-disease focus of surveillance is insufficient and that the scope of surveillance needs to be generally broadened to consider animal health in general. This would allow for the prioritisation of hazards and an assessment of the resource allocation efficiency in existing control programmes. We conclude that data on disease, economic costs and behaviour practices should be integrated to comprehensively inform animal health decision making. The systematic use of formal evaluation of both technical effectiveness and economic benefits of surveillance should help increase the general utility of surveillance and the promotion of health and wellbeing.

Key words: Animal health, economics, food safety

An evaluation matrix for One Health surveillance systems - Application to the surveillance of antibiotic resistance in Vietnam

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ABSTRACT

Objective: The One Health (OH) approach is strongly encouraged for the surveillance of health hazards at the human-animal-environment interface. It is expected that collaborations across sectors and disciplines should improve the surveillance performance and cost-effectiveness. However, existing surveillance evaluation tools do not allow to assess those collaborations. This study aimed at developing a matrix for the evaluation of the appropriateness and effectiveness of collaborations. We applied it to the OH surveillance system for antibiotic resistance (ABR) in Vietnam.

Materials and methods: Based on the results from a previous study about characterisation of OH surveillance and on attributes defined in existing evaluation tools, we developed specific attributes for the assessment of collaborations. These attributes were submitted to a panel of experts in surveillance for review and validation. We finally applied them to evaluate inter-sectoral and inter-disciplinary collaborations in the OH surveillance of ABR in Vietnam.

Results: This study first led to the development of an evaluation matrix specific to collaborations. We identified 38 relevant attributes split into 5 distinct categories. For each attribute, we identified appropriate methods to measure and evaluate them.
The evaluation of the OH surveillance system for ABR in Vietnam demonstrated that the collaborations currently in place could be improved to meet fully the surveillance objective.

Conclusion: The evaluation matrix we developed can be used standalone or combined with other evaluation tools to evaluate a OH surveillance system globally.

Based on the evaluation results obtained for the ABR surveillance in Vietnam, we proposed some recommendations to move towards a more effective model for OH surveillance organisation and operation.

Quantitative evaluation of the Scottish and Welsh surveillance systems for bovine Brucellosis

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ABSTRACT

Objective: The Scottish and Welsh surveillance systems for bovine Brucellosis were evaluated using a stochastic model. The surveillance system sensitivity (SSe) and the confidence in freedom (PFree) adjusted (PFreeAdj) for the probability of disease introduction from abroad (PIntro), were estimated quarterly (data 2016).

Materials nad methods: Different surveillance components (representing population strata of each country) were evaluated. Beef herds not tested at the regional laboratories (B-NoTest herds) were still considered as stratum where infected cattle could be imported and missed. Information on components' coverage, came from National datasets on: milk, abortion and Post Import Calving testing. Alternative design herd prevalence (Phs) were used, and the relative risk of herd infection per stratum (RRs) was assessed using the accompanying stochastic model. Then the risk based importance of each component was evaluated.

Results: In Scotland with Ph 0.2% ($\approx$ 24 infected herds, Council Directive 64/432/EEC), the quarterly median SSe was $\approx$ 100.0%, while the PFreeAdj was > 98.0%. With Ph 0.01% (1 infected herd), the median SSe ranged from 63.0 to 65.8%, while the PFreeAdj ranged from 72.5 to 74.0%. Both outputs were > 94.0% at Ph $\geq$ 0.03% (three herds).
In Wales with Ph 0.2% ($\approx$ 23 herds), the quarterly median SSe was $\approx$ 100.0%, while the PFreeAdj was $\geq$ 99.0%. At Ph 0.01% (1 herd), the median SSe ranged from 84.2 to 85.2%, while the PFreeAdj ranged from 85.6 to 86.5%. Both outputs were > 96.0% with Ph $\geq$ 0.02% (2 herds). In both countries, the component based only on milk testing showed the highest sensitivity.

Conclusion: In Scotland, confidence in freedom was lower due to: higher PIntro and lower proportion of milk tested herds (lower SSe). Additional risk based surveillance in beef herds could improve early detection in both countries; because the first infected herd was more likely allocated by the model within B-NoTest stratum.

Key words: Bovine brucellosis, surveillance system sensitivity, confidence in freedom

Companion animal infectious disease surveillance: How much is enough?

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ABSTRACT

Objective: Taking advantage of a passive, pet animal surveillance system operating since 2010 in Australia, the effect of historical data accumulation on the system's ability to describe current disease patterns was explored. Reports of parvovirus in dogs were used as a case study.

Materials and methods: Records of all parvovirus cases reported (n=7,150) between 2010 and 2014 were extracted from the surveillance database. For analysis only unvaccinated cases confirmed by diagnostic testing (predominantly ELISA) were included. Temporal (weekly) and spatial distributions of reports during 2014 were described by an autoregressive model and a permutation test, respectively. The ability of parvovirus reports during 2010, 2010-2011, 2010-2012 and 2010-2013 to accurately predict this observed data was estimated.

Results: Between 2010 and 2014, 3,280 confirmed parvovirus cases were reported as 2,720 events throughout Australia (561 cases and 461 events in 2014). In 2014, parvovirus was best described by reports in the previous 2-3 weeks, and spatial clusters included 47 postcodes. The 2014 surveillance data was best predicted (r_{SP} 0.67-0.77) by data reported in 2013; using more historical data did not improve predictions. Clustered postcodes in 2014 were best predicted using data from 2010–2011.

Conclusion: Despite its importance to animal and human health, companion animal infectious disease surveillance is under-developed and poorly researched. In particular, alert thresholds are undefined, hampering the use of existing systems for identifying disease clusters and implementing disease control. This study demonstrates the potential value and feasibility of companion animal infectious disease surveillance, and the case study undertaken suggests that only 1-2 years' data are needed to provide useful surveillance outcomes.

Key words: Infectious disease surveillance, parvovirus, spatio-temporal, model, Australia

Achieving an optimal surveillance portfolio for zoonoses in west Africa - the Ebola example

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ABSTRACT

Objective: To develop and apply an economically optimal integrated surveillance portfolio to enhance early detection of Ebola virus circulation in Liberia, West Africa.

Materials and methods: A web-based suite of Human and ANimal DIsease surveillance tools, HandiTools, was developed to evaluate surveillance options for early detection of Ebola in wild and domestic animals, and potential crossover to people, in the various ecological environments found across Liberia. Spatial mapping of factors relevant to the distribution of the virus and reservoir and spillover hosts of Ebola was undertaken to produce a risk landscape. Potential spread and detection of virus was modelled on this landscape, relating surveillance intensity and coverage to the likely distribution of the virus. Multiple surveillance methods could be applied in animals and people, and options were evaluated in the spatial model for time to detection of virus, and benefit/cost of risk-based and/or classical sampling strategies, using the economic analysis tool HandEcon. All possible portfolios combining different mixes of strategies were assessed using the optimisation procedure OptiSurv, to identify the top ranked portfolios.

Results: It proved possible to obtain eleven different spatial layers, of which altitude, landcover type, livelihood type and landscape fragmentation were used to create the risk landscape layer. Animal distribution was then considered, and different sampling methods in wildlife, dogs and people were assessed for their potential to detect Ebola virus. Optimisation was then used to rank potential surveillance portfolios to detect a future Ebola incursion into Liberia.

Conclusion: This was a further step in developing a method for identifying optimal surveillance strategies for emerging diseases. The procedure was applied in a country with limited available data sets, and will next be applied to Lassa Fever, another important zoonosis in West Africa.

Key words: Ebola, surveillance, zoonoses, economics, optimisation

Association of *Fasciola gigantica* co-infection with bovine tuberculosis infection and diagnosis in a naturally infected cattle population in Africa

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ABSTRACT

Objectives: Bovine tuberculosis (bTB) remains a major livestock and public health problem in both high and low-income countries. With the current absence of an effective vaccine, control in cattle populations is reliant on regular testing and removal of test positive animals. However, surveillance and control are hampered by imperfect diagnostic tests that have poorly described properties in naturally infected populations. Recent research in cattle co-infected with the temperate liver fluke, *Fasciola hepatica*, has raised concerns about the performance of the intradermal skin test in high fluke incidence areas. The objective of this study was to explore the impact of co-infection with the tropical liver fluke, *F. gigantica*, on bTB infections and diagnostic performance of the interferon-γ based diagnostic tests.

Materials and methods: A sample of 762 cattle slaughtered at Ngaoundere Municipal Abattoir in the Adamawa Region of Cameroon were examined for evidence of bovine TB-like lesions and liver fluke pathology. Samples were collected for culture and a whole blood samples were collected and screened using the 'Bovigam' interferon-γ assay.

Results: We observed strong evidence that fluke infected non-Fulani breeds, after adjusting for breed, age and sex, were at increased risk of having bTB-like lesions. Further, we observed a reduced variation in the IFN-γ levels in fluke infected animals compared to non-infected animals, which after controlling for demographic factors resulted in a reduced likelihood of fluke infected animals testing positive by the IFN-γ test. Finally we explored factors associated with IFN-g false negative results compared to the presence of bTB-like lesions. There was a complex interaction between cattle breed and fluke status. Fulani cattle had a higher risk of having a false negative result compared to the non-Fulani breed group. Further, the non-Fulani breed cattle had an increased risk of being false negative if also co-infected with liver fluke.

Conclusion: Co-infection with the tropical liver fluke *F. gigantica* appears to impact bTB infection risk in non-Fulani cattle increasing their risk of having bTB lesions and by implication infection. Coinfection also increases the risk of false negative IFN-g results (due to dampening of the IFN-g response) in non-Fulani cattle. In comparison, Fulani cattle had a higher risk of having bTB lesions and of false negative results compared to the non-Fulani cattle but these risks did not appear, in this population, to be affected by coinfection with liver fluke.

Key words: Bovine tuberculosis, *Fasciola gigantica*, Africa, Cameroon, cattle

Qualitative comparison of BVDV control programmes in Europe to substantiate freedom from infection

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ABSTRACT

Objective: Several European countries have implemented control or eradication programmes for non-regulated diseases such as bovine viral diarrhoea virus (BVDV). However, the diversity in such control programmes (CP) creates difficulties for intra-community trade given that the probability of freedom from e.g. BVDV will differ between countries. This poses a risk of potential movement of BVDV into free regions. An understanding of equivalence with respect to disease freedom is important when seeking to facilitate interstate animal movements, whilst also managing the risk of infection. In this project, six European countries collaborate to develop an output-based approach to assess and compare confidence of freedom resulting from different CPs. The aim was to qualitatively compare the confidence of freedom resulting from different BVDV CPs.

Materials and methods: An existing tool for harmonized description of surveillance programmes (the RISKSUR tool) was used to collect information from each participating country about BVDV status, demographic information and surveillance activities for BVDV, and expanded to also include control measures of the BVDV CPs.

Results: The design of BVDV CPs differed considerably as well as country demographics (Table 1). The aspects of the different CPs were grouped in three main topics: context (i.e. BVDV status, occurrence of risk factors), actions to obtain a BVDV free status and measures to monitor the free status.

Conclusions: The variation in context was larger than the variation in control programmes, resulting in different risk classifications for territories. The context of a country or territory is crucial information for an outcome-based comparison of BVDV CPs.

Key words: BVDV, surveillance, control programmes, non-regulated diseases, disease freedom

An innovative Surveillance analysis Tool for Outcome-based Comparison of FREEdom from infection in heterogeneous control programs

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ABSTRACT

Countries differ in existence, stage of eradication and design of control programs for non-regulated diseases. When freedom from infection is achieved, safe trade is essential to protect that status. The aim of STOC free, a collaboration between six countries, is to develop and validate a framework that enables transparent and standardized comparison of confidence of disease freedom for control programs across herds, regions or countries. The framework consists of a model (STOC free MODEL) combined with a tool to facilitate the collection of the necessary parameters (STOC free DATA). All actions taken in a control program will be included in a Bayesian model, which needs prior distributions for most parameters. Data for the distributions can be obtained from databases of control programs, demographic data and contact structures between herds. In addition, frequency of occurrence and risk estimates for factors that influence either the probability of introduction or delayed detection of the infection will be included in the model. Bovine viral diarrhea virus (BVDV) is used as an example disease. Many countries have control programs in place for this complex and detrimental disease with wide differences between application of vaccinations, combinations of diagnostic tests applied, frequency of testing and target groups. Although BVDV will be a thorough test of the initial developed framework, it should be generic enough to be adaptable to control programs for other diseases. With the introduction of the new Animal Health Law (AHL), it is anticipated that assessments of the performance of control programmes will progressively change towards output-based measures. The STOC free framework will support the AHL by providing a single general framework, adaptable to multiple diseases, which aims to enhance the safety of trade.

Key words: Surveillance, control programmes, endemic diseases, disease freedom

Controlling respiratory disease through biosecurity measures - The Norwegian control program for bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCV)

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ABSTRACT

Objective: Bovine respiratory disease is the dominating cause of veterinary-treated disease among calves, and an important cause of antimicrobial use in dairy herds. Bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCV) are both endemic in Norway and cause financial losses as well as reduced animal welfare. A voluntary control-program was therefore launched in 2016 by a joint cattle industry. The aim of this presentation is to outline the program and to present results from the first national screening for BRSV and BCV.

Material and methods: The control-program is based on classification of herds as antibody-positive or –negative using a multiplex immunoassay (MVD-Enferplex BRSV/BCV multiplex) ELISA. Initial classification of dairy herds was based on bulk tank milk testing, while pooled serum samples of young stock (5 individuals over 6 months of age) are used in beef herds or for follow-up samples in herds with a positive bulk tank milk test. The core principle of the program is to protect antibody-negative herds from introduction of virus through biosecurity measures, and the current classification of all herds is available through the Norwegian Dairy Herd Recording Scheme. Antibody-negative herds are encouraged to only purchase animals from other negative herds. Animals from negative and positive herds are transported separately, and the truck-driver is encouraged to not enter the barn at pick-up. All producers are encouraged to have biosecurity barriers in place and must provide boots and change of clothes for visitors, including veterinarians.

Results: The results from the initial bulk tank screening showed that of the dairy herds tested in March 2016, 2106/7895 (24.6%) were test-negative for BRSV and 1298/7896 (16.4%) for BCV. The herd-level prevalence varied by geographical region, with higher proportion test-negative herds in the north.

Conclusion: The first biosecurity-based national control program for BRSV and BCV is ongoing in Norway.

Key words: control program, cattle, bulk tank milk testing, biosecurity

Quantitative risk analysis for the introduction of Bovine Tuberculosis through infected cattle in Silvopastoral systems

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ABSTRACT

Bovine tuberculosis (BTb) is a chronic progressive illness of cattle and represents a serious hazard for human population because it can be transmitted through air or unpasteurized milk and milk products. Continuous efforts to control and eradicate BTb are observed worldwide. In Mexico, prevalence of BTb is reliant upon on the regional application of a national program for BTb control and eradication. This program is based on the use of tuberculin tests with culling of reactors to declare negative (free of disease) herds. To assess the risk of introduction of BTb into the Silvopastoral (SPS) cattle farms from the Tepalcatepec valley in Michoacan State in Mexico, 6 scenarios were developed based on the application of the Mexican national program and traditional commercial practices. SPS farmers in Tepalcatepec valley share a similar location, production system, and BTb herd status (free of disease); these farms were therefore considered an epidemiological unit. Using the software @Risk®, and considering the regional prevalence and the characteristics of the tests applied, a stochastic model was developed to simulate scenarios for the introduction of BTb. The highest-risk scenario calculated in this study was from acquiring animals from unknown health status source herds without testing the animals prior to introduction to the purchasing herd (risk = 0.00251 or 1 success in 398 trials). Testing cattle with the Caudal Fold Tuberculin (CFT) test prior to movement decreased the probability of introducing false negatives (infected cattle that tested negative) into the SPS farms. Moreover, if the CFT and the comparative cervical tuberculin test (CCT) were applied in parallel, the probability of introducing false negative animals decreased to a negligible level (risk = 0.00001088 or 1 success in 91,911 trials), regardless of the health status of the source herd.

Key words: Risk analysis, bovine tuberculosis, Silvopastoral, Dual purpose cattle, Michoacan, Mexico

The role of tuberculin assays on naturally infected cattle in the Irish bovine tuberculosis eradication programme

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ABSTRACT

Objective: The purpose of this paper is to give an account of the procedures, and outline the role of assays carried out on naturally infected cattle in the quality control on the Irish Bovine Eradication Programme. Potency assay should be performed in the animal species and under the conditions in which the tuberculin will be used in practice (OIE). Ireland is perhaps unique in that it is one of the few countries which carries out routine tuberculin assay in naturally infected bovines as part of the quality control of the national bovine tuberculosis eradication programme.

Materials and methods: The potency of a tuberculin is estimated by comparing the size of the reactions, elicited by an intradermal inoculation, to the size of the reactions of a 'standard' tuberculin of known potency .The potency of three test bovine tuberculin PPDs are assayed in naturally infected cattle against the Irish National Standard (INS) tuberculin PPD with an assayed potency of 33,700 IU/ml. Each tuberculin PPD is used at two dilutions corresponding to protein concentrations of 1.0mg/ml and 0.2mg/ml. The study design was a randomized Latin square design, with each of 24 cattle receiving all tuberculins and dilutions. The cattle were injected at 4 sites on each side of the neck. The outcome measure was the increase in skinfold thickness at each site after 72 hours.
Results: The results are analysed using standard statistical methods for parallel-line assays (14), using the GLM procedure in SAS v9.1. Site of injection and side of the neck are included in the final model if significant ($P<0.05$). The 95% confidence limits for the relative potency are calculated according to Fishers' method. This analysis estimates the potency of the three routine issue tuberculin PPDs as compared to the Irish standard tuberculin PPD. Potency is expressed in IU/ml, based on the potency of the Irish standard at 1.0 mg/ml of 33,700 IU/ml as calibrated previously against the International Standard
Conclusion: OIE recommends that tuberculins are assayed in the population of animals in which the eradication programme is to be carried out, but due to practical difficulties in performing potency assays in cattle they are usually assayed in guinea pigs. However, ever since inadvertently using sub-potent tuberculin some years ago the routine assay of tuberculins in naturally infected cattle is regarded as imperative to the assurance of potency of tuberculins used in the Irish bovine tuberculosis eradication programme.

Key words: Tuberculin, Purified protein derivative, Tuberculosis, *M. bovis*, Potency

Quality Control of Purified Protein Derivative Tuberculins: Essential for Effective Bovine Tuberculosis Control and Eradication Programmes

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ABSTRACT

Bovine tuberculosis (bTB) diagnosis for control/eradication programs and live animal bTB-free certification uses tuberculin tests. Optimal results require Purified Protein Derivative tuberculin (PPD) of sufficiently high potency and optimal specificity to detect most infected bovines. Potency and analytical specificity of PPDs should be determined, in accordance with the OIE required method, from Finney (1978) i.e. bioassay in *M. bovis* infected and *M. avium* sensitised guinea pigs (GP) against the bovine/avian International Standard (IS) PPD respectively.

GP bioassay reflects potency differences in PPDs from different producers, and considerable inherent variability in immune responses within the GP model. Variability in potency/source of PPDs has implications for skin-tests and the bovine *in vitro* interferon-γ (IFN-γ) assay. Notwithstanding, GP bioassay inadequacies and differences that have always existed between PPDs from different producers, the intradermal skin-test has resulted in successful bTB control and eradication in many countries.

Increasing variability has been shown both within and, as to be expected given the variety of different GP models now in use, also between laboratories with a dwindling number of independent (national) reference laboratories able to routinely and adequately perform the GP potency assay. Hardly surprising therefore, that independent GP bioassays performed in accordance with the OIE required method on commercially available PPDs suggest a worrying disparity in quality uniformity with some commercially available PPDs showing sub-optimal potency.

Indeed, bovine PPD showing extremely low potency when assayed in *M. bovis* infected GPs and showing IFN-γ response for *M. bovis* infected cattle closely resembling the avian PPD response in the same assay, has been available commercially. Sub-optimal potency PPD of questionable specificity is of no practical use for the operation of bTB control programmes nor TB-freedom certification for cattle, products and/or herds. These findings unequivocally demonstrate that tuberculin purchasers need independent quality checks of manufacturers potency claims.

Key words: Tuberculosis, bovine tuberculosis, tuberculin, PPD, potency

Quantitative epidemiological analyses from a voluntary BVDV control program supporting policymakers in the transition to national eradication in the Netherlands

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ABSTRACT

Objective: Since 1997, in the Netherlands a voluntary control program for Bovine Viral Diarrhoea Virus (BVDV) in cattle is available, yet preparations were recently made for national eradication. To design a national BVD eradication program, the voluntary program was evaluated to answer specific questions posed by policymakers. In the voluntary BVDV control program, herds can obtain a BVDV-free status when all animals have been tested BVDV-free, and during the following 10 months all newborn calves are tested BVDV-free. Monitoring of the free status is performed by (1) biannual spot-testing, i.e. sera of five youngstock are tested for antibodies, or (2) testing all newborn calves for virus.

Materials and methods: Several analyses were conducted to answer the following questions: (i) what is the positive predictive value of the spot-test in detecting a persistently infected (PI) calf, (ii) how long do BVDV-free herds maintain their free status and what is the incidence of BVDV-free herds experiencing reintroduction of BVDV, (iii) which factors determine the risk of reinfection in BVDV-free herds? Diagnostic data was available for all herds that participated in the voluntary program between 2007 and 2016, as well as records of cattle movements and geographical coordinates of all livestock enterprises in the Netherlands.

Results: Following a positive spot-test, in on average 49% of these herds a BVDV-positive animal was detected. Survival analyses showed that during a ten-year period, free herds maintained their status for 8.6 years on average and the yearly incidence of BVDV infections in free herds decreased from 7% in 2007 to 4% in 2016. Logistic regression analyses revealed that presence of non-BVDV-free neighbouring cattle herds and purchase of pregnant cattle are risk factors for a breakdown in a BVDV-free herd.

Conclusion: The results of this study have guided policy makers in the prioritization within the design of the national BVDV eradication program, which is effective in dairy herds as of April 1, 2018.

Key words: Bovine viral diarrhea virus, eradication and control, surveillance, risk factor analysis

Building the business case for bovine viral diarrhoea virus (BVD) eradication in New Zealand

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ABSTRACT

Objective: Bovine viral diarrhoea virus (BVD) is an endemic disease that costs affected New Zealand beef and dairy farmers more than $150 million annually in direct production losses. Although eradication is technically feasible, there are still many unanswered questions about the most cost-effective means of applying the available control measures under New Zealand pastoral farming conditions. In particular, it may be difficult to break the BVD cycle in beef herds since most calves are not handled until weaning at approximately 6 months of age after persistently infected (PI) animals have already potentially exposed susceptible breeding dams during the mating period. Furthermore, many beef herds in New Zealand are also co-grazed with sheep, which may be serving as reservoirs for BVD. Recognizing the importance of controlling BVD, the Ministry for Primary Industries (MPI) joined forces with industry and academia to provide over $850,000 in funding to support the BVD Free New Zealand project.

Materials and methods: This is a three-year initiative that launched in July 2017 to build the business case for BVD eradication. Over the first two years, we are conducting a number of field studies to fill in knowledge gaps around the epidemiology and economics of BVD in cattle herds and a national campaign to encourage farmers and veterinarians to share their opinions towards BVD through a novel, interactive project website. Data from these studies will be integrated into a computer simulation model of BVD transmission within and between cattle herds to explore the relative costs and benefits of different national eradication programmes.

Results: The results will be presented as a business case to industry in July 2019 so that New Zealand can select the most economically and socially acceptable option moving forward. In this presentation, we discuss the progress, findings, and challenges to date as the project has continued to evolve.

Key words: Disease Control, modelling, economics, dairy cattle, beef cattle

Risk-based strategic plans for five priority diseases in the Palestinian Authority, integrated

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ABSTRACT

Objective: Risk-based control strategies for five priority animal diseases (PDs) were developed at the request of the Palestinian Authority veterinary services and with the support of the Food and Agriculture Organization of the United Nations (FAO) through its SPS programme.

Materials and methods: Over two years (2015-2017), with seven in-country workshops and online support, risk-based strategic plans (RBSPs) were developed following the approach advocated under the Progressive Control Pathway for FMD control (PCP-FMD). A prioritization exercise was undertaken to identify the PDs. A taskforce was established for each PD. Each taskforce analysed the current situation, identifying risk hotspots and gaps. Subsequently, using a framework of considering a) surveillance, b) outbreak response and c) prevention, they defined strategic objectives, component objectives, tactics and activities. Finally, monitoring and evaluation (M&E) indicators, targets and means of verification were established.

Results: Bluetongue, lumpy skin disease, scrapie, peste des petits ruminants and salmonellosis in poultry were identified as the PDs. Despite the different species and modes of transmission involved, substantial aspects of each control plan overlapped with the others. Thus, the disease-specific RBSPs were complemented by an overarching chapter addressing issues related to capacity building of the veterinary services, private and public stakeholder engagement and M&E.

Conclusion: The development and implementation of RBSPs are intended to ensure effective use of limited resources for animal disease control. As substantial aspects of disease control relate to overarching issues, an integrated approach including multiple priority diseases is useful and efficient.

Key words: Progressive control pathway for FMD control (PCP-FMD), risk-based, integrated disease control

Insight from epidemiological and animal movement data on bovine paratuberculosis infectious dynamics at a regional scale

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ABSTRACT

Objective: Paratuberculosis, caused by *Mycobacterium avium* subsp. *paratuberculosis* (*Map*), is a worldwide enzootic disease of economic importance whose screening in the field is difficult (long incubation and low diagnostic test sensitivity). The representation of such a regional pathosystem leads to complex epidemiological models. Moreover, as often for such systems, processes behind *Map* spatio-temporal spread are partially observed and available data are incomplete. Hence, classical inference methods are not suitable as the likelihood function cannot be specified. Our objective was to estimate key parameters of a metapopulation model of *Map* spread from a longitudinal dataset collected in Brittany (France), based on an original methodological approach relevant for such data.

Materials and methods: We used a stochastic mechanistic model of *Map* spread between herds through animal trade movements. Comprehensive data on cattle movements in 12,857 dairy herds and partial data on animal infection status were available (2005-2013). Inference was performed with a Monte-Carlo approximation of a composite likelihood coupled to a numerical optimization algorithm. We estimated the proportion of initially infected herds, the within-herd prevalence distribution, the probability of purchasing infected cattle, the indirect local transmission rate, and the mean sensitivity of the diagnostic test (Se).

Results: Empirical identifiability was verified on simulated data. The optimization algorithm converged after appropriate tuning. Point estimates and empirical confidence intervals indicated a large initial proportion (> 0.80) of infected herds with a low within-herd prevalence, a low risk of introducing an infected animal (»0.10), and a low Se (»0.25).

Conclusion: Estimations of such previously unknown parameters provide new insights on bovine paratuberculosis infectious dynamics at a regional scale. The inference framework proposed here can be applied easily to other infected areas. It can also be adapted to estimate key features for other pathosystems. It is of particular interest when likelihood-free inference methods fail due to difficulties in defining relevant summary-statistics.

Key words: Parameter estimation, composite likelihood, mechanistic epidemic model, metapopulation model, Mycobacterium avium subsp. Paratuberculosis

Assessment of the bovine tuberculosis control program in Uruguay; what can we do better?

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ABSTRACT

Objective: Bovine tuberculosis (bTB) is a chronic cattle disease that imposes a major animal and public health threat. Control programs are extremely costly because they are typically based on routine testing of the animal population and culling of individual reactors or its complete herd. A formal assessment of bTB programs in endemic countries is extremely important to improve cost-effectiveness. In Uruguay, a test-and-cull program in dairies, using skin testing and slaughter inspection, is the core of the bTB program. Regardless, bTB prevalence has increased in the past 5 years. The aim of this study was to assess the epidemiology of bTB in Uruguay, and evaluate the alternative diagnostic approaches such as targeted surveillance and the use of interferon-gamma assay (IFN-γ) to improve the bTB program.

Materials and methods: We studied (a) bTB spatial clustering using spatial scan statistics and Cuzick-and-Edwards test; (b) risk factors associated with the disease using conditional logistic regression; and (c) the role of the Uruguayan cattle network in bTB dynamics using network analyses. We evaluated ten different strategies aiming to reduce testing efforts with an integrated within-between herd mathematical transmission model elaborated for Uruguay, and finally, we assessed the accuracy of IFN-γ under field conditions using a Bayesian approach.

Results: Results from these studies indicated that bTB is clustered, and large dairies with higher number of cattle purchased had a higher risk of bTB-outbreak. The modeled strategy based on eliminating testing in low-risk farms resulted in a 40% reduction in sampling effort. The IFN-γ accuracy revealed a good sensitivity (≈82%) with a poor specificity (≈75%).

Conclusion: These results suggested it is crucial to account for animal movements as targets for testing, and the use of IFN-γ as an ancillary test can improve testing sensitivity. This epidemiological assessment will help to reallocate resources and ultimately improve control and surveillance program in Uruguay.

Key words: Bovine tuberculosis, Uruguay, epidemiological tools, control programs

Escalating community participation to sustain the rabies program on Bandung, west Java province, Indonesia

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ABSTRACT

Objective: Rabies eradication constructed by the involvement of stakeholders such as government, animal health, public health and community. Community involvement on Rabies eradication is their active participation on Rabies awareness that could affect their attitude and practice to the disease. We conduct a a knowledge, attitudes and practices survey of the community who participated on Rabies awareness by Program Study of Veterinary Medicine Universitas Padjadjaran, West Java Province and district authority, and Indonesia Veterinary Medical Association.

Materials and methods: We conducted descriptive cross sectional survey using questionnaire of knowledge and practice to rabies. There 108 participant involved this study. The data analyzed with chi squared test.

Results: There 80.6% of the respondent had a good knowledge on Rabies causative factors, rabid animals and the clinical signs. However, 43.5% respondent still had a poor attitude on how to kept the animal free from Rabies, such as contact with wandering dogs, rabies vaccination of the pet animals, and their response to the dog bites. There no significant correlation on knowledge and practice of rabies by chi square test (P>0.05).

Conclusion: Community awareness program had to be keep consistently conducted especially at the non-free area, focusing on Rabies knowledge and the prevention action, that could affect the community attitude and practice to prevent the spreading this disease both in human and animals.
Key words: Rabies, community, knowledge, attitude, practice

Can FMD be controlled by risked-based partial vaccination?

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ABSTRACT

Objectives: A New Zealand funded programme (2016-20), following an Australian investment (2010-16), aims at eliminating foot and mouth disease (FMD) from Lao DPR (Lao) the Myanmar through risk-based partial vaccination, surveillance, awareness and training. This presentation uses data from baseline surveys and post-vaccination monitoring to investigate the feasibility of such a strategy.

Material and methods: Risk maps based on passively available information were used to select villages for vaccination. Survey data were analysed from two provinces of Lao DPR (CS) and two central regions of Myanmar (MS) with little prior vaccination, and one province of Lao DPR (XK) with several years of vaccination campaigns. Space and time analysis of antibody prevalence distinguishing field virus exposure from vaccination, and farmer reported signs of past clinical FMD occurrences were evaluated.

Results: Observed FMD and the seroprevalence of 6-18 months old calves ('incidence') indicated that annual exposure to FMD virus was widespread and independent of the village risk status in both Lao DPR and Myanmar. Repeated annual vaccination led to a reduction of observed FMD in XK from 8.1% to 0.8% of households while FMD incidence was similar (17%) to unvaccinated areas (21% CS; 20% MS). A single vaccination doubled the sero-prevalence in calves. Young and adult animals achieved the target threshold for herd immunity (80%). However, the antibody prevalence to vaccine types A and O was only 10% higher than to field virus. Vaccination coverage was lower in Lao DPR (23% CS, 37% XK) than Myanmar (81%) of animals included in post-vaccination monitoring surveys.

Conclusion: Reporting and investigating FMD outbreaks is still too infrequent to become an effective spatial criterion for targeting villages for vaccination. FMD virus appears to continue circulating despite vaccination reducing clinical occurrences of FMD.

Key words: Foot and Mouth Disease, risk based partial vaccination, strategy development

Impact of diagnostic criteria on the Danish plasmacytosis control program between 2000 and 2015

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ABSTRACT

Objective: Plasmacytosis in farmed mink (*Neovison vison*) is a viral infection of worldwide economic importance, causing reduced reproduction, increased kit mortality, and reduced fur quality. In Denmark, blood samples from all farms are tested annually using a standardized antibody test (counter current immuno-electrophoresis test). Sampling events with 1-3 positives and ≥4 positives lead to the farm classifications of suspected and infected, respectively. Both groups undergo restrictions on sale of animals, further testing and improved biosecurity, and infected farms are encouraged to depopulate and disinfect. The primary objectives of this study were to assess the risk of 1) maintaining infection within test positive farms, and 2) transmission between neighboring farms.

Materials and methods: A total of 46 mill blood antibody samples from 2352 farms over a 15 year period were used along with demographic data on farm size, feed supplier, and GIS coordinates to group farms within spatial areas as well as to identify neighboring farms within 5km of each other. The test data was summarized to the level of annual farm classification and analyzed using a mixed effects logistic regression model including random effects of region, spatial sector, feed supplier, year and farm in R and SAS.

Results indicated that infection was associated (OR; P) with status of infected classification for the same farm in the previous year (70; P<0.001), suspected classification for the same farm in the previous year (10; P<0.001), presence of neighboring infected farms within 5km in the previous year (2.8; P<0.001), and presence of neighboring suspected farms within 5km in the previous year (1.4; P=0.04). However, disinfected neighboring farms were not associated with infection (1; P=0.995).

Conclusion: We conclude that suspected farms likely represent a risk of transmission to uninfected neighboring farms in the following year, and that these farms should be subject to similar control measures as for infected farms.

Key words: Transition probabilities, farmed mink, surveillance

Risk factors of Extended-Spectrum β-Lactamase Producing Enterobacteriaceae occurrence in commercial farms in Reunion, Madagascar and Mayotte Islands, 2016-2017

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ABSTRACT

Objective: In the South West Indian ocean, Extended-Spectrum β-Lactamase producing Enterobacteriaceae (ESBL-E) are a main public health issue. In livestock, ESBLE burden was unknown. The aim of this study was first to estimate the prevalence of ESBL-E on beef cattle, broiler and pig commercial farms in Reunion, Mayotte and Madagascar, and identify ESBL enzymes occurrence in each production type and territory. Secondly, potential risk factors of ESBL-E occurrence in each production sector were explored.

Materials and methods: From February to August 2016, poultry, pig and beef cattle commercial farms were sampled in Reunion, Mayotte and Madagascar. Samples were collected using boot swabs Sterisox® to cover building floor surface. Interviews were performed with farmers to assess potential risk factors of ESBL-E occurrence. All samples were immediately stored in cool box at 4 °C before laboratory analyses proceeded within 48 hours. Bacteria were cultured on selective media plates and ESBL-E identification performed following EUCAST standards.

Results: Prevalences observed in all production types and territories were high (ranging from 53.3%±18.2 to 86.7%±12.4), except for beef cattle in Reunion (03.7%±05.1) which differed significantly. The most common ESBL gene identified was $bla_{CTX-M-1}$ expect in Madagascar with mainly $bla_{CTX-M-15}$. Generalized linear models explaining ESBL-E occurrence varied between livestock production sectors. Factors associated with decreasing (e.g. water quality control and detergent use for cleaning) and increasing ESBL-E occurrence (e.g. recent antibiotic use, other farmers visiting the premises, pet presence) were identified.

Conclusion: This study was the first to explore antibiotic resistance management tools in IO farms. It confirmed the need for improving biosecurity and hygienic measures as efficient means to reduce ESBL-E occurrence in livestock. Finally, it pointed out interesting hypotheses to explore ESBL-E transmission between food-producing animals and humans in Madagascar and developing countries.

Key words: Livestock, Enterobacteriaceae, antimicrobial resistance, enzymes, Indian ocean

Effects of antibiotics on bacterial resistance and serotype diversity of *Salmonella enterica* originating from lymph nodes, fecal and hide samples of feeder cattle at slaughter

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ABSTRACT

Objective: The objectives of this study were to explore the effects of antibiotic treatment on bacterial resistance and diversity of *Salmonella enterica* in cattle.

Materials and methods: Twelve pens (134 cattle) were subjected to three treatment regimens: Cattle in four pens were treated with ceftiofur, those in another four pens received tulathromycin and cattle in the final four pens remained as control animals. Feces were collected before treatment (Day 0), after treatment (Day 7) and at slaughter (Day 100+). Hide swabs and subiliac lymph nodes were collected at slaughter. Standard methods were used to isolate *Salmonella*. 399 Salmonella isolates (58 fecal isolates from Day 0, 27 fecal isolates from Day 7, 106 fecal isolates from Day 100+, 96 lymph node and 112 hide isolates) were selected for whole genome sequencing on the Illumina MiSeq platform. SeqSero, ResFinder and PlasmidFinder databases were used to identify serotypes, resistance genes, and plasmids, respectively.

Results: Prevalence of *Salmonella* on Days 0, 7 and Day 100+ for fecal samples were 43.6 % (58/133), 20.1% (27/134) and 80.3% (106/132), respectively. Hide and lymph node prevalence at slaughter were 84.8% (112/132) and 84.2% (96/114), respectively. The two most prevalent serotypes identified on Days 0, 7 and 100+ fecal isolates were Montevideo (51.7%), Anatum (62.9%) and Lubbock (40.5%), respectively. Anatum (40.6%) and Lubbock (50.8%) were the prevalent serotypes in lymph nodes and hides, respectively. Monophasic variants of Cerro, Kentucky, Newport and Norwich serotypes were also identified. 332 isolates were pan-susceptible while 67 isolates were singly resistant and harbored *tet(*A). Resistant isolates were of the Montevideo serotype and harbored an IncN plasmid.

Conclusions: Antibiotic treatments did not significantly affect the resistance profile and serotype diversity of *Salmonella* at slaughter. There was a strong pen level effect on the *Salmonella* serotypes from hide and lymph node samples.

Key words: *Salmonella enterica*, cattle, antibiotic resistance, serotype

Effects of a two-dose ceftiofur treatment for metritis on levels of antimicrobial resistance among fecal *Escherichia coli* in Holstein-Friesian dairy cows at the time of slaughter-eligibility

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ABSTRACT

Objectives: Under current U.S. product labeling, a dairy cow is eligible for slaughter 13 days after receiving their final dosage of ceftiofur crystalline-free acid (CCFA) treatment. To evaluate the microbial safety with regard to levels of antimicrobial resistance on the first eligible slaughter date, a pair-matched cohort study was implemented to monitor levels of antimicrobial resistance within fecal populations of an indicator species, *Escherichia coli,* among dairy cows on three dairies in Texas and New Mexico, USA.

Materials and methods: Cows diagnosed with post-parturient metritis (by dairy/veterinarian protocol) were pair-matched with healthy cattle of a similar age and calving date. Upon diagnosis, a baseline fecal sample was collected from both the metritis case and the control cow. A first dose of CCFA was administered, followed by a second dose 72 hours later. Subsequent fecal samples were collected on study days 6, 16, 28, and 56. After collection, fecal samples underwent microbiological processing and were spiral-plated onto plain MacConkey agar and MacConkey agar with ceftriaxone (4 µg/mL) prior to being colony counted. Samples were additionally incubated in MacConkey broth with ceftriaxone (2 µg/mL) prior to being spiral plated onto CHROMAgar ESBL. Colonies on such agar were indole and MALDI-TOF tested for *E. coli* verification and subsequent analysis.

Results: Via full-factorial linear regression, there was a significant difference ($P < 0.05$) in quantitative resistance levels among the *E. coli* populations when comparing metritis (CCFA-treated) and control (untreated) cattle on sample days 6 and 16; later, these returned to similar levels of resistance on sample days 28 and 56.

Conclusion: Our first trial replicate results suggest that at the first eligible slaughter date, there is an increased risk of sending cattle to slaughter with increased levels of antimicrobial resistance. Extended voluntary slaughter withholding could be considered an essential component of on-farm antibiotic stewardship.

Key words: Antimicrobial resistance, dairy, stewardship, ceftiofur crystalline-free acid, cohort

Genotypic and phenotypic diversity of *Salmonella enterica* isolated from patients at an equine referral hospital

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ABSTRACT

Objective: The aim of this study was to evaluate the proportional morbidity of *Salmonella enterica* serotypes and their antimicrobial resistance (AMR) from horses admitted to a referral hospital in the southern United States, using Whole Genome Sequencing (WGS).

Materials and methods: Salmonella isolates (n=255) were obtained from patients admitted to the hospital over an eight year period. Antimicrobial susceptibility was performed using the Sensititre® system. WGS was used to identify serotypes, plasmid replicons, antimicrobial resistance genes and conduct phylogenetic analyses of the *Salmonella* isolates. Sequencing libraries were prepared using the Illumina Nextera XT kit and sequenced on the Illumina MiSeq platform. Phylogenetic analyses were performed using Parsnp and FigTree.

Results: The most common serotype recovered was Newport (18%), followed by Anatum (15.2%) and Braenderup (11.8%). Most of the isolates were pansusceptible (n=219; 85.9%), 10 (3.9 %) were resistant to one or two classes of antimicrobials, while 25 (10.2%) were multidrug resistant (≥3 classes). Beta-lactamase (*bla*) genes such as bla_{TEM-1}, ESBLs (bla_{SHV-12} and $bla_{CTX-M-27}$) and AmpC (bla_{CMY-2}) were detected. Resistance and decreased susceptibility to quinolones were encoded by the plasmid-mediated quinolone resistance gene (*qnr*B), *aac(6')-Ib-cr*, and point mutations in the chromosome. Additionally, resistance genes for gentamicin, streptomycin, folate pathway inhibitors, phenicols, tetracyclines, and macrolides were identified. The main predicted incompatibility plasmid type was I1 (10%). Phylogenetic analyses on three of the main serotypes revealed related temporal and geographical outbreak clusters.

Conclusion: The presence of AMR *Salmonella* increases the risk of unsuccessful treatments on invasive diseases in horses and remain a potential hazard to public health. Understanding the epidemiology of *Salmonella* in horses admitted to referral hospitals is important for the prevention, control, and treatment of salmonellosis.

Key words: *Salmonella*, antimicrobial resistance, whole genome sequencing, horses, outbreaks

Applying machine learning techniques to antimicrobial susceptibility data

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ABSTRACT

Objective: It is challenging to identify trends in antimicrobial resistance (AMR) because AMR data often come from several sources and are typically sparse, with a few resistances and many susceptibilities. Association rule mining, an unsupervised machine learning technique, can detect high-order associations between binary variables in sparse data-sets. We used association rule mining to discover pairwise associations between resistances because the genetic elements underlying these associations may affect responses to AM use policies.

Materials and methods: We applied the Apriori association rule mining algorithm to 14,418 *Escherichia coli* isolated by the US National Antimicrobial Resistance Monitoring System between 2004 and 2012 from chicken carcasses and retail meat, with each year and source analyzed separately. The minimum support and confidence in the algorithm were set to find all resistance rules present in one or more isolates. Rules were ranked by lift $\left(\frac{P(A \cap B)}{P(A)P(B)}\right)$ and conviction $\left(\frac{P(A)P(B^c)}{P(A \cap B^c)}\right)$ to determine which resistances occurred more frequently together in the dataset than would be expected if they were independent. We compared the rules, ranked by lift, to previously identified associations from Markov networks inferred using GLASSO.

Results: Several AMR rules were found to be consistent across the years and isolate sources, including within-class beta-lactam rules and within-class fluoroquinolone rules. Lift identified consistent rules between fluoroquinolones and beta-lactams, and between chloramphenicol and beta-lactams, although these associations were driven by a few multi-drug resistant isolates. Conviction identified between-class rules involving tetracycline and aminoglycosides, and sulfisoxazole and aminoglycosides, as well as within-class aminoglycoside rules. There was fair to substantial agreement between the rules and the Markov networks (PABAK range [0.33, 0.79]), depending on the year and the lift.

Conclusion: The between-class patterns of multidrug resistance revealed in the rules are similar to those found with Markov networks. Association rule mining efficiently identifies associations between resistances to individual antimicrobials in large, sparse data sets.

Key words: Antimicrobial resistance, machine learning, chicken, *Escherichia coli*

Determining the prevalence and diversity of *Salmonella enterica* from market hogs at slaughter

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ABSTRACT

Objective: The objective of this study was to assess the prevalence and phenotypic and genotypic antimicrobial resistance profiles of *Salmonella* in head trim and cheek meat from market hogs at slaughter.

Materials and methods: One hundred head trim and 100 cheek meat samples were collected from a hog processing plant every other month from January to November of 2015. Standard selective and enrichment methods along with non-enrichment methods were used for *Salmonella* isolation. Antimicrobial resistance phenotypes were determined by microbroth dilution on the Sensititre® system and genotypes were determined by whole genome sequencing (WGS) on the Illumina MiSeq system.

Results: The prevalence of *Salmonella* was 16.7% for head trim and 15.2% for cheek meat for non-enriched samples and 65.9% and 62.8% from enriched samples for head trim and cheek meat, respectively. We identified 22 different serotypes and the most prominent serotype was Typhimurium (48.5%). There were 218 isolates that were multidrug resistant (resistance ≥ 3 classes of antibiotics) and 97 isolates exhibited reduced susceptibility to ciprofloxacin (MIC values 0.5 to 2 µg/ml). WGS revealed the presence of *tet*(A), *tet*(B), *sul*1, *sul*2, *str*A, *str*B, *flo*R, *dfr*A, bla_{CMY}, bla_{TEM}, and bla_{SHV} antimicrobial resistance genes. The plasmid mediated quinolone resistance (PMQR) gene *qnr*B was found in 19 of the 32 isolates sequenced.

Conclusion: The finding of *Salmonella* isolates from pork with elevated ciprofloxacin MIC values and PMQR genes, in addition to other AMR genes, is concerning and warrants further investigation.
Key words: *Salmonella*, swine, antibiotic resistance, pork

Does the use of lower-order beta-lactam antibiotics in food animal production over-select for higher-order beta-lactamase resistance of consequence to human health?

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ABSTRACT

Objective: Higher-order beta-lactam resistance among Gram negative bacteria in human clinical settings has progressively increased over the last decade. Though not directly licensed for use in food-producing animals, carbapenem resistance has been demonstrated in the farm environment. Extended-spectrum beta-lactamases (ESBLs) also have proliferated during the same period, often in the absence of direct selection pressure. The objective of this study was to determine the extent to which lower order beta-lactam antibiotics (e.g., aminopenicillins and cephalosporins) differentially select for higher order antibiotic resistance (e.g., to cephalosporins and cerbapenems, respectively) among representative Enterobacteriaceae. In an initial laboratory experiment to estimate three modeling parameters (i.e., lag phase, growth rate, stationary phase), wild-type bacteria harboring four tiers of beta-lactamase genes: bla_{TEM-1}, bla_{CMY-2}, $bla_{CTX-M-*}$ and bla_{KPC} were used.

Materials and methods: For each gene, thirty previously sequenced pig, cattle or human *E. coli* isolates harboring no other beta-lactam resistance genes were selected. Thirty *E. coli* isolates, lacking all known beta-lactam resistance genes were used as controls. The absolute and relative fitness parameters were estimated over 48 hours using the Bioscreen C® automated growth curve assay. Initial parameter estimates for the same groups of isolates in the presence of ampicillin (32ug/ml) and ceftriaxone (4ug/ml) are presented. Non-linear Gompertz regression was performed using Stata® 14.2.

Results: Although not completely inhibited by ceftriaxone, the growth curve parameters of cephamycinase-producing bla_{CMY-2} isolates were significantly diminished (p < 0.05) compared to baseline as well as to those strains harboring the $bla_{CTX-M-*}$ gene. Ampicillin had no measurable effect on reducing the growth of bacteria harboring either cephamycinases or ESBLs.

Conclusion: These initial findings suggest that lower order beta-lactam antibiotics can indirectly select for higher order beta-lactamase resistance even in the presence of other types of resistant isolates. By using experimental data, mathematical modeling and targeted field studies, improved animal production and enteric microbial ecology may be achieved.

Key words: Antibiotic resistance, beta-lactam resistance, fitness, selection, stewardship

OIE PVS Pathway: Tool for the evaluation and improvement of Performance of Veterinary Services from Thailand's experience

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ABSTRACT

The OIE PVS Pathway is a global programme for the sustainable improvement of a country's Veterinary Services' compliance with OIE standards on the quality of Veterinary Services. This is an important foundation for improving animal and public health and enhancing compliance with SPS standards, at the national, regional and international level. The Department of Livestock Development (DLD) of the Ministry of Agriculture and Cooperatives of Thailand has one of its priorities, amongst other tasks, to facilitate the ongoing and improved access to international markets for animals and animal products. Thailand's decision to request an OIE PVS evaluation is therefore an important step towards this goal, measuring current performance with an independent and external evaluation. The results of the OIE PVS evaluation and the OIE PVS Gap Analysis mission can feed into the veterinary services (VS) strategic planning, investment and implementation to better meet national livestock priorities and international trade.

The PVS evaluation was conducted by independent OIE experts. It revealed that Thailand has a strong veterinary services (VS), led by the high standards required of its poultry export industries to the global market. This has also tended to improve other areas and promote awareness of high quality systems of food safety and traceability systems. HPAI outbreaks and ensuing political support have also assisted in the rapid high quality development of the VS.

The VS of developing countries are in urgent need of support to provide them with the necessary infrastructure, resources and capacities. The OIE PVS Pathway will help the countries enable to benefit more fully from the WTO's SPS measures while at the same time providing greater protection for animal health and public health and reducing the threat. Improvement of VS requires a public investment in order to meet the international standards (structure, organization, resources, capacities, role of veterinary professionals/ paraprofessionals). The OIE PVS Pathway is the progressive and participatory methodology that the country can use it as the tools to define appropriate resources and organisation and to strengthen VS based on their national constraints and priorities.

Key words: Veterinary Services, PVS, OIE, HPAI, Thailand

D. One health (animal–human–environment interface)

Are foodborne illnesses due to beef contaminated with antimicrobial resistant bacteria correlated with prophylactic use of antibiotics in beef cattle?

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ABSTRACT

Objective: Amongst drivers of antimicrobial resistance (AMR), prophylactic use of antimicrobials (PAM) in livestock is considered important. Our objective was to assess the relationship between foodborne illnesses with AMR bacteria and PAM in beef cattle in the United States (US).

Materials and methods: A Bayesian model was built to estimate foodborne illness incidence per beef meal contaminated with AMR bacteria and from cattle prophylactically treated ($\lambda_{Bf,AM}$) in 1999 and 2010, the two most recent years with nationwide estimates of tetracycline and tylosin use in US feedlots. Incidence of human illnesses from beef contaminated by STEC O157, *Salmonella* spp. or *Campylobacter* spp. with resistance to ≥ 3 drug classes was derived from FoodNet, NORS, and NARMS surveillance data. Per- capita estimations of beef meals from cattle prophylactically treated used USDA-ERS, USDA-EPA, and NAHMS data. Incidences were statistically compared using the probability that $\lambda_{Bf,AM}$ was higher in one year (PrHigher$_{year}$).

Results: From 1999 to 2010, the fraction of US beef cattle treated with tetracycline decreased (30.6% to 21.2%), while it increased for tylosin (42.3% to 71.2%). In 1999, $\lambda_{Bf,tetracycline}$ for *Campylobacter*, *Salmonella,* and STEC were 9.8×10^{-9} (95%CrI: $4.6\text{-}16.6 \times 10^{-9}$), 3.9×10^{-7} ($2.2\text{-}6.2 \times 10^{-7}$) and 3.7×10^{-8} ($1.6\text{-}7.0 \times 10^{-8}$); in 2010, they were 11.6×10^{-9} ($5.5\text{-}20.3 \times 10^{-9}$), 4.3×10^{-07} ($2.3\text{-}7.4 \times 10^{-7}$) and 4.5×10^{-8} ($1.9\text{-}9.0 \times 10^{-8}$), respectively. In 1999, $\lambda_{Bf,tylosin}$ for *Campylobacter*, *Salmonella* and STEC were 7.1×10^{-9} (95%CrI: $3.3\text{-}12.0 \times 10^{-9}$), 2.8×10^{-7} ($1.6\text{-}4.5 \times 10^{-7}$) and 2.7×10^{-8} ($1.2\text{-}5.1 \times 10^{-8}$); in 2010, they were 3.4×10^{-9} ($1.7\text{-}5.3 \times 10^{-9}$), 1.3×10^{-7} ($7.5\text{-}19.0 \times 10^{-8}$) and 1.3×10^{-8} ($5.8\text{-}24.1 \times 10^{-9}$), respectively. $\lambda_{Bf,tetracycline}$ remained unchanged (all PrHigher <95%), while $\lambda_{Bf,tylosin}$ decreased from 1999 to 2010 (PrHigher$_{1999}$ of 99.9%, 100% and 99.4% for *Campylobacter*, *Salmonella* and STEC).

Conclusion: Using US surveillance data, no evidence of positive correlation was found between prophylactic use of tylosin or tetracycline in beef cattle and AMR in foodborne illnesses from beef consumption. More regular and granular data are needed to better assess the potential impact of PAM on AMR in humans.

Key words: Veterinary antimicrobial use, prophylaxis, antimicrobial resistance, foodborne illness

A novel participatory strategy to reduce antimicrobial use in agricultural systems

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ABSTRACT

Objective: This paper reports on the interim results of a three-year project using participatory development (PD) in farmer-led groups to help formulate agricultural antimicrobial use (AMU) reduction strategies in New Zealand. The ultimate goal of this project is to reduce AMU on farm by 20% by 2020, thereby contributing to the New Zealand Veterinary Association's aspirational goal of reducing AMU to zero by 2030.

Materials and methods: This project is currently active in the lower region of New Zealand. Farmers and veterinarians across the lower South Island have been invited to participate in 4 strategic farmer groups comprising up to 12 farmers per group, from sheep, beef, deer (red meat) sectors, and from the dairy sector. Each group has a facilitator, who is a trained agricultural consultant with a background in group facilitation. The groups are initially given a technical workshop to introduce them to antimicrobial resistance (AMR), and are then allowed to develop their own strategies for reducing AMU. Vets are available to the groups to provide technical support if required.

The strategies developed will then be implemented across a number of farms to effect change.

Results: The project is ongoing. At the time of submission, groups were in the process of finalising their strategies. By the time of presentation, final strategies and interim results from the field trial will be available. Conclusion: This study intends to facilitate farmers to create a range of strategies for reducing AMU which they will feel ownership of, and then to test these strategies in the field, with regard to ease of implementation, level of effect, consequences and other impact.

Key words: Antimicrobial resistance, participatory development, antimicrobial use

Understanding the role of anthropogenic landscapes in wildlife antimicrobial resistance: Merging metagenomics and spatial epidemiology

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ABSTRACT

Objective: There is growing evidence that residual antibiotics and antimicrobial resistance-encoding bacteria from clinical settings and animal-based agriculture may accumulate in natural ecosystems. These "natural reservoirs" of resistant bacteria may lead to broad dissemination of antimicrobial resistance (AR) genes and possible exchange of AR mechanisms with human and domestic animal pathogens. However, we know relatively little about the geographic distribution of AR in natural environments and how specific anthropogenic sources of AR contribute to emergence in wildlife and environmental reservoirs. Here, we use metagenomic sequencing technology to explore spatial patterns of AR genes from the microbial communities of two native owl species that may serve as sentinels of AR in the natural environment.

Materials and methods: We collected cloacal swabs from 80 owls recovered throughout Minnesota, U.S.A. and identified enterobacteria-associated AR genes using Illumina shotgun sequencing. We then applied tools from spatial epidemiology to investigate how anthropogenic landscapes shape the distribution of AR genes. Further, we compared owl AR genes to those found in 23 samples from commercial poultry farms to evaluate the extent of AR gene sharing between agricultural and wildlife samples.

Results: Preliminary data indicate that among owls exhibiting AR, we detect genes conferring resistance to a range of antibiotic classes, including clinically relevant extended-spectrum beta-lactamases. Additionally, over 50% of AR genes found in owls are also identified in poultry samples, suggesting a possible link between agricultural AR sources and wildlife. A ColV plasmid, which is a defining trait of avian *E. coli* and carries AR genes, was identified and fully assembled from these data. Initial spatial analyses suggest there was no statistically significant geographic pattern in the occurrence of AR genes in owls.

Conclusion: Our results establish baselines for monitoring the distribution of AR in natural environments and provide insight into the role anthropogenic sources may play in AR gene dissemination.

Restriction in the Use of Antimicrobials in Food Animals and its Association with Prevalence of Antimicrobial Resistance Genes – A Systematic Review

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ABSTRACT

Objective: Antimicrobial resistance (AMR) is an increasingly serious threat to public health, as it undermines current options to treat severe animal and human infections. Objective of this systematic review was to assess whether a restriction in use of antimicrobials in food animals is associated with a reduced prevalence or decreased number of antimicrobial resistance genes and determinants (ARGDs) in bacteria isolated from food-producing animals

Materials and methods: Abstracts that reported original research, described a restriction in use of antimicrobials in food animals, and reported AMR for food animals were selected for full-text review. Two metrics were used to evaluate study results: (i) number of studies showing at least one genetic element increased, decreased or with no change; and (ii) number of associations evaluated per study, determined as number of ARGDs screened in all combinations between sample/gene/bacteria used to define a population.

Results: Our search strategy identified 8,955 citations. A total of 13 studies were included, from which five reported counts of ARGs, and eight reported risks of ARGs. In 10 of the 13 studies, at least one ARG was decreased in the intervention group; the opposite effect was observed in three studies. A total of 107 associations were reported. Most associations (n = 64) indicated no difference in presence of ARGs between intervention and comparator groups. For all comparisons where the ARG screened was associated with the antimicrobial that was restricted and the comparator group was under treatment with the same antimicrobial, prevalence or number of ARGs was reduced in the intervention group

Conclusion: In summary, restricting the use of antimicrobials in food animals is associated with either a decreased or equal presence of ARGs in bacteria isolated from these animals. Knowledge of the exposure status of the comparator group is crucial to determine the effects of antimicrobial use on the presence of ARGs

Key words: Antimicrobial resistance, antimicrobial resistance genes, food-producing animals, systematic review

Antimicrobials and disease: Impact of antimicrobial misuse in chicken farming systems in Vietnam

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ABSTRACT

Objectives: We aimed to determine the fraction of disease likely to remain untreated (due to the administration of antimicrobials on non-susceptible pathogens (virus/parasites, and antimicrobial resistant bacteria) ('treatment failure') in chicken flocks in Vietnam.

Materials and methods: Weekly data on antimicrobial use and disease symptoms were collected from 88 randomly chosen chicken flocks over 124 production cycles. A naïve Bayesian mathematical model was trained to infer the probabilities of episodes been caused by each of 25 pathogens (15 bacteria, 9 viruses, 1 Eimeria spp. parasite), given the observed symptom profile, and (prior) expert knowledge on their relative incidence. Data on antimicrobial susceptibility of bacterial pathogens were compiled from a recently published review, and were complemented by expert opinion. For each episode, treatment failure was calculated as the cumulative probability of each pathogen and the probability of resistance given the choice of antimicrobials.

Results: A total of 224 episodes of disease (median 2 [IQR 1-2] per cycle) were observed, of which 44.8% were attributed to viruses (95% CI 31.1-58.4%), 54.6% (CI 40.4-68.7%) to bacteria, and 0.6% (CI 0-1.7%) to Eimeria spp. Antimicrobials were more frequently administered on weeks with disease than in weeks without disease (43.3% vs. 17.8%; p<0.001). A median of 2 [IQR 0-4] antimicrobials were used by episode. The choice of specific antimicrobials was independent on the disease status on farms. Among episodes attributed to bacteria/Eimeria, treatment failure was estimated in 13.2% (95% CI 0.12-0.14). Overall treatment failure was estimated in 57.1% (95% CI 55.2-59.0%) episodes.

Conclusion: This study underscores the limitations as effective tools to control infectious disease on farms, while making the case for better stewardship and administration of antimicrobials on farms.

Key words: Antimicrobial resistance, pathogens, poultry, Vietnam

Variation in antimicrobial resistance profile diversity of *Salmonella* Typhimurium isolates between UK chicken, cattle and pig populations

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ABSTRACT

Objective: Determine whether or not detectable differences in circulating antimicrobial resistance (AMR) profiles of *S.* Typhimurium are observed between food producing animal populations in the UK using national surveillance data.

Materials and methods: Food producing animals can act as reservoirs of *S.* Typhimurium and are subject to national surveillance in the UK. Data from *S.* Typhimurium isolated from cattle (n=1116), pigs (n=2174) and chickens (n=248) collected in the UK between 2003 and 2014 were analysed. The diversity of observed AMR profiles were compared between host species, and within production sectors of individual host species, using ecological diversity analyses and rarefaction curves.

Results: A total of 129 unique AMR profiles were observed. Three of the five most common AMR profiles for each species were shared by all hosts. In a connectivity matrix with connections between AMR profiles corresponding to a single difference in AMR profile, the majority (88%) of AMR profiles formed a single complex and AMR profiles found in multiple host species had higher mean node degrees compared to AMR profiles observed in a single host. The number of AMR profiles unique to pigs was greater than expected and the AMR profile diversity of isolates from pigs was higher than isolates from chickens across the ecological diversity measures. The diversity of AMR profiles of isolates from cattle was also higher than of isolates from chickens in three of four diversity measures. Production sector variation was noted in chicken and pig populations, with higher diversity of isolates from broiler compared to layer chickens and breeder compared to rearer and finisher pigs.

Conclusion: Observations indicate variation in AMR profile diversity between and within food producing animal populations in the UK. These findings suggest alternate sources of bacteria and/or variation in selective evolutionary pressures between the animal populations.

Key words: Antimicrobial resistance, cattle, pigs, chicken, surveillance

Livelihoods and antimicrobial stewardship among smallholder livestock farmers and animal healthcare workers in Thai Nguyen Province, Vietnam: a cross-sectional survey

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ABSTRACT

Objectives: In countries characterised by industrialised livestock systems, veterinary antimicrobial stewardship (AMS) success is largely attributed to greater regulation. Countries dominated by smallholder systems are likely to be less responsive to such 'top-down' approaches. Towards finding more context-appropriate solutions, this research aimed to identify the ways in which livelihood capitals influence AMS in smallholder livestock systems in Vietnam.

Materials and methods: A cross-sectional survey of 82 animal healthcare workers and 210 smallholder farmers was performed in Phu Binh District, where smallholders comprise approximately 86% of households. Informed by prior exploratory research, this study aimed to describe how livelihood capitals influence AMS behaviours related to examination, diagnosis, treatment, prophylaxis and animal husbandry. Descriptive and inferential statistics were performed to compare responses within and between stakeholder groups, using STATA v14.

Results: Both stakeholder groups identified that smallholder farmers played significant roles in disease management, owing to their knowledge and skills (human capital). Most explanations provided for adherence or non-adherence to AMS principles pertained to human capital. There were exceptions; farmers chose pharmacies overwhelmingly based on effectiveness of previously purchased drugs and less, on the animal healthcare worker's experience, education or customer service. This contradicted the dominant animal healthcare worker belief that their competitive advantage lay in their years of experience.

Conclusion: This iterative approach aided a more nuanced, multi-perspective understanding of local constraints and opportunities for AMS. While the ultimate goal may be for all animal healthcare systems to adhere to global AMS standards, our research addresses the question of how we might support smallholder farmers and animal healthcare workers to make better stewardship decisions within their current livelihoods context.

Key words: Antimicrobial stewardship, livestock, Vietnam, context-appropriate solutions, mixed methods

A qualitative study of antimicrobial use practices among beef cattle producers in Tennessee, USA

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ABSTRACT

Objective: To determine the following among Tennessee beef cattle by producers:
(1) the most common drivers for using antimicrobials, (2) the perceived alternatives to antimicrobials, (3) the knowledge and perceptions regarding antimicrobial resistance, and (4) the preferred avenues for receiving information on prudent antimicrobial use.

Materials and methods: Five focus group meetings with beef producers were conducted in East, Middle, and West Tennessee with a semi-structured interview guide. Each focus group was video recorded. Thematic analysis was performed using NVivo, a qualitative data analysis tool.

Results: The factors that producers considered to drive antimicrobial use were the type of cattle operation, disease and animal welfare, economic factors, veterinarian consultation, producer's experience and peer support, Veterinary Feed Directive, and perceived drug efficacy. Vaccination, proper nutrition, and other good management practices were considered alternatives to antimicrobial use. To encourage vaccine use among small producers, participants suggested packaging vaccines into smaller quantities. Antimicrobial resistance was perceived to be a problem affecting animal and public health. Participants suggested additional education for cattle producers on the prudent use of antimicrobials as a measure for improving antimicrobial use. The veterinarian, producer associations and meetings, and county extension agents emerged as trusted avenues for channeling information on prudent antimicrobial use to cattle producers.

Conclusion: Several factors drive antimicrobial use among cattle producers in Tennessee. Participants generally perceived their antimicrobial use to be discreet and only when necessary. More awareness of drivers for the development of antimicrobial resistance and continuing education on prudent antimicrobial use is needed for Tennessee beef producers.

Key words: Qualitative study, focus group, antimicrobial use, antimicrobial resistance, veterinary feed directive

Prevalence and antimicrobial resistance profiles of *Staphylococcus aureus* isolated from raw milk in pastoral areas of northern Kenya

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ABSTRACT

Objective: The aim of this study was to investigate the prevalence and antibiotic susceptibility profiles of *S. aureus* isolated from milk obtained from lactating cows, goats, sheep, camels and pooled household milk in Marsabit and Isiolo Counties, Northern Kenya.

Materials and methods: To achieve this, 603 samples of individual and pooled milk samples were obtained randomly from households in Marsabit and Isiolo counties. *S. aureus* was isolated and positively identified using morphological and biochemical test and confirmed using molecular methods. The antimicrobial resistance profiles of the isolates were also determined.

Results: Among all the samples examined, 43 of 299 raw milk samples (14%) from Marsabit and 42 of 304 (14 %,) from Isiolo were positive for *S. aureus*. Overall, eighty five PCR-confirmed *S. aureus* isolates were obtained from 603 milk samples from the study sites.
A large proportion (67%) of the isolates was resistant to tetracycline, followed by ampicillin and oxacillin. Conversely, low level resistance (4%–15%) was observed for clindamycin, cephalexin, erythromycin, kanamycin and ciprofloxacin. Multidrug resistance was observed in 20% of the isolates and methicillin resistance (MRSA) was detected in 94% of the multidrug resistant isolates.

Conclusion: The findings of this study showed that raw milk in pastoral areas on Marsabit and Isiolo counties is contaminated with antibiotic-resistant *S. aureus* including Methicillin resistant *S. aureus* (MRSA) strains. There is a need to implement appropriate control measures to reduce contamination as well as the spread of virulent *S. aureus* strains and the burden of *Staphylococcal* related illnesses in humans.

Key words: *Staphylococcus aureus*, Antimicrobial drug resistance, milk, MRSA, pastoral areas

Human exposure to antimicrobial-resistant bacteria from food animals: Findings from the IAM.AMR Project

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ABSTRACT

Objective: The goal was to describe comparative human exposure to extended-spectrum cephalosporin-resistant *Escherichia coli* (ESC-*E. coli*) and *Salmonella enterica* (ESC- *Salmonella*), and fluoroquinolone-resistant *Campylobacter* (FQ-*Campylobacter*) from beef, chicken, and pork using an integrated assessment model (IAM) approach.

Materials and methods: Farm-to-fork models for ESC-*E. coli*, ESC-*Salmonella*, and FQ-*Campylobacter* from beef cattle, chickens and pigs were constructed using data from the Canadian Integrated Program for Antimicrobial Resistance Surveillance and a comprehensive literature search. Using a branching probability tree approach, the models propagated the probability of antimicrobial resistance (AMR) modified by 1) the odds ratio between factors (e.g., antimicrobial use) and the occurrence of AMR, and 2) the frequency of occurrence of the factors through the agri-food chain. Estimates of human exposure to resistant bacteria were obtained by adjusting the calculated probabilities by Canadian consumption patterns and population (Figure 1).

Results: All models included management system (e.g., organic) and antimicrobial use. Chicken models included other factors (e.g., type of litter). Possible exposure to AMR was higher through chicken, when compared to beef or pork. From chicken, there was higher exposure to ESC-*E. coli* than to ESC-*Salmonella* or FQ-*Campylobacter*.

Conclusion: In the modelled systems, comparative human exposure to AMR bacteria was highest through chicken and was attributed in part to higher baseline probabilities of AMR, higher bacterial recovery rates at retail, and higher consumption rates. There were substantial data gaps in the models and future work includes filling data gaps, addressing other plausible pathways of AMR dissemination (e.g., environment) and incorporating whole genome sequence data.

Key words: Antimicrobial resistance, quantitative modelling, *E. coli, Salmonella, Campylobacter*
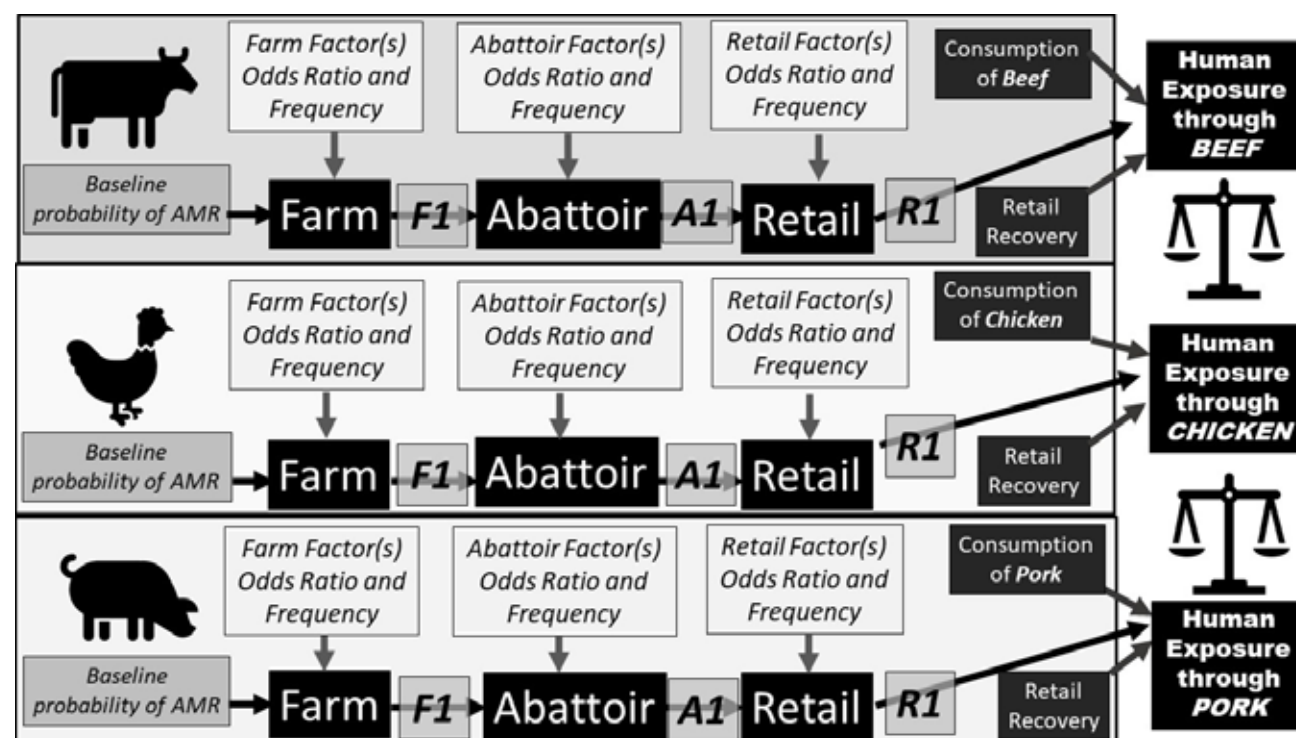
Figure 1. A qualitative representation of the quantitative models propagating the probability of antimicrobial resistance modified by factors[a] linked with antimicrobial resistance through the agri-food chain to investigate potential human exposure to resistant bacteria[b].

[a]Factors were measured observations whose relationship with antimicrobial resistance was investigated (e.g., antimicrobial use); [b]The probability of antimicrobial resistance was modified using a branching probability tree approach using 1) the odds ratio between factors and the occurrence of antimicrobial resistance, and 2) the frequency of occurrence of the factors; **F1**: updated probability of antimicrobial resistance leaving the *farm* node. This updated probability was the baseline for the *abattoir* node **A1**: updated probability of antimicrobial resistance leaving the *abattoir* node. This updated probability was the baseline for the *retail* node **R1**: updated probability of antimicrobial resistance leaving the *retail* node and was adjusted by Canadian consumption patterns and population to obtain estimates of human exposure to antimicrobial- resistant bacteria.

Antimicrobial resistance in the environment on dairy farms in Sweden

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ABSTRACT

Objective: Antimicrobial resistance (AMR) is a global public health concern and a major societal challenge for the future. An association has been found between AMR of *Escherichia coli (E. coli)* in livestock and some resistance traits in this bacterial species in humans, indicating a zoonotic spread of resistant bacteria and/ or resistance genes. The environment surrounding farms could be a source for transmission of AMR to other animals as well as humans. There are scant knowledge of AMR in environment and especially in rodents and flies, in dairy farms. To investigate the AMR pattern in the immediate environment of dairy farms.

Material and methods: Fifty-four dairy farms were visited and samples from floor drains and manure pit, bird droppings, flies and rodent droppings were collected to identify patterns of AMR in *E. coli* in the environment of dairy farms. Antibiotic susceptibility patterns were determined using a panel with 13 antibacterial agents, by use of VetMIC (MIC – Minimal Inhibitory Concentration).

Results: AMR patterns for *E. coli* from manure, drain and rodents showed some similarities, with the highest prevalence of resistance against streptomycin and sulfamethoxazole, and the lowest against florfenicol, most notably in the drain samples. The bacteria in the samples from birds showed another pattern with the highest prevalence of resistance towards kanamycin. The pattern for bacteria from flies was somewhere in the middle between these.

Conclusion: The results indicate on-farm transmission of resistant bacteria and/or resistance genes between cattle and rodents, while there were no indications of such transmission between cattle and birds or flies. However, given that the results are based on phenotypic characterization only, further study of the bacterial isolates is needed for more insight into possible transmission routes.

Key words: Antimicrobial resistance, environment, birds, rodents, flies

Antimicrobial usage and resistance surveillance strategies for developing countries

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ABSTRACT

Antimicrobial resistance (AMR) is recognised as a major threat to animal and human health. AMR surveillance is required to monitor the development and spread of resistance, but antimicrobial usage (AMU) surveillance is also needed to support stewardship programs and monitor the impact of interventions.

AMR and AMU surveillance pose particular epidemiological challenges in any context, for example, in avoiding bias and achieving estimates of adequate precision for practical decision-making. In resource poor environments of regions such as Asia and Africa, these challenges are even more complex. AMR surveillance in animals and animal products can be conducted at multiple points in the value chain: the environment, feed inputs, live health animals on the farm, animals with clinical disease, animals at slaughter or during processing, or retail products – each providing different information to address different questions, and with different costs. The number and nature of specimens collected and tests used also influence the cost and quality of surveillance.

Similarly, AMU surveillance can capture data on usage at multiple levels and resolutions – import, licensing, manufacture, wholesale, retail, in manufactured feed, veterinary supply or at the point of usage. Often, surveys are used to estimate total usage, but they generally lack precision and validity, and fail to provide the disaggregated data required to support stewardship programs.
This paper uses AMU and AMR surveillance experience in Southeast Asia to provide practical and pragmatic options to implement effective surveillance in resource poor countries with non-existent or under-developed programs. This includes recommendations on which organisms to target and practical representative sampling strategies to minimise bias. We also examine the opportunities for sustainable, high-resolution, census-based AMU monitoring as an alternative to surveys, and provide examples of systems within the southeast Asian region that may act as models for other countries.

Key words: Surveillance, antimicrobial resistance, antimicrobial usage

Harmonisation of data collection on knowledge, attitude and practices of antimicrobial use in livestock production

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ABSTRACT

Use of antimicrobials in livestock production, especially inappropriate use, is a key driver of antimicrobial resistance emergence and selection. While high-income countries have made progress in monitoring antimicrobial use, there is a distinct lack of data in low and middle-income countries. Also, knowledge, attitude and practices of livestock producers related antimicrobials is poorly understood. Adapting a One Health framework, areas relevant to understand AM use were identified during an expert workshop and translated into a KAP survey tool that was reviewed by international expert stakeholders. The aim was to develop a tool that can be used for different production systems and species in different countries to be able to collate and compare data of different sources. To encourage use of the tool and to integrate it in other surveys, attention was paid to keep the basic questionnaire below 30 minutes, requiring careful prioritisation of questions. The tool was tested in Uganda, Ethiopia and Kenya and based on feedback from interviewed farmers and of researchers conducting the interviews the tool was revised and retested. The questionnaire is available electronically in ODK format for easy compilation of data of different studies. Besides capturing data on key indicators to describe the production systems, the survey tool addresses issues such as reasons and frequency of use, source, guidance on dosage received, animals treated, experience of treatment failure, handling of expired drugs, withdrawal periods, and knowledge on antibiotics. The testing proofed the feasibility of harmonising such a survey tool and preliminary results identified areas for future interventions, mainly related to need of awareness creation and capacity building.

Antimicrobial resistance in urban mesocarnivores

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ABSTRACT

Objectives: Wildlife exposure to antimicrobial resistant (AMR) bacteria has been extensively reported, especially in human dominated landscapes. However, it is unclear whether exposure is solely driven by environmental context or whether wildlife species characteristics are also important. Disentangling these relationships is crucial for understanding how AMR bacteria are disseminated in the environment, and what the consequences might be for public and animal health. As a model for this issue, we investigated whether wildlife exposure to cefotaxime-resistant bacteria, from the family Enterobacteriaceae, was a function of spatial overlap with people and domestic dogs, or whether differences could also be explained by the type of host species sampled.

Materials and methods: Fecal samples and rectal swabs were collected from 31 raccoons, 23 opossums, and 23 coyotes, sampled from five sites (three public and two privately-owned) in north-western Chicago, USA.

Results: Cefotaxime-resistant Enterobacteriaceae were detected in 25.8% of raccoon, 21.7% of coyote, and 13% of opossum samples. While raccoons had a higher recovery prevalence, we detected no significant difference in resistance patterns by host species or by site. There was, however, a significant difference by sex, where females tended to have a higher prevalence than males, regardless of the host species sampled.

Conclusion: The lack of difference detected between areas highly used (public sites) and areas less used by people and dogs (private sites) may, in part, be due to the fact that wild animal populations in these suburban areas are well mixed and range widely, and differences are more likely to be observed across a larger scale (e.g. urban vs. suburban sites). Bacterial species identification revealed that 46.7% of resistant bacteria were Escherichia coli, 20% Enterobacter aerogenes, 20% Citrobacter freundii, and 13.3% Hafnia alvei. This suggests that multiple cefotaxime-resistant bacterial species are disseminated in the environment, and that resistance genes may be transferred between bacterial species in wildlife.

Key words: Antimicrobial resistance, dog, wildlife, urban

Assessing the transmission dynamics of antimicrobial resistant Salmonella Heidelberg in Canadian poultry production using draft genome sequence data

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ABSTRACT

Objective: We aim to identify key elements in the transmission of antimicrobial resistant *Salmonella* Heidelberg (SH), and genetic determinants of antimicrobial resistance throughout the farm-to-fork continuum in Canadian poultry production.

Materials and methods: For the present study, we selected *SH* isolates from federal surveillance programs at poultry farm, abattoir and retail levels in Ontario, Canada in 2013, and characterized them by whole genome sequencing (WGS). Using a novel *SH* core-genome multi-locus sequence typing assay, we examined the genetic diversity present in the bacterial core genome to assess the underlying population structure of *SH* circulating in the Canadian food chain.

Results: Intra-genomic diversity measured by single nucleotide variant differences in the core genomes of *SH* clustered in the same establishment was found to be greater than the inter-genomic diversity at this level. This effect was more pronounced at the farm and abattoir levels than at the retail level, where the trend was reversed. Analysis of the WGS data uncovered several genetic determinants of AMR, providing a molecular basis for results of phenotypic testing, and identifying 38% of isolates as multidrug-resistant. We identified a total of 15 chromosomal and mobile AMR determinants that included CMY-2, an *ampC* gene that encodes resistance to clinically important broad and extended-spectrum cephalosporin antibiotics. Finally, we identified a several plasmid replicon elements in our dataset, including the IncI1 plasmid, a mobile element known to be associated with the carriage of CMY-2.

Conclusion: Results from our analysis demonstrate the ability to extract meaningful information from draft genome sequence data, enhancing our understanding of the molecular basis for AMR and plasmids circulating in environments related to food production. Current results will continue to be updated with national surveillance data spanning a decade of comprehensive data collection.

Characterisation of relatedness and antibiotic resistance patterns of Escherichia coli isolated from humans and livestock in Nairobi, Kenya, by whole genome sequencing

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ABSTRACT

Objective: Evolution of microbial pathogens, including *Escherichia coli,* to evade antimicrobial treatment has been regarded as one of the most serious public health threats of this century. At present, transmission dynamics of resistant bacteria and their determinants between livestock and humans is poorly understood, particularly at the molecular level.

Using whole genome sequencing and bioinformatics analysis, our aim was to investigate patterns of genetic relatedness and to characterise antibiotic resistance profiles in *E. coli* isolates from 969 samples obtained from humans and livestock populations in Nairobi, Kenya.

Materials and methods: Our analysis identified 314 multi locus sequence types (STs), indicating a high clonal diversity within the *E. coli* population. The five most common STs were distributed across sources, indicative of frequent clonal spread.

Results: We found 53 antibiotic resistance genes (ARGs) across ten antibiotic classes. The great majority of common ARGs overlapped between humans and animals possibly reflecting overlapping antibiotic usage in human and veterinary medicine in Nairobi, or spill-over of resistance genes or bacteria between humans and animals.

Conclusion: This study demonstrated evidence of bacterial sharing and, importantly, overlapping patterns of STs and transferable ARGs, between humans and livestock in Nairobi.

Key words: Antimicrobial resistance, *Escherichia coli*, livestock, humans

Urban wildlife and the epidemiology of antimicrobial resistance in Nairobi

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ABSTRACT

Objective: In this study, we investigated the epidemiology of antimicrobial resistant Escericia coli in wildlife across the developing city of Nairobi, and related this to carriage of AMR-E. coli in sympatric livestock, humans and the environment.

Materials and methods: Faecal samples (n=2102) were collected from 78 wildlife species (n=849), 13 livestock species (n=656), humans (n=309) and the environment (n=288) from 99 households across the city. Samples were cultured for *E. coli*, and a single isolate from each sample tested for sensitivity to 13 antibiotics. Statistical models were built to answer three questions: *i)*What is the prevalence of AMR phenotypes and multi-drug resistant (MDR)-*E. coli* carriage in urban wildlife, and how does this vary between taxa? *ii)*Are urban wildlife a source of AMR diversity, when compared to other epidemiological compartments (livestock, humans, environment)? *iii)*What are the determinants for MDR-*E. coli* carriage in wildlife within households?

Results: Wildlife carried a high prevalence of MDR-E. coli [52%(252/485)], which varied between wildlife taxa (marginalR2:0.08,p<0.05). The phenotypic diversity of AMR-E. coli in wildlife was lower than in livestock, humans and the environment (p<0.01). Within households, statistical models revealed two "interfaces" for AMR exchange; i) between rodents/seed-eating birds, cattle and manure, ii) between rodents/seed-eating birds, humans and rubbish.

Conclusion: Our results show that urban wildlife carry a high burden of clinically relevant AMR-E. coli, and foraging-related life-history traits contribute to this exposure. However, compared to other compartments, wildlife are not a major source of AMR diversity in Nairobi, and could be a net 'sink' rather than source of resistance. These results provide novel insight into determinants of AMR carriage in wildlife, and routes of exposure between wildlife, livestock, humans and their shared environment.

Key words: wildlife, AMR, interface, *E. coli*, urban

Application of a new One Health evaluation framework to two research initiatives addressing antimicrobial resistance and obesity

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ABSTRACT

Objective: The "Network for Evaluation of One Health" (NEOH) has developed a new framework with tools for evaluating One Health (OH) initiatives. Aiming to illustrate the use and assess the utility of the new method for different types of OH initiatives, we applied the framework and tools to a portfolio of case studies including two OH research projects on antimicrobial resistance and obesity that are presented here.

Materials and methods: The evaluations included process assessment of six OH dimensions of 1) the „University of Copenhagen Research Centre for Control of Antibiotic Resistance (UC-Care)", a 4-year transdisciplinary research project producing new knowledge and methods to reduce the development of antimicrobial resistance, and 2) an obesity research project that was organized as a joint effort between human and animal health sector scientists across 11 European countries identifying underlying common factors associated with obesity in dog-owners and their dog(s) - a task considered unachievable by single-sector research initiatives. Information was collected by a document review (e.g. project proposal, mid-term evaluation report, publications), semi-open 1-hour-long interviews with key UC-Care consortium members and an online survey for external participants and stakeholders, as well as a survey sent to actors in the obesity study.

Results: The initiatives were described as sub-systems within their complex contexts. The theories of change including outcomes and potential impacts were deducted. Despite successful disciplinary outputs, the OH process evaluation revealed limited information and data sharing, as well as limited learning across the consortia even though they had relatively high levels of OH-thinking and systemic organisation in place. In UC-Care integrated working approaches were also limited despite proposed plans to emphasise these.

Conclusions: The application of the NEOH tools allowed identification of factors that might hinder or promote the impact in the two initiatives. The findings were presented to the project managements for consideration.

Key words: One Health, evaluation, antimicrobial resistance, obesity

Fecal *E. coli* AMR increases in mixed beef-poultry operations

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ABSTRACT

Objectives: To establish whether the practice of feeding poultry manure to cattle in mixed beef-poultry farms, together with the use of anticoccidial AM in poultry, results in fecal *E. coli* with higher levels of AMR than those of beef cattle reared without access to poultry.

Materials and methods: Twelve farms from around Harare were chosen as having either chicken only (N=4), beef only (N=4) or mixed poultry and beef on the same premises (N=4). From the cattle and chickens, rectal or cloacal swabs respectively were used to collect fecal samples from 15 randomly selected apparently healthy animals. These were cultured and *E. coli* isolates tested using disk agar diffusion (CLSI, 2017). Currently, investigations of genetic similarities between *E. coli* from cattle and chickens on the same premises that show similar AMR are underway (results to follow). Data on other management factors including previous AM use, disease problems and biosecurity measures were collected.

Results: Beef cattle kept on the same premises as broilers and fed poultry manure had significantly higher levels of resistant *E. coli* to Ampicillin ($\beta = -19.92$, df = 1, p < 0.001), Ertapenem ($\beta = -18.58$, df = 1, p < 0.001), and Ceftrioxone ($\beta = -3.066$, df = 1, p = 0.047) than beef kept as a specialized system. Broilers in mixed systems had significantly higher resistance to Ceftriaxone ($\beta = -1.743$, df = 1, p < 0.001) than broilers kept alone. Both mixed and chicken-only systems used Tetracycline, Trimethoprim-Sulphamethaxazole, and Ciprofloxacin for their broilers. All beef farmers used Tetracycline and Penicillin. Ampicillin and TMS were used by 3/4 and 2/4 specialised beef farmers. Cefepime and Ertapenem were not used in any of farms sampled. Heart water was the most important cattle disease reported in both farming systems. The biosecurity measures were lowest in beef farms.

Conclusion: AMR of fecal *E. coli* were significantly increased in beef cattle kept on the same premises as broilers and fed poultry manure. Resistance was also observed to AM that were not used in livestock.

Key words: AMR, Zimbabwe, manure

A review of veterinarypPractices and antimicrobial resistance (AMR) in Zambia

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ABSTRACT

Objective: Veterinary practices, such as the use of antibiotics in food production systems play a critical role in determining whether the development of antimicrobial resistance (AMR) occurs or not. This literature review is in line with OIE's strengthening knowledge through surveillance and research. Zambia is developing an AMR National action plan using an integrated One-Health approach. Foremost in this task is establishing a baseline for trends and practices in antimicrobial use in Zambia. The objective of this work was to review available literature on AMR as it relates to veterinary practice and/or the environment in Zambia.

Materials and methods: The literature was searched in The Web of Science article database. The following words were used: 'Veterinary', 'Zambia,' and 'Antimicrobial'. We found 1,961 published manuscripts using the above search. Only 25 manuscripts were selected for this review, the remainder were dropped either because they did not suit this review or were not in English.

Results: From the literature, the first reported manifestation of resistance was to trypanocide drugs in 1992. There was also evidence that drug administration practices were the same among both farmers and extension workers. Literature also showed that of the sampled species, pigs had the highest proportion harboring drug resistant strains. Another key finding was that antibiotic resistant strains were present not only in diseased animals but also in apparently health slaughtered animals. Attitude towards and uptake of veterinary services by small-scale cattle farmers found that more therapeutic than prophylactic services were being used. Only one study provided work on AMR in companion animals and the environment. Literature also found that the prevalence of resistant strains was had no statistical differences across farming types.

Conclusion: The existing body of literature acknowledges the presence of Antimicrobial resistance in Zambia's veterinary sector. Studies need to be undertaken to highlight the attitude, perception and knowledge of AMR in Zambia.

Key words: Zambia, AMR, Veterinary, One-Health

A European cross-sectional study identified positive associations between antimicrobial usage and resistance in broiler farms

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ABSTRACT

Objective(s): The European research project EFFORT investigates the epidemiology and ecology of antimicrobial resistance (AMR) in food-producing animals, the environment and humans to quantify AMR exposure pathways for humans. Within this project a multi-country cross-sectional study was conducted in broiler farms to identify associations at the herd level between AMR, antimicrobial usage (AMU), biosecurity and farm characteristics.

Materials and methods: In 181 herds minimum inhibitory concentrations against a panel of 14 antimicrobials were determined for a target of 10 Escherichia coli isolates per flock using microdilution. AMU was quantified using treatment incidence and Biocheck.UGent was used to assess the implementation of biosecurity measures in the farms. For resistance with the highest prevalence (ampicillin (74%), ciprofloxacine (62%), sulfamethoxazole (58%), tetracycline (57%), nalidixic acid (56%), trimethoprim (53%) and chloramphenicol (18%)) grouped logistic regression models with a random country effect were built to model the probability that an isolate was resistant to a specific antimicrobial.

Results: Positive significant associations between AMR and AMU within the respective antimicrobial classes were identified for resistance against ampicillin, ciprofloxacin and nalidixic acid; and between AMR and overall AMU for resistance against chloramphenicol, sulfamethoxazole, trimethoprim and tetracycline. Furthermore, an isolate was less likely to be resistant to a specific antimicrobial when a higher implementation of biosecurity was observed regarding animals entering and leaving the farm (ampicillin resistance) and regarding measures between compartments (trimethoprim and tetracycline resistance). On the other hand, strains were more likely to be resistant to ciprofloxacin or nalidixic acid when a higher implementation of biosecurity was observed regarding disease management.

Conclusions: This multi-country study confirms on a large scale the association between AMR and AMU for resistance against several antimicrobials. Furthermore, improving biosecurity might reduce the prevalence of AMR.

Key words: Antimicrobial resistance, antimicrobial use, biosecurity, broilers

The effect of herd health consulting on reducing antimicrobial usage in Swiss pig farms

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ABSTRACT

Objective: Antimicrobial usage for farm animals has been decreasing over recent years in many countries. However, there are only very few studies which evaluate the effect of specific interventions. The objective of our study was to evaluate the effect of herd health consulting by specialized veterinarians on antimicrobial usage and production parameters in pig farms, which regularly use oral group treatments with antimicrobials.

Materials and methods: In this controlled field study, an intervention group of 35 breeding and 35 fattening farms received quarterly visits by a trained herd health consultant over a one-year period. Health of the animals, production parameters and herd management were assessed, and potential causes for high antimicrobial use identified. At each visit, the consultant identified the three most important measures which should be implemented within the following three months. Antimicrobial usage and production data were compared to a control group of 37 breeding and 31 fattening farms, respectively.

Results: Treatment incidence in breeding farms of the intervention group decreased from a median of 321 animal daily doses per 1000 animals and day to a median of 95. The control group also decreased their usage (from 288 to 113). In fattening farms, the decrease was from 209 to 41 in the intervention, and from 248 to 179 in the control group, respectively (Figure 1). The reduction in intervention farms was significantly higher than in control farms. There was no negative effect of the intervention on production.

Conclusion: This study shows that antimicrobial use can be reduced by veterinary herd health consulting without compromising productivity.
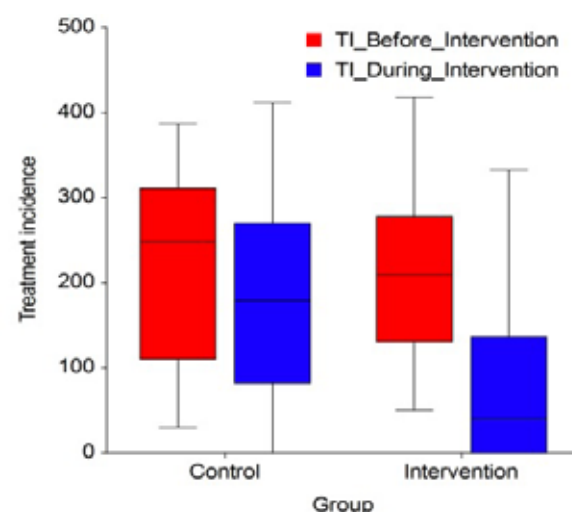
Fig 1: Treatment incidence (daily doses per 1000 animals and day) in 35 fattening farms with regular herd health consulting visits (intervention) and 31 control farms without herd health consulting.

Sow herd typologies based on biosecurity, productivity, antimicrobial and vaccine use data

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ABSTRACT

Objective: Antimicrobial use (AMU) in livestock is a global concern and many countries pursue approaches to reduce the amount used in livestock, including pig production. The EU Commission has decided to phase out use of zinc oxide in veterinary medical products by 2022, which has challenged the reduction of AMU in the European pig production. The pig producers need information about ways to comply with official AMU requirements without diminishing production and competiveness. The most efficient approaches are likely to imply a combination of multiple factors. Therefore, the objective of this study was to explore the joint effects between biosecurity, productivity, vaccination and AMU and to identify different sow herd typologies as a foundation for suggesting feasible herd health strategies under pinning an optimal level of AMU.

Materials and methods: A factor analysis was conducted on herd-level data from 152 Danish sow herds. Data consisted of several biosecurity measures, one productivity measure, herd health status, AMU for sows and weaners, and purchase of vaccines against five endemic infections.

Results: Four factors were selected based on the break-off point in the scree-plot. Factor 1 included herd type, herd size and age of farm buildings. Factor 2 covered general biosecurity, including several internal and external biosecurity measures. Factor 3 represented actions taken to prevent non-systematic swill feeding by foreign employees as part of a concern against introduction of African swine fever. Factor 4 indicated vaccination status. AMU and productivity correlated only weakly with the other variables, probably due to limited variation for both variables in the Danish study herds. This might be attributed to official restrictions on AMU contributing to a low use, and a general high level of health and biosecurity in Danish sow herds.

Conclusion: More focus on biosecurity and eradication of disease were two of the suggested strategies to improve herd health.

Key words: Pig production, antimicrobial use, vaccination, biosecurity, productivity

Antimicrobial use practices of veterinary clinicians at a veterinary teaching hospital in the United States

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ABSTRACT

Objective: To (1) identify factors influencing antimicrobial use (AMU) practices of veterinary clinicians at The University of Tennessee Veterinary Medical Center (UTVMC), (2) analyze the clinicians' preferential choices of antimicrobials, and (3) evaluate their perceptions, opinions, and concerns regarding AMU and antimicrobial resistance (AMR).

Materials and methods: A total of 121 clinicians were surveyed.

Results: Among the 62 respondents, culture and susceptibility test results and pressure from clients were the most and least important factors in their antimicrobial prescription decision-making, respectively. Compared to clinicians who obtained their veterinary degree from 1970–1999, those who graduated from 2000–2009 and 2010–2016 were 3.96 (P = 0.034) and 5.39 (P = 0.01) times less concerned about AMR, respectively.

Conclusion: There is a critical need to increase awareness about judicious AMU practices among clinicians, increase emphasis about AMR in the present veterinary curriculum, and implement antimicrobial stewardship program (AMS) in this institution. Educational activities in combination with awareness campaigns and the stewardship programs could be used to improve AMU practices at this hospital. More client education on AMR is needed.

Key word: Antimicrobial resistance, antimicrobial stewardship, antimicrobial use

Drivers for antimicrobial use in sheep farms in the UK

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ABSTRACT

Objective: In light of the global antimicrobial resistance crisis, there is particular pressure on the farming industry to reduce their usage. Although antimicrobial use (AMU) in the sheep sector is low, sheep make up around 40% of the UK livestock biomass. This means that AMU in sheep has a significant influence on the overall usage figures for livestock in the UK. Currently, little is known about sheep farmers' practices and opinions on AMU, and vets' decision-making when prescribing antimicrobials to these farmers. This study aims to understand more about AMU in the sheep sector by the implementation of two surveys.

Materials and methods: Online and paper versions of a detailed survey on production, practices and attitudes towards AMU were completed by 484 sheep farmers. A separate, factorial survey was completed by 306 vets who treat sheep and cattle. Often used in the social sciences, factorial surveys combine experimental design with survey methods to measure the judgements of professionals.

Results: Preliminary results from the farmer survey indicate that 15% (76/484) of farmers treated all lambs with oral antimicrobials prophylactically for neonatal disease. Over one third of farmers either agreed or strongly agreed that it is ok to use antimicrobials to prevent disease. Associations between farmer practices and their attitudes are being explored using multivariable logistic regression. Analysis of the vet survey identified case type, farmer relationship, other vets, time pressure, habit, willingness to pay, and confidence in the farmer as significant factors in the decision to prescribe. Males were significantly more likely to prescribe than females (P<0.05).

Conclusion: These results suggest that prophylactic use of antimicrobials during lambing is a relatively commonplace and accepted practice among sheep farmers. This was the first time a factorial survey has been implemented to understand antimicrobial prescribing practices among vets, with the aim to uncover drivers for prescribing antimicrobials to farmers.

Key words: Antimicrobial, decision, vet, sheep, survey

Assigning defined daily doses for antimicrobials registered for usage in turkeys to enable a cross-country quantification and comparison of antimicrobial consumption in 60 French, German and Spanish turkey farms

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ABSTRACT

Objective: Antimicrobial resistance (AMR) threatens our public health and is mainly driven by antimicrobial usage (AMU). For this reason the WHO calls for detailed monitoring of AMU over all sectors involved. Therefore we aimed to quantify AMU on turkey farms in France, Germany and Spain. Additionally, we aimed to determine turkey-specific Defined Daily Dose (DDD) and Defined Course Dose (DCD) values, as ESVAC values for broilers might not be applicable for turkeys.

Materials and methods: Antimicrobial treatments were registered during 1 production round on 20 turkey farms in each country. DDD and DCD values were determined for turkeys as described in previous research and compared with ESVAC values for broilers. Finally, AMU was quantified, using treatment incidence (TI) per 100 days. AMU at farm level was obtained by summing up TI_{DDD} of all treatments (TI_{DDDF}).

Results: For some active substances, turkey-specific values differed considerably from ESVAC-values for broilers. For example, DDD_{Turkey} for ampicillin$_{oral}$ was 5 times smaller than the $DDDvet_{broiler}$ value. TI_{DDDF} ranged from 0.2 to 66.6, the median TI_{DDDF} was 10.0, meaning turkeys were treated with antimicrobials on average during 10.0% of their rearing period. Seven farms did not use any antimicrobials. Aminopenicillins, polymyxins, and fluoroquinolones were responsible for 73% of total AMU. 91% of total AMU was administered in the first half of production. The average number of farms treating peaked on week 5 (18.8%) and 8 (18.6%).

Conclusion: Not all ESVAC DDDvet and DCDvet values for broilers can be applied to turkeys. However, AMU seems to be similar concerning amount and classes used. On the contrary, the timing of peaks in AMU did not match. The differences and similarities in AMU-characteristics between these different species, emphasizes the importance of studying AMU on species and farm level. Only then correct measures for a more responsible use in all food animal productions can be advised.

Key words: Antimicrobial usage, Turkeys, treatment incidence, DDD_{turkey}

Quantitative and qualitative description of antimicrobial usage in 181 broiler farms in 9 European countries

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ABSTRACT

Objective: The WHO has defined antimicrobial resistance (AMR) as one of the major threats to public health, with antimicrobial usage (AMU) as the most important driver. The broiler industry is responsible for a large share of AMU. Therefore the aim of this study was to quantify AMU on broiler farms in 9 European countries in a standardized manner to gain better insights in AMU in broilers.

Materials and methods: Data concerning AMU was collected at 181 broiler farms in Belgium, Bulgaria, Denmark, France, Germany, Italy, Poland, Spain and The Netherlands. In 20 farms per country (21 in Belgium) antimicrobial treatments were registered in detail during one production cycle. Afterwards AMU was quantified using treatment incidence (TI) per 100 days based on the Defined Daily Dose (DDDvet), Defined Course Dose or Used Daily Dose values. The total AMU on farm level was obtained by summing up the TI_{DDDvet} of all treatments on a farm ($TI_{DDDvetF}$).

Results: Overall the median $TI_{DDDvetF}$ was 9.0, meaning that on a median farm broilers were treated with antimicrobials during 9% of their rearing period. $TI_{DDDvetF}$ varied considerably on farm level with a maximum of 174.5, while all countries had at least one farm that was able to raise the broilers without any AMU. Furthermore, the average $TI_{DDDvetF}$ on country level varied, ranging from 3.3 to 36.7. Polymyxins, aminopenicillins and fluoroquinolones were the most frequently used antimicrobials with 29%, 25% and 17% of total AMU, respectively. Twenty-six percent of the farms started up treatment on day 1 of production, 49,2% of the overall AMU was administered within the first week.

Conclusion: A huge variation in AMU in terms of amount, moment and antimicrobial class, was observed both within and between countries. This suggests that in many countries there is still substantial room for improvement in the amount and type of treatments administered.

Key words: Antimicrobial usage, Broilers, Treatment incidence, DDDvet

Randomness of antimicrobial usage regarding choice of antimicrobial class and dosage on pig, poultry, turkey and veal calf farms

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ABSTRACT

Objective: Antimicrobial resistance (AMR), which is driven by antimicrobial usage (AMU), is posing a major threat to public health worldwide. To stop AMR, we do not only need to reduce AMU, we also need to promote a more responsible usage. Therefore, AMU characteristics in food animal production were explored to identify how the way these drugs are used could be improved.

Materials and methods: Within the EFFORT project, a European project investigating the epidemiology and ecology of antimicrobial resistance, details on AMU were registered on 181 broiler farms, 180 pig farms, 60 turkey farms and 61 veal calf farms. An in depth description of the set up and methodology can be found in previous EFFORT studies.

Results: When comparing the choice of antimicrobial class to treat a similar indication, totally different classes were used between countries (Figure 1), a pattern that was observed within each species. Also dosage of antimicrobials varied a lot between farms. For example, dosage of all 12 colistin treatments, administered through drinking water on the sampled broiler farms, ranged from 3.6 mg to 50.4 mg colistin per kg animal per day. This type of variation was also observed for other products and in other species.

Conclusion: These findings show a randomness of usage when it comes to choice of antimicrobial class and dosing of antimicrobial treatments. Differences in product availability and prices on regional level might explain this. Nevertheless, such randomness in AMU is no longer justifiable and should be addressed if we want to strive for a more responsible AMU.

Key words: Food animal production, antimicrobial usage, randomness, responsible usage

Figure 1. Overview of all antimicrobial classes used within each country to treat respiratory disorders on the 20 sampled pig farms in each country.
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Knowledge, attitude and practices survey on antimicrobials use and antimicrobial resistance in livestock and aquaculture production in Vietnam

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ABSTRACT

Objective: To assess level of the knowledge, attitude and practices (KAP) of pig, chicken and aquaculture producers, and stakeholders on antibiotic (AB), antimicrobial (AM), antimicrobial use (AMU) and antimicrobial resistance (AMR) in Vietnam.

Materials and methods: Structured questionnaires were used to conduct face-to-face interviews with pig, chicken and aquaculture producers (n=392) and stakeholders including veterinarians, veterinary drug and feed sellers (n=182) in Bac Giang, Phu Tho, Nam Dinh, Dong Nai, Ca Mau, An Giang provinces of Vietnam, from September 2017 to January 2018. Responses with 75% over all correct answers were defined as 'correct' knowledge, attitude or practices.

Results: Most producers and stakeholders were either familiar with AB (80% and 93%) or heard of AMR (77% and 94%). The majority of respondents received information on AMU/AMR from TV, radio and newspapers. Small proportion of producers (24-42%) and stakeholders (26-59%) had the correct understanding on AM, AB, and AMR. Some producers had 'correct' attitude on AMU (20%) and AMR (21%), while 8% and 36% of stakeholders had 'correct' attitude on AMU and AMR, respectively. Larger proportion of producers (59%) had 'correct' AMU practices than stakeholders (17%). Education and age groups, feed seller, chicken farmers were associated with lack of KAP on AMU/AMR, whereas 'incorrect' AMU practices of producers were associated to their lacking of AB knowledge (OR=1.9, 95% CI: 1.1-3.1), and 'incorrect' AMU attitude (OR=4.5, 95% CI: 2.4-8.8).

Conclusion: Results revealed the low level of knowledge, attitude, and proper practices of respondents on AMU/AMR. Veterinary authorities should develop and implement proper communication programs that target feed sellers, and chicken farmers with the goal of providing education and raise awareness. The study's methodology can be applied in other Southeast Asian countries to better understand KAP on AMR in respected countries.

Key words: Antibiotics, antimicrobial resistance, antimicrobial use, knowledge attitude and practice, Vietnam

Antimicrobial use in smallholder livestock systems in the highlands of Ethiopia

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ABSTRACT

Objective: A major factor driving the emergence of antimicrobial resistance is the high level of dependence on antimicrobial agents in animal production. However, information on antimicrobial use in livestock in Ethiopia is scarce. To understand knowledge, attitude and practice regarding antibiotic use and resistance a study involving 383 farmers is being conducted.

Materials and methods: Here we present results from piloting of the tool amongst 42 farmers and more data will be available by November. Data were analyzed both quantitatively and qualitatively.

Results: In livestock species present, farmers used antimicrobial mostly for sheep, cattle and poultry respectively. The most frequently used drugs were de-wormers (83.3 %), antibiotics (33.3 %) and vitamins (2.4 %). Tetracycline (21.4 %), penicillin and aminoglycoside (19 %) and trimethoprim-sulfonamide (4.7 %) were the most frequently used classes of antibiotics. Benzimidazoles (54.8 %) were the most frequently used anthelmintic drugs followed by triclabendazole (50%). Use of antimicrobials for group treatment for prophylactic purposes was common (90.5% of respondents). This resulted in use of broad spectrum antibiotics and de-wormers without disease been diagnosed in the herd. The most frequent reason for antimicrobial use was liver fluke followed by respiratory problems. 83.3 % of farmers had access to veterinary drugs. Most farmers (81 %) used drugs without exact diagnosis of disease cases and self-administration of the de-wormer was common. Only 24 % of farmers were able to explain correctly what antibiotics and vaccination do and 31% of farmers consume milk from their own animals who had been treated with antimicrobials.

Conclusion: The pilot study clearly shows the urgent need to understand and monitor antimicrobial use in small holder livestock keepers. Findings of the study help to target future interventions to reduce antimicrobial use and resistance in the highlands of Ethiopia. For this increasing farmers' awareness and knowledge on antimicrobial resistance will be key.

Propensity score to assess treatment practices – an application to antimicrobial prevention in broiler production

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ABSTRACT

Objectives: Preventive antimicrobial use has to be avoided in food-producing animals rearing. To achieve a significant reduction of preventive antimicrobial use, a realistic evaluation of the impact of antibiotic withdrawal would provide compelling arguments to raise awareness and convince actors. Clinical trials, the study design of reference to characterize the impact of any therapeutic option, are not easy to perform (for both ethical and practical reasons the random allocation of treatment could be refused). A propensity score approach offers an alternative and was therefore adopted to determine whether preventive administration of antibiotics at the early beginning of chicken rearing had any impact on technical performance or health characteristics of the chicken population.

Materials and methods: Historical data collected on 349 flocks of which 64 received such a treatment were analysed. Flocks were randomly selected and documented in detail regarding rearing practices and characteristics, health and treatment history through farmers interview and performance records.

Results: Administration of preventive antimicrobial treatment could be significantly related to five covariates belonging to the rearing practices and characteristics of the flocks and chicks. A theoretical probability of treatment (i.e. propensity score) was therefore estimated for each flock and used through matching or adjustment, to estimate putative treatment impact on mortality, subsequent treatments and health disorders occurrence, growth rate and condemnation rate. The analysis failed to identify any significant effect of preventive antibiotic administration on these parameters.

Conclusion: Propensity score method proved to be useful to analyse treatment practices using observational data while randomized control trials were not applicable. Early preventive antimicrobial treatment did not result in any advantage observable on flocks performance or health condition.

Key words: Antimicrobial usage, reduction, propensity score, prevention

Comparing risk-based versus random sampling in antimicrobial residue surveillance in finishing pigs in the Netherlands

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ABSTRACT

Objective: EU Member States are obliged by legislation to implement residue surveillance programs to detect illegal use or misuse of veterinary medicines in food producing animals and investigate the reasons for residue violations. These programs should be (partly) risk-based, meaning targeted towards groups of animals with the highest probability of finding residues. This study aimed to compare the effectiveness of detecting antimicrobial residues in finishing pigs with random or risk-based sampling of carcasses.

Materials and methods: A stochastic scenario tree analysis was carried out to compare the sensitivity of detecting antimicrobial residues in finishing pigs with random vs. risk-based sampling of carcasses. Two design prevalences were used: 0.03% (the expected true prevalence of residue-positive carcasses) and 0.22% (the prevalence that can be detected using the sample size laid down in EU legislation). In the random design, it was assumed that the carcasses examined for presence of antimicrobial residues were selected randomly from all finishing pigs slaughtered in a year. In the risk-based design, two risk factors were taken into account. First, a high prevalence of chronic pleuritis and pneumonia in the herd of origin was assessed. Secondly, the route of administration of antimicrobials (oral/parenteral) via visual inspection of skin lesions indicative of injectables was used as additional risk factor.

Results: Results showed that, with similar sample sizes, the probability of detecting a residue-positive carcass doubled when surveillance was targeted at pigs originating from herds with a high prevalence of chronic pleuritis and pneumonia (compared to random sampling), at similar costs of testing. Including administration route as an additional risk factor led to a negligible increase in sensitivity. Nevertheless, sensitivity values at unit level remained extremely low (<0.5%) due to the very low prevalence of antimicrobial residues in pigs.

Conclusions: In this study, risk-based alternatives to random sampling improved the cost-effectiveness of residue surveillance in slaughter pigs in the Netherlands, which could be used to enhance current programs and to increase awareness among food business operators.

Key words: Residue surveillance, scenario tree modelling, economic evaluation

National Prevalence of *Salmonella* spp. in Poultry Slaughterhouses under Federal Inspection in Brazil, 2017

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ABSTRACT

Objective: Brazil is the 2nd poultry producer and 1st exporter in the world. Due to the relevance of *Salmonella* spp. in poultry, the Ministry of Agriculture, Livestock and Food Supply (MAPA), has updated in 2016 its normative to control and monitor *Salmonella* spp. in the poultry production chain. At the poultry slaughterhouse level, the establishments monitor *Salmonella* spp. in their self-control programs and the Federal Inspection Service (SIF), verifies by official sampling cycles of poultry carcasses.

Materials and methods: We present the results of the official sampling cycles conducted from March to September/2017. In this sample collection period, 136 abattoirs slaughtered over 3 billion poultry. These establishments were classified according to poultry slaughtered per day in Small (S), Medium (M), Large (L) and Very Large (VL). The official cycles comprise 8 samples of poultry carcasses (n=8), with a maximum limit of 2 samples, where the presence of *Salmonella* spp. is detected (c=2). Sample weights were defined, which increased the validity of the data. Poultry carcass were sampled at random after chilling. A total of 1.449 samples were analyzed in official laboratories (LANAGRO) using ISO 6579 analytical reference method.

Results: The estimated prevalence of *Salmonella* spp. in poultry carcasses was 17,89 % (CI 15.50 – 20.55). Considering the representativeness of the Brazilian poultry in the global market, it is necessary to constantly evaluate and review the program to make progress in reducing the *Salmonella* prevalence.

Key words: *Salmonella*, poultry, epidemiology, Brazil

Awareness of zoonoses among small holder livestock producers in Ethiopia

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ABSTRACT

In smallholder livestock production systems humans, livestock and environment are closely interweaved. At the same time, different household members fulfil different tasks related to livestock management resulting in potential exposure to zoonoses. In order to understand the risk of exposure to different zoonoses by different household members and to get an idea on awareness of zoonoses, a mixed-methods approach was used to collect qualitative data through focus group discussions (FGD) followed by a questionnaire survey involving 432 households. Half of the 92 FGDs were conducted with women only groups and 49.3% of the respondents in the household survey were women. During FGDs, zoonoses were hardly mentioned as disease priorities with the exception of Anthrax which was ranked among the top diseases by 23 FGDs. When asked about impact of disease, human health was not perceived as very important argument for prioritizing livestock diseases. Low awareness of zoonotic diseases was confirmed in the household survey with only 46% of respondents being aware of and able to name a zoonosis. Of these respondents, 52.3% mentioned Anthrax, and most of them stated consumption of raw meat from infected animals as the main source of infection. The second most mentioned zoonosis was rabies, followed by respiratory diseases (incl. tuberculosis) and gastro-intestinal parasites such as tapeworm. The study found important misperceptions and important gaps in knowledge on zoonoses in general and on how they are transmitted in particular. The study also described the division of labour related to livestock management, which results in different risks of exposure for different household members. Findings of this study informed the design of gender responsive interventions through community conversations on gendered zoonoses risks.

Key words: Zoonoses, smallholder livestock production, anthrax, risks

The association between visual inspection of slaughter hygiene, using Hygienic Performance Rating and microbiological contamination of sheep and cattle carcasses

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ABSTRACT

Objective: The association between visual audits of slaughter hygiene by Hygienic Performance Rating (HPR) and microbiological contamination of sheep and cattle carcasses was investigated.

Materials and methods: Ten sheep and 10 cattle slaughter lines were visited in Norway, Denmark, UK, Germany, and Spain. In an HPR audit, each operation on slaughter line is assessed and given a score, which is weighted for hygienic impact and economic costs involved to improve or correct the practice. The sum of these scores yields the Total HPR score (%), where 100 % imply no deviation to what is considered best slaughter practices. Simultaneously with HPR audits, a microbiological trial and the mandatory sampling were performed. In the trial, gauze cloth swabbing of 800 cm2 (cattle) and 600 cm2 (sheep) carcasses and SimPlate® Enterobacteriaceae/E. coli (BioControl Systems Inc, Bellevue, WA, USA) was applied. Association between E. coli and Enterobacteriaceae counts (dependent variable) and scores from the individual operational sites and the Total HPR score were modelled with abattoir as random effect (generalized negative binomial). Initially, all scores, were standardized with mean zero and standard deviation of 1 to give equal weight to each score and correlation were investigated

Results: There were higher counts of Enterobacteriaceae and E. coli on sheep than on cattle carcasses and high variation between abattoirs (Figure). Moreover, there was an association between Total HPR score and Enterobacteriaceae and E. coli results obtained from the trial (but not with mandatory sampling results).

Conclusion: The HPR was demonstrated as a useful supplementary tool to document slaughter hygiene.

Key words: Slaughter hygiene, hygiene audit, sheep carcasses, cattle carcasses, E. *coli*
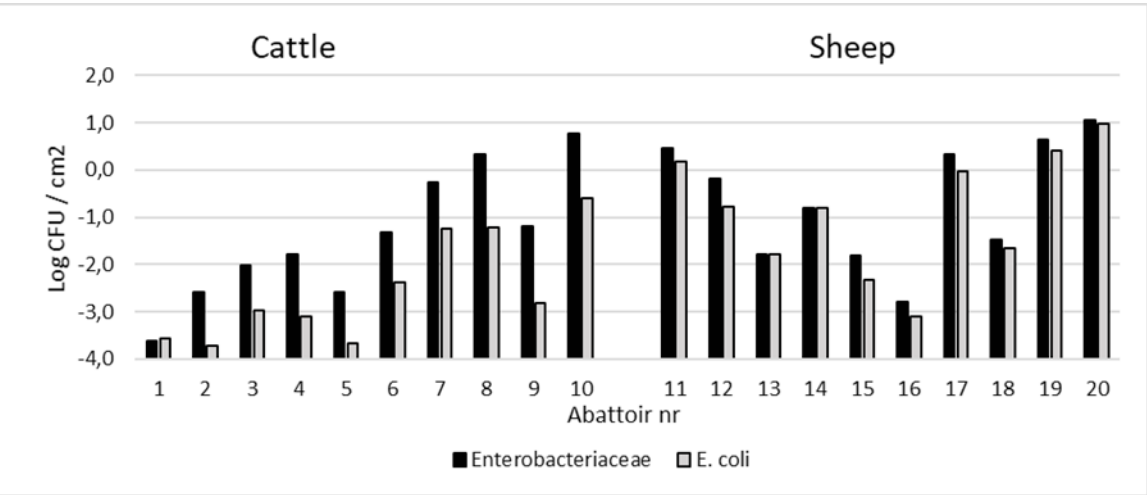
Figure. Enterobacteriaceae (black bars) and E. coli (grey bars) mean log CFU/cm^2 per abattoir (numbered from 1 to 20), for cattle to the left and sheep to the right from extended sampling.

Cross-sectional study of Crimean-Congo Haemorrhagic fever seroprevalence in sheep and farmers in Bulgaria: understanding and preparing the ground for a vaccine efficacy study

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ABSTRACT

Objective: Crimean-Congo Haemorrhagic Fever (CCHF) is a severe tick-borne disease with a high mortality rate in humans and considered a priority emerging disease. Livestock infection is asymptomatic but plays a crucial role in transmission of the virus. This study aims to inform preparations for an efficacy study of a novel vaccine by (i)estimating CCHF farm seroprevalence in young sheep, (ii)estimating within and between farm variation (iii)identifying hot spot areas for sheep exposure and factors associated with higher risk of seroprevalence and (iv)assessing exposure in farmers (as part of a parallel study)

Materials and methods: The study was conducted in two provinces of Bulgaria (Burgas and Kardzhali). Using multistage random sampling, 1200 sheep from 120 farms were selected. Sheep and farmers' blood samples, individual and farm characteristics were collected. Blood samples were tested for CCHF-IgG antibodies. Individual and farm data was analysed using mixed effects logistic regression and logistic regression with Poisson distribution respectively. Spatial scan statistic was used to identify significant clusters of farms with higher probability of having positive animals.

Results: The overall seroprevalence was 20.3% (95%C.I. 18.0–22.7%) being significantly (p<0.001) higher in Burgas. Intra-farm correlation was 0.11. Ninety six farms (80%) had at least one positive animal and were distributed throughout both provinces, but only 8 farms (6.7%) had ≥5positive animals. A significant cluster (p=0.01) of farms with higher risk of having ≥5positive animals was identified in North-West Burgas (RR=19.6; radius=21.4Km). Lambs were at higher risk of being seropositive (OR=1.51; p=0.03) compared to young sheep. Different risk factors were identified in each province reflecting differences in production systems. Three (6.8%) farmers were seropositive, two from farms located within the cluster identified.

Conclusion: These results build on the understanding of CCHF and challenge some previous assumptions. Results will provide key inputs for the study design of a vaccine trial to be conducted next year.

Key words: Crimean-Congo Haemorrhagic Fever, Bulgaria, prevalence, risk factors, high-risk areas

Emergence of a new *Leptospira* strain causes public health concerns

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ABSTRACT

Objectives: *Leptospirosis* was common in dairy farm workers in New Zealand prior to the introduction of vaccination in the 1980's. Recent reports of human leptospirosis in vaccinated dairy herds raised concerns about the level of protection. A cross-sectional study of 200 New Zealand dairy herds in 2016 showed evidence of Leptospira borgpetersenii serovar Tarassovi (TAR) not included in available vaccines and explaining most of PCR-based shedding in adult cows. We investigated TAR PCR-sequences, its emergence and impact on human leptospirosis.

Material and methods: Urine and blood of 4,000 dairy cows were tested by quantitative real-time PCR (qPCR, *gyr*B gene) and microscopic agglutination test (MAT), respectively. qPCR amplicons of 75/91 positive urine samples were sequenced and compared to reference sequences. Published prevalence studies were plotted over time to evaluate emergence. Relationships between notified human cases and their occupations were investigated.

Results: Strong associations between MAT and PCR indicated that TAR may have caused 45% of urine shedding. Amplicon sequences were not equivalent to vaccine serovars but included a unique, likely new *Leptospira borgpetersenii*-like strain that predominated (53/75, 71%) while reacting serologically as TAR. Notified human cases showed a strong association with dairy workers compared to other farming or abattoir occupations. Published prevalence studies (1953-1982) demonstrated that nine historic prevalence estimates of Tarassovi ranged 0-6% of cattle in 0-20% of herds. The 2016 survey showed 17% cows and 74% herds being seropositive for TAR.

Conclusion: The 2016 survey demonstrated exposure to an emerging non-vaccine strain that impacted strongly on urine shedding in dairy cows and clinical leptospirosis in dairy workers. This emerging strain warrants isolation and whole genome sequence analysis to understand its taxonomy and immunogenic surface antigens to inform vaccine development.

Key words: Human leptospirosis, occupational exposure, emerging strain

One Health Approach to rabies management in Manitoba

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ABSTRACT

Objective: Manitoba Rabies Central was formed in 2014 following the transfer of rabies management from federal to provincial control in Canada. The primary objective of Manitoba Rabies Central is to provide effective risk management of possible rabies exposure in humans and domestic animals in order to maintain zero recorded cases in humans.

Materials and methods: This is accomplished through the collaborative efforts of Manitoba Health, Seniors, and Active Living; Manitoba Agriculture; and Sustainable Development. These three departments of government include representation from human, veterinary, and environmental health following the One Health approach. Testing for rabies is only performed if a human or domestic animal has been exposed to a suspected rabid animal through non-intact skin contact, through a bite, exposure of mucus membranes to saliva, or if the exposure was from a bat (category II or III exposure as defined by the WHO). Samples are evaluated by direct immunofluorescence assay at a federal laboratory.

Results: Between April 2014 and February 2018 a total of 527 samples were submitted with 60 positive samples (11.4%), 16 samples which were unfit for testing (3.0%), and the remainder testing negative (85.6%). The majority of submissions were: dogs (27.9%), cats (24.1%), cows (12.9%), skunks (12.5%), bats (5.7%), and horses (3.4%), with the remainder coming from other domestic animals (2.3%) and other wildlife (11.2%). Skunks accounted for 63.3% of positive samples (n=38), and had the highest proportion of positive samples (57.6%), as compared to the overall positive proportion of samples (11.4%). The majority of positive cases were in southern Manitoba. Through the coordinated efforts of each branch of Manitoba Rabies Central, time from reported exposure to reporting of results was 3.6 days.

Conclusion: Use of a One Health approach aided in performing risk assessments, sample submission, human post-exposure prophylaxis, and animal quarantine in a timely and cost effective manner, while maintaining zero recorded human cases of Rabies in Manitoba.

Key words: Rabies, Canada, One Health

Prevalence of mental health outcomes in Canadian veterinarians

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ABSTRACT

Objective: To estimate the prevalence of depression, anxiety, compassion fatigue, compassion satisfaction, burnout, resilience, and suicidal ideation among Canadian veterinarians.

Materials and methods: A cross-sectional study was conducted from February to July 2017, using an online survey disseminated to Canadian veterinarians. Validated psychometric instruments were used to measure depression, anxiety, compassion fatigue, compassion satisfaction, burnout, and resilience. The questionnaire also included questions regarding suicidal ideation, demographics, lifestyle, and employment and career details.

Results: Responses were analysed from 1403 veterinarians in 11 provinces and territories, representing approximately 10% of the Canadian veterinarian population. The prevalence of possible 'caseness' for anxiety was 53.1% (95% confidence interval [CI]: 50.4-55.7%), and for depression, 25.2% (95% CI: 22.9-27.6%). While 31.6% (95% CI: 29.1-34.2%) of respondents had high scores for compassion satisfaction, 65.4% (95% CI: 62.8-67.9%) ranked high for secondary traumatic stress. High scores on the three components of burnout were also observed: emotional exhaustion (49.6%, 95% CI: 46.8-52.4%), depersonalization (27.9%, 95% CI: 25.4-30.4%), and personal accomplishment (43.1%, 95% CI: 40.3-45.9%). Three-quarters of respondents' resilience scores fell below the general population average. The 12-month prevalence of suicidal thoughts was 26.2% (95% CI: 23.7-28.7%), with 1.8% (95% CI: 1.1-2.6%) of respondents reporting a suicide attempt since the start of veterinary school. Male participants were older than females and fared significantly better on most mental wellness scales and subscales.

Conclusion: Participating veterinarians in Canada had higher levels of anxiety, depression, and burnout, relative to the general population. The reported prevalence of suicidal thoughts indicates that these Canadian veterinarians are a high risk group for suicide. Low resilience among veterinarians represents a crucial area for intervention, as resilience training may protect against adverse health outcomes. Overall, these results serve as a call to action for supports and educational programs directed at improving the mental wellness of veterinarians in Canada.

Key words: Veterinarian, mental wellness, mental health, suicide, resilience

Developing a comparative conditional incidence to analyze relationships between local weather and Campylobacter infections in England and Wales

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ABSTRACT

Objective: The impact of the environment on the seasonality of campylobacteriosis in humans is poorly understood, with data exhibiting puzzling patterns such as a steep increase in the incidence in England and Wales during the early summer. A key problem is that the time-varying explanatory variables are often related (collinearity). Our objective was to disentangle and quantify the contribution of each environmental factor in campylobacteriosis.

Material and Methods: We linked, using the diagnostic laboratory location, a dataset of 1.2 million Campylobacter cases over 25 years in England and Wales with meteorological datasets. Data were extracted for the date when specimen reached the laboratory and previous 90 days. Environmental variables included temperature, relative-humidity, rainfall and daylight duration. We analysed the subsets of cases when the explanatory variables were within the same narrow range (e.g., all cases with averaged rainfall and relative-humidity between 5-10 mm and 70-75%, respectively). This allowed us to: i) detect the explanatory variables and remove collinearity; ii) quantify the probability of acquiring the disease conditional on the weather variables; and iii) estimate the time lag for each environmental driver. Reconstruction of the time-series of events showed that the method accurately reproduced the empirical patterns.

Results: Rainfall was not an explanatory variable *per se*. In contrast, the steep increase in incidence in early summer and inter-annual variations were associated with temperature, relative humidity and daylight duration only. The risk of infection increased non-linearly with two-months-averaged prior maximum temperature; and varied non-monotonically with two-months-averaged prior relative humidity. In particular, the risk was highest for relative humidity between 75-80% and maximum temperature 14-16 °C.

Conclusion: We have an accurate phenomenological description of how the weather impact on Campylobacteriosis, helping our understanding of the mechanisms of transmission, *e.g.* the potential role from chicken flocks being infected from the environment in the spring.

Key words: Gastro-Intestinal diseases, environment, seasonality

Biological and anthropogenic drivers for emerging zoonoses from an interdisciplinary perspective

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ABSTRACT

Objective: As the emergence of zoonoses is influenced by social, economic, environmental, and ecological factors, a multidisciplinary and transboundary approach is required to understand, predict, prevent and control these diseases. This study aimed to identify the main drivers of emerging zoonotic pathogens and to indicate targets for prevention and intervention from an interdisciplinary perspective.

Materials and methods: Identification of drivers was based on three case studies: Lyme disease and Q-fever in the Netherlands, and classical rabies in South-America. For each case study a schematic diagram was drafted to depict drivers for emergence based on literature review and expert knowledge. Experts from different disciplinary backgrounds were asked to evaluate these diagrams, and to identify five drivers that could best be targeted for effective prevention or control (critical control points for intervention, CCPs). Two different methods were used for this expert consultation: an interactive workshop and a questionnaire using a Delphi approach.

Results: Based on the schematic diagrams for the cases studies, we distinguished nine generic clusters of drivers, five of which were classified as biological (climate, landscape, vertebrate hosts, arthropod vectors, agent aetiology) and four as anthropogenic (human behaviour, nature management, living conditions, human and veterinary medicine). Results of the expert consultation were consistent between the workshop and the Delphi study, and indicated that drivers related to human behaviour and awareness/knowledge are important CCPs for both Lyme disease and rabies. For Q-fever, drivers related to livestock farming and human and veterinary medicine were considered the most effective CCPs.

Conclusion: The multidisciplinary approach of this study enabled a robust inventory of biological and anthropogenic drivers for emergence of zoonoses, and as such contributes to improved understanding of the complex interactions between drivers. Targets for effective prevention and control of the case pathogens were mainly associated with anthropogenic drivers.

Key words: Global one health, drivers, emerging zoonoses, critical control points, expert consultation

Risk factors and spatial cluster determination for non-typhoidal *Salmonella* spp. circulating in backyard production systems raising poultry and/or swine in central Chile

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ABSTRACT

Objective: The aim of this study was to identify epidemiological risk factors and spatial distribution of *Salmonella*-infected BPS breeding poultry and/or swine in central Chile.

Materials and methods: A proportional stratified random sampling was performed at province level in three regions from central Chile. *Salmonella* isolation was carried out for 1,744 samples collected from 329 BPS in central Chile. Faecal samples were taken from swine, poultry, other domestic birds, as well as environmental faecal samples. Confirmation of *Salmonella* spp. was carried out with *invA*-PCR. A logistic regression model analysis was performed. Variables with a *p-value* ≤ 0.25 were selected for the multivariable model. Lowest log Likelihood Ratio Test (LRT) model was selected as final model, using a backward elimination procedure removing variables with non-significant coefficients ($P > 0.05$). Goodness-of-fit was assessed using the Hosmer and Lemeshow Test (HLT). The Bernoulli model of spatial scan statistic was performed for cluster detection.

Results: 25 samples (1.4% of total samples) from 15 BPS (4.6 % of total sampled BPS) were *Salmonella*-positive. Increasing the number of birds other than chickens (OR 1.04, 95% CI 1.01 – 1.07), BPS with mixed activities (agricultural and other non-agricultural) (OR 5.51, 95% CI 1.28 – 28.44) and BPS using a mixed origin for animal replacement (OR 5.23, 95% CI 1.35 – 20.19) had a significantly higher-risk of becoming *Salmonella*-positive. While BPS that takes any action when observing a disease (OR 0.19, 95% CI 0.05 – 0.69) were at significant lower risk. The model presented a good fit to the data ($P = 0.14$). Only one borderline significance cluster was detected ($P = 0.08$).

Conclusion: First evidence of epidemiological risk factors for BPS-positivity to *Salmonella* spp. in Chile and the presence of borderline significant high-risk clusters, highlighting the importance of BPS biosecurity and food safety education.

Clostridium difficile on Ohio (USA) swine farms: A comparison of swine and human environments and assessment of on-farm risk factors

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ABSTRACT

Objective: Swine are a reservoir for the pathogen *Clostridium difficile*. Although transmission of *C. difficile* from swine to human farm workers has been previously suggested, the role of farm environmental surfaces, specifically worker breakrooms, as an important route of transmission has not been explored. This study aimed to compare the prevalence of *C. difficile* and distribution of PCR-ribotypes in swine and human environments on swine farms and determine associations between biosecurity protocols and the presence of *C. difficile*.

Materials and methods: Thirteen Ohio (USA) swine farms were visited and farm surveys (demographics, biosecurity and infection control practices) and environmental samples collected. Culture, PCR and ribotyping were used to confirm and characterize *C. difficile* isolates. Responses from surveys were modeled against *C. difficile* recovery using mixed effects logistic regression.

Results: Samples (n=629) were collected from swine (e.g. floors, gates, piglet feces) and worker breakroom surfaces (e.g. refrigerators). *C. difficile* was recovered from all farms. Farrowing units exhibited the highest prevalence (60%), followed by breakrooms (50%), and nursery units (9%). Farrowing units and breakrooms were found to have significantly (p<0.0001) higher odds of *C. difficile* recovery than nursery units (OR=40.5; OR=35.6, respectively). Ribotypes 078, 412, 005, and 596 were recovered from both swine and human environments, two of which (078 and 005) have been previously implicated in human disease. *C. difficile* recovery in breakrooms was associated with high prevalence in the farm's farrowing unit (OR=3.2, p=0.027). Cleaning practices and farm size (number pigs weaned/year) were significantly associated with *C. difficile* presence.

Conclusion: The association between contamination of surfaces in the swine and human environments and high prevalence with virulent ribotypes found on surfaces in breakrooms suggest these surfaces may be an important source of *C. difficile* transmission to swine farm workers.

Key words: Swine, *Clostridium difficile*, zoonosis, biosecurity, infection control

Analysis of socio-economic factors associated with voluntary rabies control measures in Vietnam

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ABSTRACT

Objectives: Rabies is a fatal zoonosis that kills over 60,000 people annually, mostly in developing countries. In Vietnam, rabies remains problematic despite the availability of dog rabies vaccination. The purpose of this study was to clarify the socio-economic factors associated with voluntary rabies control measures among the general population using a Knowledge, Attitudes, and Practice framework to provide health and veterinary authorities in Vietnam with baseline information for better planning of policy supports.

Materials and methods: A questionnaire survey with interviews was conducted in 495 households in Thai Nguyen Province in September 2016. After the survey, uni- and multivarable analyses were performed to detect factors associated with the practices of dog rabies vaccination and tethering dogs. Structural equation modelling (SEM) was performed to understand the structures associated with practice decisions.

Results: Our results showed that the practice of dog rabies vaccination was promoted by good social status, rich knowledge, and positive attitudes toward dog rabies vaccination. Vaccination coverage in this study area was 77.4%, and mean estimation of willingness-to-pay for a vaccination was 51,959 Vietnamese dong. Although the practice of tethering of dogs was not good, willingness to confine dogs if this practice were to be enforced was excellent.

Conclusions: In conclusion, findings from this study provided valuable information on the importance and focus of public education programs. In addition, the high willingness-to-pay for dog rabies vaccination and tethering of dogs would be encouraging data for decision makers to develop dog rabies control strategies.

Key words: Rabies, dog, vaccination, risk factor, willingness-to-pay

Seroprevalence and risk factors for human brucellosis in agro-pastOral areas in Morogoro region, Tanzania

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ABSTRACT

Objective: Brucellosis is one of the most prevalent zoonotic diseases in the world. The authors had revealed the endemic situation of bovine brucellosis in agro-pastoral areas in Morogoro Region, Tanzania. This study was conducted to determine the seroprevalence of human brucellosis and to identify its risk factors.

Materials and methods: A cross-sectional study involving questionnaire survey, blood sampling and sero diagnosis by competitive enzyme-linked immunosorbent assay was conducted from January to February 2018 at 4 villages in Mvomero District in Morogoro Region, Tanzania. The participants were the farmers who participated in the previous bovine brucellosis study, their family members and others in the villages. People with willingness to participate in the research were involved.

Result: Total 132 people were included, and 53 people were from the farms which participated in the previous bovine brucellosis research. The human brucellosis prevalence was 33.3% (44/132, 95% CI: 25.5–42.1). Maasai were significantly sero-positive (56.5%) than other tribes (28.4%) (OR = 3.2, 95% CI: 1.3–8.4). Drinking raw milk was a risk factor of human brucellosis (OR = 4.0, 95% CI: 1.6–10.2). Maasai conducted more risky behaviours for human infection such as drinking raw milk (OR = 7.8, 95% CI: 2.9–22.1) or blood (OR = 7.9, 95% CI: 2.6–24.9) and helping delivery with bare hands (OR = 3.2, 95% CI: 1.2–8.4) than other tribes. Agreement (kappa value) between bovine brucellosis result of participant's farm and human brucellosis result was -0.55.

Conclusion: Maasai should be prioritized in the disease control program in the areas. Bovine and human brucellosis were not associated in participants' farms. More information about the milk value chain and the sociological aspects of Maasai is necessary.

Key words: Brucellosis, human, risk, Tanzania

Using participatory approaches to investigate the drivers, attitudes and communication networks for improving the management of zoonotic diseases among smallholder farmers in Pakistan

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ABSTRACT

Objective: The aim of this study was to investigate the knowledge, perceptions and communication networks in relation to zoonotic diseases among smallholder farmers in Pakistan.

Materials and methods: A participatory epidemiological (PE) study was conducted among smallholder farmers (n = 82) in four districts of the Punjab. The study was implemented using focus groups and data were gathered using pre-established questions, activities and group discussions. Quantitative data is presented as descriptive statistics and qualitative data analysis was carried out using coding of the open questions to find the common descriptors. These common descriptor data were analyzed using thematic analysis.

Results: The findings indicate that farmers are not concerned about zoonotic diseases, with haemorrhagic septicaemia, foot and mouth disease, and mastitis being considered the three most important diseases of concern, with economic cost being the main reason explaining this concern. Farmers reported conducting practices posing a risk of zoonotic disease, with over half of participants reporting using raw milk and raw milk products. However, approximately half of those conducting these practices considered them to pose a risk for disease transmission. The drivers for these practices included family tradition lack of resources and lack of understanding. In the event of an animal health problem farmers would self-treat or contact senior farmers in the village; with government veterinary assistants being only contacted sometimes. Similarly, in relation to human health problems, half of participants reported to use self-treatment, with 58% indicating that they would go to the village dispensary. Access to animal and human health stakeholders and to resources was the most important driver of farmer actions.

Conclusion: This study indicate there is low awareness of zoonotic diseases and a clear disconnection between risk perception and practices conducted, supporting the need of the development of targeted extension programs delivered by trusted stakeholders.

Key words: Brucellosis, Pakistan, participatory epidemiology, zoonotic diseases

Zoonotic brucellosis at the human-cattle farm interface: a One Health opportunity, Gauteng, 2016

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ABSTRACT

Objective: In South Africa, bovine brucellosis is endemic and controlled by governmental Veterinary Services through quarantine, test and slaughter and vaccination since the 1970s. Despite this, there has been an increasing trend of cattle herd prevalence over the last five years but no increase of reported human cases. This objective of this study was to determine the level of exposure and risk factors for zoonotic brucellosis in farm workers on farms with Brucella positive cattle herds as well as assess the health seeking behavior of this occupational group.

Materials and methods: A multidisciplinary field team investigated the occurrence of, and risk factors for brucellosis in farm workers on cattle farms with Brucella positive cattle herds, identified through routine veterinary surveillance between 2014 and 2016. A cross sectional seroprevalence survey was conducted on all farm workers on these farms using the RBT, Elisa IgG and BrucellaCapt serological tests. Structured questionnaires were used to capture human, social and herd management risk factors. Data were analyzed using univariate and multivariate logistic regression models (STATA 14).

Results: 208 human samples from 41 farms were tested. 48.8% farms had at least 1 seropositive person while 14.4% (n=30) of farm workers were positive to at least one test. At farm level, significant risk factors associated with seropositivity were: being of White ethnicity (p = 0.008) and the presence of goats on the farm (p = 0.004). Vaccination was associated to seronegativity in people (p = 0.004). The "White" ethnic category was significantly associated with poor health-seeking behavior (p = 0.002) and a low probability of detection at first line medical care, (0.21), which reduced further (0.06), if the occupation of the farm worker was not disclosed to the consulting doctor.

Conclusion: The high brucellosis seroprevalence (14.4%) in farm workers and the low probability of brucellosis detection in farm workers at first line medical care is a critical gap in public health that can potentially be addressed by field veterinarians. We discuss the implications of integrating Public Health with Animal Disease Control in brucellosis detection and mitigation at the human-cattle farm interface.

Key words: Brucellosis, Zoonotic Disease, One Health, human-cattle farm interface

Anthrax: a striking example of the impact of neglected zoonotic diseases

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ABSTRACT

Objective: Anthrax, while ranked amongst the major poverty-related neglected zoonotic diseases by the World Health Organization, is poorly documented in endemic settings worldwide, making it difficult to assess its impact on animal and human health, and on livelihoods. The aim of our study was to better understand the epidemiology and implications of anthrax in livestock-dependent communities in endemic areas.

Materials and methods: This study was conducted in the Ngorongoro Conservation Area (NCA) in northern Tanzania. While there were some evidences suggesting this was an affected area, prior to our study only a handful of cases were reported annually in livestock. Two hundred household surveys were conducted across seven NCA wards in 2016. Additionally, active investigation of suspected animal and human cases was carried out by a dedicated field team, including the collection of samples for molecular diagnostic testing (qPCR) and microscopic examination.

Results: Our results confirm that cases of anthrax occur frequently in livestock and humans in the NCA throughout the year, particularly in extremely dry weather conditions. Using molecular testing, Bacillus anthracis DNA was detected in more than two thirds (292/422) of the anthrax-suspect livestock carcasses sampled. More than 7% of all households surveyed reported the loss of over 100 animals due to suspected anthrax in the period between 2015 and 2016, which represents a minimal loss of more than 2500 USD per household, greater than the mean annual household income. Since many cases occur in remote areas, these figures likely underestimate the true burden of the disease.

Conclusion: Neglected zoonotic diseases such as anthrax have major but under-recognized impacts on health and livelihoods in rural communities. This case begs the question why such prevalent and impactful diseases remain so invisible. Awareness and control efforts at all levels will be essential for reducing the impact of this neglected zoonosis and the associated losses.

Key Words: Anthrax, Bacillus anthracis, One Health, surveillance, zoonosis

Understanding poultry farmer outbreak behaviour in Vietnam through the combined use of behavioural games and semi-structured interviews

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ABSTRACT

Objectives: The objectives were to (1) identify epidemiologically significant outbreak behaviours amongst small and medium-scale chicken farmers in Vietnam and the associated influencing factors and (2) assess the impact of these factors on farmer behaviour.

Materials and Methods: The study involved the use of a novel approach intended to complement existing epidemiological study designs. Data was collected in two stages in two neighbouring villages in Hải Dương Province, Vietnam. In Part 1, 30 individual semi-structured interviews were conducted followed by four focus group interviews with five farmers in each group. In Part 2, three behavioural games were individually played by 100 farmers. The games were used to experimentally assess the role of specific factors on the behaviours of interest identified during the interviews. Games 1-2 investigated the selective sharing of outbreak information and altruism. Game 3 investigated farmer willingness to either sell chickens or report outbreaks under different levels of risk and rewards during a hypothetical outbreak scenario.

Results: Several epidemiologically significant outbreak behaviours were identified from the interviews, including variable willingness to sell sick chickens, report outbreaks and share outbreak information. The games revealed inter and intra-village variation in farmer altruism and sharing (Games 1-2) and in the willingness to take risks and report outbreaks (Game 3). Influencing factors included farmer livelihood strategies, timing of outbreaks, social distance, community preferences and levels of trust in peers and the government.

Conclusion: Farmers may adopt epidemiologically significant behaviours during outbreaks and these behaviours are affected by local and context-specific factors. Disease prevention and control activities involving farmers should consider this to maximise effectiveness. The methods developed during this study can be used as a companion tool when investigating complex human-animal disease systems.

Key words: behavioural games, outbreak behaviour, poultry, avian influenza, zoonoses

What influences livestock farmers and traders to adopt behaviours to reduce zoonotic disease transmission from livestock in Myanmar?

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ABSTRACT

Objective: There is an eminent lack of information on the attitudes and behaviours of livestock farmers and traders on the prevention of zoonotic disease transmission in developing countries.

Materials and methods: Surveys were used to compile data on zoonotic disease prevention practices conducted by livestock farmers (N = 613) and traders (N = 65) in Myanmar. Multilevel generalized linear modelling was applied to the data collected in a health belief modelling framework. In addition, livestock trading density was characterised by using social network analysis and network parameters were included in the models.

Results: Livestock traders were more aware of zoonosis transmitted by cattle compared to livestock farmers ($p < 0.05$), while people, not rearing or trading small ruminants and/or poultry were less likely to be aware of the zoonotic risks associated with these livestock species ($p < 0.05$). Information on zoonosis transmitted from small ruminants was mainly promoted through farmers ($p < 0.05$), while information on zoonotic diseases that can be obtained from poultry was disseminated through farmers, local authorities and the media. The availability of information about zoonosis to traders influenced their confidence to implement preventive actions ($p < 0.05$). Appropriate hand hygiene measures (i.e. cleaning of hands after touching, cutting, cooking meat) and treating of sick animals increased the confidence of small ruminant and village chicken owners to prevent zoonotic diseases ($p < 0.05$).

Conclusion: The results of this study can be used to implement reliable and efficient strategies to reduce the likelihood of zoonotic infections on farms and at markets.
Key words: zoonoses, livestock, farmers, traders, prevention

Modelling the probability of introduction and establishment of *Salmonella* subtypes of biosecurity concern in Australia through beef imports

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ABSTRACT

Objectives: This study investigated the probability of introduction and establishment of *Salmonella* enterica Typhimurium Definite Type 104 (*Salmonella* DT104) among humans and animals in Australia via imported beef.

Methods: An exposure assessment was conducted to evaluate pathways of direct and indirect exposure of humans and animals to *Salmonella* DT104 present in imported beef, using scenario trees. Pathway probabilities were estimated using Monte Carlo simulation modelling with @RISK 6.0, considering volume of imports from different countries and different prevalence of *Salmonella* DT104 in beef. The human health implications of *Salmonella* DT104 establishment in animals were investigated estimating the additional yearly number of human cases, hospitalisations and deaths due to this establishment.

Results: The probability of entry of *Salmonella* DT104 for each exposure unit being introduced is very low for all the scenarios considered. For each infected exposure unit, defined as standard meat serve size (80-120g) being imported, the median probability of direct exposure to humans and animals is estimated to be very low (0.023) and extremely low (0.0001), respectively. When 2,000 to 20,000 infected exposure units are introduced, the expected median number of exposures in a year, ranges from 45 (95% prediction interval, 6-88) to 454 (61-856) in humans, 0 (0-1) to 2 (0-7) in wildlife and 1 (0-7) to 15 (2-60) in domestic animals. Establishment of *Salmonella* DT104 in cattle would led to less than one additional death and 30 hospitalisations per year in humans. The models predicted up to two additional deaths and 350 additional hospitalisations if *Salmonella* DT104 became established in poultry.

Conclusion: Considering the model assumptions, the likelihood of *Salmonella* DT104 entry and exposure posed by each exposure unit being imported is extremely low in humans and negligible in wildlife and domestic animals. Establishment of *Salmonella* DT104 in poultry would have the most significant human health outcomes.

Key words: Salmonella DT104, scenario trees, simulation modelling, beef

Risk factors of human cystic echinococcosis in urban areas of Aysén region in Chile

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ABSTRACT

Objective: Cystic echinococcosis (CE) is a parasitic zoonotic disease caused by the cystic stage of the cestode parasite *Echinococcus granulosus,* in which the definitive hosts are mainly domestic dogs. In Chile CE is endemic and the region with the highest incidence is the Aysén region where exists all factors for parasite maintenance such as home slaughtering, inadequate dog deworming and feeding dogs with infected livestock's viscera. The aim of this study was detect people affected with CE in households in three cities from the Aysén region in Chile and assessing risk factors for CE in the area.

Materials and methods: A cross-sectional study was carried out in Aysén, Coyhaique and Cochrane between February and March 2016 where 1,156 households were visited. An epidemiological questionnaire was applied to household owners inquiring about whether a person at household has been diagnosed/treated with CE. Confirmatory methods were proof of scan, surgery and/or medical treatment. Socioeconomic and cultural questions were made at the household and individual level. A multivariate logistic regression was conducted in R 2.12 to assess risk factors for the presence of households with people diagnosed with CE.

Results: Overall, 661 (57%) households had dogs; of these, in 51 households we recorded people who had been diagnosed with CE by health services, 36 in Coyhaique, 8 in Aysén and 7 in Cochrane. Of 21 factors explored we found that there are 3.5 times more opportunity to find households with people diagnosed where there is knowledge of the prevention of this disease. Also, we found 3.3 times more chances where dogs are present when livestock is slaughtered at household. Finally, two times more chances were found in those households that reported taking their dogs to the countryside.

Conclusion: CE is present in urban areas of Aysén region and education and de-worming is suggested to reduce incidence in urban people.

Brucellosis exposure among animal health workers in India: Risk factors and identification of hotspots for bovine brucellosis

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ABSTRACT

Objectives: This study was conducted to determine (a) risk factors for brucellosis seropositivity among animal health workers, (b) reasons for differences in brucellosis seroprevalence between veterinarians and para-veterinarians, and (c) if brucellosis seroprevalence in animal health workers could predict bovine brucellosis hotspots.

Materials and methods: Animal health workers working in a district of India were enrolled and requested to donate a blood sample and complete a questionnaire. Blood samples were tested using three Brucella serological tests. Questionnaires data and laboratory testing results were analysed using logistic regression to identify risk factors for brucellosis seropositivity. SaTScan analyses were conducted to identify significant clusters of brucellosis. Bulk milk samples were then collected from high and low seroprevalence clusters and tested using milk ring test and ELISA.

Results: Of the 279 serum samples tested, 19.7% to 53.8% were positive in three serological tests. Veterinary pharmacists and animal handlers had 10.3 and 9.6 times, respectively, the odds of testing positive than veterinarians (p = 0.009). Veterinary pharmacists reported handling a greater number of cases of retained placenta and still-birth than veterinarians (p<0.001). The numbers of years spent in veterinary practice were positively associated with brucellosis seropositivity. Four clusters were identified based on brucellosis testing results, and bulk milk samples (n = 533) were collected from 15 villages in these clusters. Brucellosis seroprevalence among animal health workers was significantly associated with the bovine herd prevalence estimated based on milk ring test (p = 0.0013) but not based on milk ELISA (p = 0.16).

Conclusion: The results provide crucial information for making policy decisions for controlling occupational brucellosis in India. Control and education programs should preferably target para-veterinarians to reduce their level of exposure.

Key words: Brucellosis, zoonosis, veterinary personnel, animal handler, India

E. Special section: Our trend and future

Use of scenario planning methodologies to explore the long-term future of the veterinary epidemiology discipline

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ABSTRACT

Objective: To facilitate strategic thinking from experts in the field about current and future challenges in veterinary epidemiology and public health.

Materials and methods: At the 2018 Society for Veterinary Epidemiology and Preventive Medicine (SVEPM) conference in Tallinn, Estonia, a participatory workshop was conducted with delegates from a wide variety of backgrounds to explore the focal question: What is the long-term future of veterinary epidemiology? Scenario planning methodologies were used to structure the dialogue given the broad scope of the question. Elements of the process included: identification of trends and key uncertainties, development of consistent and plausible scenario narratives and use of these as decision tools.

Results: Workshop participants prioritised important scientific, technological, political and environmental drivers influencing the profession and the development of epidemiological principles and approaches. These included consideration of the end-users of epidemiological evidence and how to communicate risk and uncertainty; new methodologies to generate epidemiological data; how data are shared and accessed and funding strategies for research. In a broader context, participants also highlighted the importance and uncertainty of societal and political drivers on epidemiological research networks, data sharing and communication. Developing communication skills and trusted science communication networks and proactive efforts to promote the profession were identified as necessary strategies if epidemiologists are to reinforce their valuable position within animal and human health in the future.

Conclusions: A variety of critical factors have influenced the scope and application of epidemiological research. In the next 20 years, epidemiologists may have an increasingly important part to play as knowledge brokers at the interface of "man and machine", for both policy and industry.

Key words: Epidemiology, futures, education, scenario planning

Bridging the gap – an interactive self-study tool for advanced epidemiological methods

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ABSTRACT

Objective: Epidemiology can be a challenging subject to teach. While interactive online training is increasingly used to provide first introductions into basic concepts, few self-study tools exist that support learning of more quantitative analyses. Learners mostly have the choice of costly face-to-face training or engaging in time-intensive self-study to acquire advanced skills. To overcome these challenges and to support the teaching programme at the University of Minnesota, the learning platform TOOLS/savi was developed.

Materials and methods: RStudio Shiny was selected as the base development framework which enabled publishing to the web as well as offline capability using RStudio. Analyses were coded as R scripts. D3.js graphics library, Bootstrap, JavaScript and HTML were used to extend functionality. Following the development of an initial prototype the interface was tested by users of different backgrounds using a standardised feedback form.

Results: The final version of TOOLS/savi contains three different modules – genetic analysis, OptiSample and network analysis. Users have the option to use provided example data or to upload their own. Results can be exported both in csv as well as image format. A detailed user guide and embedded context-sensitive information is provided. Video tutorials introduce each module.

Conclusion: TOOLS/savi was very positively received by test users and provides new opportunities for hands-on learning of advanced epidemiological methods. Advantages of the platform include self-guided learning, easy access, the ability to add new modules as required and options to use either one's own or example datasets. Testing of the tool was critical to ensure a seamless user experience.

Key words: Learning, analytical epidemiology, dashboard, online
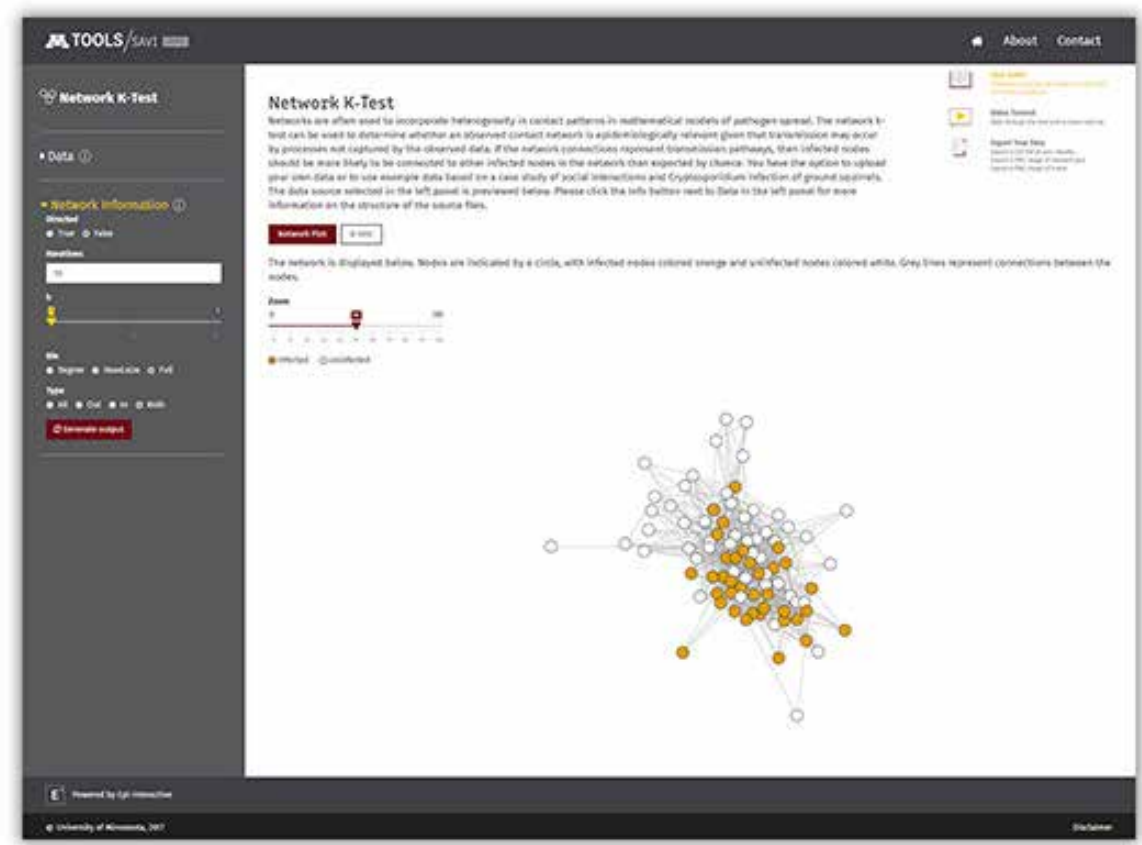
Figure 1. Screenshot of TOOLS/savi module on network analysis

A novel way of bringing One Health to veterinary and medical students

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ABSTRACT

One Health promotes the integration and collective consideration of human, animal and ecosystem health, resulting in value-adding to all disciplines. Many undergraduate curricula teach One Health and post-graduate courses also exist, to great effect. However, the mechanics of the day-to-day integration of One Health in generalist medical and veterinary practice appears difficult to influence.

Wagga Wagga is a regional city in Australia with a population of 65,000, a large rural referral hospital, numerous generalist medical and veterinary clinics, a veterinary school and two regional medical school campuses: a perfect environment to explore the interface between human and animal health. In order to do this, a "One Health Day" (1HD) is run to provide specific teaching and, moreover, to promote and facilitate interaction between medical and veterinary disciplines.

The 1HD is a full day of teaching for 5th year veterinary and medical students in the region. It is attended by all 5th year undergraduate students and a selection of specialists. In 2017, the day was attended by a GP, infectious disease specialist, cardiologist, paediatrician, public health registrar, two veterinary epidemiologists, a veterinary internal medicine specialist and a number of other clinical veterinarians. The day is structured to include minimal didactic teaching (pre-emptive lectures are delivered to veterinary and medical students prior to the day to ensure baseline knowledge), case-based learning and challenging provocative cross-group discussion. It covers infectious and non-infectious diseases, with specific reference to human-animal interaction and antimicrobial resistance. Cross-table and cross-room discussions are facilitated by staff to ensure that the synergies, differences and potential for value-adding across disciplines are adequately explored and appreciated.

We experience enthusiastic "buy-in" in the 1HD from staff and students. This represents a small, but important, step towards integration of One Health principles at the level of primary veterinary and medical practice in regional Australia.

Key words: One Health, education

Integrating Education into One Health Action: South Asian Experience

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ABSTRACT

Massey University has implemented 2-year One Health Epidemiology Fellowship Program in four South Asian countries from 2014-2016. Under this program 24 medical and veterinary doctors have been trained together as a cohort in One Health epidemiology. Participatory engagement with key government, non-government and research institutions working on detection and management of emerging and endemic zoonotic diseases, and with universities educating future public health, animal and wildlife health professionals, is a critical success factor for this One Health epidemiology capacity-building program. Central to this is establishment of a collaborative framework and engagement of host organisations from both the human health and the animal health sectors in each country to partner with Massey University in the design and implementation of in-country and regional activities structured into a 2-year program. This arrangement provided a strong and supportive in-country base for program participants, created opportunities to strengthen host and collaborating organizations' capacity through involvement in program design and delivery, and strengthens collaborative One Health relationships within and between countries. Collaboration on applied epidemiology, policy evaluation and train-the-trainer components of the program between the host organisations, government institutions and universities stimulates multidisciplinary and inter-sectoral engagement. Agile design allowed programs to be customized to suit institutional arrangements and capacity-building needs in each country, with coordination managed nationally by the host organisations and regionally by a Regional Program Coordinator.

This presentation will share the experiences and success stories of this unique education program implemented through a regional approach.

Use of R Shiny Apps for technology-assisted teaching of probabilistic modelling in animal health and food safety

M. Crotta*, E. Abu-Basha, J. Guitian

ABSTRACT

Objective: Computer technology has proven to be extremely useful in enhancing education of veterinary students by the use of interactive/dynamic representation of fundamental epidemiological and statistical concepts such as randomness, sampling procedures or the relationship error-sample size. Several studies have demonstrated how the use of interactive applications increase students' understanding, particularly for "visual learners", which are normally disadvantaged in statistical classes due to the very nature of the subject. While a variety of websites provide online tools for the most common epidemiological calculations, web-based applications specifically suited to risk analysis and probabilistic modelling are scant. As a part of the OIE Veterinary Education Twinning Programme RVC-JUST, we developed a collection of visually appealing and freely accessible Apps intended to be used as interactive tools for technology-assisted instruction of stochastic processes and basic quantitative modelling in veterinary epidemiology.

Materials and methods: The Shiny package in R 3.4.1. was used to develop a collection of Shiny apps including instructions, graphical representation and summary statistics of: (i) The basic stochastic processes: Binomial, Poisson, Hypergeometric and Multinomial; (ii) Binomial process with inclusion of Sensitivity and Specificity; (iii) The mixture distribution: Beta-Binomial and Gamma-Poisson and (v) Second-order cumulative probability plots. The apps were conceptualized to be as interactive as possible with all the distribution parameters, summary statistics and graphical features being inputted/selected by the user.

Results: A collection of nine apps covering a range of topics within risk analysis and quantitative probabilistic modelling have been made freely available at: https://mcrvc.shinyapps.io/stochastic_processes_rvc-just/. The apps are mainly designed for students in Veterinary Medicine but can be easily suited to other settings from the source code available from the corresponding author.

The set-up of an international One Health master program: the InterRisk program in Southeast Asia "Assessment and management of health risks at the human, animal and ecosystem interface"

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ABSTRACT

Southeast Asia (SEA) is at particular risk for new pathogens. Building bridges among health, environment and development sectors has been recognized by SEA countries as a major challenge. The integration of One Health (OH) into educational programs is urgently needed to put the concept into practice

Kasetsart University, the National Veterinary School of Toulouse and the CIRAD have decided to join forces for developing a new OH master curriculum in SEA. InterRisk curriculum was designed through regular interactions between academic staff, researchers, and professionals working in SEA. OH projects implemented in the region were identified, with the aim to be used for creating "real-life" teaching materials. The program was accredited by both Universities in June 2015.

The program aims at training students to conceptualize and design holistic health programs, which integrate epidemiological, ecological, and socio-economic approaches. The course comprises four study semesters, with two periods of academic work placement. Core curriculum comprises of several technical modules but also includes transdisciplinary modules dealing with ecosystemic and social/economic approaches. The implication of stakeholders from private sector, international agencies, and NGOs is helping to create inter-sectoral links. The Master is now entering its third year. A first batch of 10 students, from Vietnam, Bhutan, Cambodia, Nepal, Indonesia and France, has completed their degree in 2017. The second batch of 10, from Thailand, Vietnam, Cambodia, Germany, France and Ivory Coast is actually finishing their 6 months internship.

The international InterRisk Master is an innovative and successful answer to the challenge of training professionals to OH approaches. Using 'in situ' case studies in SEA, it provides theoretical and practical training on the analysis of health risks at human, animal and ecosystem interface.

Unlocking the potential of veterinary clinical records using a data mining approach

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ABSTRACT

Objectives: Clinical records from veterinary practices are a rich source of data for epidemiological research. These data are typically stored in veterinary practice databases in free-text, narrative and unstructured format, which are difficult to analyse using standard computational and epidemiological methods. There are a number of challenges associated with processing large volumes of such unstructured data where manual examination of records is not feasible, e.g. the lack of standardization in data entry and format, the use of different terms to describe the same concept (syntactic irregularities) and extraction of contextual information from free text. Data mining approaches have been relatively little used for accessing veterinary clinical records, in contrast to human health records, where medical informatics techniques are well-established. In this study, a natural language processing (NLP) and text mining methodology is presented to transform unstructured veterinary clinical data into structured data, to make them accessible for further analysis.

Materials and methods: Clinical entries are categorised by diagnosis and body system via an NLP and data mining approach. Standard veterinary ontologies such as Veterinary Nomenclature (VeNom) are used as a framework. These structured data are then systematically evaluated by applying algorithms for machine learning and case-based reasoning. The data are also compiled into a relational database allowing evaluation using SQL.

Results: Implementation of the method in R and Python will be described, and its efficiency and accuracy tested using a database of small animal clinical records comprising over 5 million entries.

Conclusion: The use of NLP and text mining to convert unstructured veterinary clinical records into structured data, extract clinical context and classify diagnoses can make available a wealth of data which are currently inaccessible for veterinary epidemiological analysis.

Key words: Medical informatics, natural language processing, clinical records, veterinary ontology

A framework for health informatics: Big Ideas from Big Data

T. Bernardo*, A. Campigotto, B. Ouyang

ABSTRACT

Trends in Technology and Health: Emerging technologies have disrupted many sectors (communication, publishing, music, transportation, retail, etc.), but have not yet had a profound effect on the health of individuals and populations. According to the Global Burden of Disease study, most people live with and die from chronic diseases (heart disease, stroke and cancers). A Global Burden of Animal Disease Study has been proposed. The shift of emphasis from disease to wellness, combined with technological trends (faster, cheaper, smaller, smarter and connected) provides opportunities for innovation.

Big Data Analytics: Historically, we had detailed records of individual companion animals versus large amounts of herd-level data for production animals, but this relationship is about to change. Data can now be collected or accessed from a variety of sources such as electronic medical records, social media, wearables and environmental sensors. Streams of real-time data could be combined with collections of pre-existing data to meet new challenges, such as air quality, affecting both humans and animals. A Lancet Commission reported that pollution is responsible for 9 million premature deaths, three times more than AIDS, tuberculosis and malaria combined. Open data, standards for interoperability, the ability to combine structured and non-structured data, use of ontologies (scaffolding) and artificial intelligence (analysis within the structure) represent advances in data analytics that will support the current shift from disease prevention to wellness promotion for all.

Framework: A framework for building a health informatics program will be presented, the foundation of which is evidence of the impact of big data on health and wellness, followed by a scoping review to provide a baseline of knowledge to date, as well as determining competencies for health informatics education, and research on the communication of trends. Finally, examples of leveraging community and potential applications for One Health will be described.

Using technological advances and machine learning to develop algorithms for livestock health and welfare

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ABSTRACT

Objective: Recent advances in bio-telemetry technology have made possible to generate lot of data through sensors which could be used to monitor welfare and classify behavioural activities in many different farm animals including sheep. However, little has been done w.r.t evaluating predictive ability and comparing various machine learning approaches for 'big data' (velocity in this case) and also evaluating how this change depending on sampling frequencies and position of sensors. This aim of this talk will be to discuss these challenges through presenting result from our research on development of algorithms for lameness in sheep as a use case.

Materials and methods: We developed a series of machine learning algorithms that can predict lameness in sheep using data (i.e. signals) from animal-borne sensor which contain a tri-axial accelerometer and gyroscope. Different machine learning algorithms such as: random forest, neural network, support vector machine, were used for the classification of different lameness scores in sheep and behavior activities. These algorithms were evaluated using upto 44 feature characteristics. A comparison of the performance of the different algorithms was obtained using the overall accuracy, precision, recall, F-score, and specificity values.

Results: Algorithms could classify active and non -active sheep behaviour with overall accuracy of 95% and also able to identify lame vs non-lame sheep. However, the accuracy varied by number of features used, choice of algorithm and window size used for feature generation. The results from this study show that by using machine learning algorithms using sensors have value in veterinary epidemiology and welfare monitoring.

Conclusion: Result highlight that certain types of algorithms are better suited than other and accuracy is dependent on various factors. The talk will discuss these implications.

The Use of Machine Learning for Systematic Reviews in Epidemiology under the Remit of the European Food Safety Authority

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ABSTRACT

Objective(s): Our objectives were to explore, select and evaluate Machine Learning Techniques (MLTs) and tools that could aid in the production of systematic reviews to support risk assessment work in the European Food Safety Authority (EFSA).

Materials and methods: A systematic review is a structured process that includes the identification, selection, appraisal and synthesis of all relevant evidence found in relation to a specific research question or sub-question. A systematic review (SR) involves several steps and it can be a resource intensive process, often involving several reviewers working together over a long time. This process is increasingly used by the scientific community as it is considered a cornerstone of evidence-based research. At the same time, it poses challenges due to the exponential growth in evidence and the consequent high demand in terms of time and resources. Therefore, the automation of some of the systematic review steps by using Machine Learning (ML) is highly desirable. Some methodologies falling under the broad category of Machine Learning Techniques (MLTs) are tested in specific steps of the SR process and their performance evaluated with respect to the golden standard (e.g. human expert reviewers).

Results: Several MLTs were explored; the most promising were selected, tested and compared in terms of the performance measure F1, sensitivity and specificity. Results of the use of ML in comparison with human expert reviewers were obtained. The best results for the screening part of the systematic reviews were obtained when using ensemble models with a combination of random forests, neural networks or gradient boosting machines (each adjusted for class imbalance via SMOTE or ROSE sampling). For the data extraction part of the systematic reviews, the R package Tabulizer was used. A shiny R tool was developed that aids reviewers in some steps of the SR process such as screening and data extraction.

Conclusions: Significant progress is being made worldwide with regards to the automation of systematic reviews. The critical appraisal of evidence proves to be in many cases a complex part of a systematic review that in order to be performed by machines might require deep learning and cognitive computing.

Key words: Machine Learning, Systematic Reviews, Screening, Data Extraction, Epidemiology, EFSA

Seasonal risk for avian influenza virus introductions into free-range layer farms and implications for control strategies in the Netherlands

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ABSTRACT

Objective: Free-range chicken farms in the Netherlands have a high risk for introductions of avian influenza virus (AIV), hence during the H5N8 highly pathogenic AI ((HPAI) outbreaks (2016-2017) free-range layers were confined indoors as a risk mitigation measure. Confinement lasted longer (22 weeks) than allowed (16 weeks) for eggs to be commercialised as free-range, leading to large economic losses. This experience highlighted the need to accurately identify the high risk period for introductions to guide this kind of decisions. The objective of this study was to characterise the seasonal patterns of AIV introductions into free-range layer farms.

Material and methods: Data from the low pathogenic AI (LPAI) serological surveillance programme for the period 2013-2016 was used to first estimate the time of introduction of AIV into affected farms and then assess seasonal patterns in the risk of introduction. Time of introduction was estimated by fitting a mathematical model to seroprevalence data collected longitudinally from infected farms. For the period 2015-2016, longitudinal follow up included monthly collections of eggs for serological testing from a cohort of farms. Information on the time of introduction was then used to estimate the monthly incidence and seasonality by fitting harmonic and Poisson regression models.

Results: A significant yearly seasonal risk that lasted around four months (November to February) was identified with the highest risk observed in January. The risk of introduction in this period was on average four times higher than the period of low risk around the summer months. Results were validated against the observed HPAI introductions within 2014 – 2018.

Conclusion: The model here developed can be used to estimated the time of introduction of infectious diseases using serological data. Regarding avian influenza, the results of this study can be used to optimise risk-based surveillance and guide decisions on timing and duration of indoor-confinement.

Key words: Avian influenza, seasonality, risk factors

The assessment of preventive measures against Highly Pathogenic Avian Influenza (HPAI) H5N6 infection in chicken eggs layer farms in Republic of Korea

D-S. YU*, K-N. Lee, H-C. Yoon, K-S. Kim, B-E. Park, H-M. Son

ABSTRACT

Objective: From 2016 to 2017, HPAIV H5N6 that emergently affected 11 countries damaged heavily on chicken egg layer farms in Republic of Korea causing unprecedented eggs price spike from lack of supply. This study aimed to assess effectiveness of preventive practices implemented at the farm level under different environmental and network structural condition for prevention and control.

Materials and methods: Before first HPAI H5N6 outbreak which started from 16th November 2016 to 30th March 2017, we collected information about the type of biosecurity practices implemented at chicken egg layer farms through on-site survey to avoid recall bias. Of them 174 farms where HPAI did not occur were assigned to the control group and 149 farms with HPAI H5N6 infection were assigned to the case group. 5 Types of biosecurity measures implemented in the two groups were compared by chi-square test. Direct effect of each biosecurity measures against HPAI was examined by mixed effect logistic regression with size of heard, spatial and network variables.

Result: Results of univariate analysis showed significantly difference of 3 biosecurity measure variables between cases and controls. Multivariate analysis showed taking biosecurity measure on person to visit at entry of a chicken egg layer farm was most effective one, 0.065 odds ratio (0.021-0.180 95% CI), followed by wearing single boots each of chicken barn 0.294 odds ratio (0.109-0.760) and fence installation around a chicken egg layer farms, 0.312 odds ratio (0.129-0.720). In addition, combining effect of three biosecurity action against HPAI prevention reported 0.017 odds ratio (0.003-0.079).

Conclusion: This was first study to identify effective preventive actions for producers to implement under different condition of chicken egg layer farms in Republic of Korea, which provide scientific evidence for biosecurity policy to prevent and control HPAIV outbreak.

Key words: Avian influenza, Biosecurity, Korea, spatial and network analysis

Risk based surveillance of influenza virus in wild birds in Chile

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ABSTRACT

Objectives: Wild birds (WB) are considered the main reservoirs of influenza A virus. Chile, with more than 4,000 km of coastline, has several suitable sites for local and migratory WB concentration. Yearly, thousands of migratory WB arrive from the Northern Hemisphere for nesting and feeding at these sites. The aim of this study was to gain epidemiological knowledge of avian influenza (AIV) circulating in Chile.

Materials and Methods: 192 known sites recognized as WB concentration areas in Chile were characterized, and a risk score was calculated for each site to guide surveillance in high-risk areas for AIV. From each site, environmental samples of fresh feces were collected, to allow for the identification of at least 1 positive sample assuming a prevalence of 1.5% per site. Influenza A virus matrix gene was detected by RT-qPCR. Virus isolation was attempted on samples with a Ct. <35. Isolates were confirmed by HA and RT-qPCR. Isolated virus and gene fragments were sequenced.

Results: 35,140 samples were collected from September 2015 to December 2017, identifying a global prevalence of 2.9%. Subtypes H1N1, H2Nx, H2N2, H3N4, H3N8, H4N2, H4N6, H5Nx, H5N2, H5N3, H6Nx, H6N2, H6N8, H7N3, H7N6, H8Nx, H8N4, H9Nx, H9N2, H9N7, H10Nx, H10N1, H11Nx, H11N1, H11N9, H12N5, H13Nx, H13N2, H16Nx and H16N3 have been identified. Complementarily, over 20 WB species have been identified as carriers of AIV in Chile, being *Anas georgica* and *Anas flavirostris* the species carrying the most subtype diversity, including H5Nx and H7Nx subtypes.

Conclusion: These results reveal the epidemiological importance that Chile could have in the persistence and evolution of AIV in the American continent, highlighting the importance to improve and maintain a risk-based surveillance system in WB in Chile and South America.

Key words: Influenza, wild birds, surveillance, risk

Implementation of a spatial data warehouse for avian influenza response

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ABSTRACT

Objective: This abstract illustrates the implementation of a spatial data warehouse (SDWH) to merge and organise spatial and epidemiological data from multiple distributed sources in order to quickly produce online interactive map or specific spatial applications in an emergency situation. The system described has been used to create a spatial decision support system (SDSS) applied during the H5N8 highly pathogenic avian influenza (HPAI) epidemic, which occurred in Italy in 2017-2018.

Materials and methods: The approach was developed in three phases: (i) to identify and metadata the source of data (spatial and non-spatial), (ii) to create the SDWH by implementing ETL (extract, transform and load) procedures and harmonisation protocols, and (iii) to publish the harmonised data by specific standard services (Web Feature Service – WFS or Web Map Service – WMS).
Oracle 11G software integrated with the ArcSDE engine of ESRI were the database components. Geoserver 2.4.4 was used to publish the web services and PL/SQL to implement the ETL procedure. HTML 5, Dojo and JSP were used to develop the webGIS client used as SDSS.

Results: Laboratory data, poultry farm registry data, poultry movement data, and outbreak data were daily integrated and harmonised with the spatial dimension in the SDWH by means of the ETL procedures. The SDWH data was published in terms of WFS and WMS to be used by the decision-makers as feature data. The feature data were organised geographic layers in the webGIS. The webGIS allowed the user to visualise, filter and extract the SDWH data.

Conclusion: The contribution presented the concepts of SDWH in the context of a veterinary domain. We consider SDWH a useful approach for: (i) data interoperability, integration and processing, (ii) spatial knowledge discovery, and (iii) query building and data navigation. In emergency situations the rapid availability of a SDSS is fundamental for decision-making.

Farm management and environmental village level factors influencing avian influenza circulation on backyard and commercial chicken farms in Bangladesh

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ABSTRACT

Objectives: To estimate H5 and H9 avian influenza (AI) sero- and viro-prevalence on backyard and commercial chicken farms in Bangladesh. To identify village and farm-level risk factors associated with H5 and H9 sero-prevalence.

Materials and methods: Two cross-sectional studies were conducted in two districts: (1) 144 backyard chicken farms in February-April 2016, and (2) 106 commercial broiler and 113-layer chicken farms in February-April 2017. Blood samples and oropharyngeal and cloacal swabs were collected from 576 chickens and 204 in-contact ducks on backyard, and from 954 broilers and 904 layers on commercial farms. Questionnaires were used to collect data on farm-level bird management and participatory appraisal was used to develop village maps and collect information on village-level risk factors.

Results: Flock-level sero-prevalence (at least one positive bird per flock) of unvaccinated backyard flocks was 60.4% (95% CI: 52.1-68.2) for H9 and 27.8% (95% CI: 21.0-35.7) for H5, highlighting that a large proportion of flocks was exposed to AI. More commercial farms were H9 virus positive compared to backyard farms, with 1.9% (95% CI: 0.5-7.4) and 2.0% (95% CI: 0.5-7.8) of unvaccinated commercial broiler and layer farms and 0.7% (95% CI: 0.1-4.9) of unvaccinated backyard farms being positive. No flocks were positive to H5 viral RNA. We identified separate H5 and H9 spatial clusters where backyard chickens were H5/H9 sero-positive. Farm-level management and village level environmental risk factors associated with sero-prevalence patterns were identified for backyard and commercial farms.

Conclusion: Our results indicate previous exposure of backyard flocks to H5 and H9 infection with low virus circulation rates in unvaccinated poultry and higher H9 virus circulation rates on commercial compared to backyard farms. Our results can be used to streamline and improve AI risk-based surveillance programmes in Bangladesh (e.g. focusing on specific production systems and high risk areas and management practices).

Key words: H5, H9, prevalence, chicken farm, Bangladesh

Density of wild birds is associated with risk of highly pathogenic avian influenza virus (H5N8) introduction into poultry farms

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ABSTRACT

Objectives: Highly pathogenic avian influenza (HPAI) virus can be spread across the globe by migratory birds, which have been proposed as a possible source of introduction for poultry farms. In this study we examined whether the risk of an HPAI H5N8 outbreak in a commercial poultry flock in The Netherlands was associated with the average density of wild birds around the farms.

Materials and methods: In total 9 HPAI H5N8 outbreaks were notified in 2016, which included 7 unique ecological locations. As controls we randomly selected 21 uninfected poultry farms (R-NL) from all over the Netherlands and 7 farms located in wetland areas (R-WL). Standardized bird counts from 2011/12-2015/16 were used to estimate the average numbers of wild birds in radius of 1, 3, 6 and 10 km around these farms. For five subsets of target species for AI surveillance (Commission Decision 2010/367/EC), i.e. Eurasian Wigeon, Tufted Duck, *Anatidae* (ducks, geese and swans), *Laridae* (gulls) and *Rallidae* (crakes, coots and gallinules), average densities around outbreak and control farms were compared using a linear mixed model.

Results: For each of the 4 radius the density of all five categories of birds was higher around outbreak farms compared to R-NL and R-WL farms. The difference in density was most striking for Eurasian Wigeon for the 1 km radius, for which the average density around outbreak farms was 82.8 (95% CI:3.5-1937.8) times higher compared to R-NL and 13.6 (1.3-142.5) times higher compared to R-WL farms.

Conclusion: The density of specific wild birds around a poultry farm is strongly associated with the occurrence of HPAI H5N8 outbreaks, providing further evidence for their potential role as a source of HPAI H5N8 virus. Poultry farms in wetland areas should take stringent biosecurity measures to reduce the risk of introduction of the virus onto the farm.

Optimising the surveillance of avian influenza viruses in live-bird markets

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ABSTRACT

Objectives: Live bird markets (LBMs) are major targets for avian influenza virus (AIV) surveillance programmes. While sampling LBM environment has become a widespread alternative to the labour-intensive sampling of live poultry, the design of surveillance programmes and the interpretation of their results are undermined by the lack of knowledge about the effectiveness of these sampling strategies.

Materials and methods: We used latent class models and a unique empirical dataset collated in Vietnamese LBMs to estimate the sensitivity and specificity of five different sample types to detect AIVs subtypes H5N1 and H5N6: oropharyngeal duck samples, solid and liquid wastes, poultry drinking water and faeces.

Results: Model outcomes suggest that the sensitivity of environmental samples for detecting H5N1 viruses is equivalent to that of oropharyngeal duck samples; however, taking oropharyngeal duck samples was shown to be far more effective in detecting H5N6 viruses than taking any of the four environmental samples. Results also stressed that the specificity of the current surveillance strategy in LBMs was not optimal leading to a significant number of false positive LBMs. Finally, using simulations, we identified 42 sampling strategies more parsimonious than the current strategy and highly sensitive for both viruses, all of which involved the collection of both environmental and oropharyngeal duck samples.

Conclusion: This study generated results that are crucial for making an evidence-based decision when it comes to surveillance design and provided quantitative evidence of the relevance of environmental samples for monitoring H5N1 viruses. It also presented a robust and flexible statistical modelling approach that should be applied to other contexts in order to advance our collective understanding of how HPAI surveillance should be designed in LBMs.

Bioaerosol Sampling to Detect Avian Influenza Virus in Hanoi's Largest Live Poultry Market

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ABSTRACT

Objective: We sought to introduce aerosol sampling for avian influenza viruses in Vietnam. Aerosol sampling has the advantage of screening larger areas of virus than that involved with bird or cage swabbing.

Methods: We used NIOSH two-stage aerosol samplers to monitor for and capture live avian influenza H5N1 and H7N9 viruses from the largest live poultry market in Hanoi, Vietnam during the first three weeks of October 2017. Several times a week, three NIOSH samplers were assembled on a tripod and positioned 0.5m from the ground. SKC AirChek Touch pumps were set at a flow rate of 5.0 L/min and run for four hours. Up to 20 oropharyngeal (OP) swabs were collected from chickens and ducks distanced at 0.2–1.5m from each NIOSH sampler.

Results: The three weeks of sampling yielded a total of 30 aerosol samples which 90% qRT-PCR positive for influenza A and 116 OP swab pools (5 swabs per pool) which were similarly 47% qRT-PCR positive. Egg culture yielded one influenza A virus (not H5 or H7) from aerosol and 25 influenza A viruses from OP swab pools (five were H5 positive). The agreement between sample types (over time and position) was strong, with 92% of positive OP pooled swab samples confirmed by positive aerosol samples and 81% percent of influenza A positive aerosol samples were confirmed by positive OP swab collections. Overall the agreement was 77% percent.

Conclusion: We posit that aerosol sampling might be used for early warning screening of poultry markets for novel influenza virus detection. Markets which have positive aerosol samples might be followed up with more focused individual bird or cage swabbing and later back tracing could be to specific farms to reduce highly pathogenic avian influenza virus spread.

Risk of between-herd transmission of foot-and-mouth disease virus by milk collection

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ABSTRACT

Objective: During a foot-and-mouth disease (FMD) outbreak, animal movements are prohibited to minimize the risk of between-herd transmission. Milk collection on dairy farms can, however, not be discontinued for a prolonged period. The aim of this study was to estimate the risk of between-herd transmission of FMD virus by aerosols emitted from the bulk milk tanker (BMT) during an FMD outbreak.

Materials and methods: A quantitative risk assessment was performed to estimate the infection risk of dairy herds by aerosols emitted from a BMT that has first collected milk at an infected, but not yet detected farm. A within-herd transmission model was used to estimate the time-dependent FMD virus concentration in tank milk on infected dairy farms. The output of this model was used to calculate the expected virus concentration in the BMT when collecting milk at subsequent farms. Data on aerosolization of milk during loading were available to calculate the release of FMD virus on these non-infected farms. An exponential dose-response model was used to estimate the probability that the released virus would infect at least one farm down the route of the BMT.

Results and discussion: Assuming that the FMD-infected farm is the first farm on the route of the BMT and that 10% of the aerosols released from the BMT are inhaled by cattle, there is a 5×10^{-4} to 7×10^{-4} probability that one or more farms down the route of the BMT will get infected, dependent on herd size.

Conclusion: Comparison of the calculated infection probability of dairy farms down the route of the BMT with the kernel estimate for distance-dependent between-farm transmission of FMD indicates that aerosols emitted by the BMT might substantially contribute to between-farm transmission during an FMD outbreak.

Key words: Risk assessment, foot-and-mouth disease, between-herd transmission, bulk milk tanker, aerosol

Reconstructing a transmission network and identifying risk factors of secondary transmissions in the 2010 foot-and-mouth disease epidemic in Japan

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ABSTRACT

Objectives: Estimating a transmission network, representing 'who infected whom' for an infectious disease outbreak, is useful to understand the dynamics of disease transmission. Research on transmission network models combining epidemiological and genetic data have been conducted actively in recent years. In this study, we reconstructed a transmission network of the 2010 FMD epidemic in Japan and explored farm-level risk factor associated with increased likelihood secondary transmission.

Materials and methods: A published transmission network model, Lau's systematic Bayesian model, was applied to epidemiological data of 292 infected farms (farm-type, locations, and dates of clinical onset, notification, and culling on the farms) and whole genome data of 104 infected farms. This model can make inferences for known infected farms lacking sequence data. The consensus transmission network was examined for spatial and temporal fit to the observed outbreak. Then, risk factors of farms inferred to have caused the secondary transmission was explored using multivariable Poisson regression model.

Results: The consensus network corresponded well with the spatial and temporal disease dynamics observed during the outbreak. Among 292 farms, 108 farms were inferred to have caused the secondary transmission, and the median number of secondary cases was 2 (range 1-20) farms. The farm-type (large-sized cattle and pig farms), the number of days from onset to notification, and the number of susceptible farms within a 1-kilometer radius were significantly associated with secondary transmission.

Conclusion: Transmission network analysis incorporating both epidemiological and genetic data can provide us valuable insights for understanding FMD spread. Our results suggested the potential usefulness of this approach for identifying the risk factors to target in future disease control.

Key words: Transmission network, reconstructing outbreaks, secondary transmission, foot-and-mouth disease, Japan

Clinical and infection dynamics of foot-and-mouth disease in beef feedlot cattle: An expert survey

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ABSTRACT

Objective: Foot-and-mouth disease outbreaks in FMD-free countries with large livestock populations will have severe consequences for the livestock industries. Mathematical models are powerful tools to evaluate potential outbreak control options, however, parameterization of the models is challenging due to gaps in knowledge of FMD-dynamics in susceptible populations.

Materials and methods: Expert-opinion surveys are an approach to collect data in areas where no data have been reported. We developed a survey to collect expert-opinion about key parameters of natural history, transmissibility, and clinical manifestation of FMD in beef feedlot cattle. Twenty-seven experts (virologists, epidemiologists, mathematical modelers) with experience with FMD in endemic and non-endemic settings agreed to participate and the completion rate was 59% ($n=16$ respondents). Parameters surveyed included: duration of infection and disease stages, proportion of cattle exhibiting specific clinical signs, reduction in feed consumption and its duration, and probabilities of FMDv transmission and severe clinical disease. Parameter values differentiating FMDv virulence, infection dose, and infection route were surveyed. Using the responses, best-fit mathematical distributions for the parameter values were identified and distribution statistics (*e.g.*, median, range) were computed.

Results: Estimated median probability of FMDv transmission via direct contact varied from 53% (IQ range 76-27%) from cattle infected with low-virulent strains in a low dose to 82% (IQ range 90-70%) from cattle infected with high-virulent strains in a high dose. Probability of developing clinical disease after infection varied from 82% (IQ range 90-70%) with high-virulent to 63% (IQ range 89-60%) with low-virulent strains. Reduction in feed consumption was estimated to last 5 days (SD: +/-2) in cattle infected by low-virulent strains and 7 days (SD: +/-2) in cattle infected by high-virulent strains.

Conclusion: The obtained parameter distributions can be used in combination with experimental and outbreak data to parameterize simulation models to assess intervention strategies during potential FMD-outbreaks in beef feedlot cattle.

Key words: Foot-and-mouth disease, expert survey, clinical FMD, infection disease dynamics, beef feedlot

Assessment of the risk of incursion of exotic FMD viruses into Southeast Asia

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ABSTRACT

Objective: The South-East Asia and China Food and Mouth Disease (SEACFMD) campaign recognised that foot and mouth disease viruses (FMDVs) circulating in other regions could pose serious risks to its members. This study assessed the risk of incursion of exotic FMDVs into Southeast Asia (SEA).

Materials and methods: A qualitative risk assessment was conducted according to the World Organisation for Animal Health (OIE) framework. The outcome of interest was the exposure of susceptible livestock to exotic FMDV. Data were gathered from site visits, published studies, grey literature and expert opinion. The findings were validated at a regional workshop.

Results: Ten release and six exposure pathways were characterized. Overall, the likelihood of future incursions was assessed as high. The pathways involving imports of live animals and animal products from FMD-endemic countries in neighbouring regions had the highest likelihood. Surprisingly, even FMD-free countries allow these types of imports. An incursion would likely have a negative impact on animal health and welfare and, in some cases, valuable trading markets would be jeopardised. An exotic FMDV would likely spread extensively within SEA due to intense intra-regional livestock trade, weak surveillance and lack of well-integrated and risk-based national FMD strategies.

Conclusions: Our study indicates that further incursions of exotic FMDV to SEA is not a matter of 'if' but 'when'. A risk-based approach involving public and private stakeholders at regional and national levels is recommended to reduce this risk.

Key words: Risk assessment, exotic FMD viruses, risk pathways

Spatial epidemiology, phylogenetic history, and risk factors for foot-and-mouth disease in Uganda

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ABSTRACT

Objective: East Africa has one of the most complicated foot-and-mouth disease virus (FMDV) ecologies in the world, with diverse management practices, high densities of FMDV-susceptible animals, and multiple circulating serotypes. Outbreaks of FMDV are common, yet because the local disease ecology is poorly understood, the best strategy for controlling FMDV in Uganda is unclear. The specific aims were to 1) describe the geographic distribution of FMDV, 2) identify risk factors which promote the maintenance and circulation of FMDV, and 3) elucidate the phylogeographic history of FMDV in Uganda.

Materials and methods: We conducted a four-year cross-sectional survey of over 14,000 cattle in Uganda, which included serological testing (antibody ELISA) accompanied by a questionnaire. In addition, sequences of the VP1 capsid protein coding region were obtained for a subset of cattle (323 sequences).

Results: Spatial analysis demonstrated significant geographic heterogeneity in the exposure of cattle to FMDV (see figure; high-risk cluster shaded in red), suggesting that areas in the northeast that are dominated by pastoralist management systems could be targeted for enhanced surveillance and control. A risk factor analysis revealed that factors such as proximity to international borders further predispose herds to exposure to FMDV. Using genetic data, we also identified four circulating serotypes – A, O, SAT1, and SAT2, all of which were spatially clustered. Additionally, we apply Bayesian phylogeographic analysis to reveal underlying spatial patterns in the circulation of multiple genetically-distinct lineages of serotype O.

Conclusion: Our results will guide control measures that could more effectively control FMDV in Uganda.

Epidemiological strengthening of FMD control in southern Lao PDR

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ABSTRACT

Objectives: FMD is widespread in the SE Asia sub-region, including Lao PDR. However, there is limited epidemiological data to accurately estimate prevalence. As part of sub-region wide effort to control the disease, vaccination activities are being carried out in Savannakhet and Champasak Provinces. The objectives of this study were to estimate the seroprevalence of FMD in these two provinces in order to optimise the control strategies.

Materials and methods: In this cross-sectional study, large ruminants (buffaloes and cattle) of all age groups were selected using a two-stage cluster sampling technique. A questionnaire was administered to collect risk factor information. Subsequently, serum samples were collected and tested for FMD antibodies using an ELISA test for non-structural proteins (NSP). Standardised mortality (morbidity) ratios (SMR) were estimated at the village-level and interpolated on map surfaces to identify areas with above-average seroprevalence.

Results: A total of 1,725 large ruminants were tested. The overall seroprevalence was 52.3% (CI: 46.0; 58.5) and 46.6% (CI: 44.0; 49.1) in buffaloes and cattle, respectively. District-level serporevalence ranged from 0 to 27% in Champasak and 25 to 71% in Savannkhet, resulting in a province-level seroprevalence of 41% and 51%, respectively ($p < 0.01$). These results were consistent with farmer responses to the questionnaire. There was some limited spatial heterogeneity but no consistent pattern. Farmers in Champasak consistently reported observing clinical signs of FMD in few animals than farmers in Savannakhet.

Conclusion: The combined data show that FMD is highly endemic across these two provinces. While there is some evidence to suggest spatial variation, our serological results, combined with the questionnaire, indicate that this is limited. This implies that control through risk-based or targeted vaccination is unlikely to be effective. These results are being used to redesign the control strategies.

Epidemiological study to understand livestock trading network and identify the relationship between trading connectivity and the occurrence of Foot and Mouth Disease (FMD) outbreak in Myanmar

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ABSTRACT

Objective: Myanmar possess a large number of small and large ruminants population. Animal movement contribute as a high risk for the spread of the disease. The objective of this study is to understand the attribute of trading network with cattle market which can cause a spread of livestock diseases.

Materials and methods: This study was conducted in Mon State, Yangon Region, Mandalay Region, Bago Region, Magway Region and Nay Pyi Taw council area where these areas had many complex cattle movements, highest cattle population and the most linkage with border area. Cross-sectional study was conducted in this study. A total of 174 respondents were interviewed by using preset questionnaire including movement between cattle markets in between and within the regions and they were asked to draw route of animal movements and then collected data were used for social network analysis package in R statistical environment and UCINET.

Result: The critical points were analyzed by looking at the trading social network of central dry zone and transboundary animal movement. Mandalay and Bago Regions was identified as critical point for central dry zone because these regions have many complex cattle movement. Mon State studied area was identified as transboundary animal movement critical point. It was noted that 56.1% of respondents visited cattle market with their trading partners. It was concluded that 96.5% of respondents were aware of market to market movement system. In cattle markets, the proportion of 66.7% of adult male cattle (over 4 years) were traded not only for draught but also for meat purpose. It can be concluded that various stakeholders such as traders, clients, dealer, middlemen, farmers and veterinarians involved in trading network.

Key words: FMD, epidemiology, animal movement

Use of pooled milk for foot-and-mouth disease surveillance in different production systems

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ABSTRACT

Objectives: Foot-and-mouth disease (FMD) is endemic throughout large parts of Africa and Asia, and associated with high economic impact and huge amounts of resources used for control. There are several limitations and potential biases with traditional surveillance approaches such that alternative methodologies for surveillance are desirable. Pooled milk has potentially several advantages over other samples types for FMD surveillance. Previous studies at the Pirbright Institute have demonstrated that FMD virus can be detected in the milk of experimentally and naturally infected animals by rRT-PCR. The objective of this project was to evaluate pooled milk for FMD surveillance on dairy cattle farms using an optimised rRT-PCR assay.

Materials and methods: The first study was undertaken on two heavily vaccinated, large-scale dairies in Saudi Arabia. Biweekly samples were collected opportunistically using in-line milk samplers from individual management houses and the results compared to clinical incidence data. The second study focussed on smallholder dairy farmers in Nakuru County, Kenya and combined prospective sampling of pooled milk facilities alongside periodic cross-sectional surveys for clinical disease. A third prospective study has been initiated by taking samples from bulk-milk tanks on individual farms located within a dairy complex in Tehran Province, Iran alongside serological tests for seroconversion to FMD virus.

Results: The first study revealed evidence of co-infection of different FMD viral serotypes and a likely role of subclinical infection. The second study revealed that FMD virus could be detected and serotyped at household level incidences less than 2.5% when 20-40% of farmers were members of pooled milk facilities. The third study is ongoing.

Conclusion: The results from these studies so far indicate that pooled milk has a potential use for FMD virus surveillance in endemic settings although this approach could be further optimised by utilising a strategic risk-based approach taking advantage of the milk supply chain.

Key words: Foot-and-mouth disease; milk; surveillance; endemic

Novel Insights into the evolutionary epidemiology of SAT1 and SAT2 Foot-and-Mouth Disease Virus in Eastern and Southern Africa

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ABSTRACT

Objective: The objective of this study was to explore and compare evolutionary epidemiology of SAT1 and SAT2 viruses among eastern and southeastern African countries, as well as between domesticated cattle and wild buffalos.

Materials and methods: We performed analyses on SAT1 and SAT2's VP1 gene segments collected between 1975 and 2016 using Bayesian Phylodynamic models. We used discrete-state ancestral reconstruction approach to model viruses phylogeography, among eastern and southeastern African countries, and viral transmission between host species.

Results: Our phylogeographic analyses implicate Zimbabwe as the ancestral location for SAT1 introduction in eastern Africa (P=0.67), while Kenya as the ancestral location for introduction of these SAT2 lineages to southeastern Africa (P=0.72). Important viral dispersal routes were inferred from Tanzania to Kenya and from Kenya to Uganda for SAT1 and SAT2, respectively (Bayes Factor > 10). Host species analyses strongly implicate domesticated cattle as the ancestral host (P=0.99) for SAT1 and SAT2 cattle-buffalo transmission cycles. Furthermore, results suggest that the direction of transmission from cattle to buffalo is substantially more frequent (BF > 1000) than from buffalo to cattle.

Conclusion: Our findings shed new insights into the evolutionary epidemiology of SAT1 and SAT2 in Africa and, for the first time, between host species. Inferences from the present study highlighted the role of cattle movements and related anthropological activities on shaping the evolutionary history of SAT1 and SAT2 in the region. Our results can be used to guide surveillance in the region, subsequently, and improve related intervention strategies.

Key words: Ancestral reconstruction, Phylogeography, FMD, cattle, buffalo

The effects of a Foot-and-Mouth Disease outbreak on the fertility performance of a large scale dairy herd in Kenya

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ABSTRACT

Objectives: Foot and Mouth disease (FMD) virus places major constraints on livestock production across the world, particularly in developing countries where 70% of the worlds extreme poor depend on income from livestock. A full economic impact assessment of FMD is needed to support control programs and currently there is a lack of data on the impacts of FMD on fertility due to the complexity of the data required for impact analysis. Poor fertility impairs productivity.

Materials and methods: This is a retrospective cohort study, following an FMD outbreak on a large-scale, FMD vaccinated, dairy herd in Kenya (N=328 females), assessing the impact of FMD on herd fertility.
Kaplan-Meier graphs depict differences in survival functions between exposure groups and cox regression models were used to calculate hazard ratios (HR) for associations between clinical FMD cases and fertility outcomes; 'age at first calving', 'fertility culling', 'time first service' and 'time conception'. Confounding variables controlled for were; 'age', 'breed', 'parity', 'stage of lactation/gestation' and 'eligibility for service'. A case control study was nested within the cohort to investigate the effects of FMD challenge on conception, in animals susceptible to fertility suppression at the time of the outbreak compared to animals that conceived prior to the outbreak, irrespective of case diagnosis.

Results: Clinically affected young-stock median age of first calving was 2.7 months higher than non-cases and animals susceptible to fertility suppression at the time of the outbreak had a lower conception HR = 0.56 (0.41-0.75 P = 0.01), irrespective of case diagnosis.

Conclusion: Increased age at first calving increases rearing costs and reduces future productivity and increased time to conception reduces production efficiency. These results provide strong evidence that FMD infection impairs herd fertility. The repercussions of an outbreak last longer than clinical cases and should be considered when estimating the economic impact of FMD.

Key words: Foot and Mouth Disease, fertility, economics

Determinants of household-level FMD in endemic areas of Lao and Myanmar

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ABSTRACT

Objectives: A 5-year project, funded by New Zealand and coordinated by the OIE aims at eliminating FMD in Lao PDR and Myanmar. Cross-sectional studies were conducted in 2016-17 to assess the burden and determinants of transmission of FMD in Central Myanmar (MM), Southern Lao (SL) and Northern Lao (NL).

Material and Methods: In each study region, six households per stratified-randomly selected village were enrolled. Data about FMD annual clinical incidence (ACI) and putative transmission factors were collected by interview. Blood from cattle/buffaloes was sampled and tested by NSP-ELISA to determine past exposure to FMD virus in the household. Logistic regression was used to determine risk factors associated with FMD ACI and sero-prevalence in the household.

Results: The proportion of households with sero-positive livestock was 55-78% while 1-7% households observed clinical disease in the past year. Large ruminants of a village often had contacts through communal grazing. Village level FMD occurred as both a sporadic and an outbreak pattern (Figure 1). Vaccination appeared strongly protective against clinical FMD in all study areas. In SL and MM, a large livestock population (village and/or household-level) was a risk for a higher sero-prevalence. In MM, communal grazing and presence of pigs were risk factors for ACI and sero-prevalence. In Lao, the proximity to road was associated with increased sero-prevalence

Conclusion: Determinants for household-level ACI and serological evidence of FMD tended to vary between regions and countries. Large village cattle populations and proximity to roads tended to increase the FMD risk.
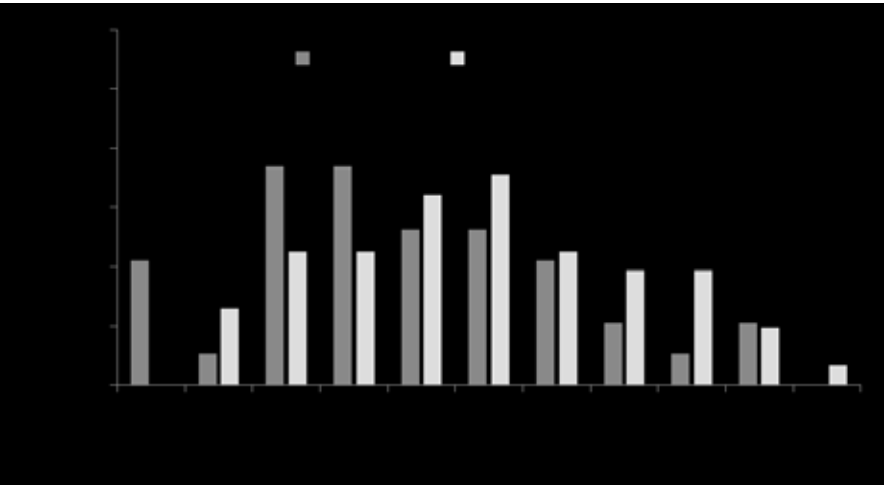
Figure 1. Pattern of farmer-reported FMD at the village-level in Southern Lao (2012-2016)

SPREAD: A high-performance computing application for near-real time determination of the source of farm-to-farm transmission during foot-and-mouth disease epidemics

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ABSTRACT

Objective: In controlling FMD epidemics, an important tool is the epidemiological investigation that seeks to determine the source of the farm-level outbreak. Traditionally this has been undertaken by veterinarians applying questionnaires during farm visits, but often the results are inconclusive. To address this we are developing a web-based application called SPREAD that will allow veterinarians to access relevant meteorological and sequence data to inform their investigations. However, to be truly useful, this "decision support system" requires the processing of large amounts of data and in near real-time.

Materials and methods: We are developing SPREAD with a "loosely coupled" architecture wherein end-user access is via the web, but any requests for undertaking data analyses and modelling are handled by intermediate "Application Programming Interface". The API then passes the request onto a high-performance computer, which following the processing of the data and the running of models, returns results back to the API, and then onto the user.

Results: SPREAD is complex software, and accordingly is being built in phases. Stage 1, which enables the visualisation of epidemics and preliminary wind-borne dispersion risk assessments has been completed, and currently the focus of Stage 2 is on FMDV genome assembly and construction of transmission networks. Datasets from historical FMD outbreaks are being collated for validation exercises.

Conclusion: The concept of integrating whole-genomic sequencing data with wind dispersion modelling was developed from the experience of the 2007 UK FMD outbreak. However, this pioneering work was undertaken retrospectively, and to date no system has been developed that will enable transmission pathways to be determined in near-real time. Whilst the SPREAD application will address this for Australia, it is being built so as potentially to be run for FMD epidemics in any country, thus encouraging international collaborative partnerships to ensure ongoing funding for maintenance and enhancements.

Key words: Farm-to-farm transmission, infectious disease networks, wind-dispersion

A sero-survey of foot and mouth disease (FMD) in cattle around Mana Pools Conservation Park of northern Zimbabwe

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ABSTRACT

Objective: FMD is a highly infectious viral disease of cloven-hoofed livestock and wildlife in Southern Africa. African buffalo (Syncerus caffer) has been demonstrated to be an asymptomatic carrier and reservoir of the serotypes that circulate in Southern Africa. Cattle are highly susceptible. In Zimbabwe, the southern provinces frequently report clinical cases of FMD, but no clinical disease has been reported from the northern provinces, despite observed buffalo/cattle contact. Our study aimed at describing FMD circulation in unvaccinated cattle herds in the periphery of the Mana Pools Transfrontier Conservation Area (TFCA) in order to design appropriate FMD management strategies.

Materials and methods: The study focused on investigating whether buffalo-cattle contact patterns observed explain the FMD serological patterns at the periphery of Mana Pools Conservation Park. A total of 1238 cattle sera were collected from the target areas in a two-stage random sampling protocol. Samples were tested for antibodies to the non-structural protein of the FMD virus using the Enzyme Linked Immunosorbent Assay (NSP-ELISA). A questionnaire was administered to interrogate selected risk factors perceived to influence FMD virus infection in cattle.

Results: A total of 3.6% (45/1238) sera tested positive for antibodies to FMD suggesting a low prevalence of the infection given the area is never vaccinated. Positive cases were spread in all three seasons in both Mbire and Hurungwe districts. Contact with buffalo, hot-dry season, and area of origin were associated with increased risk of testing positive for FMD antibodies. The results complement the findings of Jori et al in the southern part of the country. Work is underway to establish the serotype(s) at play.

Conclusion: Serological results confirmed FMD infection in cattle in the periphery of the Mana Pools TFCA, suggesting movement control policy in the north may need to be adjusted in line with the practices in the south.

Key words: Serosurvey, serotypes, antibodies, NSP ELISA

Quantifying risk factors to strategically plan control strategies for digital dermatitis in dairy cattle

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ABSTRACT

Objective: Our aim was to determine the prevalence of digital dermatitis (DD) in dairy herds in Alberta, Canada, and to identify and quantify risk factors for digital dermatitis, to support DD control decision making on farm.

Materials and methods: Cow characteristics and hoof lesion data of 17,169 cows originating from 76 farms (longitudinal study) were combined with farm characteristics (cross-sectional study) generated in the same time frame. A generalized logistic mixed model with farm as random effect was used to identify and quantify risk factors associated with the presence of DD.

Results: Of the 15 significant risk factors related to animal, environment or cow management, a deep layer of straw bedding had 0.34 higher odds for DD compared to cows housed on a thin layer of wood shavings. Footbaths need to be implemented at least once a week were 0.30 times higher compared to a frequency of less than once a week. Also, copper sulfate resulted in 10 times lower odds compared to the use of other products. Finally, lower parity cows with lower production levels were at highest risk for DD; high-yielding cows were more impacted by DD.

Conclusion: In a financially constraint farm setting, focus on deep bedding and the implementation of a proper footbath protocol has the potential to most likely reduce the odds for DD. Optimal management should be aimed towards heifers, as they were classified as having higher odds for DD.

Key words: Dairy, digital dermatitis, herd health, risk factors

Risk factors for reproductive disorders and major infectious causes of abortion in sheep in the highlands of Ethiopia

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ABSTRACT

Objective: A cross-sectional survey was conducted in 2015/16 to determine serological status of major infectious causes of abortion and associated risk factors in sheep in of the highlands of Ethiopia.

Materials and methods: A total of 120 households from three districts were enrolled in the study. Per farm, 3-4 samples of animals aged >2 years were collected. A total of 445 sera were tested for chlamydiosis, Q fever, toxoplasmosis, brucellosis and border disease virus. Zero-inflated poison regression was used to model the number abortion, number of lambs lost and number of still births in the flocks. A mixed-effects logistic regression model was fitted to identify covariates associated with prevalence of infectious causes of abortion.

Results: The study found that 20% [95% CI 12.74, 27.26] of flocks had recent experience of sheep abortion, lamb losses was at 65%[95% CI 56.34,73.65] and still birth at 10%[95%CI 4.55,15.44]. The incidence risk ratio for abortion was significantly higher in larger flocks. And lamb losses were significantly higher in Q-fever and toxoplasma positive flocks, in one of the districts, and in flocks with size with more than 30 animals. The serological analyses revealed the presence of 3 abortive infections, while none of the samples tested positive for brucellosis or border virus disease. From 120 flocks tested, 107(89.17%) were positive for chlamydiosis, 82 (68.33%) for Q-fever, and 85 (70.83%) for toxoplasmosis.

Conclusion: Our results showed the likely contribution of different infectious agents to the reproductive disorders in sheep farmers are facing. The high sero-prevalence of infectious agents, especially chlamydiosis, at both flock and animal level, warrants more in depth research to attribute reproductive problems to these pathogens.

Key words: Abortion, Ethiopia, reproductive disorders, risk factors, sheep

Developing sensible and sensitive policy: rabies response in northern Australian Indigenous communities

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ABSTRACT

Objective: Determine which proposed measures - in the event of a rabies incursion in northern Australia - are considered justifiable by Indigenous communities.

Materials and methods: Five collaborative co-compositional workshops were conducted with 1) community members in East Arnhem Land (EAL) and the Northern Peninsula Area (NPA); 2) Indigenous Rangers in EAL and NPA; and 3) residents of Cairns, the local regional centre. Storyboard methodologies - encouraging lay-people to develop and communicate their knowledge about a specific issue using stories and non-textual media - were used. In Indigenous research it helps centralize a locally relevant 'story' as a key vehicle for sharing existing data and allow meaning-making to be directed by participants.

Results: Using participatory methods, key findings include that the capacity of communities to contribute/adapt to a biosecurity response is limited by material disadvantage, dominant cultural norms and food security concerns. Key contrasts were identified in how different canids are classified and valued with participants; EAL emphasized that domestic dogs have great cultural significance as actors in their own right, whereas Cairns' residents related to dogs in terms of companion animal and ownership responsibilities. Definitions of dingoes and their relationship to dogs and people's practical capacity to enforce recommended protocols also varied. Notably, culling of healthy wild dogs or their populations was not supported by any participants in any of the three settings.

Conclusion: Different attitudes and practices were found to exist within and between northern Australia communities studied, but in the event of a rabies outbreak, key interventions might be accommodated within cultural beliefs and long-standing norms of dog management if sufficient effort is made to adapt interventions to local contexts and community preferences. The practicalities and everyday realities entailed by trying to manage dogs differently in these communities also require consideration.

Key words: Disease outbreak, rabies, response, policy, Australia

ILRI SESSION

Food safety in informal markets: what works and why

D. Grace*, K. Roesel, F. Mutua, A. Kebede, J. Lindahl, S. Alonso

ABSTRACT

Objectives: The enormous health and economic burden of foodborne disease is increasingly recognized, but there is less information on the best options for managing food safety. Africa suffers the highest burden of foodborne disease and a number of interventions have been tested in recent years.

Materials and methods: We present the results of a systematic literature review to evaluate food safety interventions in Africa. We developed a typology to set out the different type of interventions used along the value chain and at population level to improve food. A syntax was developed and CabDirect and PubMed were searched. PRISMA guidelines were followed.

Results: We screened 3,470 titles, obtained 498 abstracts, identified 84 papers and retained 67. Technologies dominated the interventions followed by training and information, then Interventions around new processes, and willingness to pay for quality assured products. There were few interventions on regulations and only one on infrastructure. Thirty four studies claimed success (significant change in beneficial outcomes), three partial success, and only three admitted failure. All willingness to pay experiments indicated consumers were willing to pay for safer food. Based on this we identify seven critical success factors: food safety interventions should be effective, have an enabling environment, be frugal (economically feasible), have incentives in place, and not worsen equity or have unwanted consequences.

Conclusion: The track record for food safety interventions is rather encouraging. The major evaluated interventions of technologies, training and information, new processes and willingness to pay for food safety given generally good results. However, major investments in infrastructure, national control systems and organizational innovation have not been well evaluated

Key words: Food safety, intervention, Africa, systematic literature review

Food safety in the pork value chain and pathways towards safer pork in Vietnam

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ABSTRACT

Objective: Food safety is one of the most pressing issues for consumers in Vietnam, more important than education or health care. The presented paper, addresses questions such as: Is pork in Vietnam safe and are the risks serious? What are feasible mitigation options?

Materials and methods: Research approaches include risk assessment for biological and chemical hazards, a cost of illness study, food safety performance and value chain assessments. Research is carried in up to 5 provinces of Northern Vietnam since 2013. Data collection follows the entire pork value chain using questionnaires, focus group discussions, key informant interviews and biological sampling for identified biological (e.g., *Salmonella*) and chemical food safety hazards (e.g., heavy metals, β-agonist and antibiotics residues) using a probabilistic sampling design

Results: Results show that pork is not safe: S*almonella* was found in 44% of pork sold at the markets in the study area and a quantitative microbial risk assessment indicated that one to two out of 10 pork consumers are at risk of *Salmonella* poisoning annually. Cost per episode treatment for Salmonella at hospital ranged from USD 2.5–7.6 million annually. Veterinary drug residues and other chemicals were only found in relatively few samples.

Conclusions: Various approaches to improving safety had been tried, largely based on systems used in developed countries e.g.: GAP, traceability, certification, and modernising retail but safe meat production has not yet take a significant share of the market (<6%). The key constraints to uptake are high cost of adoption and missing incentives. We opt for gradual improvements to the food system in place. Potential mitigation options will be presented and discussed (e.g. iron grid to avoid floor slaughter).

Key words: Pork, risk assessment, Vietnam, food safety

Aflatoxins in the dairy value chain- a challenge for the informal markets?

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ABSTRACT

Objective: In tropical regions, *Aspergillus* molds commonly infect crops, and may produce aflatoxins. The metabolite of aflatoxin B1, the most potent natural carcinogen, is aflatoxin M1, which is excreted into milk. Aflatoxins are hepatotoxic, nephrotoxic and carcinogenic to different degrees in livestock as well as humans, and can cause acute fatal disease as well as chronic. The effects on livestock of long term exposure may be reduced growth and immunosuppression, which has severe impacts on the production, which affects livelihoods and food security. Even though many countries do have regulations for aflatoxin control in both foods and feeds, resource-poor countries lack means of enforcing them, and in the informal markets, products are never tested.

Materials and methods: We sampled milk from the informal dairy market in low-income areas of Nairobi, Kenya and found that in households, 100% of samples contained the toxin and there was a positive association between the levels of aflatoxin M1 ingested and the degree of stunting in the children. In addition, up to 100% of samples collected in different rural counties exceeded the regulatory levels. We conducted a pilot study in Kenya and showed that by providing small-holder peri-urban and urban farmers with an anti-mycotoxin additive, a clay binder, the farmers could reduce the levels.

Results and conclusion: Although binders may prove to be a cost-efficient way of reducing aflatoxins in milk sold in the informal markets, more work still needs to be done, especially engaging with policy makers, to allow for formulation of policies that would guide production of safer feed products for smallholder farmers.

Research and training partnership to assist food safety in Vietnam and Cambodia

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ABSTRACT

Objective: This paper analyses a process of an initiative of researchers and institutions to work together in promoting the risk-based approach as a tool for better management of animal sourced food safety in Vietnam and Cambodia.

Materials and methods: A Taskforce of Risk Assessment for Food Safety was formed and consists of researchers working on risk assessment and food safety, and representatives of the related ministries of Health and Agriculture in Vietnam. In Cambodia, A Taskforce is being developed from the learning from Vietnamese experience and with adaption to the specific Cambodian context.

Results: In Vietnam, the Taskforce analyzed the situation of food safety policies, identified key constraints and opportunities. A series of hands-on training with selected relevant case studies were organized, risk assessment curricula have been developed and taught at universities to promote sustainability. Hand-on guidelines, text books, a special edition in a Vietnamese journal and policy briefs were published. The Taskforce has also provided technical support to key food safety assessment to the World Bank and international development partners. Case studies on food safety risk assessment were conducted in different food commodities, published, and widely communicated for risk communication and management purpose. The Taskforce has been institutionalized by a national university to have a formal role in implementing its activities. In Cambodia, the development of the Taskforce is in the framework of the "Safe Food, Fair Food for Cambodia project (SFFF)" funded by USAID under the Livestock System Innovation Lab (LSIL). The proposed way forward to establish the taskforce in Cambodia was to add the Taskforce into the existing national food safety technical working group to strengthen the existing group and optimise the synergy of, and to avoid duplication of efforts in different food safety activities in the countries

Conclusion: The Taskforce has brought experts in Vietnam to work together on prioritized topics of food safety risk assessment, assisted and informed ministries in implementing risk-based approaches for food safety management. It can be recommended as a way of institutionalizing risk-based methods in countries like Cambodia.

Key words: Food safety, risk-based approach, informal market, Vietnam, Cambodia, South-South learning.

Is my milk safe? Characterizing the quality and safety of the milk consumed in low-income households in Nairobi

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ABSTRACT

Objectives: Unprocessed milk, sold in informal markets, is the most widely consumed milk in Kenya. While unprocessed milk may be a vehicle for zoonotic pathogens, it is still one of the richest and most affordable sources of nutrients for low-income families. Although it is considered less safe compared to pasteurized milk, to date there is no compelling evidence on the health risks associated with consumption of such milk. This study characterized milk composition and consumption practices to understand the potential health risks and nutritional benefits for consumers.

Materials and methods: We conducted a survey among 200 low-income households in Nairobi to understand milk handling and consumption practices and characterize the quality and safety of the milk consumed. Samples were collected from 121 households. Laboratory analyses were done to determine total aerobic bacterial and Enterobacteriaceae counts and presence of *Listeria* spp., *Salmonella* spp., *Staphylococcus* spp. and aflatoxin M1. Milk composition was determined using FOSS MilkoScan.

Results: About 40% of the milk met the Grade I criteria (best grade) of the East African standards for raw milk. While *Listeria innocua* was present in 20% of samples, *L. monocytogenes* and *L. ivanovii* were present in just one sample. A small proportion of samples carried *Staphylococcus* spp., and none contained detectable *Salmonella* spp. Milk composition was diverse across samples. Only about 2% of the surveyed households had a fridge. Fifteen-percent of the milk had been boiled at the time of sampling and this was associated with reduced bacterial counts.

Conclusion: While bacterial contamination of milk, especially with spoilage associated bacteria, at the household level was high, boiling remains an efficient way to reduce load, especially where cold chain can't be assured. The data provides clues on the potential risk posed by milk from informal markets and gives insights of use in the promotion of milk safety at household level.

Key words: Milk, quality, safety, Nairobi, informal markets

POSTER PRESENTATION

Session A: Epidemiology studies in specific species/topics

Prevalence & therapeutic studies on diabetes mellitus in cats in & around Lahore

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ABSTRACT

Objective: The present study was hence conducted to study the prevalence of diabetes mellitus in cats (age 3 year and above) in and around Lahore, the effect of diabetes mellitus on various blood parameters and to evaluate the efficacy of insulin therapy in diabetic cats.

Materials and methods: Each cat who showed any of the following clinical signs polyuria, polyphagia, polydipsia, weight loss and of age 3 year and above was included in this study. The cat showing glucose > 250 mg/dl was considered as diabetic. Therapeutic Trails: For chemotherapy, a total of 12 cats (n=8 diabetic cats, n=4 healthy cats) were divided into three groups: A, B and C. In group A were the selected diabetic cats, Group B was kept as positive control, while, healthy cats were kept in group C. The efficacy of therapeutic trials was assessed through determination of the blood glucose values after insulin therapy. The data was analyzed by using Chi square test and T-test using statistical package for social sciences (SPSS) version 13.0.

Results: This study yielded a percentage prevalence of 3.6% diabetes mellitus in cats in and around Lahore. The study also yielded that the prevalence of diabetes mellitus in male cats was significantly ($P<0.05$) higher than that of female cats. Furthermore, the results of this study showed that the prevalence of diabetes mellitus was higher in old age cats and winter season, which occurs in a similar pattern as in human beings. Hematological Analysis: The clinical signs of polyuria, polydipsia, hyperglycemia, dehydration, and anemia were commonly observed in diabetic cats. The results of hematological study correlated well with the clinical findings. Group A exhibited the value of 367±20.28 mg/dL, Group B showed the value of 356±16.32 mg/dL, while Group C manifested blood glucose at the value of 209±10.36 mg/dl.

Conclusion: From this study, it was conclusively inferred that the prevalence of feline diabetes mellitus in Lahore, Pakistan was higher (3.6 %), as compared with previous studies. This might be due to the fact that owners do not pay much attention to the health management of their aged cats. Furthermore, male cats were found to be at higher risk for diabetes mellitus, as compared with the female cats. Seasonal variation with the disease being most prevalent during the winter season and in aged cats, was also observed from our data. Chemotherapeutic trials strongly confirmed the efficacy of NPH insulin for the treatment of diabetic cats.

Key words: Prevalence, diabetes mellitus, insulin

Culicoides-borne diseases in the Indian Ocean: Examples of Bluetongue and Epizootic Hemorrhagic Disease fever viruses in Reunion Island

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ABSTRACT

Objectives: Bluetongue (BT) and epizootic hemorrhagic disease (EHD) viruses are two important vector-borne orbiviruses with a worldwide distribution that have major impacts on livestock breeding and trade. They are transmitted by hematophagous *Culicoides* species. If epidemiological investigations in epizootic territories conducted after massive outbreaks enabled to better understand the epidemiology of these diseases, their epidemiology remain poorly studied/understood in areas of endemicity. In this context, three studies were implemented in Reunion Island located in the South Western Indian Ocean

Materials and Methods: The three studies were: (i) a virological and serological survey on cattle to identify BT and EHD viruses seasonal dynamics and prevalence, (ii) an entomological study on *Culicoides* species diversity, seasonal dynamics and spatial distribution, (iii) a viral screening in *Culicoides* species to identify and better characterize the vector species involved in the viral transmission, the level of infection in field populations and virus dynamics in *Culicoides* populations.

Results: The period with highest levels of seroconversion occurred is the hot and rainy season, when incidence of antibody acquisition reached 36.7% (IC95% = [31.7%; 41.7%]) for EHD virus and 20.7% (IC95% = [16.3% ; 25.1%]) for BT virus. Five *Culicoides* species are described on the island, and seasonal dynamics is particularly marked for three of them. Four species are involved in the transmission of each virus.

Conclusion: Overall, BT is endemic with continuous virus circulation, limited clinical cases and high serological prevalence while EHD is epizootic with a marked seasonal transmission pattern.

Key words: Bluetongue, Epizootic hemorrhagic disease, *Culicoides*, epidemiology, Indian Ocean

A genomic map for bovine tuberculosis susceptibility in *Bos indicus* breeds

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ABSTRACT

Objective: This study aims to describe the genomic variation in bovine tuberculosis susceptibility within a *Bos indicus* population.

Materials and methods: A cross-sectional study of 2346 slaughter cattle was conducted in four regions of Cameroon. bTb was detected by culture in 150/162 animals with lesions. A subset of 239 cattle (culture positive and negatives) was genotyped using a BovineHD 777K BeadChip, their genomic diversity characterized and the admixture structure of the Cameroon cattle population estimated using principle component analysis (PCA), STRUCTURE, genetic relatedness and genetic differentiation (F_{ST}) analysis. Quantitative trait loci (QTL) which had previously been identified in *Bos taurus* was compared.

Results: We found that breed (within the *Bos indicus* subspecies) is an important factor in explaining the epidemiology of bTB, with Fulani breed appearing to be more susceptible then mixed breeds. The difference in susceptibly between *Bos indicus* subspecies could be due to their admixture structure. Therefore, selective breeding could be used to decrease the susceptibility of cattle to bTB which could reduce size and duration of outbreaks, providing a new viable option for targeted genetic disease control.

Key words: Cameroon, *Bos indicus,* bovine tuberculosis, admixture, susceptibility

Strong associations of 9-point body condition scoring with survival and lifespan in cats

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ABSTRACT

Objectives: The objective of the study was to investigate the associations of a 9-point body condition score (BCS) with survival time and lifespan in cats.

Materials and methods: Electronic patient records from a cat-dominant primary practice in metropolitan Sydney, Australia, where the body condition of cats was regularly recorded using a 9-point BCS scale were obtained. The maximum BCS of each cat during the visits was used as the primary exposure variable. Two survival analyses were conducted to evaluate the associations of BCS with cats' survival and lifespan.

Results: In total, 2609 cats met the selection criteria from 4020 cats screened. The median of the maximum BCS was 6 (interquartile range [IQR]: 5–7). Compared with cats with a maximum BCS of 6, increased hazards of death were observed in cats with a maximum BCS of 3 (hazard ratio [HR]: 4.67, 95% confidence interval [CI]: 3.00–7.27), 4 (HR: 2.61, 95% CI: 1.95–3.49), 5 (HR: 1.43, 95% CI: 11.5–1.76) and 9 (HR: 1.80, 95% CI: 1.11–2.93). Median lifespan was 15.8 (IQR: 13.5–17.6) years. Compared with cats reaching a maximum BCS of 6 in the same age group, cats reaching a maximum BCS of 4 (HR: 4.15, 95% CI: 1.26–13.67) or 5 (HR: 1.75, 95% CI: 1.07–2.85) between age 1 and 3 years, and a maximum BCS of 3 (HR: 6.09, 95% CI: 1.47–25.25) and 9 (HR: 2.27, 95% CI: 1.27–4.04) between the age of 3 and 11 years had shorter lifespans.

Conclusion: There are significant associations of 9-point body condition scoring with survival and lifespan, and BCSs ≤5 and of 9 were found to be negatively associated with both. The study yielded information regarding a desirable BCS for cat longevity that veterinarians could consult with.

Key words: Cat, obesity, underweight, body condition score, survival

Seroprevalence of Rift Valley fever virus in livestock, wildlife and humans from 1968 to 2016: a systematic review

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ABSTRACT

Objective: Rift Valley fever virus (RVFV) is a zoonotic arbovirus that causes severe disease in livestock and humans. The virus has caused recurrent outbreaks in Africa and the Arabian Peninsula since its discovery in 1931. This review evaluated RVFV seroprevalence across the African continent in livestock, wildlife and humans in order to understand the spatio-temporal distribution of RVFV seroprevalence and to identify knowledge gaps requiring further research. Risk factors associated with seropositivity were identified and study designs evaluated to understand the validity of their results.

Materials and methods: The Preferred Reporting of Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines were used to produce a protocol to systematically search for RVFV seroprevalence studies in PubMed and Web of Science databases. The Strengthening the Reporting of Observational studies in Epidemiology (STROBE) statement guided the evaluation of study design and analyses.

Results: A total of 174 RVFV seroprevalence studies in 126 articles fulfilled the inclusion criteria. RVFV seroprevalence was recorded in 31 African territories from 1968 to 2018 and varied by time, species and territory. Only eight studies analysed RVFV seroprevalence in both livestock, wildlife or and humans concurrently. Higher RVFV seroprevalence was identified in animals compared to humans. Many studies did not account for study design bias or the sensitivity and specificity of diagnostic tests.

Conclusion: Future research should focus on conducting seroprevalence studies at the wildlife, livestock and human interface to better understand the nature of cross-species transmission of RVFV. Higher RVFV seroprevalences seen in animals may be a consequence of differing forces of infection. Reporting should be more transparent and biases accounted for in future seroprevalence research to understand the true burden of disease on the African continent.

Key words: Rift Valley Fever virus (RVFV), seroprevalence, risk factors, bias, Africa, livestock

Study of important infectious agents in out-migrating Fraser River Sockeye salmon

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ABSTRACT

Objective: To determine the presence, prevalence, and relative burden of 46 known or putative infectious agents in juvenile FR Sockeye salmon.

Materials and methods: 2,006 out-migrating Sockeye salmon were collected from four main regions along their migration trajectory (in freshwater and seawater) in British Colombia, during the spring of 2012 and 2013. Homogenized tissue samples (gill, brain, heart, liver, and kidney) from each fish were prepared and tested for the simultaneous detection of 46 important infectious agents using a novel high-throughput microfluidics quantitative PCR (Fluidigm BioMark™). Spatiotemporal patterns (by sampling region and year) in the prevalence and infection burden of most prevalent agents (prevalence > 5%) were also assessed using logistic and linear regression models.

Results: 26 different agents on the panel were detected at least once, including nine agents with prevalence > 5%. *Candidatus brachiomonas cysticola, Myxobolus arcticus*, and *Pacific salmon parvovirus* had the highest prevalences with 90, 60, and 57%, respectively. 82% of sampled fish were infected with at least two different agents (co-infections). A significant rise in the prevalence and burden of the prevalent agents from 2012 to 2013 was observed. The prevalence and burden of the prevalent agents increased upon entering the ocean from freshwater, but did not change substantially afterwards.

Conclusion: Our findings can contribute to the prioritization of future studies on the Fraser River Sockeye population decline, as well as to adjustments to the current fisheries management and conservation strategies.

Key words: Sockeye salmon, Fraser River, infectious agent, prevalence, high-throughput genomic screening

Investigation of Foot and Mouth Disease outbreak in cattle in Yinmarbin Township, Sagaing region, Myanmar during December 2016 - February 2017

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ABSTRACT

Introduction: In October 2016, Foot and mouth disease (FMD) occurred in Yinmarbin Township, Sagaing Region, Myanmar and was officially reported at the end of December, 2016. Investigation was carried out in late February, 2017 to understand the potential source of FMD, to identify the pattern and nature of outbreak and to measure the effectiveness of disease control programme.

Materials and methods: Household that having at least one cattle showing any clinical signs of FMD (salivation, lameness, hoof lesion, tongue lesion, stop rumination) was defined as case. Questionnaire interviews were done from 45 households at 4 villages. The collected data were analyzed for Descriptive statistics.

Results: A total of 126 (70.4%) cattle over 179 cattle in 45 households were infected FMD. The most prominent clinical signs were lameness and tongue ulcer. Sixteen (35%) respondents had experience in previous FMD outbreak between 1999 and 2016. Most of the farmer grazed their cattle on communal grazing ground and some were fed at home with mixed cattle feed. The course of the disease varied with average 21 days (minimum 4, maximum 71). The first case was occurred in 25th October, 2016. The incidence of disease was gradually increased from October and peaked in January and then decreased in the following weeks.

Conclusion: FMD was spreading to the neighboring villages and townships even disease control with vaccination to the susceptible animals and movement control activities were launched because the involvement of all stakeholders and cooperation of cattle farmers are unsatisfactory. More detailed study is needed to understand the occurrence and risk factors of the disease for the effective prevention and control of foot and mouth disease in Myanmar.

Key words: Foot-and-mouth disease, outbreak investigation, Yinmarbin Township, Myanmar

The case for and against vertical transmission of Piscine Myocarditis virus (PMCV) in Atlantic salmon

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ABSTRACT

Objective: Cardiomyopathysyndrome (CMS) has become one of the most important infectious viral diseases in the production of Atlantic salmon (AS) in the North Atlantic. One outbreak is estimated to cause economic losses around 1.9 mil. €, and in Norway alone there are more than 100 outbreaks each year. CMS is caused by *Piscine myocarditis virus* (PMCV), which was identified only in 2010. Transmission pathways for PMCV are not fully known, and in this study, we have investigated whether PMCV can be transmitted vertically.

Materials and method: Seven family groups of AS from two large salmon producers were followed, from broodfish through the different developmental stages (egg, larvae, fry) and until smoltification. At pre-testing of the broodfish, parents with different PMCV status were identified, with detected viral loads in hearts ranging from none to high. Samples were also taken from milt and ova, from eggs before and after disinfection as well as from larvae and fry. This was done atdifferent points during the production time in hatcheries. 60-120 samples were taken from each group at each timepoint, and all samples were tested with RT-qPCR.

Results: PMCV was found in the hearts of 128 out of 130 tested broodstock, while the prevalence was 69% in roe and 60% in milt. PMCV was detected in all developmental stages of the progeny, but with prevalences <25% and with low viral loads. PMCV was also detected in smolt groups both before and after seatransfer.

Conclusion: PMCV can be transmitted from broodstock to offspring through normal production routines. This suggests a possible critical control point for mitigating CMS.

Key words: Cardiomyopathy syndrome, Atlantic salmon, virus disease, vertical transmission

Broiler chicken welfare: what is the status in large-scale Kenyan farms?

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ABSTRACT

Objective: This study applied World Animal Protection welfare criteria for broilers to analyse welfare status in large-scale Kenyan farms.

Materials and methods: Data were collected from thirty contract and 31 non-contract broiler farms using a pre-tested questionnaire. Quantitative data were analysed using descriptive and inferential statistics, while qualitative data were summarized using themes.

Results: The estimated stocking density for broilers in contract farms was 21.80 kg/m^2 (95% CI: 18.2 - 25.6), while for non-contract farms, this was 22.54 kg/m^2 (95% CI: 18.4 - 26.8). The estimated daily growth rate for broilers in contract farms was 51 g (95% CI: 50.3 - 52), and 43 g (95% CI: 40 - 45.6) for non-contract farms. Age at maturity for broilers in contract farms was 34 days (95% CI: 33.8 – 34.6), and 38 days (95% CI: 36.5 – 39.9) for non-contract farms. Most farms kept Cobb 500 breed, with some non-contract farms keeping Arbor acres. Broilers were raised under deep litter system, and litter material spread throughout the shed, with no cages. Litter was mostly dry, but with moist areas around drinkers. Farms had no enrichments. In contract farms, broilers were fed on pellets and crumbles, while for non-contract farms, mash was fed. Furthermore, estimated mortality rates were 6.4% and 3.1%, and culling rates of 1 % and 0.3 % for broilers in contract and non-contract farms respectively.

Conclusion: These findings provide baseline information on broiler welfare in developing country context which is useful for policy making and support for extension.

Key words: Broiler welfare, large-scale farms, Kenya

Outbreak investigation: Identification of risk factors associated with seropositivity to goat brucellosis in Singburi province – Thailand during December 2016 - February 2017

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ABSTRACT

Objective: The study objectives were to identify magnitude of the outbreak, to identify risk factors of seropositive and to recommend the prevention and control measures.

Materials and methods: We conducted a case control study among a random sampling of 72 goat farms of the Singburi province during December 2016 – February 2017. Farmers were face to face interviewed using questionnaire regarding farm production types, husbandry, goat health managements, grazing management, breeding, carcass management and purchasing. Information from interviewing and sero-prevalence of goat brucellosis were illustrated by descriptive statistics. Multiple logistic regression was used to determine the risk factors of sero-positivity.

Results: Out of 72 farms, a total of 5,221 goats was raised with the median of 60 goats per farm (range=6-600). 90.3% were fattening farm. 80.6% (58/72) were introduced theirs new goat from Singburi province. Among these farms 39.7% (23/58) produce their own replacement goats. The highest problems that farmers complained was stillbirth 16.7% (12/72). We identified 26.4% (19/72) brucellosis seropositivity farms. Two factors were likely to be probable risk factors with univariate analysis, raising in public pasture (OR= 12.8; 95%CI = 1.6 – 102.9) and having goat with clinical signs of suspected brucellosis. (OR= 5.1; 95%CI = 1.6 – 16.4).

Conclusion: One-fourth of goat farms in Singburi province got sero-positive to goat brucellosis. To reduce transmission of the disease, we recommend that farmers should carefully seek for a suspected brucellosis goat in their farms by clinical signs/symptoms together with active sero-surveillance. Further study of knowledge, attitude and practice (KAP) among goat farmers on public sharing practice is necessary to solve goat brucellosis transmission in Singburi province.

Key words: Goat, brucellosis, seropositivity, risk factor, Thailand

Risk factors for early return to service in breeding pig herds

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ABSTRACT

Objective: Our objective was to determine risk factors associated with early return to service (ERS).

Materials and methods: Data included 998,395 service records in 904,028 parity records of 172,255 female pigs from 155 herds. The ERS was defined as return to service 11-17 days. A 1:4 matched case-control study was carried out and logistic models were applied to the data. The following factors were assessed: age at first-service, parity, number of services, service season, number of weaned piglets and lactation length.

Results: Of all the females, 1.9% experienced ERS in their lifetime (95% confidence interval: 1.81-1.94%), and the incidence rate for ERS was 3.9 cases per 1,000 pig-weeks (95% confidence interval: 3.81-4.07). Significant factors were being in gilts, re-service, winter servicing and fewer weaned piglets. For example, a gilt was 1.39-1.85 times more likely to have an occurrence of ERS than a sow ($P < 0.01$). A re-serviced pig was 1.22 times more likely to have an occurrence of ERS than a first-serviced pig ($P < 0.01$). A pig serviced in winter was 1.18-1.34 times more likely to have an occurrence of ERS than a pig serviced in the other seasons ($P \leq 0.01$). Lastly, a sow with 10 or fewer weaned piglets was 1.20-1.21 times more likely to have an occurrence of ERS than a sow with 11 or more weaned piglets ($P < 0.01$). However, there was no association between an occurrence of ERS and lactation length ($P = 0.24$). Meanwhile, the age at first-service was tended to be associated with an occurrence of ERS ($P = 0.051$). Pigs first-serviced in 234 or less days of age was 1.13 times more likely to have an occurrence of ERS than pigs first-serviced in 235-274 days of age ($P = 0.04$). Therefore, producers should keep an eye on at-risk female pigs to prevent ERS. (299 words)

Key words: Case-control study

An outbreak of classical swine fever in pigs in Bangladesh, 2015

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ABSTRACT

Objectives: In a group of 22 healthy pigs aged between 4 and 6 months, 2 pigs became ill with high fever, complete anorexia, cough and abnormal swaying movements on 22 June 2015. One of them died on June 24 and the second died on July 3. Shortly after, the remaining pigs also fell ill and died from the same illness by 10 August 2015. We investigated the aetiology, epidemiological and clinical features of the outbreak.

Materials and methods: We recorded the clinical signs and symptoms for each pig with the date of onset of illness. Veterinarians conducted *post-mortem* examinations on the 12 dead pigs, they collected tissue samples from the dead pigs and placed them in a tube containing 1 mL of nucleic acid extraction buffer (lysis buffer). We tested all the tissue samples by real-time reverse transcription polymerase chain reaction (rRT-PCR) to detect classical swine fever virus (CSFV) because the animals' symptoms matched those of this disease. We also conducted a phylogentic analysis of the nucleotide sequence of the E2 gene segment of CSFV detected in a lung tissue sample.

Results: The attack rate (22/22) and the case fatality were 100%. The predominant symptoms of the disease included high fever, cough, diarrhoea and swaying movements of the hind legs prior to death. Of the 12 pigs tissue samples tested, all had evidence of the presence of CSFV RNA by rRT-PCR. The phylogenetic analysis indicated that the virus belongs to genotype 2.2, which is closely related to CSFV genotype 2.2 reported in India.

Conclusion: Our investigation suggests that CSF is circulating in pigs, posing a risk for communities in Bangladesh that rely on pigs for economic income and dietary protein. Future research could focus on estimating the disease and economic burden of CSFV in pig rearing areas to determine if interventions might be warranted or cost-effective.

A regional outbreak of winter dysentery; effect on herd level milk production

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ABSTRACT

Objectives: In adult cattle, bovine coronavirus causes epidemics of diarrhea, called winter dysentery. The associated drop in milk production is well known in areas where this disease is a recurring problem. Despite this, quantification of effects on milk production is lacking in scientific literature. The objetive of the present study was to quantify the effect of winter dysentery on herd level milk production.

Materials and methods: During the winter 2011/2012 a regional epidemic of winter dysentery occurred in Norway. As a result, the dairy board advisory service initiated a voluntary surveillance system; a telephone 'hot-line' for veterinary and farmer reporting of herds with signs of winter dysentery. Using milk shipment data, milk production in herds that reported winter dysentery (n = 241) was compared to production in herds in the same region that did not report an outbreak (n = 2093) in a retrospective cohort study. Pseudo-outbreak dates were simulated for the group of herds with no report to ensure comparable time at risk and reduce misclassification bias due to underreporting. A linear mixed model was built with herd-level milk production (L/cow per day) as the outcome. Initial differences in production were adjusted between the two groups and a correlation structure accounted for dependence between milk shipments from the same herd.

Results: Milk production in herds with reported winter dysentery dropped considerably in the period around disease outbreak. Lowest predicted value of production occurred at day two post- reporting, when production was reduced by 15% compared to pre-outbreak levels. Production increased after day two, but affected herds did not regain pre-outbreak milk production levels within the modelled time period (< 20 days after reporting).

Conclusion: Winter dysentery has a profound impact on herd level milk production. This novel finding can motivate stakeholders and inform improvements in the prevention of between-herd spread of bovine coronavirus.

Key words: Winter dysentery, bovine coronavirus, cattle, milk production

Impact of sociocultural factors and farmers' behavior on the prevalence of brucellosis in Sri Lanka

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ABSTRACT

Objectives: Brucellosis has been prevalent for decades in Sri Lanka, causing enormous economic losses to dairy farmers. It is a threat to livelihood development and alleviate poverty in the rural areas of Sri Lanka. Our presentation aims to identify the sociocultural factors causing the spread of Brucellosis in Sri Lanka.

Materials and method: The Ampara District, which is located in the southeast region in the dry doze in Sri Lanka, was selected for our study area. Social and epidemiological surveys were conducted from May to September 2016. A total of 155 dairy farmers from the selected area were investigated by questionnaire survey. The blood samples of 1,153 cattle belonging to those farmers were collected.

Results: The seroprevalence at farm level was found to be 9.6%. Some specific farming behaviors, such as "isolation of aborted animals from others" were negatively related to brucellosis occurrence. Higher incidence of brucellosis was found among Muslim farmers compared to other ethnicities. Also, incidence was higher among farmers who brought animals from other farmers in the neighborhood. Farmers did not concern about health certificate when purchase. It was suspected that Brucella-infected cattle that had abortions were sold intentionally. Farmers' knowledge about brucellosis was significantly poor.

Conclusion: The analysis revealed that brucellosis transmission from animal to animal was influenced by socio-cultural factors and human behavior of farmers. It is effective to improve farmers' knowledge of brucellosis with high priority for susceptible ethnicity. But knowledge would cause hidden transaction of infected cattle, aggravating the condition; thus knowledge improvement with infective cattle culling compensation would be effective in controlling.

Key words: Brucellosis, Sri Lanka, knowledge, behavior, poverty

Efficacy of Diazinon ear tag in blood-sucking flies control and influence on weight gain in beef cattle

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ABSTRACT

Objective: Ear tags impregnated with 20% diazinon were evaluated for efficacy against the blood- sucking flies and influence on weight gain in beef cattle.

Materials and Methods: Forty crossbreed beef cattle were divided into 2 groups of 20 cattle by matching with weight, and sex. One group received one ear tag per cattle for 120 days while the control group remained untagged. Both group lived in an open-house stable and were allowed similar duration of access to pasture. Cattle were fed consistently with the standard practices of the facility and ad libitum water during the study. The Vavoua Trap was set in the morning and collected at the same time of the next day. Flies were collected once or twice a week for almost 1 month before ear tagging. During ear tagging period, flies were collected every 2 weeks until the tags were removed. Additional samples of flies were also collected every 2 weeks 3 more times after tags were removed.

Results: Ear tag demonstrated a highest efficacy of 89% stable fly (*Stomoxys calcitrans*) reduction at week 10 and when compared mean number of flies before ear-tagging and during ear-tagging period, mean number of flies during treatment was significantly lower than that of pre-treatment ($P<0.05$). Statistical significance influence on weight gain was also founded when compared between ear-tagged and non-tagged cattle groups among young claves.

Conclusion: Ear tag shown high efficacy in controlling population of stable fly but due to a small fly samples, further study should be done in farm with abundant number of blood-sucking flies. It has statistical significance influence on weight gain in tagged calves. Even though influence of ear-tagging has no statistical significance on weight gain among beef heifers

Key words: Ear tags, diazinon, fly control, beef cattle, weight gain

PIG DATA: Health analytics for Swiss pig farming

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ABSTRACT

Objective: Large data volumes can no longer be analyzed using conventional methods; they have to be made usable by applying new methods. So far, such methods have not had much impact on animal husbandry. Swiss pig production differs from the intensive production systems in other European countries because of its complex and small-scale structure. Although all stages of production generate animal health and production data, it is not being used in a way that brings together all the various stages of production. If this information is suitably prepared and analyzed, it will be possible to identify new links, causes and risk factors in relation to diseases and/or a drop in performance – and to identify the best strategies for combating them.

In this project, new methods aiming at gaining a better understanding of, and optimizing the structure and complexity of the pig farming and production network in Switzerland are applied.

Materials and methods: Various production data (bases) from veterinarians, companies involved in trading of pigs or feed, or in slaughtering fatteners have been assessed and integrated in a large database (called the Pig Data Space). This Pig Data Space is further fed with (retrospective and current) data about animal movements in Switzerland and climate data from the whole country. The Pig Data Space will be updated in different time intervals.

Results: This project is not only utilizing existing data but also taps into potential sources of new data in order to improve animal health, boost animal welfare and make pig production more sustainable. The results of this project enable livestock owners and veterinarians to take steps to improve animal health and prevent disease. Optimized production processes will lead to greater efficiency, sustainability and value creation. Ultimately, end users such as consumers will benefit from improvements in animal health, reduced antibiotic use and the resulting foodstuffs.

The relationship between non-nutritional factors and milk citric acid concentrations in dairy cows in western, Thailand

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ABSTRACT

Objectives: This study determined the relationship between non-nutritional factors and milk citric acid concentrations in dairy cows raised in small holder farms in western Thailand.

Materials and methods: The data were collected from 84 dairy farms belonging to the three most populated dairy provinces in western Thailand. In total, 1,117 lactating dairy cows were included in the study. Milk samples were collected from all cows and were analyzed for milk componants, somatic cell counts and citric acid concentrations using Milkoscan Analyzer at the Nong Pho Milk Quality Laboratory. Extreme values of one or more parameters were excluded from statistical analyses. Descriptive statistics for milk citric acid, parity, stage of lactation, and test-day milk yield, fat and protein were calculated. The comparison of milk citric acid concentrations between subclinical mastitis and normal were calculated by t-test. The subclinical mastitis of milk samples was classified when milk somatic cell counts were greater than 5×10^6 cell/ml.

Results: The milk citric acid concentration was highest during the early lactation, and decreased later in mid and late lactation. The milk citric acid was peak at lactation 4 and then still decreased following the number of lactation. A positive relationship existed between milk citric acid concentration and lactose, milk urea nitrogen, while negative relationships with milk protein%, milk fat% and total solid were observed. The results showed that the citric acid concentrations in subclinical mastitis (0.109 mg/dl) was significant lower than normal milk (0.115 mg/dl) (P=0.01).

Conclusion: A positive relationship was found between milk citric acid concentration and lactose and milk urea nitrogen, while negative relationships with milk protein%, milk fat% and total solid. The concentration of milk citric acids may be useful as a screening test for early warning for subclinical mastitis in dairy cattle.

Key words: Milk citric acid, non-nutrition factors, dairy cows

Bayesian statistical methodologies and experimental designs to aid investigating apparent lack of anthelmintic efficacy in cattle herds

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ABSTRACT

Objective: Anthelmintic use is increasingly under threat due to nematodes becoming resistant to products. The Faecal Egg Count Reduction Test (FECRT) is the most widely used field-based method for determining drug efficacy and as an indicator of drug resistant nematodes in cattle. This test traditionally involves a group of cattle with apparent suspected resistance or lack of efficacy, being randomised into positive treatment and untreated control groups at baseline (Day 0). Faecal egg counts (FECs) are then obtained 14 days post-treatment, through counting techniques of various degrees of sensitivity, measured in eggs per gram (epg) of faeces. Efficacy is determined by calculating the percentage reduction in FECs based on arithmetic means of the two groups with a 95% confidence interval. As part of our work, we have investigated if there are strategies to improve efficacy calculation reliability, using a Bayesian statistical framework.

Materials and methods: Using cattle FEC data that were obtained from large scale field studies in England, a simulation study was conducted using Bayesian methodologies. The study evaluated the accuracy of different efficacy calculations, involving different cattle sample sizes and FEC methodology sensitivities and presence/absence of an untreated control group.

Results: The following percentage estimate was observed to be the most accurate:

where and are the Day 0 and Day 14 FECs from the *i*-th animal in a positive treatment group and is the sample size.

Conclusion: The above percentage estimate would be recommended to use under: a paired study design with a positive treatment group only; FECs determined using a 15 epg sensitivity method; and a minimum sample size of 15 animals. The hyperlink: http://outreach.mathstat.strath.ac.uk/apps/FECRT can be accessed to carry out the recommended Bayesian analysis.

Key words: Cattle, anthelmintic efficacy, anthelmintic resistance, FECRT, Bayesian

Canine leptospirosis in the United States (2009-2016): Use of PCR testing to unravel complex spatial, temporal, human- and animal-level risk factors

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ABSTRACT

Objective: Canine leptospirosis is a reemerging zoonotic disease of concern, yet information on its epidemiology is lacking. Recent wide-scale clinical uptake of a new PCR test, which offers improved sensitivity, may provide greater insight into this complex disease. This study aimed to describe the temporal and spatial distribution of PCR-positive canine leptospirosis cases in the U.S., and to identify environmental, dog and human-level factors associated with infection.

Materials and methods: Data from 40,118 canine leptospirosis PCR tests run in the U.S. between 2009 and 2016 were acquired from IDEXX Laboratories. Data on weather, urban influence, human income and education were obtained from public databases. Maps were created to identify high-risk areas and generalized (univariable, followed by multivariable) mixed logistic regression models accounting for county and state were used to identify significant predictors and assess for confounding.

Results: Overall test-positive prevalence was highest in the midwest and was 5.4% across the U.S. - peaking in 2013 (7.7%), and steadily decreasing into 2016 (5.0%). In the final multivariable model, dogs were at higher odds of testing positive in the fall (Sept-Nov) compared to the spring (OR=2.13, P < 0.001). Dogs tested during months with moist environmental conditions (measured at the state climatological level by the Palmer Drought Severity Index) were at higher odds of testing positive compared to dry conditions (OR=1.22, P < 0.001). Females dogs were at lower odds of testing positive compared to males (OR=0.79, P < 0.001). Urban dogs were at higher odds of testing positive compared to non-urban dogs (OR=1.31, P = 0.01) in univariable analysis, but not in the final multivariable model. No human factors were significant in any model.

Conclusion: These results highlight important factors based on newly available PCR testing, allowing for an improved understanding of canine leptospirosis and targeted education and prevention efforts at clients/dogs with greatest disease risk.

Key words: Canine, leptospirosis, zoonosis, PCR testing

Bovine hydatid disease in Australia: risk factors and spatio-temporal clustering

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ABSTRACT

Objective: Bovine hydatid disease is characterised by hydatid cysts in the viscera. The objective of this study was to describe the prevalence of hydatid disease, determine risk factors, and identify spatio-temporal clusters of disease in Australian cattle.

Materials and methods: Data from approximately 280,000 beef cattle slaughtered at a northern New South Wales abattoir between 2010—2016 were examined. Regression techniques were used to assess the impact of sex (male or female), age (dentition group), and feed type (grass- or grain-fed) on the presence of hydatid disease at slaughter, with origin (Property Identification Code [PIC] region) included as a random effect. Spatio-temporal clustering of hydatid-positive cattle in PIC regions was assessed using discrete-Poisson models.

Results: Prevalence of hydatid disease in the study population was 15.5% (95% CI 15.4—15.6). Regression analysis showed that the odds of hydatid disease were highest in eight-tooth cattle (>42 months, OR 22.99, 95% CI 22.15—23.86, P<0.001, ref zero-tooth). Females (OR 2.30, 95% CI 2.24—2.36, P<0.001, ref males) and grass-fed cattle (OR 2.56, 95% CI 2.29—2.86, P<0.001, ref grain-fed) were also more likely to have hydatid disease. Two clusters of hydatid-positive regions were identified. The most likely cluster was located in north eastern New South Wales (January 2012-June 2015; log likelihood ratio statistic 5058; P<0.001). The second most likely cluster was in central Queensland (August 2015-April 2016; log likelihood ratio statistic 609; P<0.001).

Conclusion: Although the association between age and hydatid disease is consistent with previous studies, the association between sex and hydatid disease is not. This is possibly due to confounding of variables unavailable in abattoir data. The identification of clusters indicates geographical variability in the prevalence of hydatid disease. Further analysis to determine reasons for variation could assist with future control programs.

Key words: Hydatid disease, Australia, beef cattle, risk factors

Risk factors during smoltification at fresh water sites associated with High Risk Diseases (HRD) during marine phase in Coho salmon

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ABSTRACT

Objective: The smoltification process in salmonids is a critical process for productive success and sanitary condition in marine phase could be conditioned by this. To assess risk factors during smoltification at freshwater sites associated with HRD mortality in Coho Salmon (CS) that were transferred to the sea between 2011 – 2015.

Materials and methods: A retrospective study design was used with all complete production cycles of CS that started between 01/01/2011 and 31/12/2015. Official mortality counts of HRD (defined by SERNAPESCA (National Service of Fisheries and Aquaculture) informed to the service and other official databases were used. Data was available from 26 companies that contributed with 128 sites that included 2,782 cages located in the X, XI and XIV Regions. The association between risk factors and HRD counts was evaluated using a Zero-Inflated mixture model (Binomial and Poisson distributions) using R. Three models were build, one for each segment of the marine cycle (smolts, juveniles and adults).

Results: Smolts: Count model: Variables associated with increased counts were:
Type of water body (smolts reared in lakes and open flow) relative to estuarine.
Variables associated with decrease counts were:
To vaccinate relative to not vaccinate
Zero-inflated model: all non-significant.
Juveniles, Count model: Variables associated with increased counts were:
Type of water body (smolts reared in lakes, rivers and open flow) relative to estuarine.
Neighbourhoods (the area where the site was located related to neighbourhood #1)
Variables associated with decrease counts were:
To vaccinate relative to not vaccinate
Zero-inflated model: statistical significant differences between cages.
Adults: Similar results as for juveniles.

Conclusion: Several risk factors were identified that will allow to adjust national policies.

Key words: Zero-inflated models, coho salmon, smoltification, risk factors

Transection as faster means to release the suspensory ligament during canine ovariohysterectomy

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ABSTRACT

Objectives: The objective of this study was to conduct a pilot randomized controlled trial to estimate surgical time, safety, intra-operative nociception and post-operative pain of digital strumming (DS) compared to sharp transection (ST) of the suspensory ligament. We hypothesized that: (1) ST of the suspensory ligament is a faster technique to elevate the ovarian pedicle from the canine abdomen; (2) ST will decrease intra-operative nociception.

Materials and methods: Thirty adult female dogs were randomly assigned to ST or DS procedures. Measures of nociception were assessed through baseline measurements of pre- and intra-operative heart rate specifically during manipulation of the suspensory ligament. Measures of pain were assessed through pre- and post-operative pain scores using the Glasgow Pain Score. Assessment of the time of each procedure was measured through total surgical time and the time it took to rupture the suspensory ligament as an isolated event (i.e. the time it takes from clamping the proper ligament to placing the first hemostat on the ovarian pedicle). During suspensory ligament manipulation, the change in heart rate (HR) was measured as the increase in HR from the time the proper ligament was clamped to the peak HR during suspensory ligament manipulation.

Results: Accounting for body weight, the total surgical time for ST was 1.1 minutes faster than DS and each additional kg of body weight increased total surgical time by 0.1 minutes. DS had 30.6 times the odds of taking greater than 1 minute compared to ST. The difference in heart rate from baseline to peak was 7.4 bpm lower in the ST treatment group than in the DS treatment group. No perioperative complications were observed and there was no difference in post-operative pain score between treatments.

Conclusion: We concluded that ST provides less intense nociceptive input compared to DS. ST was also faster than DS.

Key words: Canine, spay, suspensory ligament, surgery

Evaluation of efficiency of environmental sampling in the national surveillance for Mycobacterium avium subspecies paratuberculosis in Japan

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ABSTRACT

Objectives: Since 1998, individual serum tests have been conducted for all dairy cattle at least every five years as a national paratuberculosis control program in Japan. The test-and-cull strategy with sequential follow-up tests in detected farms has contributed to reducing the number of cases to a very low level. Meanwhile, sampling from individual cattle nationwide is costly in labor and financial perspective. Therefore, we examined the testing strategy using environmental samples from farms as an alternative screening tests in the control program.

Materials and methods: An individual-based transmission model was developed using parameters estimated from field epidemiological data on paratuberculosis. In the model three transmission routes were considered; vertical, dam-calf horizontal and horizontal transmission from contaminated environment. Contamination of environment was modeled considering the concentration of Mycobacterium avium subspecies paratuberculosis (MAP) in feces, reduction of MAP by cleaning and biological decay of MAP. Then, within-farm transmission caused by introduction of an infected heifer was simulated for 40 years for 1,000 iterations.

Results: When the individual test was conducted without follow-up tests, infection continues until the end of simulation. When the individual test was conducted with the follow-up tests as the current strategy, eradication from the herd was achieved almost within 10 years. The environmental sampling seemed less labor intensive and assumed to be conducted every year with the follow-up tests. Under this scenario, eradication was achieved earlier than the current strategy.

Conclusion: Tests using environmental samples can be an alternative in the national control program. This testing strategy greatly reduce the number of test samples and less labor intensive. As a result, the overall cost of the control program will be reduced significantly.

Key words: Mycobacterium avium subspecies paratuberculosis, surveillance, environmental sampling, individual based model

Evaluation of economic losses due to paratuberculosis in a bovine dairy herd in Northern Italy, 2012-2016

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ABSTRACT

Objective: Mycobacterium avium subsp. paratuberculosis (MAP) is the causative agent of Johne's disease (JD), a chronic gastrointestinal inflammation affecting especially ruminant species worldwide. JD causes substantial economic losses in dairy sector. Moreover, due to the concern over the zoonotic potential of MAP, specific trading warranties have been required by some extra-UE countries.
This work aimed at estimating the economic impact of JD in an infected dairy herd located in Northern Italy.

Materials and methods: In an infected farm, between 2012 and 2016, we selected 120 cows older than 36 months using serological (every six months) and fecal culture (once a year) tests. We considered an animal which resulted positive to at least one test as MAP-positive, while animals tested at least twice and resulted always negative as MAP-negative. The study population included 45 MAP-positive and 75 MAP-negative. Data on animal characteristics and production were obtained from different databases.

Results: We estimated an average unrealized income of 3340.06 EUR per infected animal due to the lower mean lifetime milk production (-3207.16 EUR) and to the lower average slaughter weight (-132.90 EUR). The relative risk of death on the farm for MAP-positive animals was 8.33 (95% CI, 1.01-69.08) compared to their negative herdmates (p<0.05).We estimated an additional mean loss of 892.80 EUR per year, due to direct mortality-related costs in infected cows. Due to the shorter production life in infected cows, we estimated the need to purchase four additional replacement heifers per year, thus increasing the mean replacement cost of 7200 EUR per year.

Conclusions: This is the first study of JD economic impact in Southern Europe. Our results indicate that MAP infection causes considerable economic losses to dairy producers and suggest the need to carry out farm control programs.

Key words: Johne's disease, economic losses, bovine dairy production

Characterization of small dairy farmers in Central Chile: general aspects, organizational structures and farmers expectations

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ABSTRACT

Objective: This study was carried out in small dairy producers from the O'Higgins Region, Chile, to characterize their production systems.

Materials and methods: A semi-structured survey was applied to 25 small dairy producers: Data was analyzed based on descriptive statistics.

Results: Most farms are managed by men. The average age of the producers was 57 years, which are predominantly landowners who work as dairy farmers supported by other complementary activities. Producers work mainly with Holstein cattle, most milking only once a day and using stainless steel containers for milk storage, for cheese production. Producers keep only reproductive records. The reproductive management techniques used are artificial insemination, pregnancy diagnosis and heat detection. There are also other managements such as animal dehorning, done by most producers before six months of age, with a saw. On the other hand, mastitis was named like the most common disease, as it means loss of milk production. In turn, an important fraction of the producers does mastitis treatments on their own. In organizational terms, most producers are not linked to any organization, mainly because of mistrust. Producers identify their animals as the most important positive aspect of their productive system, whereas infrastructure was the most substantial negative aspect of it. Most of the producers consider that their productive system is relevant for the area where they belong, which they believe turn into a high local demand.

Conclusion: Farmers were characterized in this study. Most appreciate their activity and consider mastitis as a key disease, while lack of appropriate infrastructure is considered it main challenge. Propper records are scarce and appear to be a main weakness of this production group.

Key words: family farming, dairy, characteristics

Scoping review of the literature and meta-analysis of risk factors for bovine respiratory disease in beef cattle

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ABSTRACT

Objective: Bovine Respiratory Disease (BRD) is a disease syndrome in cattle that consists of a complex combination of multiple causative agents and risk factors. To date, however, no scoping review has been performed to summarize the main risk factors associated with BRD morbidity and mortality. Our objective was to gather and synthesize literature from primary research to identify risk factors for BRD in cattle in the United States using a scoping review approach.

Materials and methods: Our research question was "What quantitative data on risk factors are available for BRD health and performance outcomes in commercial feedlot cattle in the United States?". We performed a search on Agricola, Pubmed, CAB and Scopus databases during April 2017. No restriction for publication year, language, or location was applied. After retrieving the abstracts, a relevance screening was conducted. Exclusion criteria included: diseases other than BRD, other than risk factors for BRD, non-original research, challenge studies and studies conducted on dairy, veal calves, or bulls.

Results: Of the total 2,213 abstracts originally obtained: 582 were duplicates, 468 were not related to BRD, 694 did not pertain to risk factors, 28 were not peer-reviewed, 125 were review articles, 183 had other exclusion criteria (demographic characteristics), and 27 had non-retrievable abstracts. Relevance screening passed 127 abstracts that were deemed acceptable to be summarized. Articles included during data extraction consisted of observational and experimental studies that were published between 1973 and 2017, with 2009 as the median year of publication. The main factors associated with BRD morbidity and mortality were shipping distance, gender, season, preconditioning methods (vaccination, weaning, and castration), commingling and marketing methods, metaphylaxis, and initial weight.

Conclusion: This study provides key information on risk factors to populate a risk analysis model simulating risk and control measures. This would support improved decision-making for cattle feeders and their veterinarians.

Key words: Bovine Respiratory Disease, scoping review, risk factors, beef cattle

Assessment of the potential of mid-season targeted selective anthelmintic treatment based on flexible gain threshold for gastrointestinal nematode infection control

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ABSTRACT

Objective: In first grazing season calves, the anthelmintic treatments used to control the negative impact of gastrointestinal nematodes (GIN) on growth must be rationalized to preserve their long-term efficacy. In this way, the suitability of a single mid-season targeted selective treatment (TST) for gastrointestinal nematodes control, based on flexible average daily weight gain (ADWG) thresholds, was investigated in 23 groups of first grazing season calves.

Materials and methods: Each group was divided in two sub-groups and animals randomly allocated to one of these two sub-groups intended for two different mid-season anthelmintic treatment strategies: (1) a treatment of all calves (whole-group treatment-WT) or (2) a targeted selective weight gain-based treatment (TST). TST was based of those animals showing an individual pre-treatment ADWG inferior to the mean pre-treatment ADWG of the corresponding WT sub-group. Anthelmintic treatment (levamisole 7.5 mg/kg body-weight) was performed 3 to 4 months after turnout. At housing, two parasitological parameters (the anti-*Ostertagia ostertagi* antibody level and the pepsinogen level) and a clinical parameter (the breech soiling score) were assessed at individual level in each group.

Results: Among TST sub-groups, the ADWG thresholds for treatment varied from 338 to 941 g/day and the percentage of treated animals from 28% to 75%. Pre- and post-treatment ADWG as well as parasitological and clinical parameters measured at housing were similar between TST and WT sub-groups. In the 6 highest GIN exposed groups (mean pepsinogen level $\geq$2.5 U Tyr), the average effect of treatment on post-treatment ADWG was the highest and estimated up to 14 kg after a grazing duration of 4 months. In contrast, in 6 other groups showing mean anti-*Ostertagia ostertagi* antibody level <0.7 in untreated animals, no effect of treatment was seen suggesting an absence of production losses related to a low level of infection.

Conclusion: This study highlighted the suitability of a convenient mid-season TST strategy for first grazing season calves, based on the use of flexible thresholds of ADWG, allowing similar growth compared with a whole-group treatment while keeping a nematode population in refugia through heifers left untreated.

Key words: Dairy calves, gastrointestinal nematodes, average daily weight gain, targeted selective treatment, mid-season

Using R-Shiny package to visualize laying hen movement patterns

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ABSTRACT

Objective: The development of tools to collect different types of animal data is generating large amount of data, which have the potential to provide better understanding of animals and their disease state within production systems. It may also provide a new perspective for observing animals, the way we perceive them, their needs, behaviors and can be helpful to identify diseases or changes in welfare. Monitoring individual and group level animal movements has recently been gaining popularity, under the banner of Precision Livestock Farming. These systems generate vast amounts of data that can be difficult to deal with analytically, due to size and complexity of datasets. One approach to learn about large complex datasets is to create easy to use data visualization tools, that researchers can use to discover patterns in the data. The purpose of this study was to develop a web app for visualizing laying hen movement patterns. We aimed to see if the R-Shiny package could help to develop a web app to identify individual hen and group level movement patterns.

Materials and methods: A custom designed system was developed to monitor the movements of laying hens in a commercial production environment. We used R-Shiny to create a highly customizable web app with large number of interactive plots of movements of each hen (N = 120), during the daylight period for 11 distinct six-day periods.

Results: Data visualization allowed easy identification of unique individual bird movement patterns, consistent over the short term. It also allowed us to identify sudden and long term changes in the movement patterns, over the production cycle.

Conclusion: R-Shiny package is a valuable tool for data visualization, providing a platform to easily identify complex patterns in data and helping to understand the movement behavior of laying hens.

Key words: Animal behavior, R-shiny, precision livestock farming

Seroprevalence of Verocytotoxigenic *Escherichia coli* (VTEC) Serotypes in Poultry Farms in Abuja, Nigeria

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ABSTRACT

Objective: The seroprevalence of both O157 and non- O157 Verocytotoxigenic *Escherichia coli* (VTEC) serotypes were investigated in poultry farms in Abuja, Nigeria.

Materials and methods: Feacal samples collected from the poultry farms were analyzed for the presence of VTEC serotypes after culturing in a supplemented enrichment media. Confirmation of typical *E. coli* isolates were carried out using Eosin Methylene Blue (EMB) agar and specific biochemical tests. *E. coli* isolates ex-EMB were sub-cultured into Cefixine-Tellurite Sorbitol MacConkey (CT-SMAC) agar to identify sorbitol and non-sorbitol fermenting isolates which were further characterized serologically using commercially procured latex-agglutination test kits from Oxoid, England.

Results: A total of 574 samples were tested and a prevalence of 6 (1.05%) for O157 and 9 (1.56%) for non-O157 (specifically O26, O103 and O11) were recorded. The distribution of the infection with season was also carried out using Fisher's exact test. There was no significant association ($p > 0.05$) between season and infection with VTEC O157 and non O157 in Poultry.

Conclusion: The detection of various zoonotic serotypes of VTEC in poultry in Abuja, FCT is an indication that poultry may serve as a source of infection to man. VTEC disease manifests itself in a range of severity from mild diarrhea to severe bloody diarrhea to complications such Haemolytic Uraemic Syndrome (HUS) that can result in death in humans. There is need to intensify hygienic and other control measures in poultry farms and environments.

Key words: Seroprevalence, verocytotoxigenic, *E. coli*, serotypes, poultry

Similar development of cecal microbiota diversity within four broiler houses at two different farms

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ABSTRACT

Objective: Gut microbiota influences health and production performance of broiler chickens. A fundamental knowledge of whether and how the microbiota differs during a production round between flocks and farms of the same breed, however, is lacking. Therefore, we studied the longitudinal development of cecal microbiota diversity in four broiler houses at two different farms.

Materials and methods: The two farms had a different feed supplier and management, but the broiler flocks in the two houses within the same farm were from the same breed (Ross 308), hatchery and parent flock and received the same feed and management. Coccidiostatic drugs were standardly applied in the feed in all flocks. During one production round cecal content was collected from nine birds per poultry house at the chicks' day of arrival and on days 2, 7, 14, 21, 28, and 35. All four flocks showed excellent production performance, and no antibiotic treatments were applied. The diversity of the cecal microbiota was assessed by 16S ribosomal RNA gene amplicon Illumina HiSeq sequencing.

Results: From the second week of age onwards, the within sample (alfa) diversity, the richness, and evenness of the cecal microbiota seemed to stabilize at both farms. The weighted UniFrac distances showed that the age of the broilers most strongly affected cecal microbiota between samples (beta) diversity. Furthermore, unweighted UniFrac distances were slightly higher than the corresponding weighted UniFrac distances between the two farms. This suggested that the abundant taxa of the two farms are phylogenetically related. The two broiler houses within the same farm showed similar cecal microbiota diversity.

Conclusion: The cecal microbiota development of the two different farms was comparable, despite the different feed supplier and management. In all broiler houses, the age of the broilers within the production round had a similarly large effect on gut microbiota dynamics.

Key words: Broilers, microbiota, 16S rRNA, field study

Spatial distribution of Leptospira serovars in horse populations in Latin America: Estimation of animal serovar prevalence and associated risk factors

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ABSTRACT

Objectives: Leptospirosis is a zoonotic disease of global importance with scattered geographically distribution in the horse populations. The control of leptospirosis is often difficult and requires host specific measures, therefore, methods for disease control will vary according to the infecting strain and, host susceptibility status. The objective of this study was to determine the serovar specific prevalence and geographic distribution in the horse populations in the state of Rio Grande do Sul - Brazil and, to determine possible risk factors.

Materials and methods: A cross-sectional serosurvey was bases in a random sample from entire horse population of Rio Grande do Sul state. The occurrence of leptospirosis was calculated and further for each serovar, at both animal and farm levels. Animals tested positive for at least one serovar had a minimum title of 1:100. The logit method of confidence interval estimation for the prevalence by horse and the design effect were calculated. Information on the origin of the animal, age, husbandry, presence of weir within the limits of the farm and, environmental characteristics (ecoregion, soil type, temperature, rainfall, altitude) were also considered in the analysis.

Results: The top three most prevalent serovars at the animal level were L. wolffi 24.4% (CI95%: 13.3-40.0%), L. tarassovi 14.3% (CI95%: 6.6-28.0%) and L. hebdomadis 7.3% (CI95%: 4,8- 11.0%). The risk factors associated with horse leptospirosis were driven by the northwestern region (OR = 3.44) and northeastern region (OR = 2.35), in addition to precipitation (OR = 3.09), more specific precipitations between 1,260-8,233 mm (OR = 3.82), finally soil type "Neolithic litolithic" (OR = 2.17) also showed significant association.

Conclusion: Equine leptospirosis is distributed throughout the study area. The disease maps generated may help stakeholders with disease prevention, as well as highlight the potential public health concerns due the close relation people have with horses.

Key words: Disease mapping, spatial epidemiology, equine leptospirosis, Latin America

A Case-control Study of an outbreak of Newcastle Disease in poultry at the farm level in Pemagatshel district, eastern Bhutan

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ABSTRACT

Objective: Newcastle disease (ND) is a highly contagious viral disease of domestic and wild birds, and have huge economic impacts to the poultry farmers. Using a case control study design, we identified farm level risk factors for ND outbreak in two villages under Pemagatshel district, eastern Bhutan.

Materials and methods: Thirty households that experienced an ND outbreaks in 2014 and 2016 were identified as case. For each case two controls were selected from the same village. The data were retrospectively collected using questionnaire in February and March 2017. A univariable and multivariable logistic regression model were built to identify risk factors of ND outbreaks. Ninety household (30 case and 60 control) were selected and interviewed.

Results: Twelve of the 48 variables were found to be associated with ND outbreak on univariable analysis while the final model (multivariable analysis) identified three variables to be a risk factors for ND outbreaks. The odd of ND occurrences in a farm that were easily accessible by wild birds was 13.08 times (95% CI: (2.96-57.78) more than those farm that are not accessible to wild bird. Significant higher odds (adjusted odd ratio: 10.66; 95%CI: 2.3-49.5) of outbreak were reported in the farms that have larger flock size (>10) than the smaller farm (<10). The farm which were located near to the road (<500m) were 3.85 times (95% CI: 0.95-15.63) more likely to get the disease comparing to those that are located far from road (>500m). Routine cleaning of litter materials from the shed [(OR: 0.16 (95%CI: 0.04-0.66)] and farmers knowledge on vaccinations [(OR: 0.16 (95% CI: 0.03-0.79)] had protective effects to ND outbreaks.

Conclusion: Improving the farm biosecurity and cleanliness would reduce the incidences of ND outbreak. Awareness and regular vaccination against ND should be conducted to prevent disease outbreaks.

Key words: Newcastle disease, case control study, risk factors, Bhutan

Post-operation wound healing complication and associated factors under dog and cat population control of Chiang Mai Municipality in 2017

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ABSTRACT

Objective: Dog and cat population control program is a crucial activity for rabies elimination in Chiang Mai Municipality. Surgical operation has been applied in this program by the Municipality. With limited resources under field condition, post-operation wound healing complication was the most concern under the program. This study aimed to describe the incidence of wound healing complication and evaluate its risk factors.

Materials and methods: The prospective study was conducted in owners and animals that participated in Chiang Mai Municipality animal birth control program during March – June 2017. Information of wound healing complication and possible risk factors were recorded. Incidence of the complication measured seven days after operation was described and its possible risk factors were measured by Risk Ratio with 95% level of confidence. 141 owners of 252 animals were included in this study

Results: Fifteen animals (5.95%) had wound healing complication. Using procaine penicillin with dihydrostreptomycin as prophylaxis had 2.75 times (95%CI=1.03–7.31) higher chance to get would healing complication than using cefazolin. Animals that received drug completely after operation can reduce risk of wound healing complication (RR 0.15; 95% CI 0.05–0.43). For female animals, mid-line incision had lower incidence than flank incision (RR=0.22, 95% CI=0.07- 0.71).

Conclusion: The surgical operation had low incidence of wound healing complication after operation and wound healing complication monitoring should be continuously evaluated.

Key words: Sterilization, wound healing complication, Chiang Mai Municipality, Thailand

Risk factors associated with the seroprevalence of Leptospirosis amongst at risk groups in Tanga city, Tanzania

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ABSTRACT

Objective: The epidemiologic status of leptospirosis in Tanzania has not been well defined because of the low disease awareness and difficulties in undertaking diagnosis. The objectives of the present study were to estimate the *Leptospira* serovars antibody prevalence in various occupational risk groups of apparent healthy inhabitants in Tanga city, Tanzania. The overall purpose was to collect baseline epidemiological data in order that appropriate disease control interventions can be recommended.

Materials and methods: A cross-sectional seroprevalence study on leptospirosis, using the microscopic agglutination test (MAT), was conducted in various occupational groups from Tanga city during November 2005. A titre of $\geq 1:160$ was taken as an index of seropositivity in this study. Questionnaire and laboratory data were handled and analysed using Epi-info (version 6.04) (CDC, Atlanta, USA). The differences in *Leptospira* serovars antibody prevalences were compared across the investigated variables using the Mantel-Haenszel chi-square. A value of $p < 0.05$ was considered significant.

Results: The overall prevalence of *Leptospira* infection among 199 persons sampled was 15% (95% confidence interval [CI]: 10.4-20.8). The prevalence of antibodies to individual *Leptospira interrogans* serovar were 36.6% for Icterohaemorrhagiae, 30% for Bataviae, 20% for Hardjo, 6.6% for Tarrassovi, 3.3% for Ballum and 3.3% for Pomona, respectively. Amongst the occupational groups examined, the livestock keepers, animal health workers and abattoir workers were found to be most at risk with a prevalence rate of 19%, 18% and 17%, respectively. Subjects reporting keeping milking cattle were significantly associated with increased sero-positivity to *Leptospira* infection (Odd ratio [OR] = 3.44; CI: 1.76-6.75, P<0.001).

Conclusion: These findings indicate that a significant proportion of the population of Tanga city is being exposed to pathogenic *Leptospira*. Public health actions for leptospirosis control will need to target not only the occupational groups at risk of infection with severe forms of this disease, but also the general population at large

Key words: *Leptospira*, human, risk, Tanzania

Prevalence and factors associated with echinococcosis/ taenid eggs presence in dogs in Ibadan, Oyo state, Nigeria

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ABSTRACT

Objectives: Echinococcosis, a parasitic zoonosis affecting both humans and dogs, causes disability in humans which include brain damage, epilepsy, severe liver disease, and fatalities. Human association with infected dogs could pose risk of infection. Some studies have reported the prevalence of echinococcosis/ taenid infections in dogs in Nigeria. Few of these studies have reported some intrinsic factors associated with the prevalence. However, none of these studies have attempted to determine extrinsic factors associated with the prevalence. This study, therefore, was done to determine the presence of echinococcosis/ taenid eggs in faeces and its associated intrinsic and extrinsic factors in dogs presented at the veterinary clinics or hospitals in Ibadan, Oyo state, Nigeria.

Materials and methods: A total of 185 faecal samples were obtained and tested using the faecal floatation method. Questionnaire was used to obtain data on intrinsic factors such as age, gender, breed; and extrinsic factors such as management and hygienic practices and environmental factors from participating dog owners. Data obtained were analysed using descriptive statistics and Fisher's exact test at $\alpha_{0.05}$.

Results: The mean age of the respondents was 35.7 ± 11.3 years, while the median age of the dogs was 20 months (range 2 – 96). The prevalence of echinococcosis/ taenid infection was 4.87%. Extrinsic factors such as the water source – tap water (OR: 5.5; 95% CI: 1.01, 36.8) and the feed types – dry foods (OR: 11.4; 95% CI: 1.1, 159.3) were significantly associated with echinococcosis/ taenid infection. None of the intrinsic factors was significantly associated with echinococcosis/ taenid infection.

Conclusion: Echinococcosis/taenid infection is low in dogs in the study area. Dogs taking tap water and dry foods have higher likelihood of infection than those taking borehole water and home-made or canned foods. Provision of clean water source and feeding of home-made or canned foods could help reduce echinococcosis/ taenid infection in dogs.

Key words: Echinococcosis/ taenid eggs, associated factors, zoonosis, dogs, Nigeria

What do we know about the antimicrobial resistance of bacteria isolated from dogs with otitis in France?

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ABSTRACT

Objective(s): Resistant bacteria can be cross-transmitted and close contact between pets and people might foster dissemination of antimicrobial resistance (AMR) determinants. The aim of our study was to describe the AMR pattern of the major causative agents of canine otitis - one of the most common diseases in dogs - in France.

Materials and methods: This retrospective study was based on the analyses of data collected between 2012 and 2016 by the French national surveillance network of AMR referred to as RESAPATH. Proportions of mono and multidrug resistance to relevant antibiotics were calculated over the whole period. For the combination bacteria-antibiotic with enough available data, the multidrug resistance was mapped to explore geographical distribution. Resistance trends were investigated using non-linear analysis (generalized additive models).

Results: A total of 7,021 antibiograms were analyzed. The four major causative agents of canine otitis in France were coagulase positive staphylococci, *Pseudomonas aeruginosa*, *Proteus mirabilis* and streptococci. Over the whole period the resistance to penicillin was very high for both *Staphylococcus pseudintermedius* (68.5%) and *Staphylococcus aureus* (70.9%). *P. aeruginosa*, a germ harbouring numerous natural resistances, showed the highest proportion of resistance to fluoroquinolones (67.7%). 19.4% of *P. aeruginosa* isolates were resistant to both enrofloxacin and gentamicin and regions in the south of France showed the highest levels of resistance to those two antibiotics. The multidrug resistance proportions ranged between 11.9% for *Proteus mirabilis* and 16.0% for *S. pseudintermedius*. Since 2013, resistance trends to fluoroquinolones decreased in both *P. aeruginosa* and *S. pseudintermedius* isolates.

Conclusions: These results are essential to guide prudent use of antibiotics in veterinary medicine. They can also help in designing efficient control strategies and policies and to measure their effectiveness. In a risk assessment perspective, this study underscored the importance of an ongoing surveillance network for AMR in companion animal.

Key words: antimicrobial resistance, dog, canine otitis, time-series, RESAPATH.

Avian Influenza Outbreak and Prevalence in Live Bird Market, Quangninh province, Vietnam from 2015 to 2017

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ABSTRACT

Objectives: This study aimed to describe AI situation using information from AI outbreaks and LBM surveillance result in Quangninh province during 2015-2017 and identify its risk factors.

Materials and methods: Data from AI outbreaks, LBMs surveillance and molecular analysis in Quangninh province were gathered from Regional Animal Health Office II of Vietnam. AI outbreak and prevalence in LBMs were described. Risk factors of AI in LBMs were measured by Odds Ratio with 95% level of confidence. Results: Ten outbreaks of AI were reported mainly in areas bordering with Bacgiang province and China. AI prevalence in LBMs was 37.33% (227/608). Out of these, 2.63 % (16/608) were positive to AI H5N6. All 608 samples were negative to AI H5N1 and H7. We found that poultry originated from Bacgiang province had higher chance to infect with AI (OR=1.44, 95%CI=1.01-2.04).

Conclusion: Quangninh province was at high risk for AI and LBMs contributed to the AI spreading from nearby areas. More restriction of poultry movement control in LBMs and between provinces and from China should be immediately implemented.

Key words: Avian influenza, H5N6, live bird market, Quangninh province, Vietnam

Long-term effect of subclinical Bacterial Kidney Disease (BKD) on performance of farmed Atlantic Salmon (*Salmo salar* L.): a 2-stage hierarchical interrupted time-series (ITS) approach

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ABSTRACT

Objective: To quantify the effect of subclinical BKD in Atlantic salmon populations cultured in open marine cages, on the following production indicators: mortality, growth and food conversion ratio (FCR).

Materials and methods: We used a 2-stage hierarchical interrupted time series (ITS) analysis. The first stage consisted of time series analysis of pens within sites and included one model per production cycle per site. The interruption was the change from BKD free to BKD infected. The second stage was a meta-analysis in which we compared the sites and investigated the effect of site-level predictors on the variation between sites.

Results: For all three outcomes, some sites had positive effects, others negative. Overall, no effect of BKD on mortality and growth was detected, while a very small, negative effect on FCR was observed. The only site-level predictors that affected variation in performance was the effect of harvesting year on growth.

Conclusion: Surprisingly, we did not find any obvious long-term effects of BKD on performance of Atlantic salmon. Because BKD is known to transmit vertically, it could be that R. salmoninarum causes minimal interference with performance resulting in increased probability of the pathogen being passed to the next generation. Alternatively, other unmeasured mechanisms may cause variation in production indicators, thus masking potential growth and efficiency effects of infection with R. salmoninarum. Large time-series data sets available from current farm management records systems continue to generate opportunities to investigate potential effects of chronic, subclinical infections on aquaculture productivity.

Key words: Time-series regression (TSR), subclinical, Bacterial Kidney Disease (BKD)

Evaluating sensitivity of surveillance strategies for the detection of proliferative gill disease (PGD) in Atlantic salmon in Scotland

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ABSTRACT

Objective: Proliferative gill disease (PGD) is an important disease of farmed salmon in Scotland. Proliferative gill inflammation (PGI) is a similar condition, characterised by histopathological presentation in the gills of tissue proliferation, vascular changes, inflammation, and cell death. The terms "PGI" and "PGD" are often interchangeably used, although inflammation might be inconsistently observed or absent in PGD cases in Scotland. Surveillance for PGD/PGI is based on the use of non-invasive gross-gill scores, determined from visual inspection of gills. Our objective in this study was to investigate the sensitivity of this surveillance approach for the detection of PGD/PGI in salmon pens.

Materials and methods: Six fish per one pen in two farms in Scotland were sampled on a bi-weekly basis between February 2016 and March 2017. Gross gill scores and histological characteristics were recorded. Eight sampling events were considered to represent a PGI/PGD positive pen because at least one fish had all four histopathological characteristics of PGI. PGI-positive fish were removed from the sample dataset, and sensitivities of presence of gross signs or histological characteristics to detect PGI were determined across the remaining fish in each sample, using characteristics of different combinations of fish within the sample.

Results: Use of gross gill scores from individual fish led to an overall test sensitivity of 63%. When three fish were combined, using all four histological characteristics for PGI lead to a mean sensitivity of over 60%, and when inflammation was not included to over 80%. Pooling of all four histological characteristics from 5 fish increased mean sensitivity to over 80%.

Conclusion: This descriptive pilot study demonstrates that three or more fish might provide reasonable accuracy for PGI/PGD surveillance. As inflammation was part of the definition of the reference standard, values presented here might apply mainly to more severe and chronic cases. Larger studies are needed to provide more precision.

Key words: Time-series regression (TSR), subclinical, Bacterial Kidney Disease (BKD)

How do winter housing and management factors impact Norwegian sheep health and production?

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ABSTRACT

Objective: This study aimed to quantify the effect of winter housing and management factors on outcomes of Norwegian sheep health, including clinical mastitis (CM).

Materials and methods: Data on sheep housing conditions, such as insulated vs. non-insulated, newly built vs. modernized buildings, flooring type, and management practices were collected from 1204 producers in Norway using an electronic questionnaire. Of these, 1078 (89.5 %) farms were members of the Norwegian Sheep Recording System (NSRS), which collates individual animal health and production records. Farms were retained in the dataset according to consent to access NSRS data and assessment of data quality. Mixed effect logistic regression modelling included farm and ewe identity as random effects. Interaction effects were examined.

Results: The final dataset consisted of 785 flocks, 108,352 ewes, 201,807 lambing events and 2470 first cases of CM (1.3 %) occurring one week prior to three weeks following the registered lambing date. In general, ewes aged two years and over had a higher CM risk compared to yearlings. There was a significant interaction between ewe age and litter size. Ewes aged six years and over who delivered three or more lambs had a CM odds ratio (OR) of 7 (95% CI 4-11). Whereas, yearling ewes delivering three or more lambs had an OR of 4 (95% CI 2.3-8.5). Short-tailed Norwegian breeds had a lower CM risk compared to long-tailed Norwegian breeds. Ewes receiving lambing assistance had a slightly higher CM risk (OR 1.4, 95% CI 1.2-1.7) compared to those lambing unaided. There was no significant effect of housing insulation type, or new vs. modernized buildings on CM risk. Management on deep litter bedding halved the odds of CM compared to ewes on metal grated floors (95% CI 0.3-0.8).

Conclusion: Individual ewe and flock factors were stronger predictors of CM than housing factors.

Temporal and spatio-temporal patterns of Caligidosis and Piscirickettsiosis co-occurrence in salmon farms in Chile

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ABSTRACT

Objectives: Currently, Caligidosis and Piscirickettsiosis are the diseases with the greatest economic impact for the Chilean salmon industry. Caligidosis is caused by the ectoparasite *Caligus rogercresseyi*, while Piscirickettsiosis is caused by the bacteria *Piscirickettsia salmonis*. Studies on parasite-bacteria models suggest parasites increase fish susceptibility to bacterial infections, which may be driving Caligidosis and Piscirickettsiosis co-occurrence in Chile. The objectives of this study were: 1) to describe temporal and spatio-temporal patterns of Caligidosis and Piscirickettsiosis co-occurrence in salmon farms in Chile, and 2) to identify epidemiological factors associated to space-time disease clusters.

Materials and methods: Using weekly monitoring data on *C. rogercresseyi* counts and Piscirickettsiosis mortality from Jan. 2015 to Dec. 2016, we classified farms at a given week in one of the following categories: i) Caligidosis (CL)– /Piscirickettsiosis (PR)–, ii) CL+/PR–, iii) CL–/PR+, and iv) CL+/PR+, depending on whether or not the disease surpassed a defined threshold (CL: farm average of 3 gravid females/fish; PR: farm-level mortality of 0.035%). Temporal and spatio-temporal co-occurrence disease clusters were evaluated using a multinomial space-time scan statistic. Associations between co-occurrence categories and epidemiological factors were assessed using a multinomial logistic regression.

Results: Results indicate there is a greater risk that Caligidosis and Piscirickettsiosis co-occur in mid production cycle (Atlantic salmon: 35 to 89; rainbow trout: 29 to 64 weeks from stocking). Caligidosis and Piscirickettsiosis were concurrent in the central part of Chiloé island and in the Hornopirén area in Los Lagos region, during summer and early fall, and forming smaller clusters scattered all over the Aysén region, in summer, fall and winter. The regression analysis indicated that Caligidosis and Piscirickettsiosis co-occurrence was significantly influenced by the salmon species, fish weight and water salinity.

Conclusion: During 2015 and 2016 Caligidosis and Piscirickettsiosis co-occurrence showed strong temporal and spatio-temporal variability in Chile and depended on management and environmental factors.

Epidemiological investigations into infectious hematopoietic necrosis in South Germany

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ABSTRACT

Objective: Epidemiological investigations were conducted to identify the connections between the farms and the source of infection.

Material and Methods: All contacts were traced backwards and forwards for extended periods of time on each of the affected farms. Samples were taken and examined for the presence of IHN virus and the isolates were sequenced. Farms were visited and data collected in structured interviews using standard questionnaires filled in together with the farm managers.

Results: Identification of the high-risk period for tracing back and forwards was difficult because water temperatures rose during summer, thus providing opportunities for the virus to be present on the farm without showing clinical signs. Combining epidemiological investigations with data on virus genome sequences, several links between the farms could be identified. Direct transport of fish was identified as the main source of infection. On some farms, separate units were infected subsequently, indicating that indirect contact, despite high biosecurity measures, were responsible for transmission. Other farms bought fish from farms declared free of IHN, so that it has been speculated that the fish may have been exposed during transportation.

Conclusion: Despite extended epidemiological investigations, the source of the epidemic could not unambiguously be identified. Several potential gaps in the biosecurity measures were identified on some farms, such as the collection of dead fish for rendering, the procedures of unloading fish brought onto the farm and the disinfection of sport fishing gear. All farms have been cleared and disinfected before restocking.

Key words: infectious hematopoietic necrosis, salmon, Germany, biosecurity

First report of the sea louse Caligus rogercresseyi found in farmed Atlantic salmon in the Magallanes region (south 49°16' S), Chile

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ABSTRACT

Objective: Caligus rogercresseyi is a marine copepod causing Caligidosis which is considered the most challenging parasitic disease for the salmon industry in Chile. Historically, C. rogercresseyi had been widely distributed in coastal waters of northern Patagonia (40°15'S to 49°16' S) where most of farmed salmonids are located. In 2017, C. rogercresseyi was detected in farmed Atlantic salmon south 49°16' S, in the Magallanes region, affecting salmon farms that had not dealt with Caligidosis until then. The objective of this study was to report the measures and activities conducted by the Chilean Fisheries and Aquaculture Service during this emergency.

Materials and methods: The main activities were verification of the diagnosis and confirmation of the outbreak, improvement of surveillance, implementation of control measures, evaluation of measures taken and communication of findings. The presence of C. rogercresseyi on Atlantic salmon was confirmed through both morphological and genomic analyses.

Results: According to the case definition, there were 8 farms affected (out of 31) by the parasite in the region during 2017. Surveillance was improved by increasing the frequency of data reporting from monthly to weekly and training private and public personnel in identification and count of C. rogercresseyi on fish. Most of case farms were required to treat their fish in order to avoid potential C. rogercresseyi spread over the region. Pharmacologic delousing treatments were highly effective, but in some cases, lice re-infected the farm in the following weeks.

Conclusion: We hypothesize the C. rogercresseyi outbreak in the area could have been due to i) the pathogen extended its geographical range recently (resulting from a natural phenomenon or an anthropogenic action), or ii) the parasite was present in the area before 2017, but in that year the epidemiological conditions changed making possible the parasite detection. Further research is needed to evaluate consequences for the local salmon industry.

Factors associated with the movement of cows and replacement heifers in dairy herds in France: implications for disease surveillance

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ABSTRACT

Objective: Although diseases are primarily introduced into and spread among bovine herds due to inter-herd movements, there is limited knowledge on the factors that drive farmers' decisions to purchase or sell animals and on the volume of such exchanges. The aim of this study was to identify and quantify the variables influencing the trade of reproductive females (cows and replacement heifers) in dairy herds.

Materials and methods: We applied a hurdle model to identify factors associated to the act of selling or buying and to the numbers of sales or purchases when appropriate for two periods without major cattle epizootics in France (2010-2011 and 2013-2014). We tested a set of variables describing herd management practices (presence of a feedlot, number of fattening bovines, herd size, three-year trend in herd size) and herd performances (annual mortality rates, three-year trend in mortality rates, average calving interval, turn-over rate) computed from the French National Cattle Register. We also included a cluster variable obtained from a herd classification approach based on social network indicators (betweenness, in-closeness, out-closeness and closeness).

Results: Several factors related to management practices (the presence of a feedlot, the short-term trend in herd size, and the proportion of first-calving females), herd performances (risk of mortality), and herd position within the network of cattle farms were revealed to be important drivers of reproductive female exchanges, with consistent results in both study periods.

Conclusion: Even if the role of most of these factors was already well-known, our study allows quantifying their effect. As we selected two study periods without movement restriction policy, our models could be used to predict number of sales and purchases in "normal" conditions. These findings are of interest for animal health stakeholders in order to direct surveillance towards high-risk herds and implement preventive measures to limit their vulnerability to diseases being introduced.

Key words: Bovine exchange, Hurdle model, disease introduction

A multi-site randomized field trial to evaluate the effect of lactoferrin on the health of dairy calves with diarrhea

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ABSTRACT

Objective: Neonatal calf diarrhea remains the most common cause of mortality and antimicrobial use in dairy calves. Lactoferrin, an iron-binding protein found in colostrum, has been shown to improve growth and reduce mortality in pre-weaned heifer calves. The objective of this study was to investigate the effect of lactoferrin when administered to pre-weaned dairy heifer calves with diarrhea.

Materials and methods: A randomized controlled field trial was conducted on five commercial dairy farms in Ohio. In total, 485 calves (≤ 21 d of age) were enrolled after first diagnosis of diarrhea, and randomly assigned to receive lactoferrin or water (control) for 3 consecutive days. Health assessments were conducted on the day of enrollment and 1, 2, 3, 7, 14, 21, 28, and 35 d post-enrollment. A Poisson regression model (PROC GENMOD, SAS) was used to test differences in the frequency of disease through 35 d post-enrollment.

Results: The median age at enrollment was 11 d, and ranged from 1 to 21 days of age. On the day of enrollment, 51.3% (123/240) and 52.2% (128/245) of calves in the control and lactoferrin treatment groups, respectively, were diagnosed with severe diarrhea (fecal score = 4). The frequency of diarrhea through 35 d post-enrollment did not differ between control and lactoferrin treatment groups (RR: 1.01, 95% CI: 0.93-1.08; $P = 0.87$). Further, depression (depression score ≥ 2 defined as marked depression to moribund, unable to rise) was not different for calves supplemented with lactoferrin compared to calves in the control group (RR: 0.85, 95% CI: 0.59-1.22; $P = 0.37$).

Conclusion: This study suggests supplementing lactoferrin to dairy calves with diarrhea does not influence the frequency of diarrhea or depression 5 wk post-diagnosis; however additional analyses of secondary outcomes and future research may uncover longer-term benefits of supplemental lactoferrin on morbidity and mortality in dairy heifer calves.

Key words: Calf diarrhea, lactoferrin, antimicrobial alternative

Evaluation of risk due to sea lice infestation in wild juvenile Pacific salmon populations

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ABSTRACT

Objective: Decreased wild salmon returns to certain rivers has been observed on the British Columbia (BC) coast of western Canada, and sea lice have been implicated as a potential factor associated with these declines. Scientific evidence indicates that fish can develop innate immune responses against sea lice, and that the parasite's impact on the health of wild juvenile salmonids depends on the number of sea lice and the size of the infested fish. Various infestation thresholds have been suggested for risk assessment on wild hosts; e.g. no more than one motile *Lepeophtheirus salmonis*, on small (< 0.5 g) salmon. However, these have rarely been tested using field-based empirical data. The objective of this study was to evaluate risk of sea lice to wild salmon based on a range of infestation thresholds.

Materials and methods: We analysed 15 years of data from sea lice monitoring programs along the BC coast. The proportion of fish with sea lice levels over the threshold was calculated for each sampling area and sampling year.

Results: The proportion of fish with sea lice levels over the threshold increased as we progressed from the modest to more conservative criteria. However, there was also significant spatial and temporal variation in the proportion of wild fish deemed to be at risk. In all years other than 2004, at least 95%, and often more, of wild fish sampled exhibited infestation below even the more conservative thresholds.

Conclusion: Assessing infestation levels based on risk thresholds may help us better understand the true impact of sea lice and improve targeted strategies to control these parasites in wild and farmed salmon populations.

Key words: Sea lice, *Lepeophtheirus salmonis*, salmon, infestation threshold, Canada

Factors affecting an occurrence of a hypo-prolific sow in Brazilian breeding swine herds

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ABSTRACT

Objective: Hypo-prolificacy of sows is a major hidden concern for pig production efficiency because of relatively huge variation in female reproductive performance in a modern swine industry. The present study was aimed to investigate factors affecting hypo-prolificacy of female pigs.

Materials and methods: Between 2011 and 2016, 186,195 parity records from 35,522 female records in the 15 Brazilian herds were obtained from PigCHAMP record-keeping system. A hypo-prolific sow was defined as who possess the lower 10th percentile of the number of piglets born alive (PBA, 8 pigs or fewer, 9 pigs or fewer, or 9 pigs or fewer) farrowed at parity 1 (PY1); the remain was for the ordinary sow. According to definitions of the hypo-prolific sow, three mixed-effects logistic regression models were used to examine factors affecting an occurrence of the hypo-prolific sows.

Results: The odds for becoming the hypo-prolific sows were significantly higher for gilts having re-service event (OR=1.29, P-value=0.011). The odds for that were statistically higher in relating to service seasons (summer, OR=1.13, P-value=0.013 and spring OR=1.16, P-value=0.005 compared to autumn). In addition, the interaction between re-service and multiple numbers of mating in service (OR=1.66, P-value=0.005) compared to non-re-service and single numbers of mating in service.

Conclusion: To mitigate an occurrence of a hypo-prolific sow at PY1, producers should inseminate gilts with the best service practice as well as good quality of heat detection and keep scrutinizing those gilts who were serviced in summer and spring seasons.

Key words: Hypo-prolificacy, risk factors, sows

Using multiple correspondence analysis (MCA) to identify risk and protective factors for on farm mortality in a sample of sow herds in Finland

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ABSTRACT

Objective(s): This study aimed to establish associations between an extensive list of farm characteristics, housing conditions, management practices and sow on-farm mortality (euthanasia and spontaneous death) in a sample of Finnish commercial farms.

Materials and methods: Client farms from the three largest slaughterhouse companies were included either voluntary (n=12) or after being convenience-sampled (n=31). Cross-sectional type of study using questionnaire survey and field visit was carried out between February and October 2014. To determine annual mortality percentages for each farm, data from the National Swine Herd Register were obtained. Multiple correspondence analysis (MCA) was applied to identify complex underlying typologies based on all the collected categorical and categorized continuous variables. Sow mortality was dichotomized by different thresholds and added as supplementary variables to interpret relationships with farm descriptors. Wilcoxon rank sum test was used to compare farm clusters located in different parts of the generated graphs.

Results: The first three MCA dimensions explained almost 40% of the variability among the farms. Most prominently, number of sows per worker, farm size, manure management, amount of solid floor and degree of pen dirtiness, use of bedding, rooting and nesting materials, stocking density, feeding systems and the level of parturition induction contributed to the inertia of the first two factorial axes (F1, F2). The overall mean mortality percentage was 9.7 (95% CI 7.9-11.5). The coordinates representing increasing mortality shifted along the F1 towards the more negative side. The identified farm clusters either having a negative coordinate on F1 or positive coordinates on both F1 and F2, differed for mortality (p<0.05).

Conclusions: This study indicates the need to consider potential factor combinations instead of individual risk factors to control sow on farm mortality.

Key words: sow, mortality, farm descriptors, MCA

Development of a clinical scoring system for bovine respiratory disease (BRD) in postweaned dairy calves

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ABSTRACT

Objective: The objective of this study was to develop a clinical scoring system for bovine respiratory disease in postweaned dairy calves.

Materials and methods: A prevalent case-control study using field data from 689 dairy calves in group pens on five dairies in California was performed. Of the 689 calves in the study, 89 were selected because they appeared sick based on display of lethargy, depression or separation from the group, while the remaining 600 were randomly selected. Clinical signs were recorded for all calves and BRD case status was determined by thoracic auscultation and ultrasound examinations, using parallel testing strategy. Of the 689 calves, 238 were BRD cases. Five survey-adjusted generalized linear mixed models with a logit link function were fitted to a training set of 551 observations with calf as the unit of analysis, dairy as a random intercept, and their performance assessed using 3-fold cross validation

Results: The best model chosen based on performance and parsimony contained the variables cough (2 points), abnormal respiration (1 point), low body condition (5 points), sunken eyes (4 points) and 24-hour ambient temperature range on enrollment day of > 15°C (1 point) with a 2-point cutoff for a for a BRD suspect score. The best model was validated on 138 observations not used for model training and resulted in 77.0% screening sensitivity, 100% diagnostic sensitivity and 61.9% specificity. Adding rectal temperature > 39.2°C as a second-tier test for score positive animals improved specificity to 76.7%.

Conclusion: Use of the California BRD postweaning scoring system may provide a new tool to monitor BRD in group housed dairy calves. The use of rectal temperature in series with the scoring system may reduce unnecessary treatments of animals with antimicrobials.

Key words: Dairy calf, bovine respiratory disease, clinical scoring system

Effects of feeding a novel amino acid-complexed trace mineral supplement on productivity and digital dermatitis mitigation in growing-finishing feedlot heifers

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ABSTRACT

Objective: To evaluate efficacy at reducing incidence and severity of digital dermatitis (DD) in growing-finishing feedlot heifers, nutritional supplements providing trace minerals (CTM; zinc (Zn), manganese (Mn), and copper (Cu) as amino acid complexes and cobalt glucoheptonate were compared to supplements with predominantly inorganic sources of minerals (Control; CON).

Materials and methods: Source of all iodine was ethylenediamine dihydroiodide (EDDI). Site of the study was a commercial feedlot with a history of DD. After 30 d starting period, 1,120 heifers (BW = 277 kg) were randomly allotted to 8 pens (140 heifers / pen; 4 CON and 4 CTM pens). The same basal diet was provided, with ractopamine (300 mg·hd^{-1}·d^{-1} fed during last 30 d before harvesting. On d 189, terminal slaughter groups into 323 (Heavier group) and 387 (Lighter group) heifers were formed. Heifers were scored for DD lesion incidence and severity using M-stages (M0, M2 and M4 lesions) five times (d0; d 70; d 148; d 189; d 248).

Results: Baseline prevalence of DD lesions was 0 on d0 and d70 with greatest prevalence observed post d 188. DD prevalence in CTM pens (active M2+chronic M4 lesions; $P \leq 0.001$) increased less compared to CON. Total weight gain for the entire trial was increased by 8 kg ($P \leq 0.09$) and carcass weight increased by 5.9 kg ($P \leq 0.10$) for CTM compared to CON heifers. Logistic regression analyses indicated an increase in individual animal carcass weight (HCW) of 11.8 kg (95% C.I. 5.40 – 18.7 kg) for CTM compared to CON heifers.

Conclusion: Increase in prevalence of active M2 +chronic M4 DD lesions observed over days on feed was significantly reduced in CTM pens compared to CON pens. We confirmed that CTM improved growth performance and carcass yield compared to CON pens resulting in economic benefits.

Key words: Digital dermatitis; feedlot, trace mineral supplementation

Identifying poor metabolic adaptation to negative energy balance during early lactation in dairy cows using cluster analysis

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ABSTRACT

Objective: The objective was to characterize PMAS using a cluster analysis of commonly-used measures of metabolic health that were available [i.e., milk fat to protein ratio, blood beta-hydroxybutyrate acid (BHBA), blood non-esterified fatty acids (NEFA)], and identify the best diagnostic indicator for PMAS.

Materials and methods: Veterinarians performed physical exams and collected blood and milk samples from cows between 5 and 50 days in milk on 26 Bavarian AMS farms during weekly visits for an average of 7 weeks. Principal component analysis was performed on the metabolic measures of 790 observations, followed by k-means cluster analysis. Clusters were ascribed to "Low", "Intermediate" or "High" PMAS classes based on their degree of agreement with expected PMAS indicators and characteristics (e.g., older, higher producing cows earlier during lactation with greater BCS at the start of lactation with elevated liver enzymes and bilirubin, and decreased rumen fill, rumen contractions, and milk production). Next, we evaluated limit values for the best diagnostic indicator that separate PMAS classes.

Results: Out of 5 resulting clusters, 1 cluster was ascribed to a "High" PMAS class and 2 were ascribed to both "Low" and the "Intermediate" PMAS classes. PMAS classes were best differentiated by blood NEFA levels. A NEFA value < 0.39 [95% CI: 0.360 - 0.410] mmol/L separated the Low PMAS observations from the Intermediate class, and NEFA values $\geq$ 0.7 [95% CI: 0.650 - 0.775] mmol/L separated the High PMAS observations.

Conclusion: These results suggests that NEFA should be used to identify cows currently needing veterinary attention due to poor metabolic adaptation to NEB during early lactation.

Key words: Metabolic adaptation, negative energy balance, non-esterified fatty acid, ketosis, beta-hydroxybutyrate acid

East Coast Fever control at the livestock / wildlife interface in Northern Tanzania

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ABSTRACT

Objectives: East Coast Fever (ECF) in cattle is caused by the protozoan *Theileria parva,* transmitted by *Rhipicephalus appendiculatus* ticks. In cattle ECF is often fatal, causing annual losses >$300 million. The African buffalo (*Syncerus caffer*) is the natural host for *T.parva*. Disease transmission and control in livestock/ wildlife interface areas are poorly understood. The aims were to determine the prevalence of *T.parva* in cattle, in a 30km zone adjacent to the Serengeti National Park, Tanzania, where livestock interact with buffalo, and to ascertain herd vector control practices.

Materials and methods: A randomised cross-sectional cattle survey and questionnaire survey of vector control practices were conducted. Cattle were sampled (n=770) from 48 herds and blood samples analysed by nested PCR to establish *T. parva* prevalence. Half body tick counts were recorded on every cow. Farmers were interviewed (n= 120) in the study area, including the sampled herds, to obtain data on vector control practices. Local workshops were held to discuss findings and validate results.

Results: Overall prevalence of *T.parva* was 5.2%, lower than in other hyperendemic areas. Although 100% farmers reported seeing ticks on their cattle, tick counts were very low with 78% cattle having zero ticks. Questionnaire analysis indicated significant acaricide use with 79% of farmers reporting spraying and 41% dipping cattle routinely. Some farmers reported very frequent spraying, as often as every four days. All acaricides used were from the same synthetic pyrethroid drug class, alphacypermethrin.

Conclusion: These data indicate high levels of acaricide use, which may be responsible for the low observed tick burdens and low ECF prevalence. This vector control is farmer-led and aimed at both ticks and tsetse flies. The levels of acaricide use raise concerns regarding sustainability; resistance development is a risk. An integrated control strategy may alleviate acaricide dependence but *Theileria* population genotyping is required to establish vaccination efficacy at this interface.

Key words: *Theileria parva, Rhipicephalus appendiculatus,* East Coast Fever, vector, acaricide

A welfare assurance programme for dairy calves in New Zealand

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ABSTRACT

Objectives: Following significant public pressure to improve young calf welfare, a veterinarian-led calf welfare assurance scheme was developed to help guide dairy producers and allow them to better benchmark their practices and identify areas for improvement. This paper presents 2017 data from this scheme, which was first piloted in 2016.

Materials and methods: Twenty-three seasonal (spring) calving pasture-based dairy farms in the Southland region of New Zealand were enrolled in this programme in 2017. Both qualitative and quantitative data on calf rearing set-up and practices were collected by veterinarians and veterinary technicians both prior to and twice within the first 2 months of calving. Farmers were also encouraged to report some parameters daily through an online form. Quantitative measurements included colostrum quality and colostral transfer; and qualitative measures included assessments of housing and shelter such as quality of bedding, quality of feeding management, and environmental conditions. Measurements were grouped into four areas for benchmarking: colostrum management, biosecurity, preventive health, and calf welfare. Farmers received real-time feedback, including key recommendations for improving outcomes; benchmarked reports following each visit; and a final summary report.

Results: The average percentage of farms achieving best practice targets across all measures within each of the four categories assessed was highest for welfare (80%) and colostrum management (78%) and lowest for biosecurity (53%) and preventive health (55%). The majority of farms (15/21 with two post-calving visits) decreased or maintained the proportion of calves that had failure of passive transfer (FPT, total protein < 5.5g/ dL). Other detailed results will be presented at the conference.

Conclusion: This project demonstrated the value to farmers of monitoring and benchmarking animal health and welfare, with rapid (within-season) improvements demonstrably possible.

Key words: Welfare, assurance, calf rearing, monitoring

Tail damage of dairy cattle in New Zealand

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ABSTRACT

Objectives: Estimate the prevalence of tail damage in dairy cattle in New Zealand to help quantify the magnitude of this welfare issue.

Materials and methods: Data were collected from dairy farms over 3 years (seasons). Tail scoring was performed once per season on each farm. Tails were scored as either normal (healthy, undamaged), broken (evidence of a fresh or past fracture), docked too short (higher than the last 2-3 vertebrae), or damaged (any other forms of tail damage). Scoring was performed by trained veterinarians or veterinary technicians. Results were reported back to each farm as the proportion of cows in the herd with normal tails, benchmarked regionally and nationally (all five regions represented collectively).

Results: 267 whole-herd, tail scores were completed over three seasons, representing 134,054 cattle individually scored. The average proportion of cows with normal tails was 0.85, with significant variation across seasons (range 0.81-0.87) and regions (range 0.73-0.93). Within-herd prevalence of abnormal tails ranged from 0-100% with 99% of herds found to have some cattle with abnormal tails. Herd size did not have a significant effect on within-herd prevalence. The most common type of tail damage was tail fractures (0.08), followed by tails docked too short (0.05) and then other damage (0.03). There was some significant regional and seasonal variation in the type of tail damage found.

Conclusion: This paper reports the first known objective data on the prevalence of tail damage in dairy cattle in New Zealand. On average, 15% of dairy cattle surveyed showed evidence of some form of tail damage during their lifetime, with almost every herd contributing to what this survey suggests is a significant animal welfare concern.

Key words: Welfare, tail damage, dairy cattle, prevalence

Puppy acquisition behaviour – preliminary data from the 'Generation Pup' birth cohort

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ABSTRACT

Objectives: In the UK, it is advised that puppies should be viewed with their mother and not leave their mother until eight weeks of age. Preliminary analysis of puppy acquisition behaviour within a UK birth cohort of puppies (Generation Pup) was conducted to investigate compliance with these recommendations.

Materials and methods: Owner-completed questionnaire data (for 1074 puppies aged ≤16 weeks) were available for analysis. One study dog/household was used to avoid clustering at household level, reducing the dataset to 1028 puppies. Excluding homebred puppies (n=44), the percentage of dogs acquired according to current recommendations (aged ≥8 weeks, viewed with the puppy's mother) were calculated. Chi-squared tests were used to test for association between these two variables and owner-reported source of puppy (professional or Kennel Club Assured Breeders Scheme (KC ABS) breeder/hobby or occasional breeder). Puppies acquired from rehoming centres (n=49) and other sources (n=62) were excluded from the chi-squared analysis. SPSS Statistics v25 was used for analysis. Significance was set at P<0.05.

Results: Of 984 puppies, 26.1% were acquired before eight weeks of age and 13.0% were not viewed with their mother. Excluding 62 puppies whose source could not be ascertained, most (49.1%) were obtained from hobby/occasional breeders, 27.1% acquired from KC ABS breeders, 18.4% from professional breeders and 5.4% from rehoming centres. Chi-squared tests provided no evidence that source of puppy was associated with the likelihood that puppies were obtained aged ≥8 weeks or viewed with their mothers.

Conclusion: Despite the potential for our cohort to be well-informed regarding puppy purchase, substantial non-compliance with puppy-buying recommendations was apparent. Future research will test associations between puppy-buying behaviour and health/behaviour outcomes of dogs within this cohort.

Key words: Cohort, longitudinal, dogs, canine, welfare

How many ways to spay? Improving student confidence and competence in performing desexing surgeries at the time of graduation

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ABSTRACT

Objective: Although desexing surgeries are considered a core clinical skill for small animal veterinary practice, it can be challenging for veterinary schools to provide students with adequate training opportunities within the traditional curriculum. At the Massey University School of Veterinary Science, we recently established an innovative extracurricular volunteer programme designed to have students teaching other students under veterinary supervision how to perform different elements of desexing procedures as they progress though their degree.

Materials and methods: This includes administrative and assistant roles for first year students (responsible for client communication, patient restraint, and medical record keeping), physical exam and recovery roles for second year students (responsible for assessing patient fitness for surgery, drawing up anaesthetic drugs, and monitoring patients in recovery), anaesthesia and neuter surgeon roles for third year students (responsible for inducing, preparing, and monitoring spay patients and performing cat neuter surgeries), and spay surgeon role for fourth year students (responsible for performing cat spay surgeries, discharging patients, and following up with clients to assess patient recovery).

Results: This programme has been highly successful in improving student confidence and competence while also providing a valuable low-cost desexing service to the local community. We are currently running several research studies to formally evaluate the impact of this programme on students and recently conducted a national survey of practicing veterinarians in New Zealand to collect baseline data on the different techniques they use in practice to perform desexing surgeries as well as their experiences with teaching desexing surgeries to veterinary students during their final year private practice clinical rotations.

Conclusion: These findings will be used to improve the desexing surgery training programme and the teaching and evaluation framework we have established would be useful for other veterinary schools looking to expand desexing surgery training opportunities for students.

Key words: Spay, neuter, surgery, students, clinical skills

Clostridium difficile in dogs: Risk factors for colonization and infection

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ABSTRACT

Objective: The zoonotic potential of Clostridium difficile is not well studied, and while dogs have been implicated in transmission, their role has been poorly defined. This study aimed to identify husbandry, owner and dog risk factors for C. difficile colonization in dogs, with an emphasis on the transmission potential between humans recently diagnosed with C. difficile infection and dogs living in the household.

Materials and methods: Dog-owners recently tested for C. difficile were recruited. A survey collected data on health status of people, their dogs, and husbandry factors; a follow-up survey was sent 1 month later. Paired human and canine fecal samples were requested at time of recruitment, with an additional canine sample 1 month later. Culture and PCR were used to confirm and characterize C. difficile isolates. Responses from surveys were modeled against dog C. difficile recovery using logistic regression.

Results: Fecal samples from 30 people and their dogs (n=41) were submitted. One-month follow-up samples were submitted for 20 dogs. C. difficile was identified in 25% of the human samples, 22% of the initial canine samples and 10% of the follow-up canine samples. When C. difficile was identified, toxin-producing genes A or B (toxigenic C. difficile) were frequently identified in human samples (76%), but less common in canine samples (10%). Gastrointestinal illness was not reported in any of the dogs from which C. difficile was recovered. No significant husbandry, owner or dog factors were associated with C. difficile presence (all P>0.3). Whole genome sequencing (WGS) of C. difficile isolates and investigation into human-dog pairs is currently in progress.

Conclusion: Toxigenic C. difficile colonization was infrequently identified in dogs living with humans recently diagnosed with C. difficile infection, suggesting a very low risk for human-dog transmission. Analysis of WGS and human-dog pairs may provide further insight into transmission risks.

Key words: Dog, Clostridium difficile, zoonosis, infection control

Causal effect of milking practices to sub-clinical mastitis in Mbarara dairy farms, Uganda

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ABSTRACT

Objectives: A project has been being conducted to improve dairy farming productivity in Mbarara, Uganda sponsored by Japan International Cooperation Agency. In this study, risk factor analyses for sub-clinical mastitis were performed.

Materials and methods: In 30 farms, California mastitis tests (CMTs) were conducted for 608 milking cows including 2411 quarters from February to May 2017. Teat end scoring was performed (n = 2062). Milk samples whose CMT score were 2 or above (n = 576) were collected for bacterial culture. Herd-level milking practices were surveyed using check-list. For risk factor analysis, univariable analyses were performed to analyze relations between mastitis and milking practice, between mastitis and teat score, and between contagious mastitis and milking practices, using generalized mixed effect models. Multivariable models were built to estimate causal effects of significant variables in the univariable analyses including confounders defined by causal diagrams.

Results: The cow-level sub-clinical mastitis prevalence was 68.6% (417/608) and the quarter-level was 39.2% (946/2411). For risk factor analyses, confounders were adjusted, and cows relaxed at the end of milking had lower prevalence on cow-level (OR = 0.19, 95% CI = 0.05-0.68, p = 0.01), also on quarter-level (OR = 0.30, 95% CI = 0.11-0.86; p = 0.02). Quarters whose teat score were 3 had higher prevalence on quarter-level than those of score 1 (OR = 4.92, 95% CI = 1.34-18.02, p = 0.02). Quarters for which one towel was used for one cow to wipe teats had lower prevalence of mastitis caused by contagious pathogens (OR = 0.31, 95% CI = 0.12-0.77, p = 0.01).

Conclusion: The high prevalence of sub-clinical mastitis was observed in Mbarara from which production loss is concerned. From the evidence, an intervention study will be held for the future study.

Key words: Dairy cattle, milking practices, risk factor, sub-clinical mastitis, Uganda

Analysis of the effect of feedback feeding on farm-level porcine epidemic diarrhea occurrence in Kagoshima and Miyazaki Prefectures in Japan

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ABSTRACT

Objective(s): A large scale epidemic of porcine epidemic diarrhea (PED) occurred in October 2013 in Japan. During the epidemic period, feedback feeding (feeding feces and gut tissues of infected piglets) was attempted to grant immunity to sows to immunize nursing piglets through their milk. This study was carried out to evaluate the effect of feedback feeding on PED control.

Materials and methods: A questionnaire survey on PED and feedback feeding was conducted in Kagoshima and Miyazaki Prefecture in 2014, and the questionnaires were returned from 172 farmers. Epidemic data were provided by the both prefectures. Generalized linear models with gamma errors and Poisson errors were used to analyze the association between conduct of feedback feeding and epidemic period and the number of dead piglets at the farm-level.

Results: The epidemic period was longer (difference in reciprocal = -0.01, se = 5.6×10^{-3}, p = 0.012), and the number of dead piglets was higher (difference in log =0.5, se = 0.3, p =0.063) in the farms conducted feedback feeding than those not. The within-farm epidemic period (slope of reciprocal = 1.1×10^{-4}, se = 5.5×10^{-5}, p = 0.061) and the number of dead piglets (slope of reciprocal = -0.01, se =3.0×10^{-3}, p < 0.001) declined over time of the epidemic course in the region.

Conclusions: The epidemic situations of farms conducted feedback were worse than farms that did not. However, among the farms conducted feedback, the damage of PED decreased over time, suggesting feedback feeding method stabilized at the later stage.

Key words: Swine - Porcine epidemic diarrhea – Feedback – Japan

Critical elements of a successful disease control programme: The case of Bovine Johne's disease

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ABSTRACT

Bovine Johne's disease (BJD), caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP), is a contagious chronic granulomatous enteritis characterised by diarrhoea, progressive emaciation and death in cattle. Infection in dairy cattle reduces farm productivity and MAP has been implicated as a possible causative agent of Crohn's disease in humans. This has driven the development of national control programmes throughout the world; however, the disease remains difficult to control.

National control programmes throughout the world have many of the critical elements for a successful disease control programme, such as adequate veterinary infrastructure and specific and valid reasons for control; however, the unique epidemiology of MAP has meant that traditional regulatory control programmes tend to fail and alternative approaches are required. Test performance and the critical role of sub-clinical shedders in disease spread are all challenging factors to contend with, but the social, political and economic aspects of BJD control is often the biggest hurdle to success.

This presentation will provide an overview of critical elements of a BJD control programme that can improve the chance of success, such as identification and promotion of drivers for industry and producer engagement and support. Provision of training, education and extension activities should seek to alter farm management practices in relation to MAP control and help farmers recognise that they are ultimately responsible for herd health and biosecurity practices. Government or private companies can assist farmer decision-making by providing tailored individual farm risk assessment and management recommendations to minimise introduction of infection to uninfected herds and within-herd transmission in affected herds. Ideally, this should be part of broader on-farm biosecurity efforts. Voluntary programmes that categorise herd risk levels should support producers so that they can identify low-risk herds from which to source replacement stock and high-risk or infected herds to promote on-farm control.

Key words: Johne's disease, paratuberculosis, Mycobacterium, MAP, control programme

Association between temporal patterns in continuously monitored reticuloruminal pH data and production characteristics in dairy cows

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ABSTRACT

Objectives: Bolus devices allow reticuloruminal pH to be continuously monitored over an extended time period, which has the potential to inform precision livestock management. Our aim was to describe pH patterns in clinically healthy dairy cattle and to assess their potential for predicting reduced productivity.

Materials and methods: Remotely sensed pH data were recorded at 600 second intervals over a period of 45 consecutive days from 24 apparently healthy, co-managed cattle on a single dairy herd. The data were analysed using a non-linear model with a modified sinusoidal function that allowed the rate of increase in pH to differ from the rate of decrease in pH for modified sine functions with a daily frequency and a frequency determined by the interval between milking times. Longer term changes in pH were accounted for by alternating the non-linear model fit with a generalised additive model. All animals were modelled separately. Residuals from the fitted model were then summarised at daily intervals and correlated to future deviations in observed milk yield and dry matter intake.

Results: There were strong similarities but also important differences in the daily pH patterns observed between the co-managed animals. Depending on the animal, between 20-40% of the observed variation was predicted by the time of day, and an additional 10-25% was predicted by fluctuation between milking times. Days with less predictable pH observations (higher mean absolute residual) were found to be significantly correlated to both reduced milk yield (p<0.001) and dry matter intake (p<0.001) at a subsequent time point.

Conclusion: Remotely sensed pH data has the potential to be used for monitoring productivity in dairy cows. Further work to provide real-time warnings of a predicted reduction in milk yield using dynamic linear models is ongoing.

Key words: Reticuloruminal pH, remote sensing data, big data, statistical modelling, dairy production

Cat management and residents' attitude of cat by-laws in local councils in Adelaide, South Australia

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ABSTRACT

Objectives: Both owned and unowned cats can potentially be associated with issues such as causing nuisance to residents. In some areas cat management regulations (bylaws) have been used in order to reduce this, however few studies have looked at the effects of these regulations. Mitcham Council in Adelaide was the first council in South Australia to introduce cat by-laws, including cat registration in 2011. This study investigated public attitudes to cat registration and cat related complaints in a council with cat bylaws versus two councils without cat bylaws.

Materials and methods: A questionnaire was developed asking information on demographics of respondents, attitudes to cat registration and perception of nuisance issues with cats. Questionnaires were made public on social media and through council websites. After data management, data were analysed by Generalised linear model in SPSS.

Results: A total of 518 responses were included in the analyses. No difference in age or sex were seen between councils in descriptive analyses and overall 69% of respondents were in support of cat registration with no significant difference in support between councils with and without cat registration. More residents in councils without registration had overall nuisance issues with roaming cats but there was no difference in residents' perception of number of stray cats between the different councils. Respondents in councils with cat registration had less issues with cat noise and trespassing but more issues with cats attacking wildlife than respondents in councils without registration.

Conclusion: Results from this study, can be used in cat management. It appears that cat registration is not enough to decrease number of stray cats in South Australia but it might reduce overall nuisance caused by cats.

Key words: Cat, management, Nuisance

A cohort study on the milk production loss associated with bovine leukemia virus infection in dairy production in Hokkaido, Japan

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ABSTRACT

Objectives: Bovine leukemia virus (BLV) infection is a global health problem in cattle but was overlooked in Japan due to unapparent economic damage. This study was conducted to quantify the milk production loss from the disease in dairy farms to understand the actual significance for the dairy industry if the disease is not controlled.

Materials and methods: A cohort study was conducted with 10 commercial dairy farms in which infection of BLV was confirmed within the Nemuro and Kushiro region of Hokkaido, Japan in 2015 and 2017. Of the ten farms, nine have participated in Hokkaido Dairy Milk Recording & Testing Association. With the farmers' consents, milk production data were collected from this Association. For the analysis of the impact of BLV infection on milk production, Generalized Linear Models (GLM) with gamma errors and linear regression were used for the univariable and multivariable analyses. For the analysis of the effect of BLV infection on the frequencies of mastitis, Generalized Linear Models (GLM) with zero-inflated Poisson errors were used.

Results: An asymptomatic cow produced milk production 47.6kg less milk per lactation period and a high viremia cow 19.5kg less milk per lactation period compared to a non-infected cow. The frequency of mastitis during secretion of milk period in a high viremia cow was significantly higher than asymptomatic or aleukemic or non-infected cows (p=0.03, risk ratio = 1.37).

Conclusions: Considering milk production loss and frequency of mastitis, a high viremia cow was confirmed to cause significant economic loss in dairy farms. The expected values of economic losses are still under analysis and will be shown in the talk at the conference.

Key words: Bovine leukemia virus (BLV), mastitis, milk production

Individual-based infectious disease modelling for Bovine Leukemia Virus infection in a dairy farm in Hokkaido, Japan

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ABSTRACT

Objective: Bovine Leukemia virus (BLV) is the causative agent of Enzootic Bovine Leukosis (EBL). BLV sero-prevalence in Japan is quite high; 40% for dairy cattle and 30% for beef cattle. The objective of this study is to assess cost-effectiveness of BLV control measures through modelling approach.

Materials and methods: An individual infectious disease model was developed based on the data from a tie-stall dairy farm in Hokkaido, the largest dairy area in Japan. The farm was previously tested for BLV infection and 7 out of 48 delivered cows were BLV-positive. The following points were considered in life cycle of cows: birth, death, sale, culling, age, sex, lactation stage, and pregnancy stage BLV infection status was classified into non-infected, asymptomatic, persistent lymphocytosis or EBL. Parameters on infectivity were taken from literatures, and the effect of rectal palpation without changing gloves for several cows was examined. The monthly, five-years-long simulations were run and changes of prevalence over the period were monitored.

Results: BLV prevalence in the farm after the five years increased more than twice initial prevalence. If gloves for rectal palpation were not changed each time, about 25 cows were infected by rectal palpation when the simulation finished and final BLV prevalence increased about 2.5 times as when the gloves were changed each time.

Conclusion: It was revealed that risk of not changing gloves for rectal palpation on BLV transmission was very high. The model is being developed further to accommodate the effects of several control measures such as pest management, buying-in BLV free stocks, segregation, and test and slaughter; and for several types of dairy farms. The models we are developing will help farmers making decisions on appropriate BLV control measures.

Key words: Bovine leukemia virus, enzootic bovine luekosis, infectious disease modeling, dairy farm

Collared peccary (*pecari tajacu*) are susceptible to porcine reproductive and respiratory syndrome virus (PRRSV)

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ABSTRACT

Objective: Collared peccary (*Pecari tajacu*) and pigs (*Sus scrofa*) are members of superfamily *Suoidea*, coexist in the Americas, and share some of the same viral infections. PRRSV is among the most impactful pathogens of swine worldwide, and the susceptibility of peccaries to PRRSV is unknown. Therefore, the objective of this experiment was to evaluate the susceptibility of collared peccaries to PRRSV and contribute to the discussion of the role of peccaries in the epidemiology of swine diseases.

Materials and methods: Three peccaries were intramuscularly inoculated with PRRSV. One PRRSV-inoculated pig served as a positive control and two pigs and one peccary as negative controls. Serum samples were collected at regular intervals over a 23-day observation period and tested by PRRSV rtRT-PCR and isotype-specific (IgM, IgA, IgG) PRRSV ELISAs.

Result: The development of viremia and a PRRSV-specific humoral immune response (see graphic) demonstrated that collared peccary are susceptible to PRRSV.

Conclusion: The results raise questions regarding the natural history of PRRSV in non-*Sus* members of superfamily *Suoidea*, and more broadly, their role in the evolution, transmission, and ecology of PRRSV.

An intervention study to investigate the impact of raised hygiene in the perinatal period on mastitis and health in housed ewes

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ABSTRACT

Objective: Mastitis is a bacterial infection, costing the UK sheep industry an estimated £120M/annum. Mastitis causes decreased milk yield and can lead to death or premature culling of ewes. An intervention study was conducted on one flock in England to test the impact of raising hygiene in the perinatal period on occurrence of acute mastitis (AM).

Materials and methods: Ewes were allocated to control (n = 422) or intervention (n = 315) groups at lambing. Researchers managed the intervention ewes; antibacterial hand gel was used before handling ewes and overalls and boots disinfected daily. Intervention ewes were put in pens post-lambing which had antibacterial bedding powder beneath straw bedding and were cleaned daily. Data on the presence of intramammary mass (IMM) an indicator of chronic mastitis, were collected on five occasions: during pregnancy, at lambing, early and late lactation, and pre-tupping. Occurrence of AM, lambing assistance and ewe death were recorded.

Results: The period prevalence of ewes with an IMM was 37.5% and incidence rate of AM was 5.5%. There was no difference in percentage with IMM or AM between intervention and control groups. Ewe death was associated with lambing assistance (OR = 7.22), 41.7% of control ewes and 100% of intervention ewes that died were given lambing assistance. IMMs were associated with previously detected AM (OR = 17.10) and IMM (OR = 3.25). AM was more likely to occur in ewes where an IMM was detected at a previous examination (OR = 15.49).

Conclusion: Whilst increased hygiene procedures were not significantly associated with reduced AM or IMM, ewes were mixed after housing which may have confounded the intervention. The link between lambing assistance and death is an important finding for welfare and cost to farmers and needs further investigation.

Key words: Ovine mastitis, epidemiology, animal welfare, clinical trial, suckler ewes

Seroprevalence and risk factors associated to horse and wild bird infection by West Nile virus in Madagascar

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ABSTRACT

Objective: West Nile virus (WNV) is considered as the most prevalent arbovirus in Madagascar, yet few studies have focused on WNV circulation in wild birds and horses. The aims of this study are (i) to provide recent estimates of WNV seroprevalence and incidence in horses, (ii) to assess which wild bird species are exposed to WNV and (iii) to identify risk factors associated with exposure in horses and wild birds.

Materials and methods: Horses from 4 regions of Madagascar were sampled before and after the 2015-2016 rainy season to estimate prevalence and incidence. Stable and horse characteristics were collected through a questionnaire. A wide range of wild birds species from the same regions were sampled in 2016-2017. Antibodies against WNV in horses and birds were tested using a competition ELISA test; results of a subset of samples were further confirmed using either a specific microsphere immunoassay for horses or a viral neutralization assay for birds. Logistic models were developed to identify risk factors.

Results: Overall seroprevalence in horses was 33.5% (n=254) and incidence during the rainy season was 8.8% (n=147). Age, presence of ponds, use of insecticides and combined presence of rice fields and ruminants in the vicinity of stables were identified as risk factors. Overall, 352 birds (belonging to 41 species) were tested and 12.5% (belonging to 19 species) were seropositive. Birds caught outside wetlands, in Alaotra Mangoro region, belonging to the Passeriformes order, and species with an area of distribution in the Indian Ocean islands were significantly more exposed to WNV.

Conclusion: This study confirms that WNV is endemic with high levels of circulation in horses, although no clinical cases were recorded. For the first time in Madagascar, 19 species of wild birds (among which 12 of the 21 Passeriformes species) were shown to be exposed to WNV.

Key words: West Nile Virus, Madagascar, horses, wild birds, risk factors, seroprevalence

Evaluation of the economic impact of coccidiosis and necrotic enteritis using an integrated biological-economic model of host-pathogen interaction.

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ABSTRACT

Coccidiosis imposes significant costs on poultry systems worldwide. Ionophores, together with chemical coccidiostats, and vaccines have formed the pillars of coccidiosis control for the past 50 years for broiler and layer chickens, respectively. The status quo may not be sustainable however as ionophore coccidiostats have been drawn into the wider debate on antimicrobial resistance developing in livestock systems.

This has refocused attention on new vaccines suitable for use in broiler systems. Ionophore coccidiostats are also crucial to the control of C. perfringens, the causative agent of necrotic enteritis. To provide evidence for the economic feasibility of the use of vaccines in broilers, a model is presented here which combines published experimental data on the biological effects of infection at individual bird level by two species of Eimeria, E. acervulina and E. tenella, with production inputs and financial costs to estimate the gross loss and productivity change at flock level associated with these pathogens. Pathogen replication and immunogenicity are simulated to recreate infection dynamics throughout the production cycle, validated against field data from European broiler systems. This is combined with a deterministic spreadsheet model of necrotic enteritis outbreak. The scenarios modelled provide the impact of Eimeria, with or without treatment with a combination ionophore coccidiostat, and with or without a concurrent necrotic enteritis outbreak.

These scenarios result in losses of 5.3% of total flock mass by day 36 of production in the untreated-Eimeria-positive group, 8.4% in the untreated, Eimeria and C. perfringens-positive group, and 2.9% in the ionophore treated, Eimeria-positive group. Additionally, changes in feed conversion ratio are recorded relative to the uninfected control, resulting in increases of 0.079, 0.091 and 0.041 respectively by group. Further work will include modelling new vaccine protocols as a replacement for ionophore coccidiostats; these results provide a baseline against which vaccine impact can be calculated.

Genetic and epidemiological characteristics of *Sarcocystis spp.* in sika deer (*Cervus nippon*) in Japan

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ABSTRACT

Objective: It is reported that raw horsemeat contaminated with *Sarcocystis fayeri* has caused food poisoning in Japan. Recently, consumption of raw venison contaminated with *Sarcocystis* also caused similar food poisoning. Although the fact that distribution of *Sarcocystis* in sika deer is obscure, the consumption of venison has been increasing steadily in Japan. The objective of this study is to clarify the distribution of *Sarcocystis* spp. in wild sika deer in Japan.

Materials and methods: 30 muscle tissue samples from three subspecies of sika deer in four regions in Japan (*Cervus nippon yesoensis* in Hokkaido, *C. n. centralis* in Chiba and Mie, *C. n. nippon* in Nagasaki prefecture) were used. Sarcocyst was isolated individually from muscle tissue samples and examined by molecular methods including polymerase chain reaction (PCR) amplification and DNA sequencing targeting variable region of 18S rRNA gene and the partial cytochrome c oxidase subunit I gene (cox1).

Results: As the result, *S sp.* HM050622, *S. pilosa*, *S. tarandi*-like, *S. taeniata*-like, *S. scandinavica*-like were detected from sika deer in Japan. Furthermore, *S sp.* HM050622 was separated into two clusters by phylogenetic analysis. The positive rates were as follows: 52% (42/81) for *S sp.* HM050622, 34% (27/81) for *S. pilosa*, and 12% (10/81) for *S. tarandi*-like. There was no statistically significant difference in positive rates of *Sarcocystis* species, sika deer subspecies and habitats.

Conclusion: This is the first report of proposal of new *Sarcocystis* species in wild sika deer in Japan based on cox1 sequences.

Key words: *Sarcocystis*, cox1, sika deer, coinfection, Genetic analysis

Disease occurrence, culling rate and production profile in Iranian Holstein dairy cattle during the early postpartum period

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ABSTRACT

Objective: The purpose of this study was to identify the production profile, incidence of periparturient diseases, culling rate and risk factor of them in the period of 60-days after parturition.

Materials and methods: Eight industrial dairy herds which were under supervision of a full time veterinarian located in north eastern of Iran were selected. In a prospective manner, 1464 dairy cows which were calved from June 22 to December 22, 2016 were observed for a period of 60 days after parturition. For each cow, monthly milk yield records, the exact date of disease occurrence and culling were recorded. Cox proportional hazards model and logistic regression were used to evaluate the factors influencing on culling and disease occurrence.

Results: Incidence of diseases for 60 days following period were as follow: Dystocia or calving assistance 46%, uterine inflammation 14%, retained placenta 9.9%, clinical mastitis 8.3%, lameness 3.6%, milk fever 2%, clinical ketosis 1/2%, replacement of abomasum 0.7%, fatty liver 0% and other diseases 9%. Average milk production was 40.19 ± 4.44 and 39.49 ± 3.99 kg in the first and second records, respectively. The rate of culling was 4.4%. Parity was positively correlated with chance of ketosis, milk fever and culling ($P<0.05$) Metritis increased chance of subsequent clinical ketosis (OR=6.02; p=0.002). Also, retained placenta increases the chance of Metritis (OR=8.8; $P<0.001$) and displacement of abomasum (OR=6.75; P=0.016).

Conclusion: Milk yield and health status in industrial dairy herd located in this area of Iran are in acceptable condition. However, implementation of strategy to decrease reproductive disorders early after parturition will result in lower subsequent problems and less obligatory culling.

Key words: Periparturient diseases, culling, milk production, dairy cattle, Iran

Determination of shedding levels of *Mycobacterium avium paratuberculosis* in New Zealand sheep farms using a direct faecal qPCR method

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ABSTRACT

Objectives: Infection with *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is endemic in New Zealand (NZ) sheep flocks (farm-level prevalence 76%). MAP can cause ovine Johne's disease (OJD) associated with production loss in affected flocks. Infected animals shed varying amounts of MAP into the environment through faeces. The presence of super- shedders (shedding disproportionately high numbers of MAP) might drive the dynamics of infection at the farm level. Knowledge about the proportion of super-shedders in typical commercial sheep flocks is a desirable input for realistic simulation modelling. This might in turn contribute to determine effective OJD control strategies in NZ. We aim to estimate the distribution of MAP shedding in NZ commercial sheep farms by testing faecal samples of individual animals. A secondary objective is to compare serum ELISA measurements and qPCR for detection of super shedders.

Materials and methods: A total of 880 individual sheep faecal samples from 44 commercial sheep farms (20 per farm) will be tested by direct faecal qPCR. These samples were originally collected for a nationwide survey of MAP infection prevalence in 2009 and have been stored at -80◦C since then. The multistage PCR protocol involves recovery of MAP cells from a faecal suspension, bead beading for cell disruption and DNA extraction using magnetic beads (low input work flow Magmax core mechanical lysis module®, Thermo Fisher Scientific), followed by IS900 quantitative PCR. Additionally, frozen sera samples will be tested using ELISA and the two tests compared using latent class analysis.

Results: The qPCR testing of faecal samples is currently ongoing. Results are expected by the end of May 2018.

Conclusion: Findings from this study will inform on-farm control of OJD.

Herd-level risk factors associated with infections of pathogenic *leptospira,* in lactating dairy cattle from Southern Chile

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ABSTRACT

Objective: The leptospirosis is one infectious disease widely distributed, present in feral and domestics animals and it affects dairy cattle producing milk production losses and lower reproductive efficiency. The aim of the study was to assess risk factors associated with seropositivity to nine pathogenic *leptospira* at herd-level, that were located at X and XIV Regions of Chile

Materials and methods: A multilevel-stratified (by herd size) sampling design of herds was used, using only adult females in production age. An infected herds was defined when at least one animal was seroreactor to Microscopic Agglutination Test titre ≥1: 200 and ≥1: 800 for unvaccinated and vaccinated herds, respectively. An epidemiological survey was applied to owners on; information about characteristics and management system. Information was analyzed by a mixed-effects logistic regression model using a forward algorithm and confounder variables were included in the final model.

Results: Apparent Herd Prevalence was 42%, 95%CI (34.2-50.2). The serogroups Hardjo, Pomona and Tarassovi were the more prevalent in the area. The final model included 4 variables and it is described in Table 1.

Conclusion: Some risk factors were identified that could be included for farmer advisory.

Key words: Herd level prevalence, Leptospira, reproductive disease, loss production, microscopic agglutination test

Concentration of antibiotics in tissue during oral treatments in farmed salmonids

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ABSTRACT

Objective: The growth of aquaculture in Chile has been marred with increasing health Challenges. One of these challenges is piscirickettsiosis, a bacterial disease caused by *Piscirickettsia salmonis*. Despite efforts made by authorities and farmers, the control of this disease has been challenging and, to date, heavily relied on the use of antibiotics. However, antibiotic treatments are not always successful. Antimicrobial resistance is frequently suggested as one of the causes of treatment failure, but recent studies suggest infection with resistant strains is far less frequent than the observed rate of treatment failure. An alternative source of treatment failure may be insufficient concentration of antimicrobial in tissue. Our objective was to assess a) the factors that influence the level of antibiotics in muscle-skin tissue samples obtained during and immediately after in-feed oral treatments against piscirickettsiosis, and b) whether these levels were adequate to inhibit the growth of *P. salmonis*.

Materials and methods: We used industry-provided data on florfenicol and oxytetracycline tissue concentration in 2231 muscle-skin samples obtained from individual fish during (day 7) and immediately after (day 14) antibiotic treatments against piscirickettsiosis delivered between June 2010 and February 2016. A mixed-effects linear mixed model was used to assess the association of tissue concentrations with individual, pen, treatment, and farm-level factors. We derived MIC90's for florfenicol and oxytetracycline from published data (Henriquez et al., 2016) and compared with our tissue levels to assess whether fish attain adequate antibiotic levels in tissue using mixed-effects logistic models.

Results: There is a wide variation in tissue concentrations, specially within the same pen (56% variance) and between treatments (26% variance). In our models, the day of the sample, fish weight, and species were associated with tissue concentrations. We also found that 42% and 10% of the samples were below the MIC90 for florfenicol and oxytetracycline respectively. In fish treated with florfenicol, species, weight category (below average, average, above average), and day of treatment were significantly associated with tissue concentrations above MIC90.

Conclusion: Tissue concentration of antibiotics during oral treatments vary greatly between individuals, and this variation is associated with fish size and its effects on the hierarchical behavior of salmonids. Within a fish population, smaller individuals attain lower concentration of antibiotics and are more likely to have below MIC90 levels. Conversely, larger individuals attain tissue concentrations several times above adequate levels. These findings are even more evident when antibiotics with short half-life, such as florfenicol are used, and suggest that differences in concentration maybe associated with uneven consumption of feed.

Key words: Antibiotic in-feed treatment, antibiotic tissue concentration, florfenicol, oxytetracycline, MIC90

Expatriation of animal experiments from Switzerland

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ABSTRACT

Objective: Animal experimentation is a common step within the research process worldwide. However, there are no universally accepted standardized regulations and differences between countries exist. Recent reports in the non-scientific press suggested that some researchers from countries where animal experimentation regulations are strict, might be shifting their experimental research to countries with less stringent regulations. We used a systematic literature search to determine whether there may be an increasing trend in the expatriation of Swiss funded animal experimentation on non-human primates for the years from 2004 to 2017.

Materials and methods: We conducted a search in Web of Science for articles written in English, using the project applicants' names from projects that were financed by the Swiss National Science Foundation (SNSF) between 2004 and 2016 as search terms. We included only publications describing laboratory experiments with non-human primates. For each publication, we recorded the place of experimentation, funding source, number of animals, species and statement of ethical approval and classified the publications accordingly.

Results: We identified 83 publications, from all years between 2004 and 2017, that matched our inclusion criteria. These studies involved 1062 animals. *Macaca mulatta* and *Macaca fascicularis* were the most common species.

Conclusion: Although some experiments were done outside of Switzerland, our findings did not demonstrate an increasing trend in movement of Swiss funded experiments to other countries. In recent years we found an increasing trend in the number of studies where authors stated they received ethical approval and in addition also stated the ethical approval number.

Key words: Animal experimentation, non-human primates, ethics

Factors associated with Pet Attitude Scale (PAS) among pet dog and their owners in Korea

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ABSTRACT

Objective: Animal companion is an integral aspect of life in Korea, with approximately 64.5% of households experiencing raising companion animals. The aim of this cross-sectional study was to look for different patterns of owner-dog relationship and to identify those owners and dog dependent factors, which influence the owner's pet attitude toward their dogs.

Materials and methods: The survey group population was constructed by Research and Research, Inc. (Seoul, South Korea). From September to October 2017, we contacted pet owner in Seoul, Korea by sending emails with questionnaire which consisted of the characteristics of pet owners and their pet ownership. A total of 654 young adults participated who were 19-39 years old, living in Seoul, and owning the dogs. Univariate and multivariate logistic regression were conducted to identify factor associated with high PAS scoring in pet owners.

Results: Five variables were significantly associated with high PAS group in multivariate logistic regression model: spending more than 4 hours for a dog (OR= 2.697), visiting veterinary hospital more than 4 times in a year (OR=1.743), small dog owner (<=10kg) (OR= 1.718), not having the other species pet in the house (OR= 1.672), and pet source: adapted (OR=1.538).

Conclusion: This study was the first to provide information about the demographics of the pet dog owner and dog population in Korea and identified factors for PAS. We believe that this study highlights the pet owner's positive pet attitude was associated with pet ownership pattern and pet health status.

Key words: Pet Attitude Scale, pet owners, pet dog, owner-dog relationship

Investigation of association between bovine viral diarrhoea virus and cervid herpesvirus type-1, and abortion in New Zealand farmed deer

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ABSTRACT

The deer industry exports from New Zealand are valued at NZD 266 million. An investigation into sub-optimal reproductive performance in rising two-year-old (R2) and mixed-aged (MA) adult hinds was undertaken. R2 (n=22,130) and MA (n= 36,223) hinds from 87 and 71 herds, respectively, throughout New Zealand were pregnancy tested using ultrasound early in gestation (Scan-1) and 55-89 days later (Scan-2) to detect mid-term abortions. Within-herd mean daily abortion rates of 0.043% and 0.025% in R2 and MA herds, respectively, equating to 3.9% in R2 and 2.2% in MA herds for 90 mid-term gestation days were reported.

Sera from aborted and non-aborted hinds were tested for BVD and CvHV-1 using virus neutralisation tests. Available fetuses and uteri and vaginal samples from aborted hinds and uteri from hinds not rearing a calf to weaning were tested for herpesvirus DNA. A logistic regression model, adjusted for within-herd clustering, was used to assess association between abortion and sero-status (BVD or CvHV-1).

In herds with aborted hinds, 10.3% of 639 R2 and 17.2% of 302 MA hinds were sero-positive for BVD and 18.6% of 613 R2 and 68.5% of 232 MA hinds were sero-positive for CvHV-1. There was no association between BVD sero-status and abortion (R2 p=0.36, MA p=0.76) whereas CvHV-1 sero-positivity was negatively associated with abortion in MA hinds (p=0.01) but not in R2 hinds (p=0.36). Eleven of 108 uteri from aborted R2 hinds but no MA hinds were positive for herpesvirus DNA. Vaginal samples from aborted hinds were negative for herpesvirus DNA. A Cervid Rhadinovirus type-2 (CRhV-2) was identified in seven PCR positive uteri samples.

Findings suggest that BVD and CvHV-1 may not be associated with abortion in R2 hinds, but association needs to be tested further in MA hinds. Investigation into other potential abortifacients is warranted. The role of CRhV-2 requires clarification.

Key words: Red deer, abortion, bovine viral diarrhoea virus, Cervid herpesvirus type-1, Cervid Rhadinovirus type-2, virus neutralisation test

Making big data small to improve clinical decision-making on farm

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ABSTRACT

Objective: Big data has become one of the big buzzwords in the animal health research space and there have been many recent initiatives looking to collate information from different passive and active data streams into a central location where it can be analysed to uncover trends in disease epidemiology. However, given that there are often limited incentives for farmers and veterinarians to participate, there have been many issues with the quality, completeness, and representativeness of these data, which significantly limits their use for disease surveillance and research purposes. In order to make systems like these sustainable, we need a better understanding of how farmers and veterinarians currently use big data to make decisions and how we can present the analyses back to make big data practically useful. In this preliminary study, we are conducting qualitative interviews with 15 farm animal veterinarians to collect information on (1) what data sources they currently use to help them identify on-farm problems and devise interventions, (2) how they communicate this information back to farmers to motivate action, and (3) what additional information or tools would improve the decision-making process on farms.

Materials and methods: The interviews will ask veterinarians to consider recent clinical cases where they had to advise farmers about making animal health decisions and describe the processes they used to reach a final action.

Result: This will also provide valuable information on the characteristics of farmer and veterinarian communication that may help lead to positive behavioural change. The results will be used to inform the design of a new centralized animal health data system in New Zealand.

Key words: Decision support, farmer behaviour, qualitative research, communication, animal health

Analysis of within-facility factors associated with survival in Australian southern rock lobster

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ABSTRACT

Objective: A retrospective investigation into risk factors for post-harvest survival at an Australian southern rock lobster (SRL, *Jasus edwardsii*) holding facility was undertaken using stock records from the 2016/17 fishing season.

Materials and methods: The facility consisted of four independent holding tanks with 5-6 compartments in each tank. Daily survival data from September 2016 to August 2017 was accessed for each compartment. Ancillary information included supplier and source location, arrival date, stocking density, SRL size class, holding tank and compartment within tank. Potential association with daily survival was explored using a fractional logit model and estimated as odds ratios (OR). Clustering within holding compartment and tank was accounted for when necessary.

Results: The facility experienced a seasonal cumulative mortality of 1.6%. In the final model, the daily survival was significantly higher with stock travelling shorter distances (OR=0.49, p<0.001), in higher class size stock (> 0.6 kg) (OR=1.9, p<0.001), decreasing stock density (OR=0.83, p<0.001), and during winter and spring (OR=2.67, p<0.001). The results suggest that higher transport duration and transport during warmer months may lead to an increase in mortality potentially due to increased physiological stress resulting from thermal stress and increased air exposure. Within facility, the increase in stocking density may be contributing to the physiological stress experienced by SRL in holding tanks.

Conclusion: The findings from this study will assist in risk management of SRL survivorship in holding facilities. Moreover, improvement in management of SRL transport from source location to holding facility may contribute towards optimising post-harvest survival during summer months.

Cross-sectional study of cow comfort and risk factors of lying time and cleanliness of smallholder dairy cows in Kenya

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ABSTRACT

Objective: The objective of this cross-sectional study was to determine the management practices affecting lying time and cleanliness in smallholder dairy cows in Kenya in 2017.

Materials and Methods: A total of 106 milking cows from 73 farms were assessed for daily lying time through data loggers attached to a hind leg for three days. Leg, udder, and stall hygiene were assessed, along with knee wetness and impact tests, and housing design problems potentially contributing to cow comfort issues. Information on management practices were acquired using a questionnaire. Univariable and multivariable linear and logistic models were used to analyse factors associated with lying time and cleanliness of the cows and stalls, respectively.

Results: Mean daily lying time was 10.9±2.2 hours. A total of 65% of stalls were categorised as dirty (>2.5), while 21% and 50% of the cows had udder and leg hygiene scores >2.5, respectively. From multivariable models, at the cow-level, stall hygiene scores >2.5 (β=-1.12), and poorly positioned neck rails (β=-1.505, P=0.011) were associated with decreased lying time of cows, and two farm-level variables were also in the final model: delayed removal of manure (β=-1.53) and delayed addition of new bedding (β=-1.22). Delayed cleaning of the alley (OR=6.1), lack of bedding on the stall floor surface (OR= 4.97) and standing idly and/or backwards in the stall (OR=10.83) were herd-level risk factors for stall dirtiness. Stalls categorized as dirty (OR=3.38) and adding new bedding less than once a week (OR=3.31) were cow- and herd-level risk factors for dirtiness of the udder, respectively, while the stall being dirty was a cow-level risk factor for leg hygiene scores >2.5.

Conclusion: Stall design and management practices have a significant impact on stall hygiene and cleanliness of cows and their lying time.

Key words: Cow comfort, lying behavior, hygiene, dairy cows, Kenya

Estimating the effect of intervention on contagious mastitis pathogens within herd using transmission rates derived from Bayesian analysis of a Hidden Markov Model

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ABSTRACT

Objective: Numerous different interventions can be used to manage and control contagious mastitis within dairy herds. The effect of such interventions is often estimated by assessing the change in incidence of clinical cases or somatic cell counts, but this is prone to inclusion bias and lacks specificity for the pathogen. A more direct approach is to estimate the transmission rates before and after intervention using a Hidden Markov Model (HMM). We assessed the effect of two different hygiene procedures on the transmission of contagious mastitis pathogens in two herds using automated milking systems each with an intervention group and a control group.

Materials and methods: A total of 611 cows were sampled between 1 and 8 times over a 4 month period, yielding a total of more than 2,300 cow-level qPCR observations on milk. A discrete time HMM model was implemented within a Bayesian framework to estimate transmission parameters based on qPCR observations of imperfectly detected infection status for *Staph. aureus* and *Strep. agalactia*. This model assumes that the true state of the individual at a given time point is latent but can be observed indirectly via observations with imperfect sensitivity and specificity. The cyclic threshold (ct) value chosen for *Strep. agalactia* and *Staph. aureus* were <40 and <32 to dichotomize the ct-values into infected and non-infected.

Results: The crude prevalences in the two herds before intervention were 4.3% and 21.7% for *Strep. agalactia* and 4.9% and 21.0% for *Staph. aureus*. After intervention the prevalences were 5.8% and 11.7% for *Strep. agalactia* and 2.6% and 12.1% for *Staph. aureus* in the two herds. However, the crude prevalences from test round to test round within both herds and for both pathogens were very variable and there were no difference between the intervention and control group.

Conclusion: Preliminary results suggest that there is no effect of the improved hygiene measures in the automated milking systems.

Key words: Mastitis, transmission rates, Hidden Markow Model

Cost/benefit analyses on indicator-based intervention on physiological imbalance in dairy cows

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ABSTRACT

Objective: Physiological Imbalance is a pre-clinical disease state in dairy cows that cannot be directly observed but is assumed to precede subclinical and clinical diseases in the beginning of lactation in dairy cows. It is possible to detect the state of physiological imbalance using Fourier transform mid-infrared spectroscopy (FT-MIR) in milk but there are issues related to the accuracy of this prediction. The objective of this study was to estimate the costs and benefits associated with an indicator-based intervention against Physiological Imbalance with different indicator accuracies, herd prevalences and prices.

Materials and methods: We used a mechanistic, dynamic, and stochastic dairy herd model that simulates the production and state changes of dairy cows (SimHerd) to estimate the negative effects associated with the diseases that were mediated through Physiological Imbalance and developed an effect chart to quantify the cost and benefits associated with the outcome of the FT-MIR results and based on those a deterministic cost-benefit analysis. We assumed that the negative effects of Physiological Imbalance were prevented by supplementing the cows with propylene glycol for 5 days. We simulated the negative effects of disease and production mediated through Physiological Imbalance to be € 121 per case.

Results: The results showed that if the FT-MIR based indicator was accurate (Se=0.9/Sp=0.95) and the prevalence of physiological imbalance was 50% a total of € 42/cow/yr could be expected to be gained for paying for the indicator-based system.

Conclusion: In conclusion the results shows that final economic results to be highly variable to the prevalence of Physiological Imbalance, the costs associated with treatment and the cost associated with treating false positives and not treating false negatives. In addition, this study highlights the benefits of simulation to pinpoint where additional information is needed to further quantify the economic value and required accuracy of an indicator-based intervention system.

Key words: Intervention, dairy herd, physiological imbalance, economics

Cross-sectional study of productive and reproductive performance, and factors associated with milk production of lactating dairy cattle in smallholder dairy farms in Kenya

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ABSTRACT

Objectives: Our objective was to determine milk production and reproductive performance of cows on smallholder dairy farms (SDF) in Kenya, and to determine factors associated with milk production.

Materials and Methods: A census of 318 lactating cows was sampled from 200 randomly selected SDF in Naari, Kenya. Questionnaires were used to collect management and demographic information, and physical examinations were used to obtain biodata. Descriptive statistical analyses were conducted, and mixed model regression was used to determine associations with the natural log of daily milk production.

Results: The cows that were cycling and non-pregnant (n=71) had a mean of 309.4 days in milk, while those cows that were anestrous (n=98) had a mean of 212.9 days in milk. As days in milk increased beyond the first hundred days in milk, milk production was lower. The highest producing breed was Holstein-Friesian crosses, producing 7.5 kg of milk per day, while Zebu crosses only gave 4.9 kg per day. Cows with recent history of mastitis had 7% lower milk production than those without mastitis. Milk production in cows that received dairy meal in the last month of gestation was 33% higher compared to those that did not receive any. Presence of other sources of farm income was associated with 5.6% lower milk yield compared to farmers who did not have other sources of income. The percentage of land allocated to dairy feed was positively associated with the cow's milk yield per day, with a 14.3% increase for every 25% increase in land set aside for growing forages for dairy cows.

Conclusion: With the low milk production observed, improved mastitis control, reproductive management, and nutrition are recommended, such as feeding dairy meal during the last month of gestation, and enhanced on-farm forage production.

Key words: Smallholder dairy farms, productive, reproductive, Kenya

Development of a generic model for assessing the risk of introduction and spread of viral diseases within marine farms in the Mediterranean basin

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ABSTRACT

Objective: The study is part of the project entitled Mediterranean Aquaculture Integrated Development (MedAID) funded by European Commission, Horizon 2020. The study focuses on diseases and health management of two main species produced in Mediterranean marine aquaculture i.e. seabass (European seabass: *Dicentrarchus labrax*) and seabream (Gilthead seabream: *Sparus aurata*). Viral nervous necrosis (VNN) is used as considered the most serious viral infection of seabass and seabream. The objectives of this study are to quantitatively assess the risk of introduction and spread of the virus infection within a farm, and identify probable prevention and control measures to minimize the risk and losses in production and performance.

Materials and methods: The approach used in the study is multidisciplinary combing a quantitative analysis of risk profiling for a farm, and a simulation modelling of infectious diseases within a farm. Data are collected from various sources including on-farm databases, literature review, scientific reports, reference and national diagnostic labs, and expert opinion.

Results: Results indicate important pathways for acquiring and spreading VNN within a farm and a range of risk factors and their values contributing to each pathway. A simulated spread of VNN within a farm provides a visualization of epidemic course over time. Time dependent mortality and reproduction number are monitored and compared for different measures e.g. use of vaccines, deliverance of live fish from known sources, improved hygiene and biosecurity year-class separation and fallowing, effect of rearing density, etc.

Conclusion: A platform for quantitative risk estimation of viral disease introduction and spread in Mediterranean marine seabass/seabream is developed and can be used to facilitate the decision making process of the industry, veterinary authorities, and other stakeholders.

Key words: Mediterranean aquaculture, risk assessment, Viral Nervous Necrosis (VNN), European seabass, Gilthead seabream, MedAID

Prevalence of bovine norovirus and nebovirus and risk factors for infection in Swedish dairy calves

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ABSTRACT

Objectives: The objective of the study was to determine the prevalence of bovine norovirus (BNV) and nebovirus in young calves in dairy herds and to investigate risk factors for infection on calf and herd level.

Materials and methods: Rectal fecal samples were obtained from five milk-fed calves per herd in 50 dairy herds. Herds were randomly selected in proportion to cattle density in five geographic regions across Sweden. Samples were analyzed by RT-PCR specific for BNV and nebovirus, respectively. Specific amplicons were confirmed by sequencing.

Results: Fifty calves (20%) in 24 (48%) herds were positive for BNV. In 17 herds, $\geq$ 2 calves were BNV positive. Thirteen calves (5.2%) in 8 (16%) herds were positive for nebovirus. Thirty-six calves (14%) showed diarrhea at the time of sampling. Median age of BNV-positive calves was 7 days vs. 16 days for BNV-negative. Median age of nebovirus-positive calves was 21 days vs. 13 days for nebovirus-negative. Median age of calves with diarrhea was 11.5 days vs. 14.5 days for calves without diarrhea. Multivariable analyses showed that norovirus infection was associated with herds located in southern Sweden, with colostrum intake by spontaneous suckling from dam vs. bucket feeding, with increasing no. of calves in the herd and with housing calves in single pens vs. group pens. No significant risk factors for nebovirus were detected, most likely due to the low no. of positives. Diarrhea was not associated with detection of BNV or nebovirus in this study.

Canadian national dairy study: Heifer calf health and management

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ABSTRACT

Objective: The objectives of this study were to use questions in the 2015 Canadian National Dairy Study to examine heifer calf health and management, and explore factors associated with different rearing strategies.

Materials and methods: The questionnaire was open to all licensed dairy producers in Canada and had a 12% response rate (n=1,373).

Seventy-seven percent of respondents reported calving and stillbirth information for 2014; mean reported stillbirth rate was 4.9% (SD=3.3). Forty percent housed calves in individual pens, 34% in group pens, 21% in individual hutches, 2% reported tethering calves, and 1% used group hutches. Of those who housed calves in groups, 59% reported the maximum group size was 3–10 calves, 31% a pair of calves per pen or hutch, and 10% a group >10 calves. Fifty percent of respondents reported useable mortality data; mean preweaned mortality was 6.4% (SD=8.3), and postweaned mortality was 2.4% (SD = 4.4). Over 95% of producers reported disbudding practices; 86% used cautery, 11% used surgical amputation, and 9% used caustic paste. Twenty-eight percent reported disbudding at less than 3 wk of age, 60% at 3 to 8 wk, 22% at 8 to 16 wk, and 5% reported dehorning at more than 16 wk of age. Sixty-six percent of cautery users reported use of local anesthetic, 33% used sedation, and 25% used a non-steroidal anti-inflammatory drug.

Conclusion: Multi-variable regression models showed that the use of local anesthetic when disbudding calves was associated with social media activity and high-speed internet access, whereas sedation was associated with geographic region, and NSAID use was associated with disbudding at more than 3 weeks of age. Exploring heifer rearing management practices, including adoption of best practices, may help focus future education and extension efforts. Poor reporting of mortality data may reflect a lack of record keeping on farm.

Key words: Survey, calf, disbudding, mortality

Retrospective analysis of factors affecting clinical outcome following CHOP-based chemotherapy in dogs with primary nodal diffuse large B-cell lymphoma

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ABSTRACT

Objective: Numerous factors are known to affect the prognosis of dogs with chemotherapy-treated lymphomas. However, prognostic factors for dogs with specific subtypes of lymphoma are less clearly defined. The objective of this study was to identify prognostic factors for dogs receiving CHOP-based chemotherapy for primary nodal diffuse large B-cell lymphoma (DLBCL).

Materials and methods: Medical records of dogs treated for DLBCL at the Purdue Veterinary Teaching Hospital from 2006-2016 were reviewed. Factors potentially related to prognosis were analyzed using multivariable statistical methods.

Results: Ninety-eight dogs were included in the study. Best overall response to chemotherapy was complete remission in 80 dogs (81.6%) and partial remission in 18 (18.4%). Median progression-free survival (PFS) for the entire population was 252 days (range 19-1068). Factors significantly associated with achieving partial (rather than complete) remission following CHOP included presence of thrombocytopenia at diagnosis (OR 6.88; 95% CI 1.98-23.93; $P = 0.002$), baseline serum globulin concentration (OR 2.63; 95% CI 1.03-6.75; $P = 0.044$), and age at diagnosis (OR 1.36; 95% CI 1.08-1.71; $P = 0.009$). Factors significantly associated with PFS in the lowest quartile (≤ 93 days) included presence of thrombocytopenia at diagnosis (OR 8.72; 95% CI 1.54-49.33; $P = 0.014$), age at diagnosis (OR 1.47; 95% CI 1.12-1.94; $P = 0.005$), and baseline neutrophil count (OR 1.18; 95% CI 1.02-1.37; $P = 0.025$).

Conclusion: Presence of thrombocytopenia, greater age, higher neutrophil count, and higher serum globulin concentration all may be associated with a particularly poor outcome in dogs receiving CHOP-based chemotherapy for DLBCL.

The epidemiology of stifle joint disease in a population of insured Swedish dogs

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ABSTRACT

Objective: To determine the incidence and risk factors of stifle joint disease in a population of insured Swedish dogs. Determination of various risk factors for stifle joint disease is of great importance since it can increase awareness of the diseases in a clinical situation and provide information about why some individuals and breeds are affected to a greater extent than others.

Materials and methods: The study was based on a historical cohort originating from dogs insured in Agria Animal Insurance during 2011-2016. Incidence of veterinary care events were expressed as a rate per 10,000 dog-years at risk (DYAR), where time at risk was from beginning of study period (1 January 2011) or start date of insurance, if after 1 January 2011, until end of study period (31 December 2016), death or cancellation of insurance policy. Multivariable logistic regression models was used to assess risk factors.

Results: The cohort included a total of >1.7 million DYAR. Nontraumatic stifle joint disease occurred at 54 per 10000 DYAR and the relative risk (RR) of being affected differed significantly between breeds. High risk breeds were English Bulldog, Dogue de Bordeaux, American Bulldog, Chow Chow and Pomeranian, where RR ranged between 3.7 and 6.1, relative to median risk breeds.

Conclusion: The results showed that breed affected the occurrence of nontraumatic stifle joint disease. More risk factors such as sex and age need to be further investigated.

Key words: Incidence; Risk factors; Canine; Insurance

Using Google Trends as a free, independent additional data source; An example from the Dogslife project

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ABSTRACT

Objectives: In parallel with human health, the internet is an important resource for veterinary health information, with increasing numbers of animal owners turning to the web for advice. Our aim was to use search query data from Google Trends to investigate patterns in canine veterinary health related public internet browsing and to identify whether these results agree with data obtained from a large questionnaire database (the Dogslife project).

Materials and methods: Dogslife is an internet-based, longitudinal study of UK Kennel-Club registered Labrador Retrievers that collects a variety of information from owners. To decide which search-terms to investigate, we identified common spelling mistakes for the word we were interested in, asked a sample of owners participating in Dogslife to tell us what search-terms they use when using the internet to obtain veterinary health advice and mined free-text boxes in Dogslife questionnaires using the 'tidytext' R software package to identify commonly used canine disease terminology. Data about these search-terms of interest were then extracted from Google Trends using the 'gtrendsR' R software package over the same time-period (since July 2010) and location (the UK) as Dogslife.

Results: We successfully harvested temporal and geographical data about veterinary health search terms from Google Trends and used this information to complement Dogslife data. The data provided a new perception of seasonal and longer-term trends in public veterinary advice-seeking behavior within specific locations and geographical areas over the course of Dogslife.

Conclusion: Search engine queries are a valuable source of information for researchers interested in population behaviour and disease. Google Trends data allows you to understand latent terminology used by the lay public to describe disease and can be a useful additional source of information to validate, compliment and provide new insights into veterinary epidemiological studies.

Key words: Google, search-terms, canine, big-data, surveillance

Neosporosis Seroprevalence in beef cattle in Uruguay

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ABSTRACT

Objective: The objective of this study was to determine the seroprevalence and distribution of *Neospora caninum* (*N. caninum*) in beef cattle in Uruguay.

Materials and methods: In the second semester of 2015, a cross-sectional study was developed with a two steps random sample: in the first step beef herds were divided into three strata according to the bovine population size (from 1 to 200, 201 to 800 and more than 800 cattle). In the second step, 20 beef breeding cows were sampled within each herd.

Results: A total of 9464 serum samples from 496 herds were analyzing by indirect ELISA test, under the manufacturer's recommendations. Sampling design was used to estimate population prevalence. Beef cow seroprevalence of *N. caninum* was 14.3 ± 0.7 % (95% confidence interval (IC), 13.4–20.6%), and at herd level was 86.5 ± 2.9 % (95% IC, 80.8–92.2%). Cow seroprevalence increased when the size of the herd decreased (p=0.04). No significant differences in the estimated seroprevalence at herd level among strata were detected. Also intra-herd seroprevalence were not different between strata, and had a range between 0 and 75%.

Conclusion: These results show that although the individual seroprevalence has remained stable over the years, infection with *N. caninum* is widespread in Uruguayan beef cattle. Therefore, the strategies applied to prevent and control the neosporosis were not useful to decrease prevalence in Uruguay, and it will necessary to identify risk factors that collaborate in the design of new control measures.

Key words: *Neospora caninum*, sero-prevalence, beef cattle, Uruguay, cattle abortion.

Paratuberculosis in goat herds in Quebec: prevalence, risk factors and diagnosis approaches

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ABSTRACT

Objectives: Paratuberculosis is a chronic debilitating disease of ruminants caused by *Mycobacterium avium* ssp. p*aratuberculosis* (MAP). In Québec, this disease has been identified as a major cause of death or premature culling in dairy goats, but little is known on its prevalence and distribution. This study was undertaken to estimate 1) the prevalence of MAP infection in Québec dairy goat herds, at the individual and herd level 2) the association between the risk of infection and management practices and 3) the performance of various testing strategies to determine herd status.

Materials and methods: A cross-sectional study was conducted in 2017 in dairy goat herds of the province of Québec, Canada. In each herd, 30 goats having kidded at least once were randomly selected, in addition to 5 goats targeted for their poor body condition. For each goat, a fecal and blood samples were collected for PCR and ELISA testing, respectively, and information was collected on the breed, age, body score and color of the eye mucous membrane. Fecal samples were tested individually and in pools. A bulk tank milk and environmental sample were also collected and tested by PCR for each herd. A questionnaire on management practices was completed during the farm visit. Multi-level logistic and binomial-negative regression analyses were used for modeling of risk factors.

Results: A total of 45 dairy goat herds were recruited. The infection was detected by PCR and/or ELISA in 19% of goats and 91% or herds. Some management practices were associated with a higher intra-herd prevalence of infection: presence of other ruminant species on the farm, animal introductions and kidding management. The different testing strategies and type of samples used had variable sensitivities for the detection of the infection at the herd level.

Key words: Paratuberculosis, goat, risk factor, prevalence, diagnosis, Canada

Incidence of fecal excretion of *Mycobacterium avium* subsp. *paratuberculosis* in dairy cows before and after the enrolment in the Québec Voluntary Program

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ABSTRACT

Objectives: This cohort study aim to: 1) describe changes of the incidence density rate of individual fecal excretion of *Mycobacterium avium* subsp. *paratuberculosis* (MAP) in 2 cohorts of cows – cows born before and after farm enrolment in the Québec Voluntary Paratuberculosis Prevention and Control Program (QVPPCP); 2) determine the impact of the risk score of within-herd transmission of MAP (measured by a risk assessment questionnaire) on the incidence of individual fecal excretion of MAP; and 3) evaluate the impact of calf rearing management practices on the incidence of individual fecal excretion of MAP.

Materials and methods: Eighteen MAP-positive herds enrolled in the QVPPCP were visited annually from 2011 to 2015. MAP was cultured from individual fecal samples from all adult cows collected at each visit. A risk assessment questionnaire was completed upon enrolment in the QVPPCP and at each visit. Cox proportional hazards models were used to estimate the hazard ratios (HR) for the exposure variables. Herd clustering was taken into account using robust standard errors.

Results: A total of 2158 cows were included (cohort born before *n*=919; cohort born after *n*=1239). The incidence and hazard of fecal excretion were significantly lower for the cohort-after than the cohort-before (incidence rate ratio=0.38; 95% CI: 0.18-0.78 and HR=0.48; 95% CI: 0.23-0.98). The HR of fecal excretion for cows exposed to a high RAS was 2.20 times (95% CI: 1.21-3.99) that of cows exposed to a low RAS. Poor calving cow hygiene (HR=3.41; 95% CI: 1.40-8.31) and contact between pre-weaned heifers and adult cows or their feces were significantly associated with an increased hazard of fecal excretion of MAP (HR=2.66; 95% CI: 1.08-6.56).

Conclusion: Our results suggest that enrolment in the QVPPCP reduces the risk of individual MAP fecal excretion. Contact between calves and adult cows or their feces increases MAP transmission.

Can SMS change farmers knowlege and practices? A randomized control trial in Uganda

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ABSTRACT

Objectives: In developing countries, knowledge transfer to communities in rural areas has been traditionally challenged by poor accessibility, resources and low literacy levels. The current large mobile phone coverage offers an opportunity for knowledge dissemination. We conducted a cluster randomized control trial to test the effectiveness of short message service (SMS) to improve knowledge and pig husbandry practices in one of the poorest districts in Uganda.

Materials and methods: Fifteen simple and actionable messages on pig nutrition, care and health were developed to address knowlege gaps and sub-optimal pig farming practices previously identified in the communities. Sixty villages were randomly allocated to one of 3 groups: unidirectional (messages pushed to participants), interactive (messages received upon request by farmer) and control. Messages were sent in predefined intervals over three months. Outcomes, including changes in knowlege and pig husbandry practices, were measured at the farmer level at baseline and between one and two months after the intervention was completed. Gender-disaggregated focus group discussions (FGDs) were conducted at the end of the trial to gather participants' perceptions on the intervention, process and messages. Item response theory model was used to assess the ability of the questions to define the latent knowledge trait of participants.

Results: Complete data was available for 687 farmers. Results compare the difference in knowledge score and change in proportion of farmers adopting optimal practices between treatments and control. The data from the FGDs revealed why participants use mobile phones for their pig business, limitations of the intervention including literacy in reading and operating phones, suggestions on how to improve the system and willingness to pay for such a service.

Conclusion: The project shows the potential for SMS to change farming practices, but also the limitations of mobile based technologies for livestock extension services and ideas for improvement.

Key words: SMS, RCT, pig, Uganda, extension

Evaluation of the main risk factors associated with White Spot Syndrome Virus occurrence in Sinaloa, Mexico, using a Bayesian Model

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ABSTRACT

Objectives: White spot syndrome virus (WSSV) has heavily impacted shrimp industry worldwide in the last decades. Through this study, we aimed to first assess the prevalence of the WSSV in the northern coast of Mexico (Sinaloa region). We also identified major management and biosecurity practices at farm level that could affect the presence of WSS outbreaks.

Materials and methods: We used data from a survey designed and implemented in 2015 by the "Comité Estatal de Sanidad Acuícola de Sinaloa" under a MEXUS project. Initial variable reduction was performed using classification and regression (CART) from an original set of 122 variables. Pre-selected variables were then used as predictors in a Bayesian multi-level binary logistic regression model with a varying municipality effect to account for clustering.

Results: Overall, 327 shrimp farmers participated in the survey, out of which 65.3% mentioned having at least one WSSV outbreak. The model identified eight predictors that were associated with and could potentially affect the presence of WSSV outbreaks. These variables are related to waste management, water and tank treatments and shrimp larvae importation.

Conclusion: Results of this study will directly benefit decision makers within farming industry in establishing targeted actions to prevent future outbreaks, and reduce the risk of spreading to other regions in Mexico or neighboring countries.

Key words: Aquatic epidemiology, Bayesian inference, multi-level models, Stan, CART

Simulating the silent spread of African swine fever in Great Britain

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ABSTRACT

Objective: Since 2007, the pig industry in Eastern Europe has experienced severe African swine fever (ASF) outbreaks. Knowledge gaps remain on how fast and extensive ASF virus (ASFV) spread is between herds, although this is important when assessing the effectiveness of intervention strategies. The objective of this study was to assess the spread of ASFV between herds via pig movements, with a focus on identifying the type and location of premises at risk during the silent spread period.

Materials and methods: The spread of ASFV between-premises was simulated using a stochastic compartmental susceptible-infected-infectious-dead (SEIR) model. The spread was assumed to occur solely through the daily movements of pigs in 2012 as recorded in the national movement databases (AMLS, ScotEID) of Great Britain. The model was parameterised with parameters estimated in the literature. Incursion events were simulated from two regions (Aberdeenshire and East Anglia), representing two main pig production hotspots.

Results: Results demonstrate that the likelihood of epidemic take-off was around 4% and 13% from one index case located in East Anglia and Aberdeenshire, respectively. If epidemics take off, ASFV infection would affect a small number of premises, around 20 and 24, respectively. Accordingly, the likelihood of observing less than 10 infected premises reached 95%. The distributions of the distances travelled by pig batches showed they were mainly moved over short distances, showing the dominance of intra-regional movements.

Conclusion: This study allowed investigating the spread patterns of ASFV between premises in detail, through simulations based on the movement network. Improved data accuracy will improve the validity of outputs from this model and therefore will optimise the identification of the premises at risk for potential future ASF outbreaks. It is crucial that simulation models for ASFV spread are developed and utilised in advance of any outbreaks to help decision making.

Key words: African swine fever, simulation modelling, pigs, disease control, silent spread

Epidemiology of pseudorabies in intensive pig farms in Shanghai, China: Herd sero-prevalence and risk factors

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ABSTRACT

Objective: Pseudorabies (PR), also known as Aujeszky's disease, is a highly contagious disease affecting pigs and a wide range of animals. Pseudorabies is enzootic in many countries. In China, PR is a priority animal disease for control and eradication. Disease frequency data on Pseudorabies virus (PRV) in intensive pig farms and the information on associated risk factors is lacking.

Materials and methods: A cross-sectional study of intensive pig farms ($\geq$350 sows) in Shanghai was conducted to determine herd prevalence of PRV and associated risk factors. Following a two-stage random sampling design, a total of 1,349 sow serum samples were tested by gpI-ELISA from a total of 91 intensive pig farms in Shanghai. Information on putative risk factors was collected using questionnaires to pig farm owners or veterinarians. A logistic model with a binomial outcome was built to identify risk factors for herd sero-positivity.

Results: Our results indicated that the true herd PRV sero-prevalence was 62.8% (95% CI$\square$52.8 - 72.7). In the multivariable logistic regression model using backward stepwise process, two variables were found to be significantly associated with PRV sero-positive farms: breeding with introduced sows in the last 12 months (OR = 3.5, 95% CI:1.2 -10.3, p =0.02), and the presence of stray dogs or cats (OR = 4.0, 95% CI:1.2 – 13.6, p = 0.02). The multivariable logistic model fitted the data well and presented a very good predictive ability.

Conclusion: This study suggested that PR was highly endemic in intensive pig farms in Shanghai. The risk factors identified in this study could be useful to improve the prevention policy of PR in Shanghai.

Key words: Pseudorabies virus, herd sero-prevalence, risk factors, intensive pig farms, cross-sectional, Shanghai

Occurrence of trypanosome infections in cattle in relation to season, livestock movement and management practices of Maasai pastoralists in Northern Tanzania

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ABSTRACT

Objective: African animal trypanosomosis (AAT) is one of the greatest constraints to cattle production in Tanzania. There is insufficient information on seasonal occurrence of AAT and management practices in Monduli District of the Maasai Steppe ecosystem to guide and prioritize AAT control programs.

Materials and methods: A cross-sectional survey was undertaken in 10 randomly selected villages. Information on seasonal animal movements was gathered using a standardized questionnaire with 130 pastoralists. An entomological survey was also undertaken. Polymerase chain reaction was used for parasite identification in cattle blood and in tsetse flies.

Results: The overall apparent prevalence of AAT in cattle was 5.8% (95% CI of 4.1-8.3) and 4.2% (95% CI of 2.7-6.3) during the wet and dry reasons, respectively. *Trypanosoma vivax* was the most common species identified in cattle. Tsetse fly infection status was determined to be 6.9%; (CI 95% of 3.7-8.7%) with nearly 50% of infections due to *T. congolense*. The trypanocides, Novidium® and Berenil®, were the most frequently reported commercial drugs and were used by 42% of cattle owners. Vector control by hand spraying was reported by the majority (90.8%) of cattle owners, while dipping and deployment of insecticide-impregnated targets were reported by few cattle owners (16.2% and 5.4%, respectively). The majority of cattle owners (83.1%) reported to move cattle away from home villages during the dry season with many migrating to areas in close proximity to wildlife parks.

Conclusion: This study confirms the presence of circulating pathogenic trypanosomes in tsetse flies which continue to pose a threat for the Maasai cattle. The seasonal movement of cattle during dry season was associated with more clinical cases of cattle trypanosomosis. This study demonstrates the need to strengthen surveillance and control strategies for AAT.

Key words: Cattle trypanosomosis, tsetse flies, management practices, seasonality, Northern Tanzania

Factors affecting the efficacy of antimicrobial treatment of Salmon Rickettsial Septicaemia in Chile: Analysis of an integrated industry data platform

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ABSTRACT

Objective: Salmon Rickettsial Septicaemia (SRS) is an important disease of farmed salmonid fish in Chile. In addition to direct losses from SRS-attributed mortality, consumer concern about the widespread use of antimicrobials to treat SRS contributes to a lower value of Chilean salmon in global markets. This study aims to evaluate factors affecting the efficacy of antimicrobials to treat SRS in farmed salmonid fish in Chile.

Materials and methods: This study takes a novel approach to the investigation of antimicrobial efficacy in a commercial aquaculture setting. Rather than designing a controlled trial—with high costs and necessity to include a small fraction of the industry—this study is supported by a cloud-based data platform that integrates data directly from the commercial data management systems of numerous salmon-producing companies. This enables powerful analysis of data from across the industry, captured in real-time and fine spatial and temporal resolution. In addition to a descriptive component, hypotheses about risk factors for antibiotic efficacy are tested with a range of statistical models.

Results: Results of particular interest relate to the effects of treatment factors (antimicrobial type, dose and route of administration), protocols for drug administration (including different feeding regimes for oral administration), timing and duration of treatment relative to onset of SRS-attributed mortality and start of the sea-water phase of production, and other host, management and environmental factors.

Conclusion: Global concerns about antimicrobial resistance are driving efforts to understand and manipulate to positive affect the factors that influence antimicrobial efficacy. The Chilean salmon industry represents an ideal test case for new approaches, given its size and the richness of data collected and managed by highly organised commercial companies. The integration and analysis of industry data provides a powerful and sustainable way to improve the effective use of antimicrobials in aquaculture.

Key words: Antimicrobial, SRS, platform, salmon, industry, sustainable

Sea lice infestation of farmed salmonid fish in Chile: distribution and analysis of risk factors using regulatory data

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ABSTRACT

Objective: Infestation with the sea louse *Caligus rogercresseyi* has a major impact on the production of farmed salmonid fish in Chile. The objectives of this study are to describe the spatiotemporal distribution of sea lice in farmed salmonids in Chile, to identify and describe risk factors for sea lice infestation, and to evaluate the utility of regulatory data for the purposes of epidemiological research.

Materials and methods: The Chilean government regulates the industry and requires companies to provide weekly reports of sea lice numbers at every sea site. Data on sea lice numbers (based on the sampling of individual fish in multiple cages in each sea site), mortality (by attributable cause), treatments, population characteristics and environmental data were extracted from government-managed databases for the period 2011–2017. Spatiotemporal description of lice abundance, density and 'high-infestation events' was followed by the development of models to evaluate risk factors. The latter part of the analysis included the development of directed acyclic graphs and *a priori* hypotheses about causal relationships, and subsequent implementation of spatial models to test these hypotheses.

Results: Key findings include seasonal patterns of lice abundance consistent with faster lice development in warmer sea temperatures, the positive association between lice abundance and duration of exposure (as measured in cumulative degree days) and the resistance of Coho salmon relative to other farmed species. Lice abundance was lower in more easterly locations (closer to the Chilean mainland) and—unexpectedly—higher stocking density was associated with lower lice abundance.

Conclusion: This study yields a range of epidemiological insights about sea lice infestation of farmed salmon that were gained from analysis of regulatory data. It illustrates the value of analysing large regulatory datasets, but also highlights the constraints inherent in using health data that was initially collected for regulatory purposes, rather than research.

Key words: Sea lice, Caligus, salmon, risk factors, Chile

Serological screening of Dutch slaughter pigs to estimate the seroprevalence of *Toxoplasma gondii* infections at farms

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ABSTRACT

Objectives: *Toxoplasma gondii* is the cause of the parasitic disease toxoplasmosis, and is an important foodborne zoonosis. Pig meat is one of the sources of toxoplasmosis in humans. *T. gondii* tissue cysts cannot be detected by visual meat inspection. Therefore, serological screening for antibodies against a *Toxoplasma* infection might be useful to identify farms with a high risk for *Toxoplasma* introduction. The objective of this study was to estimate the seroprevalence of *Toxoplasma* in Dutch slaughter pigs.

Materials and methods: For this study we used blood samples from an ongoing monitoring programme, collected from pigs, slaughtered in five Dutch pig slaughterhouses from 2012 to 2016. Pigs were originating from conventional pig farms (no outdoor access) and organic farms (compulsory outdoor access). Samples were tested serologically for the presence of antibodies against *Toxoplasma*. From the serological results a yearly prevalence was estimated with a logistic regression model, in which year, farming system and province were used as explanatory variables. The results were adjusted for the different sample sizes per farm/year/province. Data were also analyzed for seasonality in the seroprevalence by using a harmonic regression model.

Results: During the five year period a total of 226,340 samples were collected from pigs originating from 3,114 farms. For conventionally raised pigs the adjusted seroprevalence varied between 1.4 and 2.6% per calendar year, and for organically raised pigs between 2.0 and 5.3%. The analysis for seasonality showed dominant annual periodicity with a peak in seroprevalence around week 1, and a minimum around week 27.

Conclusion: This study provided seroprevalence and seasonality estimates of *Toxoplasma* in Dutch slaughter pigs, based on a large sample number collected over a five-year-period. Further research will include the causes of the seasonality and the risk factors for *Toxoplasma* in pig farms.

Key words: *Toxoplasma gondii*, pig, serology, prevalence

A ten-year trend in piglet death occurrences in early, mid or late lactation on Spanish farms

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ABSTRACT

Objectives: The objectives of this study were to quantify factors associated with piglet death occurrences during three stage of lactation: 0-1 (early), 2-8 (mid) and 9 days or more (late), and to assess recent annual trends.

Materials and methods: Data included 936,965 parity records of 213,752 sows on 44 Spanish farms that had 10-year records between 2007 and 2016. Mixed-effects logistic regression models were applied to the data.

Results: Mean piglet death occurrences in early, mid and late lactation ($\pm$ SEM) were 29.4 ± 0.05, 22.0 ± 0.04 and $23.6 \pm 0.04\%$, respectively. Between 2007 and 2016, death occurrences in early and mid lactation increased by 9.1 and 6.9%, respectively ($P < 0.05$). However, death occurrences in late lactation decreased by 10.6% between 2010 and 2016 ($P < 0.05$). Higher death occurrences in any lactation periods were associated with farrowing more pigs born alive, stillborn piglets, and low or high parity ($P < 0.05$). In particular, as the number of pigs born alive increased from 4 to 19 pigs, death occurrences in early, mid and late lactation increased by 29.4, 8.1 and 6.5%, respectively ($P < 0.05$). In addition, sows that had farrowed 1 or more stillborn piglets had 1.1-3.6% more death occurrences during each stage of lactation than those with no stillborn piglets ($P < 0.05$). Sows in parity 1 had 0.8-1.6% more death occurrences in early lactation than those in parity 3 or higher ($P < 0.05$). In mid or late lactation, sows in parity 2 had 1.7-5.2% more death occurrences than those in parity 3 or higher ($P < 0.05$).

Conclusion: Producers should pay attention to rising deaths during lactation, especially in parity 1 or 2 sows farrowed high PBA and stillborn piglets.

Key words: Piglets, pre-weaning mortality, year trend

A comprehensive on-farm risk assessment tool for bovine respiratory disease (BRD) in preweaned dairy calves

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ABSTRACT

Objective: We report here on the development of a comprehensive BRD risk assessment (RA) tool to modify farm-specific management practices associated with BRD in preweaned dairy calves.

Materials and methods: Results of a longitudinal and a cross-sectional study are the foundation of the RA tool's scores. The longitudinal study included 11,470 calves on five dairies between March 2015 and July 2016, while the cross-sectional study included 4,636 calves on 100 dairies in California evaluated between May 2014 and April 2016. Both studies captured data via a survey questionnaire on the management of maternity pens, colostrum, vaccinations, milk feeding and housing of calves. The RA questions' scores are based on beta-coefficients from shared frailty models and survey-weighted generalized linear mixed models. Preference was given to coefficients from the longitudinal over the cross-sectional study and from multivariable over univariable analyses, the later after adjusting for confounders as necessary.

Results: Examples for factors associated with BRD include feeding only whole milk (no milk replacer) (HR: 0.54, 95% CI: 0.42-0.70), pasteurizing whole milk (OR 0.10, 95% CI: 0.02-0.46), and number of bedding changes in the maternity pen per month (HR 0.98, 95% CI: 0.97-0.99).

Conclusion: Based on high BRD risk management practices identified, the user can formulate and assign mitigation strategies to reduce the disease burden in the preweaned calf population investigated. Follow-up RA and prevalence estimation allows for monitoring implementation of modifications and changes in BRD prevalence. The resulting RA tool may offer a novel and comprehensive way to reduce BRD in preweaned calves.

Key words: Bovine respiratory disease (BRD), dairy calves, risk assessment

An evaluation of management practices associated with the presence of *Salmonella* Heidelberg infections in U.S. dairy calves

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ABSTRACT

Objective: A case-control study was conducted to evaluate management practices among dairy operations with and without *S.* Heidelberg detected in calves at necropsy.

Materials and methods: Case operations were defined as operations on which *S.* Heidelberg had been isolated from tissue or fecal samples from at least one calf; samples were voluntarily submitted to the Wisconsin Veterinary Diagnostic Laboratory. Control operations voluntarily submitted specimens from sick or dead calves that were not diagnosed with *S.* Heidelberg. Participating operations completed a questionnaire that focused on herd additions, biosecurity, and included data on the sources of purchased calves, the distance calves traveled to the operation, as well as feeding and housing practices.

Results: In total, 12 case and 11 control operations completed the questionnaire. Completed questionnaires revealed an association with the presence of *S.* Heidelberg and newly introduced calves (primarily preweaned), purchasing calves from a dealer or market, and transporting calves more than 80 km. Interestingly, a higher percentage of case operations than control operations cleaned transport trailers and calf housing areas; however, the efficacy of cleaning and disinfection for pathogens was not evaluated.

Conclusion: Results of this study highlight the impact source and stress has during transport of preweaned calves. Practices designed to reduce calves' exposure to fecal pathogens and stress during transport are likely important in preventing *S.* Heidelberg outbreaks.

Key words: Dairy calves, *Salmonella* Heidelberg, transport

Management practices associated with morbidity and mortality in preweaned dairy heifer calves

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ABSTRACT

Objective: The objective of this study was to evaluate morbidity and mortality in preweaned dairy heifer calves based on different health, feeding, and management practices, as well as environmental factors.

Materials and methods: This study included 104 operations in 13 states (2,545 total heifer calves) that participated in the 18-month longitudinal calf component of the National Animal Health Monitoring System's Dairy 2014 study. The percentage morbidity for all calves enrolled in the study was 33.9% and the percentage mortality was 5.0%. Backward elimination model selection was used after univariate screening to determine which factors significantly impacted morbidity and mortality.

Results: After controlling for independent variables in the morbidity model, calves born at a higher birth weight had a lower predicted risk of morbidity than calves with a lower birth weight. An increase in serum IgG concentration was associated with decreased morbidity. Calves housed in positive or cross-ventilated systems had a 2.2 times higher odds of developing disease compared with calves housed in natural ventilation systems. Average THI during the preweaning period was inversely correlated with morbidity; as THI increased, the predicted morbidity risk decreased. After controlling for independent variables in the mortality model, calves born at a higher birth weight had a lower risk of mortality. An increase in serum IgG concentration decreased the risk of mortality. The odds of mortality were 3.1 times higher in calves fed ≤0.15 kg of fat/d in the liquid diet compared with calves fed ≥0.22 kg of fat/d. The odds of mortality were 4.7 times higher in calves that experienced any disease throughout the preweaning period than calves with no disease.

Conclusion: In conclusion, increasing calf birth weight and serum IgG concentrations, and ensuring a warm and well ventilated environment can help minimize morbidity and mortality on U.S. dairy operations.

Key words: Preweaned calves, morbidity, treatment, mortality

Management practices associated with higher average daily gain in preweaned dairy heifers

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ABSTRACT

Objective: The study objective was to evaluate average daily gain (ADG) in dairy heifer calves based on health, feeding, management practices, and environmental factors.

Materials and methods: This study included 102 operations in 13 states (1,410 total Holstein heifer calves) that participated in the 18-month longitudinal calf component of the National Animal Health Monitoring System's Dairy 2014 study. The mean ADG from birth to final weight was 0.74 kg/d. Backward elimination model selection in Proc Mixed after univariate screening determined factors that significantly impacted ADG.

Results: After controlling for other independent variables in the model, calves born to first lactation dams gained less than calves from second or greater lactation dams. Singleton calves gained more than twins. Calves bedded with sand or no bedding gained less than all other bedding types. Calves that were fecal-negative for *Cryptosporidium* or *Giardia* at the time of sampling gained more than calves that were fecal-positive for *Cryptosporidium* or *Giardia*. Calves with no disease events gained more than calves with one or more disease events. Calves experiencing an average THI less than 50 during the preweaning period gained more than calves experiencing an average THI greater than or equal to 50. Within the range of observed kilograms of protein fed per day in the liquid diet, every additional 0.1 kg of protein fed per day equated to 0.02 kg/d of gain. Calves fed milk replacer with a direct-fed microbial gained less than calves fed milk replacer without a direct-fed microbial and calves fed pasteurized or unpasteurized milk regardless of direct-fed microbial use.

Conclusion: These results highlight the importance of feeding a quantity and quality of a liquid diet to achieve optimal growth, keeping calves free of disease, the type or status of bedding, and mitigating the effects of temperature and humidity on preweaning ADG.

Key words: Average daily gain, Holstein heifer calves, liquid diet.

Evaluation of trace elements status of cattle and buffalo in Haryana, India

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ABSTRACT

Objectives: i) to analyze some of the trace elements concentration in serum of cattle and buffalo in Haryana, India.

Materials and methods: A total of 767 serum samples (cattle – 381, Buffalo - 386) were collected from different districts of Haryana. Serum samples were analyzed for determination of cobalt (Co), copper (Cu), iron (Fe) and zinc (Zn) concentrations using Atomic Absorption Spectrophotometer (AAS-Perkin Elmer) after digestion with di-acid mixture.

Results: In cattle, mean±s.d levels of Co, Cu, Fe and Zn were 0.405±0.457, 0.438±0.485, 9.583±3.082 and 1.628±0.081 ppm, respectively; whereas, in buffalo the mean levels were 0.453±0.460, 0.515±0.559, 9.296±3.261 and 1.876±0.088 ppm for Co, Cu, Fe and Zn, respectively. One way analysis of Variance (ANOVA) was calculated to assess the difference between cattle and buffalo in different districts, agro-climatic zones and Haryana. In Haryana significant difference between cattle and buffalo was observed only for concentration of serum Zn level (p=0.0428). The analysis was significant for all the trace elements in relation to districts ($p<0.0001$), whereas, in relation to zones significant difference was observed for Co in western zone ($p<0.0001$), Cu, Fe and Zn eastern zone (p=0.0371; 0.0168 and 0.0113). There was a statistically significant interaction between the effects of species and zone on iron, $F(1, 593) = 5.55$, $p = 0.0188$ and Cobalt, $F(1, 500) = 16.85$, $p = 0.0000$. Also, there was a statistically significant interaction between the effects of species and district on zinc, $F(15, 683) = 2.76$, $p = 0.0004$; iron, $F(15, 666) = 8.93$, $p = 0.000$ and cobalt, $F(15, 621) = 8.24$, $p = 0.0000$.

Conclusions: Trace elements concentration in serum of cattle and buffalo in Haryana affected by the type of animal, district and agro-climatic zone.

Key words: trace elements, agro-climatic zone, Copper, Cobalt, Iron, Zinc, Haryana

Swedish dairy farmers' intentions to reduce use of antibiotics

U. Emanuelson*, N. Fall, K. Sjöström, S. Sternberg Lewerin

ABSTRACT

Objective: Our objective was to investigate the intention of Swedish dairy farmers to reduce their use of antibiotics and to identify potential predictors for this intention.

Material and methods: A questionnaire study was conducted to collect information on farm and farmer characteristics, management routines, views on antibiotics and antibiotic use. An intention construct, related to improved health and decreased use of antibiotics, was defined based on 5 questions scored on 6-point Likert scales, where 1 corresponded to "don't agree" and 6 to "agree completely", and with a "don't know" option. The internal reliability of the construct was assessed with Chronback's α. The questionnaire was sent to a random sample of 300 organic and 500 conventional farmers. Imputation of missing values, using the non-parametric Random Forest methodology applied in the R-package missForest, version 1.4, was done before analysis. Associations between predictor variables and the intention variable was assessed with a multivariable linear regression model, guided by a directed acyclic graph.

Results: A total of 192 usable questionnaires were received, giving a 24% response rate. Median herd size was 80 cows (inter-quartile range (IQR) 60-130), 47% were organic and 38% had automatic milking systems. Forty-three percent of respondents were female, median age was 51 (IQR 43-58) and 53% had post-secondary school education. The median intention was 4.40 (IQR 3.75-5.00) with 10% having 5.6 or higher on the 6-point scale. Herds with organic production and a dedicated herd veterinarian showed a higher intention to reduce the use of antibiotics, as did younger farmers. The farmers' perceived risks with and benefits of antibiotics, or experience of antibiotic resistance, was not found to be associated with the intention.

Conclusion: Swedish dairy farmers show a relatively high intention to reduce their use of antibiotics, despite already having the lowest use in the European Union.

Key words: Antibiotic, antimicrobial, intentional, believes, cows

Increased levels of hair cortisol found in calves not coping with competition

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ABSTRACT

Objective: Analyzing hair cortisol content offers a non-invasive possibility to measure retrospective levels of circulating cortisol, a potential indicator of chronic stress and animal welfare applicable in population studies. The objective of this study was to evaluate the associations between hair cortisol and welfare indicators of dairy calves.

Materials and methods: The welfare of 206 calves (1-43 weeks of age) from 12 Swedish dairy farms was assessed using animal-based measures and behavioural observations. Hair samples were collected from their tails. Samples were washed, scored for remaining dirt, dried and homogenized. Cortisol was extracted in methanol and the concentration determined with an ELISA kit designed for salivary cortisol (Salimetrics®). Statistical analysis was performed in R using Elastic Net Regression, for initial variable selection, and Generalized Linear Mixed Models including herd and pen as random effects.

Results: The largest effect on cortisol content was the dirtiness of the hair after washing. Significantly higher levels of cortisol were also seen in calves that were displaced by others, had low ruminal fill and were exposed to rubbing from other calves as well as calves that were less fearful and observed playing. Lower cortisol levels were seen in calves resisting displacement when butted and that were observed coughing. Cortisol content decreased slightly with age.

Conclusion: These results indicate that measuring hair cortisol may identify individuals exposed to, and less successful in dealing with, competition. However behaviour associated with positive arousal e.g. play, also increased cortisol content, which reduces the specificity of the indicator. The underlying cause of the effect of dirtiness of hair requires further study, but may reflect unmeasured parameters on the farm e.g. related to management or the environment, or be due to methodological issues.

Key words: Welfare, stress, indicator, cattle

Network analysis of cattle movements as an assessment of risk potential of disease spread in Slovenia

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ABSTRACT

Objective: It is well known that movement of animals between premises is one of the main factors contributing to the spread of infectious diseases in livestock. Objectives of this study were to gain insight into the structure of cattle trade network in Slovenia and the evaluation of risk potential for disease spread for each individual premises.

Materials and methods: The data on cattle movements were obtained from the Administration of the Republic of Slovenia for Food Safety, Veterinary Sector and Plant Protection. We analysed movements that occurred between 1st August 2010 and 31st July 2016. All export movements and movements to end nodes (e.g. animal waste processing centres, slaughterhouses, corpse collection centres) were excluded from the study. The weighted network was analysed in Pajek program. Moreover, we generated monthly and yearly networks to check for consistency of cattle movements through time.

Results: The studied network consisted of 37,124 different cattle premises between which approximately 1.5 million individual animal movements were documented. Weights were assigned to links based on number of animals moved between two premises on a daily resolution. The characteristics of yearly networks are quite constant over selected period. Nevertheless, a decrease in the average shortest path length and diameter and an increase in the largest strongly connected component was noticeable regardless of the aggregation period. This could be explained with an increase in the intensity of production and the average size of agricultural holdings in Slovenia in the last few years. Based on centrality measures and consistency, premises were assigned into different risk classes.

Conclusion: The identification of premises with higher risk enables targeted surveillance and control measures. Network analysis represents a valuable support for optimizing disease control and prevention, however when offering advice the latest available data should be used.

Key words: Cattle movements, network analysis, targeted surveillance

National sero-epidemiological survey for cattle brucellosis in Uruguay

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ABSTRACT

Objective: Cattle production is the main agricultural activity in Uruguay and *Brucella abortus* is endemic in the country. As many countries, the national veterinary services implement a control program based on testing and culling of positive animals. All susceptible dairy cattle are compulsorily tested every year, and the surveillance in beef cattle is based on slaughterhouse sampling of cows. The objective of our study was to determine cow and farm level prevalence (defined as at least one positive cow) for bovine brucellosis in Uruguay.

Materials and methods: We performed a two stage random sample: in the first step, we stratified herds into six strata according to the bovine population size and the production system (dairy or beef). On the second step, 60 random cows were sampled within each herd. A total of 29790 serum samples from 602 herds were analyzed in series with rose bengal test as a screening and fluorescent polarization assay as a confirmatory. Seroprevalence was estimated adjusting for the sampling design.

Results: Cow seroprevalence was 0.036% with a 95% CI superior limit of 0.076%, whereas the proportion of farms with at least 1 positive cow was 0.31% (95% CI 0.002-0.622%). There were no statistical differences on the farm or animal prevalence between dairy and beef production systems. These results showed that brucellosis is on an advanced control stage in Uruguay, however, these results do not differ with previous studies.

Conclusion: In conclusion, there has not been an improvement on brucellosis control since our last national seroprevalence study, and our recommendation is to increase the surveillance and the laboratory tests to try to eradicate it in the future.

Key words: *Brucella abortus*, zoonosis, cattle brucellosis, Uruguay, survey

Seroprevalence of brucellosis in dairy cattle in three selected districts of Punjab, Pakistan

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ABSTRACT

Objective: Brucellosis is one of the major problems of milk producing animals in most part of the world including Pakistan which deteriorates the health of livestock. It is a disease of zoonotic significance which is capable of producing disease in humans leading to infertility, orchitis, abortions and synovitis. Main objective of the study is to determine the seroprevalence of brucellosis in dairy cattle (Sahiwal) endangered temperature resistant species of Pakistan.

Materials and Methods: In this study, a total of (N=300) serum samples of cattle were collected from three selected districts of Punjab, Pakistan including district Chiniot, Sargodha and Sahiwal. Serum samples were screened through Rose Bengal Plate agglutination test (RBPT) and quantified with Indirect Enzyme Linked Immunosorbent Assay (iELISA). RBPT results indicated that 12.66% animals were seropositive. The serum samples positive by RBPT were further confirmed by the use of most specific and sensitive serological test known as iELISA. 11% animals were confirmed as seropositive.

Results: Our results indicate high seroprevalence of brucellosis in cattle as compared to buffalos. Based on the findings of study, there is high prevalence of brucellosis in dairy cattle.

Conclusion: So it is demand of the time to educate the local farmers and laymen about the economic as well as zoonotic aspects of disease. Government and public authorities should set the legislation and continuous screening of dairy cattle for brucellosis.

Key words: Seroprevalence, brucellosis, serum, RBPT, iELISA, risk factors

Antimicrobial use in Canadian beef cattle: extent, indications, and risk factors for treatment

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ABSTRACT

Objective: Antimicrobial drugs (AMDs) are used in Canadian feedlot cattle production systems to support and maintain health and as therapy for illness. Historically, comprehensive data on types of AMDs used, extent of use, common use indications, and demographics of the cattle population receiving antimicrobials have been limited. Antimicrobial stewardship is a priority for the Canadian Beef Industry, and a thorough understanding of baseline factors is important for meaningful assessment of associated public health risk and to inform stewardship activities.

Materials and methods: This project will provide robust Canadian feedlot cattle AMU estimates, interpret AMU data and relate it to Canadian feedlot production practices, validate Population Corrected Unit estimates for Canadian feedlot cattle, and assess how a standardized collection method/system might be applied nationally.

Results: Detailed AMU data (2,615,082 cattle from 36 feedlots in western Canada) were collected over 4 years (2008-2012). The majority of cattle entering feedlots were male (63%; 1,643,528), considered low risk for developing bovine respiratory disease (BRD; 61%; 1,593,443), identified as yearlings at feedlot entry (55%; 1,434,583), and arrived during the fall/winter (62%; 1,616,686). Descriptive AMU data (parenteral and in-feed) will include use trends over time, use based on Health Canada category of public health importance, and use by antimicrobial class (e.g., quinolones, macrolides, tetracyclines, etc). AMU comparisons will be made between sexes, geographical regions (provinces) and seasons. Use indications will be stratified by animal classification at feedlot arrival for risk of developing BRD (high or low), and by antimicrobial class; to allow detailed insight into AMU practices in Canadian beef production and antimicrobial exposure in Canadian feedlot cattle.

Conclusion: This presentation will highlight the importance of accessing these types of data if the Canadian Beef Industry is to be proactive in the fight against antimicrobial resistance, to continue leadership in antimicrobial stewardship and to be transparent related to access to global markets.

Cross-sectional study to estimate the dog population and economic impact on the use of mass rabies vaccine in Nay Pyi Taw Council area of Myanmar

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ABSTRACT

Objective: Rabies has been addressed as an important disease in the Law issued by the Government of Myanmar. Due to the annual report of animal and human cases, the Veterinary Department is conducting prevention and control of rabies with the support of OIE STANDZ project.

Materials and methods: Before and during the STANDZ Rabies pilot campaign, a cross sectional study was conducted to understand the dog population estimates and economic impact on the application of mass vaccination campaign. Multiple cross-sectional studies were done at Lewe Townships of Nay Pyi Taw Council area and questionnaire interviews were (n=200) from randomly selected 20 villages and additional information was taken from participatory approaches (n=415). A year after, additional questionnaire interviews (n=446) were conducted in 18 villages to obtain the cost of post exposure treatment and that of vaccination to the dogs.

Result: The overall ratio of dog and human population was 1:6 and estimated dog population was approximately 40,000 heads at the study area and dog population and human population were linearly associated. Finding for the economic impacts were that the cost of rabies vaccine per dog was about 2000 Kyats(~1.53 USD) to 5000 Kyats (~3.84 USD) whereas for the PEP treatment, it cost 7000 Kyats (5.38 USD) to 11000 Kyats (8.46 USD) for additional expenses because PEP treatments were subsidized by the government.

Conclusion: By referring the estimated dog population of 7 million in Myanmar, the cost for the mass dog vaccination was less than that of PEP treatment. Nevertheless, the vaccination can be recommended as the efficient disease preventive measure and for the development of mass vaccination campaign, selection of targeted high-risk areas based on the report and expert opinion is recommended.

Key words: Rabies, epidemiology, economic impact, population estimate

Mutations associated to synthetic pyrethroids and fipronil resistance in *Rhipicephalus microplus* from Uruguay and Brazil

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ABSTRACT

Objective: *Rhipicephalus microplus* is the most important pest of livestock in the tropics and sub-tropics and acaricide resistant is a severe problem. The objective of this study was to identify mutations associated to acaricide resistance.

Materials and methods: Larvae and adults from 15 field tick populations of Uruguay and Brazil (Rio Grande do Sul) resistant to synthetic pyrethroids and fipronil were analyzed. A PCR multiplex was standardized to detect two nucleotide substitutions in the domain II of the para-sodium channel gene associated to pyrethroids-resistance (C190A; G215T) and a mutation in the GABA-Cl gene (*rdl*) associated to fipronil resistance (GC858TC/TT).

Results: For the sodium channel, the mutation C190A was present in all resistant field populations, and the homozygous genotype was the most frequent. Therefore, some individuals were wild-type. The mutation G215T was not detected in any individuals, from Uruguay and Rio Grande do Sul. All fipronil-resistant populations (n=9) presented at least on mutant tick, and more frequently in heterozygosis. The first diagnoses of pyrethroid resistance in Uruguay and Brazil were reported in the 1990s. To increase the efficacy of this group, mixtures with organophosphates or piperonyl butoxide were released on the market. It should be noted that in some locations, the use of these mixtures might have contributed to the maintenance of these resistant genotypes.

Conclusion: The results confirm that the resistance is disperse in the region and is very strong due the high frequency of *kdr* homozygous individuals. It may be an advantage to have found the same mutations in both countries. In Uruguay, the control of the tick is legislated. So, to avoid maintaining or increasing resistant genotypes that can compromise the success of the tick control campaign, the use of the mixtures should be done only in specific cases.

Key words: *Rhipicephalus microplus*, acaricide resistance, molecular diagnoses, synthetic pyretroids, fipronil

Temporal patterns and spatial-temporal clustering of porcine reproductive and respiratory syndrome (PRRS) in Vietnam from 2008 through 2016

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ABSTRACT

Objective: The main objective of this study was to identify the temporal patterns and space-time clusters of PRRS from 2008 to 2016 using national surveillance data in Vietnam.

Materials and methods: The number of cases and outbreak dates from communes from 2008 to 2016 were obtained from the Department of Animal Health (DAH), Vietnam. Monthly cumulative cases of PRRS were calculated for the study period. Space-time cluster analysis was conducted using the SaTScan.

Results: A total of 518,028 cases were reported from 2008 to 2016. In the Red River Delta (RRD) region, cases were predominantly reported in April followed by March and May. In the Northeast/west regions, most of the cases were observed in May and March, respectively. In the Mekong River Delta (MRD), highest cases were detected in September followed by October and July. Other regions (North/South Central Coast, Central Highlands and Southeast) showed that most of the cases were detected in July and August. The first (radius: 82.17 km; ratios: 5.5) and second (radius: 50.8 km; ratios: 10.61) clusters were observed in the RRD and MRD regions, respectively and four other clusters were observed in the central and Southern parts under maximum geographical cluster size. In the Northeast/west regions, most of the cases were observed in May and March, respectively. For temporal cluster analysis, in the MRD, most cases were detected in September followed by October and July. Other regions (North/South Central Coast, Central Highlands and Southeast) had most cases in July and August.

Conclusion: Our findings provide better insight into the distribution of clusters and temporal patterns of PRRS in Vietnam. This study may be helpful for policy makers to provide valuable information on the hotspot areas and timing of outbreaks.

Key words: Vietnam, PRRS, temporal patterns and space-time cluster analysis

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Isolation and real-time PCR detection of *Brucella abortus* in lymph node in serologically positive cows in Uruguay

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ABSTRACT

Objective: Brucellosis is a serious infectious disease in cattle and other species, including man. Brucellosis is endemic in Uruguay; cow seroprevalence was estimated in 0.036%. RB51 vaccine is used in brucellosis outbreak at farm level, in Uruguay. The objective of this study is isolation and real-timePCR detection of *Brucella abortus* in lymph node from serologically positive cows.

Materials and methods: In the period September-December 2017, 63 lymph nodes were processed from animals with positive serology. For isolation, Farrell medium modified was used. Samples were also processed and analyzed by real-time PCR using *B.abortus* Primer StandardKit (Genesig®). Four grams of each lymph node were stomacher using 5 mL of 1x PBS; 1 mL was taken and centrifuged at 10000xg for 15 min, at room temperature. Digestion was performed with proteinase K and subsequent extraction of DNA was done with MagMAX™ Pathogen DNAKit (Thermo Fisher Scientific).

Results: Out of the 63 lymph nodes, 6 samples had bacterial isolation and 57 were negative; 5 isolates were *B.abortus* wild type and one isolate was *B.abortus* RB51 vaccine strain. By real-timePCR, 9 samples were positive, 13 had inhibition and 41 were negative. Five out of 6 lymph node with isolation showed inhibition and only one was positive by PCR. Eight PCR positive samples do not have isolation. Surprisingly, the PCR kit detect as positive both *B.abortus* (Wild type / RB51). PCR detected more positive samples compared to the culture, which has a low sensitivity even though those are primary data.

Conclusion: It is important to design a multiplex PCR that differentiates the wild strain from the vaccine one, especially in countries where the vaccine is used as a control tool. Given the very low prevalence, it is expected a low positive predictive value. Therefore, it is essential to improve laboratory test to eradicate the disease.

Key words: *Brucella abortus*, PCR, isolate, cattle

Leptospirosis seroprevalence in beef cattle in Uruguay

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ABSTRACT

Objective: Leptospirosis is a zoonotic disease of worldwide distribution; it affects the majority of domestic mammals and wild animals. The last seroprevalence study conducted in Uruguay dates more than ten years ago. The objective of this study was to determine the seroprevalence of *Leptospira spp* pathogenic in beef cattle.

Materials and methods: In the second semester of 2015, a cross-sectional study was carried out. The random survey was designed in two steps: first beef herds were divided into three strata according to bovine population (from 1 to 200, 201 to 800 and more than 800 cattle) and the second step up to 25 cows were sampled in each herd. A total of 6,702 serum samples from 487 herds were analyzing by microaglutination test, 4 serovars were tested: Pomona, Hardjo-bovis, Hardjo-prajitno and Wolffii. The cut off used was 1/200 for individuals and 1 positive cow for herds. The sampling design was taken into account to calculate the prevalence.

Results: Herd level prevalence was 69.22% (95%CI 60.90-77.55%) and cow level prevalence was 23.38% (95%CI 20.93-25.83). There is a trend that as the number of animals in the herds increases, it also increases the seroprevalence. There is a predominance of the serogroup Sejroe (15.57 %) in relation to Pomona (3.63%); probably, because bovines are the reservoir of the serovar Hardjo. Cow seroprevalence in relation to year 2005 was lower, 23.38 % against 38.50%, and vaccination history increased in the last years (29.88% against 4.2% in 2005).

Conclusion: In conclusion, leptospirosis continues to be an endemic disease, and it would be advisable to determine the impact in public health and the farms economic.

Key words: Uruguay, *Leptospira*, cattle, seroprevalence

Evaluation of parity as a delaying factor to reach PRRSv stability in a sow farms

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ABSTRACT

A common strategy to control and eliminate the porcine respiratory and reproductive syndrome virus (PRRSV) from sow farms is through the combination of herd closure and whole herd exposure to a live virus. This process is known as load-close-expose (LCE). The time between closure/exposure and weaning of PRRSV free piglets is known as time to stability (TTS). Usually, after four negative PCR tests, a month apart, in at least 30 piglets at weaning is required to declare a herd as stable. Recently, fluid of processing tissues (i.e. tails and testicles) was observed to provide accurate information on the herd PRRS status; particularly under low prevalence conditions (highly sensitive). Additionally, preliminary data showed a tendency for lower parity litters to have a higher percentage of PRRSV positive results. Although other factors, as the method of virus exposure (i.e. live virus inoculation or modified live vaccine) used in the herd or the season when the outbreak occurred can affect the TTS, the role of PRRSV persistence in gilt litters and their impact on the TTS has not been assessed to date. Therefore, this study aims to evaluate the role of low parity litters in maintaining PRRSV infection in sow herds. Eight farms that experienced a recent PRRS outbreak will be purposely selected. Litters of parity 1 (n=15), parity 2 (n=15) and parity 3+ (n=15) sows will be sampled at processing weekly during 32 weeks. Processing tissues of each litter will be collected in Ziploc bags and send to the laboratory for testing. Pooled samples per parity per farm will be RT-PCR tested. The proportion of positive litters in each parity group will be described and compared using logistic regression accounting for the effect of farm. Sampling started Mach 30th, 2018. Full results will be presented at the conference.

Australia's national wild surveillance program for white spot syndrome virus

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ABSTRACT

Objectives: To meet this threat a nationally coordinated surveillance program for white spot syndrome virus, the causative agent, was required. Australian aquatic animal health authorities responded with a national surveillance plan with common purpose meeting consistent standards of evidence with the primary objective of demonstrating national freedom from WSD.

Materials and methods: A national surveillance working group (WG) was tasked with proposing a coordinated national surveillance plan to provide a staged approach to demonstrate whether Australia is free from WSSV. Study populations were chosen based on the qualitative risk factors for farmed and wild animal populations and the design prevalence, confidence, diagnostic sensitivity and specificity for surveillance of apparently healthy prawns were determined at the Australian Animal Health Laboratory in accordance with the OIE Manual Chapter 1.1.2.

Results: A total of 29 epidemiological units were chosen Australia-wide. For each epidemiological unit, at least 184 prawns were sampled and tested. All samples tested were negative. Within the restricted movement area and samples from, Logan River and the Brisbane River sites, within Moreton Bay, tested negative. However, prawn and crab samples from northern Moreton Bay tested positive for WSSV. These positive test sites are within the same area that positive results previously came from in 2017. Australia's response to this disease followed a well-designed national response to implement movement controls, destruction and disposal of infected stocks, fallowing and surveillance. Elucidation of the coordinated national response highlights the interactions between epidemiologists, policy makers and industry and the difficult considerations that were faced. We illustrate how the success of this emergency response and the subsequent surveillance program relies heavily on collaboration between federal, state and territory governments. Declaration of disease freedom should follow at least two surveys per year for at least two consecutive years to be conducted three or more months apart. We will report surveillance progress, particularly in relation to how the federal government managed prawn fisheries.

Key words: White spot syndrome virus, prawns, wild surveillance, risk factors, emergency disease response

Farming factors affecting calicivirus infection in dairy farms in Sweden

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ABSTRACT

Objective: We aim to estimate the prevalence of caliciviruses (nebovirus and bovine norovirus, BNV) and relation to farm management factors and also calf level factors on Swedish dairy herds.

Materials and methods: Sampling was conducted in 26 herds during one indoor season (2009-2010). In each herd, 10 pre-weaned calves were to be sampled at one occasion. DNA was extracted from 130 faecal samples (5 calves per herd, median 17 days of age) using QIAamp viral RNA kit (Qiagen) and caliciviruses were detected with reverse transcription-polymerase chain reaction (RT-PCR). Management routines were recorded at farm inspection (41 variables). Biosecurity routines and calf management were collected through a questionnaire (29 variables). Multivariable random-effects mix model for factors associated with Calicivirus positive calves were carried out using STATA software. Two types of bovine enteric calicivirus were identified; BNV in 23.1% of the calves, and nebovirus in 7.7% of the animals. Prevalence of calicivirus was not correlated with other common infections (Giardia and Chryptosporidium spp) previously determined in the same herds. Calves presented optimum body condition (grades 3–3.5), and cleanliness (grades 1–2). Half of the positive calves presented normal faecal consistency.

Results: From the farm inspection and questionnaires, calves in single or group pens were unequally BNV-infected, with more infections when calves were moved to group pens at 2 weeks of age than older. Calves were significantly less infected on farms with all in/all out system and automatic feeders, but more infections were significantly associated with a higher maximum number of animals per pen and more cleanliness of bedding material (p<0.05). Nebovirus positive calves were associated with a higher maximum number of animals per pen (p<0.05). Less infection was observed with higher cleanliness and more bedding material in calf pens (p<0.05).

Conclusion: Swedish dairy herds can benefit from the study findings through improved biosecurity measures and calf management.

Key words: Calf diarrhea; risk factors; zoonosis; faecal consistency; biosecurity

Infectious Salmon Anaemia virus (ISAv) surveillance: An approach to enhanced surveillance for early detection of disease

N. O'Brien*, D. Whelan,

ABSTRACT

Objective: Infectious Salmon Anaemia virus (ISAv), an orthomyxovirus, causes the disease Infectious Salmon Anaemia (ISA) in Atlantic salmon. The disease will cause varying degrees of morbidity and mortality depending on the genotype. ISA virus occurs globally with periodic or regular outbreaks. Surveillance at the marine cage site is crucial for early detection and to prevent spread of the pathogen. Combined targeted and passive surveillance are used to determine ISAv status in Newfoundland and Labrador, Canada. The objective of the surveillance system is primarily for early detection.

Materials and methods: A stochastic simulation model was used to simulate the pathway for detection of ISAv through active surveillance. Active surveillance showed that the mean probability of freedom from disease exceeded 95% after 4 months if sampling occurred every 30 days. This information was then utilized to refine the surveillance program to incorporate varying probability of introduction. The probability of introduction was impacted by components such as oceanographic/hydrographic data and Bay Management Areas. This information was then used to evaluate the overall system surveillance.

Results: Preliminary data shows that factors such as sample size, sample frequency and diagnostic tests can have an impact on surveillance and therefore can be utilized to develop a surveillance program that is risk based.

Conclusion: In conclusion, ISAv surveillance can utilize relative risk to enhance early detection of ISAv at marine cage sites.

Key words: Aquaculture, ISAv, Infectious Salmon Anaemia, surveillance, salmon

Knowledge and understanding of owners on orthopedic problems in clinically overweight neutered dogs

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ABSTRACT

Objective: Obesity is a general problem in pets around the world. An obesity problem can be also found in uncontrol feed and non-exercised neutered dogs. Surgical neutering is the best way for population control in dog, it can prevent some specific health problems. However, neutered dogs tend to easily develop obesity which lead to some orthopedic problems.

Materials and methods: In this study, we collected data from dog owners who visited Small Animal Teaching Hospital, Faculty of Veterinary Science, Chulalongkorn University, Thailand, using questionnaires and face-to face interviews.

Results: A set of four hundred and two responding was collected during October 2016 to May 2017. From those, 80.1% of owners understood about possibility of being overweight after neutering while 59.2% of them knew that overweight can cause orthopedic problems. Both groups showed significantly relations (P<0.001). The data showed that dog owners had good understanding on the possibility of their dogs being overweight after neutering but they had only moderate knowledge that overweight can cause some orthopedic problems. Obesity of neutered dogs was common information for the owners while some orthopedic problems in neutered and obese dogs were too complicated for them to identify.

Conclusion: From all data and parameters, we concluded that the understanding of the owner in this topic was still in moderate level. Therefore, veterinarians have an important role to concern and emphasize more on giving owner educations for prevention of the overweight after neutering and decline the consequence orthopedics and health problems of their dogs in the future.

Key words: Understanding, neutering, overweight, orthopedic problem, dog owner

An investigation for risk factors of donkey abortion and foal dying in Shandong province

Yi Zhang[*]

ABSTRACT

Background: From March to April in 2015, the rate of abortion and mortality of foals in a farm of Donge country was extremely higher than usual, and the main symptom of donkey foals was diarrhea. The morbidity is 59.3%, and the mortality is 25.3%.

Materials and methods: In order to find out the etiology, and explore the risk factors, we carried out a field investigation, make an interview with the veterinarian, and collected data about feeding, breeding, and treating in the farm. Through field survey and logistic analysis with the data.

Results: The result was speculated that the mouldy feed may be the main cause of abortions and foal deaths.

Conclusion: The immunity and resistance of the young animal is poor, so in the nursery stage, the feed safety must be paid more attention.

Developing a predictive model for vesicular stomatitis: a USDA-ARS Grand Challenge project

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ABSTRACT

Objective: The USDA Agricultural Research Service (ARS) Grand Challenge calls for collaboration across projects, locations, and scientific disciplines to address the nation's agricultural research needs. One specific need is to combat agricultural pathogens, such as vesicular stomatitis virus (VSV), which damages livestock health, depletes veterinary resources, and disrupts trade. A trans-disciplinary team of researchers—from veterinary science, entomology, epidemiology, microbial genomics, hydrology, ecology, economics, and rangeland livestock management— has formed to elucidate virus-vector-host interactions and ecological factors associated with VSV outbreaks in the western U.S.

Materials and methods: The VSV Grand Challenge team is using big data, spatio-temporal modeling, and machine-learning to test hypotheses about phylogeographic relationships, landscape-level characteristics, and premises-level conditions associated with VSV occurrence among cattle and horses. A "data-cube" containing 1550 VSV occurrences and 300 environmental variables have been constructed on a daily, seasonal, or annual time-step over a 1 million km^2 area of the western U.S. The data-cube informs vector distribution and regression models of VSV occurrence.

Results: The month of VS onset was estimated based on latitude, elevation, and precipitation. Relationships between VS occurrence and environmental conditions differ for incursion years versus expansion years. During incursion years, rainfall, vegetation, surface runoff, streamflow, and nighttime temperatures are significant predictors (R^2=0.23). All first-incidents of VS occurred following peak annual streamflow, with 89% occurring after streams returned to baseflow conditions. During expansion years, rainfall, vegetation, soil moisture, and daytime temperatures are significant (R^2=0.73).

Conclusion: These results ultimately inform the team's on-going development of a VSV early warning system, while providing management-relevant insights for land managers, livestock owners and veterinarians. Two years into a five-year project, practical recommendations have also emerged for building an effective and productive trans-disciplinary Grand Challenge team.

Key words: Ig data, cattle, early-warning, equine, streamflow, trans-disciplinary, vector-borne

The detection of *Sarcocystis* spp. in fetus of sika deer (*Cervus nippon yesoensis*) in Japan

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ABSTRACT

Objective: Recently, undercooked venison contaminated with *Sarcocystis* spp. caused food poisoning in Japan. Previously, we have reported that positive rates of *Sarcocystis* in sika deer in Japan is 94.4 % (389/412), and even fawn under 12 months shows similar positive rate. High positive rate may suggest that the infection occurred during pregnancy or after birth through breast feeding from mother.

Materials and methods: The uterus, fetus, breast tissue and milk of sika deer (*Cervus nippon yesoensis*) were sampled. To detect *Sarcocystis* spp. in each sample, qualitative polymerase chain reaction (PCR) amplification and DNA sequencing targeting 18S rRNA gene of genus *Sarcocystis* were performed.

Results: The positive rates of *Sarcocystis* spp. were 33.3 % (5/15) in fetal skeletal muscle, 15.4 % (2/15) in fetal blood samples, 26.7 % (4/15) in placenta, 50.0 % (2/4) in fetal feces, 14.3 % (1/7) in fetal kidneys, 33.3 % (4/12) in amniotic fluid samples, 18.2 % (2/11) in allantoic fluid samples and 30.8 % (4/13) in mother's blood samples but breast tissue and milk samples were negative. DNA sequencing analysis detected *S. truncata* or *S. silva* from all kinds of sample except kidney and allantoic fluid. *S. tarandi* or *S. elongata* from all kinds of sample, *S. fayeri* from fetal blood, *S. venaroria* from allantoic fluid and *S. pilosa* from mother's blood, respectively.

Conclusions: From these results, we suspect that *Sarcocystis* spp. in *Cervus nippon yesoensis* may transplacentally infect the fetus. On the other hand, it may not migrate to breast and milk. This study showed the possibility of transplacental infection of *Sarcocystis* spp. in sika deer in Japan. However, since positive rate of *Sarcocystis* infection in fetus is still low compared to that of *Sarcocystis* in fawn, there may be another infection route to fawn except transmission via breast milk.

Key words: *Sarcocystis* spp., sika deer, vertical transmission, 18S r RNA, genetic analysis

Transmission of waterborne fish and plant pathogens and engineered control methods in aquaponics: a systematic mixed-studies review

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ABSTRACT

Objectives: Aquaponics has the potential to be a sustainable means of food production, as it uses much less land and water than traditional agriculture. But even though pathogens can jeopardize the health of these systems, a systematic review of literature regarding the spread of such pathogens and their management using engineered methods does not yet exist. Therefore, the objective of this article is to provide such a review to provide a basis for future studies.

Materials and methods: In order to be included, articles must be primary research articles about hydroponics, aquaculture, or aquaponics systems. They must discuss transmission of waterborne fish or plant pathogens and/or engineered control methods. The literature search started by searching combinations of keywords, including "aquaponics", "aquaculture", and "pathogen." Abstracts were assessed for relevance, and articles with relevant abstracts were read. The references of relevant articles were searched for additional articles, and the process repeated iteratively until no additional articles were identified. Pertinent databases and journals, such as *Aquaculture* and *Acta Horticulturae,* were also hand-searched. When no additional relevant sources were identified, the collection of articles were examined and analyzed. A bias assessment was conducted using a Mixed Methods Appraisal Tool. All information was compiled.

Results: Preliminary results show that heat treatment, UV sterilization, electrooxidation, membrane filtration, slow sand filtration, corona plasma, and ultrasound are used as water disinfection methods in these systems. The most common treatments are UV sterilization and slow sand filtration, with ultrasound and corona plasma systems being the least common. None of these methods appear to have negative impacts of fish or plant health.

Discussion: The preliminary conclusion is that engineered pathogen control methods are effective and applicable outside of the lab. Cost-efficacy studies are needed to determine the best methods for each system.

Keywords: Aquaponics, systematic review, disease control

Genetic diversity of *Leishmania infantum* suggest a common transmission cycle in humans, dogs and wildlife in Southeast Spain

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ABSTRACT

Objectives: *Leishmania infantum* is widespread in wildlife in Mediterranean countries, however their role in the domestic transmission cycle involving dogs and humans is unknown. The aims were to characterize *L infantum* strains from wildlife, dogs and humans by analyzing genetic diversity in kinetoplast DNA (kDNA) and ribosomal Internal Transcribed Spacer 2 (ITS2) DNA.

Materials and methods: Target genes from 108 *L.infantum* infected domestic and wild hosts were PCR amplified and sequenced and genetic variability was investigated by determining Single Nucleotide Polymorphisms (SNPs) and Restriction Fragment Length Polymorphism (RFLP) analysis, with further phylogenetic analysis performed in variable kDNA sequences.

Results: Differently from ITS-2, 11 sequences were identified for kDNA target, including those unique to humans (n=5), dogs (n=3), humans and dogs (n=1), humans, dogs and wildlife (n=1) and wildlife and dogs (n=1), respectively. The phylogenetic tree revealed three main groups, clustering five *L.infantum* human strains in two paraphyletic clades, excluding two other humans strains retrieved also in wild and domestic animals. RFLP analysis closely matched these clusters.

Conclusion: Genetic variability in *L.infantum* kDNA from synanthropic hosts is large. Identical *L.infantum* kDNA-sequences among humans and wildlife may suggest for the latter host a likely role as reservoir in the transmission cycle of this parasite.

Key words: *Leishmania*, molecular epidemiology, wildlife, dogs, humans

Identification of zoonotic *Giardia intestinalis* in Korean native calves with normal feces

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ABSTRACT

Objective: This study was to determine the prevalence and conduct molecular characterization of *G. intestinalis* in pre-weaned Korean native calves among selected farms.

Methods: In 2017, a total of 90 fecal samples were collected from pre-weaned Korean native calves (1-60 days) raised in seven different regions (Gimje, Namwon, Samrye, Youngju, Sangju, Mungyung, and Asan) in the central region of the ROK. The type of feces was recorded and classified as normal, pasty, watery, or hemorrhagic according to its physical characteristics. Genomic DNA was extracted from 200 mg of washed fecal samples using the QIAamp DNA Stool Mini Kit. To amplify the *b-giardin* gene, nested PCR was conducted.

Results: Of the 90 fecal samples, 9 (10%, 9/90) were positive for *G. intestinalis* by PCR using the *b-giardin* gene. Phylogenetic analysis identified assemblages A and E of *G. intestinalis* in the farms examined. Interestingly, in one farm, both assemblages A and E were detected simultaneously. Assemblage A was detected in calves with normal feces, while assemblage E was frequently identified in calves with diarrhea. This is the first report of the identification of assemblage A in pre-weaned Korean native calves with normal feces. These results suggest that *G. intestinalis* infection is closely associated with calf age and management systems including overcrowding, age-mixed grouping, and hygiene.

Conclusion: Thus, giardiasis in calves is an important disease because of its zoonotic significance and must be detected in young animals. Further studies are necessary to elucidate the transmission route of the zoonotic potential of *G. intestinals*.

Investigating kid mortality on Ontario dairy goat farms

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ABSTRACT

Objectives: 1) To determine average herd-level mortality in Ontario dairy goat kids. 2) To identify important causes of death of kids by describing: a) The distribution of mortality within each age cohort. b) The gross causes of death as identified on post-mortem and the distribution within the cohort. c) The etiologic agent(s) associated with the identified disease on a sub-set of gross pathology samples. 3) Determine herd-level risk factors that are associated with higher kid mortality rates

Materials and Methods: Mortality in kids less than 4 months has been estimated to be approximately 20% in Ontario. There is little published literature with respect to causes of dairy goat kid deaths. Our study is attempting to investigate kid mortality on Ontario dairy goat farms. Phase I, is characterized by a comprehensive questionnaire and on-farm assessment. The questionnaire was designed to capture various management aspects on farm to elucidate major risk factors for preweaning mortality. This questionnaire has been offered to a random sample of all licensed Ontario dairy goat producers with a goal of recruiting 75-100 responses stratified by herd size. An on-farm assessment is also being conducted that evaluates parameters such as stocking densities, ventilation and housing. In the second phase of the study, 30 farms from the phase I respondents are recruited and followed for a 12-month period. These producers will collect the carcasses from all kids that die on-farm under the age of 4 months. The collected carcasses will undergo post-mortem analysis at the University of Guelph. From the data acquired from both the questionnaire and on farm assessments, we intend to conduct a multivariate analysis to identify herd-level risk factors that are associated with higher kid mortality rates.

Results: TBD

Conclusions: By conducting this study, we are raising awareness about kid mortality with producers and through training for participation, leaving a footprint on each farm regarding perinatal record-keeping, quantification of kid mortality, and developing protocols for diagnosing the causes of mortalities. While the project has primarily been conducted in Ontario to date, we feel the results are able to be extrapolated to dairy goat industries globally.

Key Words: Mortality, goat, kid, dairy, Ontario

Inter-observer agreement in categorization of racehorse necropsy reports

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ABSTRACT

Since 1990, racehorses that die at sanctioned racetracks in California must be necropsied to determine the cause of death. Approximately 200-250 necropsies are performed at four different laboratory locations by approximately 10 pathologists during any year. As a consequence, the terminology and level of detail used in free-text necropsy reports are highly variable. Variability makes comparison of case findings over time or by different pathologists challenging. This project assessed agreement among observers who reviewed and coded racehorse necropsy reports. 434 reports from January 1995 to December 1996 were reviewed and classified by four observers with expertise in racehorse anatomy, pathology, and injury assessment. Coding guidelines were developed by the observers and updated as needed. Each necropsy record was classified by two observers, with descriptors for circumstances, injury site (e.g. limb), syndrome (e.g. fracture, joint luxation, etc.), and anatomic structure (e.g. carpus). Additional descriptors were included for "fetlock failure" injuries, the most common group of fatal injuries in California racehorses. Inter-observer agreement was assessed using Cohen's kappa statistic. Necropsies were performed by 15 pathologists, each performing 1 to 83 necropsies. Agreement between observers on all aspects of a necropsy report ranged from 73.4% to 82.0%, with better agreement on limb affected than on descriptors with minimal variability such as occurrence of first phalangeal fracture. . Recording standardized variables from free-text fields remains subjective, even for knowledgeable observers using coding guidelines. Classifying racehorse necropsy reports using defined guidelines and a series of categorical variables may provide standardized data.

Key words: Racehorse injury, inter-observer variation, necropsy

Molecular markers in *Amblyomma sculptum* acaricide resistance

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ABSTRACT

Objectives: The aim of this study was to identify, in samples of *Amblyomma sculptum*, genes responsible for resistance to acaricide based on pyrethroids and organophosphates.

Materials and methods: Ticks were collected in the southern region of Minas Gerais/Brazil. Specimens were transferred to cryotubes and frozen to -80 °C. 24 samples were macerated with the aid of Cryocooler® to extract the total RNA (SV kit Total RNA Isolation System:Promega®). The RNA integrity was assessed by 2% agarose gel electrophoresis and stained with Gel Red™. Concentrations and purity were determined by spectrophotometry (NaNovix®). Complementary DNA synthesis was performed by the GoScript™ Kit Reverse Transcription System (Promega®). The PCR reaction for each primer consisted of 1X buffer, 2mM MgCl2, 0.4mM of each dNTP, 40ng cDNA, 0.2μM of each primer, 2.5U Taq polymerase. The PCR products were electrophoresed on 1.8% agarose gel, stained with Gel Red™ and the bands visualized and photographed under ultraviolet light.

Results: Pyrethroids and organophosphates are acaricide widely used in many parts of the world, for over 25 years. Resistance to both is quite often considering the control of insects, and Rhipicephalus (Boophilus) microplus tick. However, the knowledge of resistance in the genus Amblyomma (Acari: Ixodidae) is not widely studied. Due to the fact that they are trioxene ticks and they naturally require a higher concentration of the acaricidal products when compared to R. (B) microplus, the presence of resistance is not so easily perceived. The primers produced amplicons of the following sizes: primer 1.344bp; primer 2,362bp; primer 3,318pb and primer 4,479bp. In the electrophoresis it was possible to observe some bands. Organophosphates, 29 samples were positive and for pyrethroids, 32 samples positives.

Conclusion: Results suggest that genes related to resistance to pyrethroids and organophosphates were identified in *A. sculptum* samples collected in horses from Minas Gerais, Brazil.

Key words: PCR, *Amblyomma cajennense*, pyrethroid, organophosphorus, Equidae

Productivity and economic benefits of improving farm management and biosecurity on smallholder broiler farms in Indonesia

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ABSTRACT

Objective: A study was undertaken over a 2-year period to assess the productivity and economic effects of improving biosecurity and management in smallholder broiler farming systems.

Materials and methods: Nine project farms and four control farms were monitored before and after recommended interventions were agreed to, and implemented on project farms. The interventions included training in vaccination and water management, brooding and grower management, disease management, and structural and operational biosecurity.

Results: The results indicate that by improving farmer capacity, farm management and biosecurity, smallholder broiler farmers can improve their productivity and, depending on the type of improvement and the type of production contract receive financial benefits. The Performance Index (PI) on project farms increased from 301 to 310 (a 3% increase) while the PI on control farms during the same period declined by 2.6%. This indicates that the PI on project farms was 5.6% higher than it would have been without the biosecurity and management improvements. This improved efficiency translated into higher enterprise returns. Project farmers received an additional USD45/1,000 birds, while in the same period control farms experienced reduced income of USD33/1,000 birds. The total economic benefit, therefore, of implementing the interventions was US$78/1,000 birds. This benefit was attained with farmer investments of only USD2/1,000 birds.

Conclusion: The type of contract will determine the proportion of benefits that accrue to the farmer and the proportion that is appropriated by the integrator company. Smallholder broiler farm productivity can be improved by integrator companies working in partnership with their farmers to improve biosecurity, farm management and vaccination programs. The results of these improving partnerships will be the supply of safe food products at a price that encourages investments in biosecurity and farmer capacity.

Key words: Broiler, biosecurity, cost benefit

Session B: Epidemiologic principles and methods

Modelling the spread of Japanese Encephalitis virus in swine farms in Cambodia: Exploring for control strategies and cost-effectiveness

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ABSTRACT

Objective: Despite human vaccination, Japanese Encephalitis (JE) remains the most important cause of human encephalitis in Southeast Asia. JE virus is a *Flavivirus* transmitted from pigs to human by mosquito bites. Direct transmission between pigs can occur via direct contact. Causing abortions, JE may negatively affect swine production. Beside human vaccination, several control measures may reduce JE incidence in pigs, thus the risk of human disease: (i) vaccination of sows, that may not be sustainable alone due to a rapid turnover in pigs and a high cost; (ii) herd management that may help raising a high proportion of immune pigs thus, reducing viral circulation, and (iii) vector control. In a previous study, we proposed a deterministic compartmental model of JE transmission in pigs taking into account direct and indirect transmission. Starting from this model, we developed a new one incorporating pig batch management. It is a hybrid model assuming continuous-time for virus spreading and discrete-time for pig dynamics.

Materials and methods: We assessed the effect of combinations of control of JE incidence and abortions in pigs (JE-IAP), as well as on the risk of transmission to farmers and workers of slaughterhouses (FWS). A sensitivity analysis was performed to determine which parameters mostly influence model outputs. We assessed the relative cost-efficacy of control measures.

Results: Results showed that herd management alone had a low impact on JE incidence in pigs. Although vaccination alone led to a disappearance of abortions (as expected), its effect on JE incidence in pigs and on the transmission risk to human (FWS) was low. However, a high level of vector control (around 80% of reduction in mosquito population) led to a 100% annual reduction in JE-IAP. Paradoxically, a reduction of 20-70% of the population of mosquitoes without implementation of vaccination increased by 15 % the incidence of abortions.

Key words: Japanese Encephalitis (JE), modelling, control, swine management, Cambodia

Differentiated development of contact network - is the spread potential of the future deviated among pig and cattle production sectors in Finland

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ABSTRACT

The animal transport network determine partially the dynamics and potential of contagious animal disease spread. The animal transport network in Finland will be much more concentrated in the future than earlier, due to a reduction in the number of farms and an increase in farm size. Logistic development is dependent how increased farm size and the need to transport more animals from the farm is translated in the frequency of transports and transported batch size.

Number of cattle farms has reduced by 20 % and number of pig farms over 40%. The production has not decreased in the same volume and the total number of transported animals has even increased by 5.5 % in pig sector. As a result the number of contacts has reacted for the changed production structure.

The development in cattle and pig sector is going into different directions. In the cattle sector the number of transports has increased slightly and the development has indicated that in the future the spread potential will be increasing. On the contrary, in pig sector the development has been different. While the number of pig farms has been decreased even more rapidly than in cattle sector, the increase in batch size has eliminated the pressure against more frequent contacts and thus indicated that the spread potential in pig sector is lower in the future. Variation in the number of trade partners has remain stable or reduced in both sector, indicating that the partnership network have simultaneously come more stable. This development may help the usefulness of contact information in epidemiological applications such as risk based surveillance planning. The reasons for differentiated development will be discussed.

Cross-contamination and recontamination during a household barbecue: estimation of the consumer exposure to methicillin-resistant Staphylococcus aureus

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ABSTRACT

Objective: In order to evaluate the importance of the good hygiene practices during a household barbecue, a quantitative analysis was carried out to estimate the likelihood and extent of cross-contamination and recontamination of methicillin-resistant Staphylococcus aureus (MRSA) from contaminated raw chicken breasts via hands and kitchen utensils in a serving.

Materials and methods: A probabilistic mathematical model describing the cross-contamination and recontamination process during a household barbecue was developed by applying Monte Carlo simulations. A modular design was used, taking into account the chronological order of the routines during the barbecue event. Available data on the prevalence and burden of MRSA in chicken meat at retail in Germany were used as starting point and were incorporated in the model as probability distributions. Besides, the probabilities and extent of bacterial transfer between food items and kitchen utensils and the routines performed during food preparation specified by their probabilities of occurrence were incorporated as the main input parameters.

Results: The model presented here is capable of predicting: (i) whether or not transfer of MRSA takes place, (ii) the amount of MRSA transferred, (iii) probability of consumer exposure and level of exposure due to cross-contamination and recontamination events, from eating one portion of bread and grilled chicken, possibly contaminated by MRSA originating from raw chicken breasts, both served in the same meal that is prepared during a household barbecue.

Conclusion: The present study contributes to the quantification of consumer exposure to MRSA through food consumption once contaminated food has entered the household kitchen. Even when the MRSA prevalence and bacterial load in retail chicken meat in Germany is low, resistant bacteria can reach the consumer due to cross-contamination and recontamination processes. This study therefore highlights the importance of keeping good hygiene practices during the household food manipulation for reducing the spread of MRSA.

Key words: Cross-contamination, kitchen hygiene, model, MRSA, antimicrobial resistance

A spatial temporal epidemiological model of sheep scab in Great Britain

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ABSTRACT

Objectives: To produce a spatial, temporal, epidemiological model of sheep scab transmission between farms. To explore the effectiveness of various intervention strategies at different geographical scales within Great Britain.

Materials and methods: Data from the literature is used to parameterise an extension of the traditional SIR model adapted for sheep scab (Psoroptic mange) which is built using the Spatial Temporal Epidemiological Modeler (STEM). The effectiveness of the timing of interventions, including the use of organophosphate dips and injection of macrocyclic lactones, is simulated at different spatial scales, from within one farm, to across the whole of Great Britain.

Results: Initial results show that the model can simulate sheep scab transmission and the impact of basic interventions as expected based on data from the literature. At a two-farm scale it seems that coordinating treatment is important in local eradication. More results are expected to be produced between the submission of this abstract and the conference.

Conclusion: In order to combat sheep scab, decision-makers should consider using results from this model, which will be valuable in predicting disease patterns and the impact of interventions.

Key words: Sheep scab, control measures, spatial epidemiology, SIR model

Investigating the epidemiology of EI epidemic spread in the province of Khyber Pakhtunkhwa, Pakistan in 2015-16

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ABSTRACT

Objective: EI in non-vaccinated population causes disruption and economic losses. To identify the risk factors associated with the EI epidemics in equids in Pakistan, case control study was conducted during 2015–2016.

Materials and methods: 1:1 matched case control study was conducted during 2015–2016. Including a total of 197 laboratory confirmed cases and negative controls, matched on the basis of geography, time of sampling, specie and age. A piloted questionnaire was used to collect data regarding risk factors associated with the occurrence of EI in face to face interviews. Conditional logistic regression was performed to analyse the data.

Results: A total of 16 out of 23 variables were found associated as risk factors in Univariable conditional logistic regression analysis. Multivariable conditional logistic-regression analysis was also performed. Monthly removal of manure doubles the risk of EI (EI) compared to its daily removal. Due to lack of vaccination; the spread of disease was favoured by high equine density. Investigating the index-case it was recorded that infected cases were imported from Afghanistan. Most of these risk factors related to biosecurity and management were due to low awareness level regarding EI amongst the respondents.

Conclusion: These findings are in line with the results of many other studies identifying similar risk factors for EI infection in various countries. Adopting protective practices, vaccination and controlling the risk factors identified in the present study could reduce the spread and future outbreaks of EI in Pakistan.

Key words: Equine, Influenza, epidemic and epidemiology

Managing Big Data on a PC: Modeling body weight and age of over 13 million cats

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ABSTRACT

Objective: This study's objective was to determine how to manage and analyze a large dataset (over 50 million data points) on a personal computer (PC) to produce models for explanatory and predictive purposes. As the data consisted of historical information on cat weight, a secondary objective was to explore the relationship between signalment and weight of cats.

Materials and Methods: Signalment and weight data from electronic medical records were made available from a veterinary diagnostic company (IDEXX Laboratories, Inc). The data consisted of breed, sex, reproductive status, age, weight, and date of measurement from domestic felines from 3972 veterinary clinics in the United States of America and Canada between the years 1981 and 2016. Using open-source Python modules (statsmodels, pandas, numpy), data was cleaned, descriptive analysis was performed and linear regression models were created using ordinary least squares and stochastic gradient descent. There were 19,416,753 records to process, with 13,715,510 remaining after cleaning. Predictive accuracy was evaluated on a validation dataset.

Results: All signalment parameters had a statistically significant impact on the average body weight of a cat. When using the same variables, the ability to predict weight based on signalment was comparable for the two models, with both producing a root mean square error of 1.433 and a mean absolute error of 1.085.

Conclusion: This study shows that by using a PC, big data can be analyzed to provide vital new information in companion animal health. The results of analysis on a PC can be used as a proof of concept prior to expending more resources setting up a server. It can also directly provide evidence: in this case, for discussion with owners concerning weight management.

Key Words: Modeling, big data, linear regression, cat

Are movements epidemiologically important in the transmission of bovine tuberculosis in Castilla y Leon, Spain?

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ABSTRACT

Objectives: Here, we characterized the cattle movement network of Castilla y Leon, a high bTB-prevalence (1.9% at the farm-level in 2015) region in Spain, over six years (2010-2015) and analyzed the distribution of bTB to ultimately assess the likelihood of spatial and movement-mediated transmission.

Material and methods: We analyzed movements from or into units within the region, and bTB data from 27,633 units located in the region, of which 87% were involved in ~1.4 million movements of ~8.8 million animals. We constructed cumulative and annual contact networks, and calculated farm and network-level metrics. We performed a permutation-based procedure to determine whether the observed distribution of the bTB-positive farms in the movement network and in geographic space are likely to be a result of the contact pattern.

Results: Network-level connectivity was low, although a few highly connected units were identified. Up to 15% of the herds became bTB-positive at some point during the study, with the highest percentage found in bullfighting and beef herds. Although bTB-positive herds had a significantly higher degree and moved more cattle than negative herds, results suggested that positive farms were not significantly clustered in the movement network. Location was a likely risk factor as bTB-positive farms tended to be located within 5km from each other.

Conclusion: Results suggested that movements may be a source of bTB in cattle in Spain, although contact network did not influence bTB spread. The description of the movement network in Castilla y Leon may be valuable for bTB surveillance in Spain. Moreover, results may be used to assess the movement-associated risk for multiple diseases.

Key words: Bovine tuberculosis, cattle movement, *Mycobacterium bovis*, social networks, spatial analysis

Integrated periodic and reactive vaccination strategies can be more effective in the prevention of Rift Valley fever epidemics than either of the two approaches – a modelling study

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ABSTRACT

Objective: Livestock vaccination is the most effective Rift Valley fever (RVF) control measure but strategies for its delivery have not been determined. Reactive vaccination strategies are an integral part of the emergency responses that governments deploy to manage RVF epidemics in eastern Africa. Their implementation is, however, limited by logistical requirements for vaccinating a critical number of livestock over a short period of time, coupled with poor accessibility of affected areas due to flooding during RVF outbreaks. We set out to to predict the impacts of reactive, biannually or annually vaccination strategies.

Material and methods: Using R software, we modelled the transmission of RVF virus (RVFV) between two livestock hosts (cattle and sheep) and mosquito species (*Aedes* and *Culex* spp) based on empirical data collected in a RVF hotspot in Kenya and used the model to predict the impacts of the alternative delivery strategies.

Result: The model replicates the 2006/2007 RVF epidemic and other seasonal transmission events empirically reported in the area. Reactive vaccination strategies considerably reduce the possibility of an epidemic as a vaccination coverage of 25% achieves a reduction in RVFV incidence of at least 22% in each host species. Vaccinating 25%, 50% and 75% of hosts at the onset of the epidemic compared to 24 weeks earlier results in 3%, 5% and 9% reduction in the cumulative incidence in cattle and 5%, 7% and 7% in sheep, respectively. If low biannual/annual coverage, e.g. of 5% is supplemented with a reactive vaccine coverage of 25%, then 50% and 35% of cases would be averted in a routine biannual or annual strategy respectively implying a massive reduction in the threshold required for a reactive vaccination to prevent an epidemic.

Conclusion: Our analyses suggest that periodic and reactive vaccination can be integrated to effectively prevent and control the RVF epidemics.

Key words: Rift Valley fever, vaccination, strategies, reactive, periodic

Estimating the introduction time window of highly pathogenic avian influenza virus into poultry flocks

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ABSTRACT

Objectives: For highly-pathogenic avian influenza (HPAI), daily mortality records in outbreak flocks offer the opportunity to estimate a farm-specific time window for virus introduction. This time window can be used to increase the efficiency and efficacy of disease control measures such as contact tracing. The aims of this research are therefore to 1) develop an accurate method for estimating the virus introduction time window and 2) evaluate this method by applying it to 11 outbreaks of H5N8 on Dutch poultry farms during the years 2014 and 2016.

Materials and methods: We use a stochastic model framework with susceptible, exposed, infectious and removed/ recovered disease stages (SEIR) to generate distributions for the time interval of virus introduction to detection. The SEIR model is parameterized using data from the literature, except for the within-flock transmission rate (β), which is estimated from disease-induced mortality data using a maximum-likelihood approach.

Results: For the H5N8 viruses affecting Dutch poultry flocks in 2014 and 2016, we find that the time interval from estimated introduction to outbreak detection depends strongly on the species (chicken vs ducks) and also on the strain (2014 vs. 2016). Due to a lower transmission rate, this time interval is longer for duck farms than for chicken farms. Within a given species, strain-specific differences in the transmission rate and lengths of the latent period result in a longer estimated time interval from introduction to detection in 2014 than in 2016.

Conclusion: Estimation of the virus introduction window from daily mortality records in HPAI outbreak flocks can be achieved using the method developed, even when data is scarce.

Key words: Virus introduction window, highly-pathogenic avian influenza, poultry farms, disease control, contact tracing

Surveillance of Porcine Reproductive and Respiratory Syndrome (PRRS) Virus Strains – New Tools for Practicing Veterinarians in Support to Control Initiatives

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ABSTRACT

PRRS sequencing (ORF5) is widely used in Quebec, Canada. Through several signed agreements with veterinarians, a structure was established allowing near real-time transfer of sequences to our research team from 3 different laboratories in Quebec. As a result, our database has grown to nearly 6000 sequences (average annual increase of 450 sequences). This database has allowed the development of several useful tools for surveillance.

Among them is an on-line application available for practicing veterinarians, who, through a "secured" access, may obtain comparisons with all sequences in our database along with nominative data for sequences that he/she had submitted (farm name, address). For all other sequences, only name of submitting veterinarian appears in the comparison, so the latter can be contacted for information sharing as part of an outbreak investigation. Veterinarians involved in regional control programs also have access to an interactive mapping system integrating production site and sequence information: genetic similarities (%) between sequences from other sites participating in the control project can be viewed geographically.

Another application was developed to identify introduction of new PRRS strain(s) in breeding herds based on current and historical sequencing data. Threshold for declaring new introduction was a genetic similarity <92% with historical data for that herd. When no previous sequence data were available, the attending veterinarian was contacted to confirm that the site was initially negative.

Over a 3-year period, 165 new viral introductions were identified, 19 of them through regular monitoring even though these herds had not shown any clinical signs, and 6 others were related to a vaccine-type strain (farms previously negative and not using any vaccine).

With these tools, incidence of new viral introduction in herds can be estimated provincially and regionally and PRRS outbreak can be investigated in a timelier fashion in a clinical context or for research needs.

Key words: PRRS, surveillance, sequence

Mathematical modelling and economic analysis of controls strategies for brucellosis and bovine tuberculosis

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ABSTRACT

Objective: The goal of this research is to evaluate different strategies to control brucellosis and tuberculosis in Brazilian bovine herds.

Materials and methods: Using two deterministic and compartmental models, one for each disease, the authors estimate, from an economical point of view: optimal vaccination coverage against brucellosis; optimal alternation points between vaccination strategies and test-and-slaughter eradication schemes and minimal efficiency of risk-based surveillance in eradication scenarios. The Brazilian States are the basis of the economic analysis and, using as gains the increase in meat and milk productivity and as expenses the vaccines, diagnostic tests, animal replacement and the cost of official veterinary service, two economic indicators are calculated to evaluate the strategies: net present value and benefit-cost ratio.

Results: Partial results point to a scenario where vaccination coverages above 80% have minimal effect in the final prevalence over a period of 10 to 20 years. However, this minimal vaccination coverage must be confirmed by the economic analysis. Vaccination is a great tool to reduce elevated brucellosis prevalence, yet it becomes inefficient in low prevalence scenarios, with animal replacement being one of the main costs in eradication schemes, the optimal cut-point should be calculated to assist the decision making in the process of adopting test-and-slaughter strategies.

Key words: Theoretical Model, Cost Benefit Analysis, Brucella abortus, Mycobacterium bovis, Brazil

Chemical clarification of oral fluids does not affect PRRSV IgG ELISA

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ABSTRACT

Objective: Routine surveillance using individual animal samples (serum, nasal swabs) is labor intensive and expensive. In contrast, oral fluids (OF) are easily collected and welfare-friendly. However, OF often contains feed, feces, and other undesirable contaminants/particulates. Processing (filtration or ultracentrifugation) of OF is not practical in high-throughput laboratories, e.g., Iowa State University-VDL performs around 200,000 OF tests annually. The objective of this study was to determine whether clarification of OF by the use of chitosan, a highly reactive flocculant, would affect PRRSV IgG ELISA detection

Materials and methods: OF of known status were generated by vaccinating pigs (n = 17) with a PRRSV MLV vaccine. Individual pig samples were collected from day post vaccination -7 to 42 and subdivided into 4 aliquots. Each aliquot was treated with one chitosan formulation (A, B, C) with the 4th aliquot serving as an untreated control (NC). All samples were tested with a commercial PRRSV OF IgG ELISA immediately after treatment (day post-treatment DPT 0), then held at 4°C and, re-tested on DPTs 2, 4, 6, and 14.

Results: statistical analyses (Kruskal-Wallis and Cochran's Q tests, $p > 0.05$) detected neither an immediate effect (DPT 0) nor residual effects (DPT 2, 4, 6, 14) of clarification treatments on the PRRSV oral fluid IgG ELISA quantitative (S/P) or qualitative (positive-negative status) results.

Conclusion: clarification of OF using chitosan-based formulations did not affect PRRSV IgG ELISA results either immediately or over time. These results suggested that chitosan (or other chemicals) could clarify OF without affecting antibody detection. This approach could be adapted for use in the field or used in the laboratory prior to testing. Further, this process may improve other diagnostic specimens, e.g. feces.

Key words: Clarification, chitosan, oral fluids, PRRSV ELISA, swine

Identification of spatial clustering in Uruguayan farms from a reproductive disease survey

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ABSTRACT

Objective: In Uruguay, beef breeding farms are based on grass feeding and the presence and distribution of reproductive disease are almost unknown by farmers' managers. In 2015, a national survey of farms and cows to estimate seroprevalence of the most important bovine reproductive diseases: neosporosis, leptospirosis, infectious bovine rhinotracheitis (IBR), bovine viral diarrhea (BVD), and brucellosis was carried out. It is known that most of infection contagious diseases usually are not random distributed, so they clustering in space and time.

Materials and methods: Cluster analysis is a method that allows the identification of areas with a significant aggregation of events of interest; and it is useful to characterize patterns of disease occurrence and to identify zones with high risk of disease. The objective of this study was to detect spatial clusters of farms in function of sero-prevalence of the reproductive diseases. A two steps random survey study was performed using data from 590 farms and 6,445 animal's serum samples. Sera were studied for bovine reproductive diseases sero-prevalence agents mentioned, and farms were classified based on this lab results. Laboratory data were combined with GIS data using the locations of the farms and spatial scan statistics were used to identify significant clusters of farms for these diseases. The Poisson and Bernulli scan statistical model of the SATSCAN® software was used.

Results: High prevalence cluster for leptospirosis were detected in beef cows. In the other diseases studied, no spatial clusters of farms sero-prevalence were identifyed. Exclude bovine brucellosis, this situation is probably determined by the wide geographic distribution of the agents, and also for the particular way of disease transmission among farms.

Conclusion: In conclusion, it is necessary more epidemiological studies of the agents to identify potential risk factors useful for a control strategy.

Key words: Reproductive diseases, bovine, survey, Uruguay, spatial analysis

Evolutionary Characteristics of Equine Influenza Virus identified from 2011 to 2017 in the US by Bayesian phylodynamic analysis of the Hemagglutinin gene

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ABSTRACT

Objective: EIV is a major infectious pathogen causing respiratory signs of equids. The recent investigation of EIVs in the US revealed that contemporary EIVs H3N8 were identified from horses with respiratory infections, even with a vaccination history. The antigenic drift of the Hemagglutinin (HA) gene may contribute to low vaccine effectiveness. Our study aimed to investigate the evolution of EIVs circulating from 2011 to 2017 in the US by Bayesian phylodynamic analysis of the HA gene.

Materials and methods: The HA gene of 70 EIV isolated from 26 US states were sequenced and combined with 286 published HA gene sequences identified from 1963 to 2017 over the world. The HKY85+G was selected as the best candidate phylogenetic model and Uncorrelated Lognormal relaxed clock model were used to estimate the divergence time by RevBayes. The synonymous and nonsynonymous ratio (ds/dn) and Tajima's D were used to measure evolutionary selection pressure.

Result: Phylogenetic analysis showed that all 70 EIV isolates belonged to the Florida sub-lineage clade 1 and identified common ancestors of US and non-US origin EIV strains. The amino acid substitution of HA protein allows significant positive selection (p-value of Tajima's D= 0.04) especially in two codons (2nd and 6th, p-value of dN/dS < 0.05).

Conclusion: EIVs in the US (Florida sub-lineage clade 1) and Europe (Florida sub-lineage clade 2) have evolved separately and accumulated substitutions in the HA protein by the process of positive selection. The antigenic drift may contribute to current low vaccine effectiveness. Results of this study will help to better understand the phylogeographic patterns of EIV to prevent its spread and support the update of vaccine strains.

Key word: Equine Influenza Virus, phylodynamics, molecular epidemiology, Bayesian approach, RevBayes

Health informatics: a scoping review of the veterinary and animal health literature

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ABSTRACT

Objective: Health informatics is an emerging field in human medicine. The purpose of this scoping review was to better understand what constitutes health informatics in animal health and veterinary medicine. It looked at how the terms "big data", "informatics" and "bioinformatics" have been used in the literature, for what species and what type of research was conducted.

Materials and methods: A scoping review was conducted in accordance with best practices developed by Arksey and O'Malley. The search strategy was developed by a team of animal health and veterinary medical professionals, veterinary epidemiologists, a computer programmer and a library scientist. The search was conducted in Agricola, Web of Science, PubMed, ProQuest Theses and Dissertations and IEEE Xplorer. Two reviewers performed relevance screening on the title, abstract and keywords (full text when necessary), followed by data characterization on articles which met inclusion criteria. The search strategy yielded 8,304 articles. After relevance screening, 1,675 articles remained.

Results: Preliminary findings show that "bioinformatics" studies comprise the majority of the studies found, followed by "informatics". "Big data" is rarely used. Studies that contain the term "informatics" most commonly reference "geographic information systems". The amount of available health data is increasing from a variety of sources such as electronic medical records, social media and sensors (wearables and environmental sensors). Terms such as "big data", "informatics" and "bioinformatics" have been used to describe fields that produce, collect, analyze and apply such data. There has been little work done in the animal health and veterinary medical literature to characterize these terms.

Conclusion: This study will help to define what constitutes health informatics as applied to animal health and veterinary medicine to date. It may also provide insight into new opportunities to utilize data generated by emerging technologies in creative ways.

A daily Monte-Carlo dairy simulation model with multi-trait genetics that quantifies the reduction in herd mastitis incidence rate and ensuing herd performance achievable through genomic selection

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ABSTRACT

Objective: Mastitis is the most costly dairy disease manifested through reduced milk production and quality and the need for the treatment and replacement of animals. The introduction of mastitis resistance trait into the routine genetic selection indices across the globe has provided dairy farmers an opportunity to reduce mastitis incidence over time through affordable genomic selection strategies. To maximize the herd performance by the reduction of mastitis incidence, decision-makers require detailed dairy simulation models which can compare different profitable strategies.

Materials and methods: We developed a whole-herd dairy simulation model, in which the performance of individual animals was affected by the economic traits included in the Lifetime Net Merit Index 2018. Each animal in the herd had an underlying base probability to contract mastitis during lactation. On top of this base probability, the genetic and environmental components of mastitis resistance as well as somatic cell score traits of each animal, determined the probability to contract pathogen-specific clinical and subclinical mastitis during the course of lactation, were added. The phenotypic penalties in milk volume, fat, protein and SCC for each pathogen-specific mastitis was modelled based on previous studies conducted by our group. Likewise, lower conception as well as higher culling risk due to pathogen specific mastitis were modelled.

Results: We simulated various genomic replacement selection strategies with a special focus on mastitis resistance trait to illustrate how the mastitis incidence could be reduced over the course of 15 years in typical Holstein herds. Also, various herd performance statistics were collected on a daily basis and tabulated annually to study the technical and economic performance of herds, focusing on genomic selection strategies for reducing mastitis incidence.

Conclusion: The tool developed can be used by decision makers as a prototype to study the herd performance of genomic selection strategies aimed at reducing mastitis incidence in various dairy populations.

Key words: Mastitis resistance, genomic selection, agent-based modeling, herd management

The location of the index case is essential to mobilize sufficient resources for active surveillance in case of emergence of ASF in France

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ABSTRACT

Objectives: Being a notifiable disease, the emergence of African swine fever in disease-free countries has huge economic consequences mainly due to export ban. Moreover, with a case fatality rate close to 100%, ASF represents a major threat for the swine industry. Recent ASF outbreaks in eastern Europe revealed the need of prospective approaches to analyse the consequences of the emergence and spread of ASF at the country level. We therefore used a modelling framework to analyse the consequences of potential ASF emergence in France to evaluate the responsiveness in terms of detection and control measures.

Materials and methods: The national swine identification database, reporting the herd location and all movements of live pigs in France, was analysed to obtain statistics related to the contact structure and distance related probabilities of contact occurrence between the different actors of the swine production network. These specific data were further used to feed a simulation model developed in Denmark (Halasa et al., 2016) representing the spread of ASF within and between farms along with realistic control measures defined in the national emergency plan (movements restriction, establishment of protection and surveillance zones, depopulation).

Results: The analysis of herd locations showed a high heterogeneity in the density of swine production units in France and 10 herd types were identified. We analysed the epidemics characteristics depending on the density-zone of the index case. Although only slight variations were found in terms of detection-delay, the number of surveillance visits was dramatically increased in densely populated areas.

Conclusion: The required resources for active surveillance in case of emergence of ASF in France is strongly related to the location of the index case and should be taken into account at the state of preparedness of the different scenarios of outbreak occurrence at the country level.

Key words: African swine fever virus, Emergence, control measures

Different control options for Foot-and-Mouth Disease in a highly densely livestock populated area in Germany

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ABSTRACT

Objectives: The objectives of this study were to evaluate different control strategies for FMD with respect to their effect on the duration of the epidemic and the number of animals to be culled compared between areas with high versus medium livestock density.

Material and Methods: A stochastic simulation model (DADS), which was originally adapted and applied to Denmark, was modified to take the conditions of Lower Saxony into account, the most densely livestock-populated area within Germany. Ten different control scenarios were compared between two regions of Lower Saxony. In the East 0.6 farms/km^2 and around 70 cloven-hoofed animals/km^2 were present, while in the West 1.4 farms/km^2 and 470 animals/km^2 respectively.

Results: The results depended on the density of livestock animals. In areas with a lower livestock population, depopulation was always the best strategy. In areas with a high livestock density, emergency vaccination with subsequent culling resulted in a relatively smaller proportion of animals to be culled as compared to depopulation. An economic assessment showed a high dependence on expected trade restrictions.

Conclusion: Depopulation and emergency vaccination provide efficient tools to control FMD outbreaks in Lower Saxony, Germany. The selection of the control strategy depends on the livestock density and several other factors, including the societal acceptance of particular control options. Export values had the greatest influence on the economic assessment of the different control strategies.

Key words: FMD, control measures, vaccination, livestock density

Improving classical swine fever control strategy using mathematical modeling in Ecuador

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ABSTRACT

Objective: The objective of this study was analyze the impact of the immunization strategies against classical swine fever (CSF), generate better understanding of population dynamics and epidemiological effects by public policy implementation.

Materials and methods: Between 2014 - 2017, Ecuadorian government initiate the first public fund project to control CSF, swine producers through associations were also co-participants of the national initiative. Historic official data available at the national Veterinary Service (Agrocalidad) was analyzed by means of descriptive epidemiology, contact rate estimation and compartmental modelling for different coverage scenarios.

Results: Descriptive analysis showed meaningful interactions and epidemiological relations between productive systems, geographic, economic and social interactions among producers. Simulations were adjusted by historic data available at the national veterinary service, fitting the natural occurrence, allowing a better understanding of epidemics. Using mathematical modeling, scenarios were generated to assist the comprehension of the disease dynamics and the future overview. Contact (β) and death (γ) rates, were monthly estimated as 4.0706 and 2.7941, respectively. In order to control and eradicate CSF, simulations show the necessity of maintaining a high vaccine coverage to eradicate the disease, also the importance to improve the surveillance approach, and also pay special attention to chronic and congenital infections.

Conclusion: Risk base surveillance techniques specifically designed for backyard and industrial producers, could assist in the new phase of the project to support the eradication objective. Facing constant budget reduction for disease programs not only in endemic developing countries like Ecuador, and the need to support sanitary programs with solid scientific evidence, mathematical modelling offers concrete based data analysis at low cost, available to developing nations in the decision and policy making process.

Key words: Classical swine fever, mathematical modelling, national veterinary service, policy-making

Simulation of herd sensitivity and specificity values of a diagnostic test for bovine tuberculosis using a composite reference standard as the comparison standard

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ABSTRACT

Objective: To compare theoretical herd-level sensitivity (HSe) and specificity (HSp) values for a new PCR diagnostic test for bovine tuberculosis using composite reference standard (CRS) for simulated scenarios.
Method: We simulated test results for 1,000 cattle herds (each with 10,000 cows) for two component tests with perfect specificity: bacterial culture (moderate Se), and conventional PCR (high Se), and the new test (very high Se and Sp). Then created scenarios based on: number of animals tested, number of reactors, and herd and animal level prevalence. The HSe and HSp of the new test was estimated using CRS, based on the two component tests, and the "OR" rule.
Results: Number of sampled animals was highly influential on the estimates of Hsp, prevalence and area under the curve. HSe increased with larger sample sizes and reached 100% when animal level prevalence was ≥ 0.1. However, herd level prevalence did not influence any of the estimated parameters for the new test, while lower animal level prevalence (<0.1) resulted in small variability in all the four parameters estimated.
Conclusion: Our simulation suggests that sampling 50-100 animals per herd provides better herd level test accuracy estimates if none of the tests have perfect sensitivity but results in underestimation of prevalence when the animal level prevalence is low.
Key words: Composite reference standard, diagnostic accuracy, herd sensitivity, herd specificity, pseudo-gold standard

Environmental transmission and management of *Mycobacterium avium ssp. paratuberculosis*: an individual based modeling approach

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ABSTRACT

Objective: Understanding how animals become infected with *Mycobacterium avium subsp. paratuberculosis* (MAP), the causative agent of Johne's disease is essential in evaluating control strategies to reduce its prevalence on dairy farms. It is well documented that animals become infected with MAP from ingesting contaminated material in their environment, but there are very few models that describe the role of the environment in transmission. Individual based models (IBMs) allow for flexibility in describing the behavior and interactions of individual agents and can be used to simulate the complex dynamics of infectious disease transmission on a dairy farm. Our objective was to determine if Johne's disease could be eradicated by implementing management strategies focused on improving farm hygiene.

Materials and methods: Using parameters estimated from a hidden Markov model created from longitudinal data from a Vermont, USA dairy we built an IBM that simulates both basic dairy herd age and behavioral characteristics as well as MAP infection characteristics including explicit environmental transmission. With this simulated farm we evaluated the ability of management programs focused on farm hygiene to control and eliminate MAP transmission on the farm.

Results: We found that MAP eradication is possible with vigorous cleaning alone, but the level of hygiene necessary for eradication is likely impossible to achieve in a true herd.

Conclusion: This model more accurately describes transmission pathways than previous models because it considers the environment explicitly as a major source of infection and includes herd and infection dynamics at the individual level. Our model can be a useful tool for farmers to control MAP prevalence and can be used as a framework for future research. This work was funded by the National Institute of Food and Agriculture of the United States Department of Agriculture through NIFA Award No. 2014-67015-2240.

Key words: Johne's disease, Paratuberculosis, epidemiologic modeling, individual based modeling

Waste milk movements from dairy farms

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ABSTRACT

Objectives: A pilot survey to estimate how far and how often waste milk (any milk that is not picked up by the milk supply company) moves off dairy farms was conducted in Southland, New Zealand in March 2018 to assist with *Mycoplasma bovis* outbreak modelling and response.

Materials and methods: Farmers were purposively selected based on availability and willingness to participate and interviewed to gather information on their management of waste milk, including movements on or off their farm. Records for each movement of milk included date, distance (km), volume (L), type (hospital, vat or colostrum) and end use (species). Frequency distributions for both distance moved (10 km increments) and timing of movements (2 week increments since the planned start of calving) were produced.

Results: Data from 15 dairy farmers were gathered and summarized; 14 from the Southland region and 1 from Waikato region. Seven traded milk for use in calves (5 sellers, 2 buyers), 4 sold milk for use in other species (pigs, sheep), and 4 didn't trade milk. Almost all milk traded for feeding to calves was moved during August and September (84%), with the remainder spread fairly evenly from October to January. For the remainder of the year waste milk was reportedly dumped or traded for feeding to other species (e.g. pigs). The approximate distance over which milk for calves was traded ranged from 10-130 km, and was positively skewed, with a median of 27 km.

Conclusion: This survey found that the majority of dairy farmers in the Southland region of New Zealand trade waste milk, particularly during the first 2 months of calving. As this trade is difficult to trace, further research is warranted to provide more robust estimates for input into disease modelling for diseases that can be spread via milk.

Key words: Waste milk, tracing, disease modelling, *Mycoplasma bovis*

Contact structure of cattle farms in southern Chile

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ABSTRACT

Objective: In 2005, the National Program of Livestock Traceability (NPLT) was established in Chile, however, it has not been analyzed yet the importance of the cattle movements for the risk of pathogens transmission. The objective of this study is to characterize the contact structure between bovine herds from southern Chile as potential risk of between-herd pathogens transmission.

Materials and methods: Network analysis (NA) was performed over a subnetwork of 16.821 holdings from the Los Rios region and neighbor regions (Los Lagos and Araucania) and movements from farms of those regions to Los Rios farms were also considered. Movements were obtained from the databases of the NPLT, from January 2016 to December 2017 (n=121,842) and includes: animal movement identification, nodes attributes such as location, type of holding, herd size. NA was based over the complete time and network metrics were estimated such as: density, degree, betweenness, cluster coefficient among others.

Results: Seventy-four percent (12.448) of the nodes involving movements in the target region belongs neighbor regions meanwhile the 76% (93.469) of the movements to Los Rios region are coming from neighbor Regions. The network presented a very low density, 0.04% of the total possible contacts being present and only the 13% of the nodes connects reciprocally. The trademarkets were the nodes with higher out-degree, in-degree and betweennes centrality, contacts fit a power law distribution. The overall cluster coefficient (CC) is extremely low (CC=0.02) mostly to the desegregating effect produced by the trademarkets.

Conclusion: The influence of the trademarkets and holdings from other region must be considered in decision making policies and surveillance. Further results regarding nodes attributes such as, size, type, location and temporal effects should be assessed.

Key words: Network analysis, cattle movements, Chile, infectious diseases

Role of duck contact networks in shaping disease transmission during the 2016-2017 epidemic of H5N8 avian influenza

C. Guinat*, B. Durand, A. Bronner, J.L. Guérin, M.C. Paul

ABSTRACT

Objective: In winter 2016-2017, Highly Pathogenic Avian Influenza (HPAI) H5N8 virus spread across France, causing a severe and unprecedented epidemic. Duck movements between holdings have been recently cited as an important means for H5N8 transmission. This study aimed to combine social network analysis and epidemiological data to evaluate the role of duck movements on the occurrence of H5N8 outbreaks in France.

Materials and methods: A directed and weighted network was built, considering each premises as a node and each daily duck flock movement between two premises as an edge. If duck flock movements were a major contributor to H5N8 transmission in France, then we would expect that positive farms would be significantly more inter-linked in the network than expected by chance. Thus, we used a novel permutation-based approach, the network k-test, to assess the epidemiological relevance of movement networks to the distribution of positive farms observed during the winter 2016-2017. In addition, associations between network centrality measures and infection status of farms were explored using a generalized linear model.

Results: Results showed that infected farms were connected to a mean of approximately one other infected farms, which according to the k-test, is substantially greater than expected if HPAI-H5N8 was distributed randomly in the network (p< 0.001). Network parameters, such as the in-degree of farms, were found to be statistically associated with HPAI-H5N8 farm infection (p < 0.05).

Conclusion: These findings suggest that the pattern of H5N8 outbreaks within the observed duck contact network are likely to have resulted from transmission processes in the network. The findings also show that farms having at-risk movements from infected farms should be monitored in addition to those located in the restrictions zones.

Key words: Highly pathogenic avian influenza, social network analysis, epidemiological data, risk-based surveillance

Modelling risk factors associated with developing clinical cardiomyopathy syndrome in salmon farms

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ABSTRACT

Objective: Cardiomyopathy syndrome (CMS) is a significant cause of mortality in Norwegian farmed salmon. Estimated costs of CMS for the industry was approximately 78 mio € in 2015. Control is based on mitigation of risk factors, since no treatment or vaccine is available. The objective of this study is to identify risk factors leading to the development of CMS.

Materials and methods: Daily production data (e.g. sea temperature, fish weight, treatments) from individual cages in more than 120 salmon farms along the coast of Norway from fish put to sea in 2012-2014 was collected. The data included cause-specific mortalities, which was used to identify outbreaks of CMS, as well as tracking data to allow us to track fish cohorts (fish from a single cage) as they are moved between cages. A survivability model was made to study how long a cohort of salmon would go without observing mortality due to CMS. Parameters were chosen to maximise the probability of the observed occurrences.

Results: Each spring ponded cohort was found to have an overall probability of developing CMS at about 1 in 2200. Fish put to sea in the fall was found to be about twice as likely to develop CMS. Fish in the southern part of Norway have a higher risk of developing CMS than fish in the northern part of Norway, by an order of magnitude. Recent outbreaks in neighbouring cages at the same farm is also identified as a considerable risk factor, as the cages often develop CMS within one week of one another.

Conclusion: The model was able to identify important risk factors, which may be used by farmers for mitigation of CMS. Some are mentioned in the above paragraph, more will be presented at the conference.

Key words: Farmed salmon, CMS, cardiomyopathy syndrome, modelling

Molecular Epidemiology of the Two Internal Genes of Equine Influenza H3N8 Virus Isolated in Pakistan 2015-16

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ABSTRACT

Objective: An outbreak of equine influenza was detected in Khyber Pakhtunkhwa during the year 2015-16. To understand the molecular epidemiology of the virus isolated from the infected area antigenic characterization of the internal genes was performed.

Materials and methods: The isolated viruses were typed for the first time in Pakistan as H3N8 and grouped with the Clade 1 viruses of Florida sub-lineages based on Hemagglutinin (HA) and Neuraminidase (NA) gene sequence analysis. Here we described the genetic analysis of two internal genes (nucleoprotein and Matrix) of the Pakistani isolates.

Results: 19 EI influenza isolated viruses were sequenced. Comparison of the nucleotide sequences of the two internal gens of the isolates showed 99.7-100% similarity with an avian influenza virus (Avian/Pakistan/H7N3/2004) isolated in Pakistan. Two major substitutions i.e. F63L and K243R were recorded in Matrix gene of the isolates. Notably NP gene did not acquire any amino acid substitution on comparison with contemporary isolates. All isolates showed 99.5-99.9% homology with the reference sequences on alignment. Epidemiological investigation of the outbreak suggested that re-assortment of EIV H3N8 with avian influenza A H7N3 most probably, might be due to the mix farming system here.

Conclusion: In conclusion, Phylogenetic analysis of the internal genes reported here will help in early detection and control of EI.

Key words: EIV, internal genes, sequence, epidemic, epidemiology

Transmission is mainly indirect: modification of the SIR model for statistical analysis

M.C.M. De Jong*

ABSTRACT

Indirect transmission has consequences both for estimating the transmission parameters and for extrapolating these estimates to other situations. The consequences of indirect rather that direct transmission can be clearly observed in the following simple situations: (1) when a new source of infection is entering a clean environment with recipients being present and (2) when all infection sources are removed from the environment and after that non-infected recipients are added. In situation (1) the infectivity will build up and relative to the standard SIR model the transmission rate parameter will appear to increase. This will also occur during each change in number of sources of infection in a closed population: each time the number of source animals increases it will be seen that the transmission rate will increase only later relative to the standard SIR model. On the other hand when the number of source animals goes down also the decrease in transmission rate will occur later. In the extreme case all sources can have disappeared and still new cases will occur. Using statistical methods to accommodate for these results from these such simple experiments it will be shown how to analyse accounting for indirect transmission. Moreover, the consequences for estimation in more complex situations will be discussed using datasets on observations on farms.

Social network analysis of duck trade movements in France: Implications for avian influenza surveillance

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ABSTRACT

Objective: Social network analysis is increasingly used in veterinary epidemiology to better understand the structure of animal movements and its impact on disease spread. It also helps assessing the most efficient control strategies, which is especially useful for emerging diseases such as avian influenza. Here we explored the fattening duck flock movement networks throughout France from 2016 to 2017 with a view to identify spatial and temporal patterns, characterise the monthly network topology and identify trade communities.

Materials and methods: Data were obtained through the French Ministry of Agriculture, and analysed using descriptive and network approaches. A directed and weighted monthly network was built, considering each premises as a node and each daily duck flock movement between two premises as an edge.

Results: Over the study period, the duck flock movements included 1,916 active premises and 21,700 movements, involving 22,500,000 ducks. The distance covered by 50%, 75% and 95% of the duck flock movements was 40km, 72km and 125km, respectively. A seasonal pattern was observed, with increased trade movements occurring in summer and autumn. Southwest France represented the major sources and receivers in term of number of movements and ducks. The monthly network exhibited both scale-free and small-world properties. The largest trade communities were identified and associated with specific regions, providing a basis for defining zoning areas.

Conclusion: This study demonstrates how the duck trade network in France can be investigated to reveals hot spots in time and space for disease spread. This information can be used to parameterise epidemic models and also to directly inform the design of targeted disease control strategies.

Key words: Highly pathogenic avian influenza, social network analysis, hot-spots, risk-based surveillance

Assessment of the duck-trade network characteristics prior to recent highly pathogenic Avian Influenza (HPAI) outbreaks in France

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ABSTRACT

Objective: Animal movements between farms represent a major route of pathogen spread within the poultry production sector and peculiarly within the duck for "foie gras" production's one. This is particularly the case for avian influenza viruses, for which trade-related movements offer additional long-ranged spreading potential as compared with other transmission routes more dependent on geographical distance (via fomites, people, synanthropic wildlife and airborne route). This study aims at describing the "foie gras" duck movement network focusing on the one- year period before the emergence and spread of HPAI viruses in France in November 2015.

Materials and methods: Up to May 2016, poultry movements were not systematically recorded at national scale. We therefore collected movement data from some integrated "foie gras" duck production and transport operators from November 2014 to May 2016 to achieve a representative sight of the national trading network accounting for truck transit between the different production sites. Social network analysis was performed to identify the central actors in the production system and to assess the impact of truck transit on network topology.

Results: Based on the first results obtained from the analysis of data from one of the major operators of the integrated "foie gras" duck production sector, raising duck premises are the main outgoing nodes with 2215 outgoing movements on the whole period from 175 duck farm sites. The network appeared only slightly modified when accounting for truck transit, with rounds disserving on average 1.3 farms' sites. Temporal analysis at monthly scale revealed periods with relatively low number of movements, especially in December and August. Conversely, the network density was higher in October and November.

Conclusion: Comparing the network topologies before and after the set-up of emergency measures would allow describing the modification of the network topology at national scale due the set-up of emergency measures after detection of HPAI outbreak in France.

Key words: Animal movement network, poultry, duck, avian influenza (AI)

A spatial entry assessment model framework for incursion of exotic disease into the European Union (SPARE)

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ABSTRACT

Objectives: The threat of incursion of exotic pathogens into European Union Member States (EU MSs) is dynamic and, therefore, needs to be continually re-assessed. Shifts in factors affecting routes of entry such as trade and wild animal movement will affect the overall probability of pathogen incursion, areas which represent the greatest threat, primary mechanisms of arrival and which pathogen has the highest probability of entry.

Materials and methods: We propose a model that makes use of global datasets to predict the probability of entry of exotic pathogens to EU MSs. The model indicates which pathogens are most likely to enter the EU, by which route and into which areas within Europe. The model is demonstrated through four case study pathogens: African swine fever, Classical swine fever, Bluetongue and Rabies. It is designed to be easy to update with new data and the development of a web based visualisation tool allows users to interrogate the model results.

Results: The model results, highlight the differences in risk between routes, pathogens and EU MSs. The greatest risk was predominantly from within the EU. Scenario analyses suggested that the risk was heavily influenced by the pathogen prevalence in the country of origin.

Conclusion: As the model relies heavily on the quality of the input data and has a wide scope, it is inevitable that some degree of accuracy is lost. Thus, we believe that the model can be best used in conjunction with current qualitative early warning systems, helping to drive risk-based surveillance activities.

Key words: Spatial model, exotic disease, European Union, incursion, release assessment

Estimating vector risk through a joint epidemiological and spatiotemporal approach

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ABSTRACT

Vector-borne disease modeling is particularly important in situations in which there is little knowledge of the vector population. Using data from the Bluetongue outbreak in Great Britain 2007/2008, we developed a Bayesian epidemic forecasting approach for emergency response to vector-borne disease outbreaks. This method combines a SIR epidemic model (Susceptible, Infected, Removed) with a vector-risk-surface model, which is based on the concept of Gaussian Processes. As Bluetongue is only transmitted through biting midges, it is classified as a purely vector-borne diseases. Hence, in order to make inference about the presence and the risk coming from the unknown vector we took covariates into account, such as humidity, mean/max/min temperature, ndvi and landscape properties. By linking local disease incidence in affected areas of the country to remotely-sensed environmental data, we were able to predict the likelihood of the disease arriving in different parts of the country together with the vector population's propensity to spread the disease once it has arrived. Our model further estimated key disease dynamic parameters, such as transmission and infection-to-detection rates, as well as a vector risk surface across the country. This promising approach is especially designed for making inference when there is little knowledge of the vector population and extends existing methodology

Key words: Bluetongue, vector-borne disease, Gaussian Processes, risk prediction

Modelling the spread of resistance to anthelmintic drugs in sheep nematodes

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ABSTRACT

Objective: Helminth infections (e.g. *Haemonchus contortus* or *Telgadorsagia circumcincta*) are a widespread problem for livestock. Resistance to routinely used anthelmintic drugs such as the benzimidazoles, ivermectin and levamisole is a growing problem which presents a challenge for disease control. Currently, the mechanisms of resistance, how they impinge on the epidemiology of resistance and how they influence strategies to minimise resistance are poorly understood. Population genetics studies demonstrate that resistance may be dominant or recessive and controlled by multiple loci, but most models to date have assumed only a single locus and recessive resistance. Our goal is to examine the spread of resistance genes through a population, and to explore the effects of both the number of loci associated with resistance, and the potential effects of dominance.

Materials and methods: We developed a mathematical model with resistance as a quantitative trait that depends on a variable number of loci, where allele fitnesses are additive and may be recessive or dominant. We specified allele fitness and dominance in both the presence and absence of an anthelmintic drug based on biologically plausible values. All possible resistance trait genotypes were enumerated and a metapopulation model was used to track the number of worms of each genotype within each host under different treatment regimens.

Results: Comparison of simple model scenarios showed that dominant alleles are less likely to reach fixation than recessive alleles and will equilibrate at lower frequencies. Resistance spread more quickly as a single locus trait, and more slowly as a multilocus trait.

Conclusion: We have created a flexible modelling framework for considering the emergence and detection of resistance. This could be used to optimise management and treatment regimens with the aim of limiting the spread of anthelmintic resistance.

Key words: mathematical model, anthelmintic resistance, quantitative trait locus, multilocus trait, dominance

Simulating the spread and control of classical swine fever in the United States: analysis of emergency vaccination strategies

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ABSTRACT

Objectives: In the event of a classical swine fever (CSF) outbreak in the United States, vaccination may be considered as part of the emergency response. With an inventory of approximately 66 million animals, the scale of the United States commercial swine industry presents challenges to effective implementation of emergency CSF vaccination. Furthermore, the integrated population structure of the swine industry adds uncertainty about the potential behavior of a CSF outbreak and implications for control measures that might be applied to those systems. The objectives of this study were to use epidemic simulation models to 1) evaluate the impact of emergency vaccination on CSF spread in the United States, and 2) evaluate the impact that an integrated swine industry population structure has on disease spread and control measures.

Materials and methods: A national scale, stochastic simulation model was used to simulate CSF spread among swine premises. The premises were categorized into multiple integrated systems with varying rates for within-system and between-system contacts. The baseline scenario represented a stamping out strategy of CSF control using depopulation, active surveillance and movement controls. Alternative scenarios added emergency vaccination to baseline control measures with variations in vaccine dose availability, efficiency of vaccine administration in the field, and selective vaccination of different animal age groups.

Results: Results demonstrate circumstances in which emergency CSF vaccination in the United States can be effective in reducing the duration and severity of outbreaks. The impact of an integrated swine population structure on simulation results compared to a non-integrated swine population highlight the importance of considering population structure when evaluating CSF spread and control measures.

Conclusion: The impact of resource availability on the effectiveness of emergency CSF vaccination presents several implications for disease response preparedness. Epidemiologic models provide a way to explore potential strategies that can inform decision making.

Key words: Epidemiologic modeling, classical swine fever, emergency vaccination, disease response, population structure

Identifying host species driving transmission in a multi-host system: Developing and parameterising a model of zoonotic hybrid schistosome transmission in West Africa

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ABSTRACT

Objectives: Schistosomiasis, the disease caused by parasitic worms of the *Schistosoma* genus, represents a significant burden of human disease in many countries across sub-Saharan Africa. Schistosomiasis is also an important disease of livestock, and the zoonotic potential of animal schistosomes through viable, fertile hybridizations with human *Schistosoma* species has previously been demonstrated. However the burden of animal disease and the zoonotic risk of livestock schistosomes to humans via hybridizations has previously remained largely unquantified. Focusing on Northern Senegal, in areas where high prevalence of human schistosomiasis has persisted despite longstanding interventions targeting the human population, the objective is to develop and parameterise a mathematical model representing the flow of parasite transmission within and between livestock and human populations.

Materials and methods: Extensive epidemiological and parasitological surveys of definitive (livestock and human) and intermediate (freshwater mollusc) hosts have been carried out over three years in Northern Senegal. Multi-locus molecular analysis of parasitological specimens has been applied to identify the *Schistosoma* species and the presence of zoonotic hybrids. Using this data a Bayesian framework has been developed for model parameter estimation, including prevalence and dispersion of different parasites genotypes in the host populations.

Results: Our epidemiological studies demonstrated high prevalence of livestock schistosomiasis, estimated to be as high as 96% in some livestock populations. Molecular analysis has also confirmed presence of widespread hybridization between *Schistosoma* species of animals and humans, indicating ongoing zoonotic transmission of parasites.

Conclusion: The continuing risk of zoonotic transmission of schistosomiasis from livestock to humans via hybridizations demonstrates the need for an integrated One Health approach to control of schistosomiasis. It is anticipated that the fully parameterised multi-host, multi- species model, will provide novel insights regarding the role of the different host species in maintaining schistosomiasis transmission, including the potential impact of interventions targeting the animal population.

Key words: *Schistosoma* spp., zoonoses, multi-host, hybridization, modelling

Networks from space: how satellite imagery and GIS data can help predict disease spread

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ABSTRACT

Objectives: Our objective was to leverage fine-scale satellite imagery, GIS datasets, and population mobility models to simulate regional disease spread via road transportation. This model will be useful in predicting disease spread in humans upon the spillover of infectious agents from other animal hosts.

Materials and methods: We used fine-grained satellite data on urban areas and high-resolution population data to build a network upon which to model disease spread. Using the resulting geospatial network and the population attributes of its individual components, we estimated the commuting rates between road-connected urban areas and incorporated mobility patterns in the network. We demonstrated the above process for Rwanda and simulated the spread of 2009 pandemic Influenza A H1N1. We compared our forecast with the observed spread of the disease in 2009-10 and also determined the effects of vaccination campaigns on outbreak spread and impact.

Results: Incorporating the fine-scale network allowed for more accurate forecasting of disease spread in terms of outbreak length and the order in which areas were infected: our results were comparable to data collected during the actual outbreak of pandemic influenza in Rwanda. The probability of outbreak occurrence reduced when areas of infection origin were vaccinated, especially with increasing vaccination coverages and efficacies. At the same time, outbreak impact, defined by the number of individuals infected with influenza, was lower when larger urban areas were vaccinated.

Conclusion: Our modeling approach predicted influenza comparably to the actual outbreak and can be valuable for future planning and control purposes in real-time disease situations. We highlight the effectiveness of controlling outbreaks by targeting mitigation efforts at their points of origin, a process that can be made possible by increased surveillance and quicker outbreak response times. This framework can readily be applied to other infectious diseases as well, such as Ebola in West Africa.

Key words: Geospatial, outbreak spread, satellite, network

Using normalisation process theory to understand embedding new technologies in veterinary epidemiology

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ABSTRACT

Objective: Big data is creating lot of opportunities in veterinary epidemiology as we are able to gain insights into health and welfare of populations. Advancements in technology and computational power have meant that we are now able to generate, assimilate, store and process this 'big' data. Precision livestock technologies or precision livestock farming has been a growing area for the past decade and is very much linked to this revolution of big data generation and processing to improve livestock health and welfare. Whilst this has huge implication on how we gather and deliver information in veterinary epidemiology, we need to understand farmers' perception and understanding around technology, its use on farm and in farming. There are no studies in this domain that have investigated this.

Materials and methods: To explore this question, we designed and conducted a qualitative study using social science methodology. A total of 50 face to face interviews with farmers having different exposure to technology for decision making /data recording on farm. Data was explored in the sociological framework of normalization process theory. Thematic analysis of the interviews was conducted, and key themes were identified.

Results: Results suggest two key areas are important for embedding and adoption of technology on farms: first, utility of the technology and its ability to fit with existing structures and practices and the belief held by farmers that the use of the device may result in a loss of skill in future - that of the farmer knowing his animals.

Conclusion: The talk will discuss these findings and its implication for technology adoption, big data in veterinary epidemiology.

GEM: software for Generalised Epidemic Modelling

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ABSTRACT

Responding to epidemics is a Grand Challenge of the 21st century, as diseases evolve alongside changes in climate, environment, and human behaviour. Computer modelling of outbreaks has become a powerful tool for predicting how diseases spread, and for testing disease interventions in a safe, virtual environment. However, it is currently a highly specialist task, demanding advanced multidisciplinary skills: computer programming, mathematics, and statistics as well as epidemiology and biology - a skills gap bridged by few. OutbreakDS crosses this gap as the first comprehensive toolkit for real-time disease outbreak analysis, forecasting and decision support, providing a translational software package, allowing epidemiological researchers to focus on building epidemic models to analyse past or current outbreaks using cutting edge statistical inference and simulation methods.

OutbreakDS is implemented in Python, and provides a user-friendly interface for defining epidemic models for individual-level or aggregate populations. A model specification language enables transparent expression of epidemic models and associated data, together with tested algorithms for parameter estimation given outbreak data and simulation for forecasting. The software has methods translation at its heart. For the epidemiologist, the user interface focuses on model design, data assimilation and reproducibility. Building block algorithms and mathematics code to implement the model are dynamically assembled by the software to work on the requested model, and run across a wide range of hardware platforms. A developer interface will allow extension and improvement to meet new application demands, and serve to accelerate the rate at which novel analytic methods are adopted by application-domain researchers.

A Bayesian latent hierarchical model for estimating mean MIC and detecting MIC creep or decline

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ABSTRACT

Public health officials seek to properly interpret the volumes of data generated by surveillance programs such as the US National Antimicrobial Resistance Monitoring Scheme (NARMS), there is a critical need to develop new/alternative approaches to the statistical analysis of antimicrobial resistance (AMR) data that will detect development of resistance in a timely manner and enable the quick implementation of mitigation measures. AMR data are collected through surveillance programs and describe the concentration of an antibiotic at which an organism ceases to grow and proliferate i.e. a minimum inhibitory concentration (MIC). For statistical analysis, proportion of bacteria in the resistant category is used as an indicator of changes in resistance. The central hypothesis of our project is that statistical analysis based on MIC breakpoints, while simple to conduct, does not facilitate timely detection of changes in resistance. The major issue with statistical analysis based on proportion in the breakpoint categories, is that the average MIC can be increasing long before changes in the proportion above the threshold are statistically detectable i.e. MIC creep. The objective with the project was to develop the statistical methods that facilitate timely detection of MIC creep. We developed a statistical model to detect MIC creep and test the hypothesis that the number of years required to detect MIC creep using a Bayesian latent class hierarchical model is less than an analysis based on the MIC breakpoint-based categories analysis. For this project we demonstrated the method using NARMS human data for Salmonella. We found that MIC values for non-resistant category were statistically significant increasing from 1996 to 2014 for Typhimurium serotype tested on chloramphenicol antibiotic, while no significance was detected on the proportion of non-resistant category. Also our proposed pair-wise comparison for MIC values between consecutive years could mimic the observed MIC trend reasonably well. This analysis enables more timely detection of emerging resistance. The impact will be, that public health officials can implement targeted antimicrobial stewardship programs sooner.

Evaluation of interferon γ test for bovine tuberculosis diagnosis in Uruguay

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ABSTRACT

Objectives: In Uruguay, the diagnostic and surveillance of bovine tuberculosis is based on caudal fold tuberculin (CFT) as a screening test and cervical compared (CCT) as a confirmatory test. The aim of the study was evaluate the performance of the Interferon γ test (2G PRIONICS) in relation to tuberculin tests.

Materials and methods: Two groups of animals were used from farms with tuberculosis and and a group of a free farm.

Results: Two hundred and forty-four tuberculine positives were selected (CFT + and CCT +), 179 positive to CFT and negative to the CCT and 123 negative CFT. In the first group the Interferon γ test detected 194 positive animals, with a relative sensitivity of 79.5% (95% CI: 73.9 - 84.4%). In the second group 102 were positive to the Interferon γ, 57.0% (95% CI: 49.4 - 64.3%). In the third group 9 animals were positive to the Interferon γ. The relative specificity was 92.7% (95% CI: 86.6 - 96.6%). Epidemiologically, the most important group is the animals CFT + and CCP- , that in the current program remain in the farm and in the case of being false negative keeps the disease in the herd. In this group, 57% were reactive to the Interferon γ test, which is the result of a mixture of false negatives to CCT and false positives to the Interferon γ test. Considering that with a 97% of confidence the relative specificity of the Interferon γ test is higher than 86.6%, most of the reactants in this group are false negatives to CCT, and therefore Interferon γ behaves as more sensitive.

Conclusion: Interferon γ is a useful tool to be used in parallel with the CCT in CFT + animals in herds with the presence of the disease.

Developing the international classification of animal diseases

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ABSTRACT

Objective: Livestock diseases affect productivity through decreased yield and work output, as well as direct mortality. To improve resource allocation directed at improving animal health, a systematic way to capture these losses at a global level is needed. This requires a widely accessible electronic information system that regularly creates, processes, retrieves, integrates, and validates animal health data, namely the International Classification of Animal Diseases (ICAD). An essential feature of the system will be its ability to utilise the current digital environment, while being flexible enough to adapt to future technological advances. The aim of this study is to develop a framework for the ICAD system and examine its utility.

Materials and methods: A review of current classification systems and natural language processing in animal health was conducted. This formed the basis of the framework for the ICAD system which contains three data components: (i) a hierarchy of disease and injury; (ii) effect on productivity; and (iii) livestock production system. Lameness in cattle was used as a case study to examine the utility of ICAD for creating a global burden of animal disease.

Results: The proposed ICAD system integrates many disparate data sources, linking alternative names and ontologies for the same concept and identifies useful relationships between different concepts. Using these links, the system then combines information from the three data components to create a disease burden metric. A range of values associated with lameness in cattle were estimated, which varied according to aetiology, disease severity, and production system. However, the disease severity index was not an adequate proxy for effect on productivity.

Conclusion: Proof-of-concept for ICAD was demonstrated, however future iterations should be extended to include a severity index that more succinctly captures production losses. This will provide more informative values of productivity losses for estimating the global burden of animal diseases.

Key words: Disease classification, electronic information system, disease impact

The use of egg yolk to detect antibody in poultry flocks in Indonesia

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ABSTRACT

Objective: Layer farms commonly have lengthy vaccination programs with several booster vaccinations for common poultry diseases. Post vaccination flock monitoring to determine immunization efficacy is desirable but in some cases farmers do not allow blood sampling due to the stress caused, fear of a drop-in egg production or farm biosecurity risks. Testing eggs for antibodies may be a more acceptable alternative for farmers as it does not require blood collection.

Materials and methods: To test this method 45 eggs were collected from nine layer farms in Central Java. The farms had vaccinated against highly pathogenic avian influenza (HPAI) H5N1 clade 2.1.3 and clade 2.3.2 viruses, Newcastle Disease (ND) and low pathogenic avian influenza (LPAI) H9N2. The method separates antibody (IgY) from egg yolk through a precipitation process. There are two important steps in separating the IgY; the first removes the lipids and the second precipitates the IgY from the supernatant. After dialysis, the purity of the egg yolk extract may reach 80% and contains the antibody to be tested for in the HI test.

Results: Antibody was detected in the yolk of sampled eggs and the HI titers varied for HPAI H5N1 clade 2.1.3 from 0 to 256; for HPAI H5N1 clade 2.3.2 from 0 to 128; for LPAI H9N2 from 8 to 2048 and for ND from 2 to 512. The average titer was above 16 for the different pathogens which indicated sufficient flock protection on these layer farms.

Conclusion: These results show that the purified egg yolk extract could be used for antibody detection for HPAI, LPAI and ND. The method could be developed for other poultry diseases for post vaccination monitoring and could be used in un-vaccinated flocks to detect previous field infection.

Key words: Egg yolk, antibody, HPAI H5N1 clade 2.1.3 and 2.3.2, LPAI H9N2, ND

Accuracy of leukocyte esterase, endometrial cytology and vaginal discharge score to diagnose reproductive tract diseases in dairy cows, using a hierarchical Bayesian latent class model

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ABSTRACT

Objectives: The main objective of this retrospective study was to determine the accuracy of the leukocyte esterase test (LE), the endometrial cytology (CYTO) and the vaginal discharge score (VDS) for the diagnosis of reproductive tract diseases in dairy cows. A secondary objective was to quantify herd prevalence of these diseases in dairy farms from Quebec, Canada.

Materials and methods: Data from 2092 cows (39 commercial dairy herds in Quebec, Canada) enrolled in two previously conducted research studies were included. In these studies, cows were examined at 35 (±7) days in milk using LE, CYTO, and VDS tests to determine their reproductive tract health status. For the initial modelling, thresholds of ≥1, of ≥6%, and of ≥3 were used for the LE, CYTO, and VDS, respectively, to define presence of reproductive tract disease. A hierarchical Bayesian latent class model for three tests was built assuming CYTO and LE to be dependent conditionally on the reproductive tract health status of the cows. Non-informative priors were used for the sensitivity and specificity of LE, CYTO, and VDS, while prior information for disease prevalence was obtained from expert opinions (mode=20%, 5th percentile=10%). Posterior inferences (median and 95% credibility intervals; CI) were obtained for each parameter using the WinBUGS statistical freeware.

Results: Median sensitivity (and 95% CI) for LE, CYTO and VDS were 84.0% (81.7-86.8), 49.9% (45.8-54.3) and 48.9% (44.0-54.5), respectively. Median specificity (and 95% CI) was 53.6% (49.1-58.5) for LE, 96.2% (93.4-98.6) for CYTO and 99.4% (97.6-100) for VDS. The median reproductive tract diseases herd prevalence in Quebec's dairies was 46.9% (38.5-55.4).

Conclusion: Using a threshold of ≥1, LE had the highest sensitivity and the lowest specificity among the tests. We are now planning to investigate how changing the thresholds for each test, to define presence of reproductive tract diseases, may affect test accuracy.

Environmental sample characteristics and herd size associated with decreased herd-level prevalence of *Mycobacterium avium* subspecies *paratuberculosis*

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ABSTRACT

Objectives: Environmental sampling is an effective method for estimating regional dairy herd-level prevalence of infection with *Mycobacterium avium* subsp. *paratuberculosis* (MAP). However, factors affecting prevalence estimates based on environmental samples are not known. The objective was to determine whether odds of environmental samples collected on farm changed culture status over 2 sampling times and if changes were specific for location and type of housing (free-stall, tie-stall or loose housing), the sample collected (i.e. manure of lactating, dry or sick cows; namely, cow group), and effects of herd size.

Materials and methods: In 2012-2013 (sampling 1 (S1)) and 2015-2017 (sampling 2 (S2)), 6 environmental samples were collected and cultured for MAP from all 167 (99%) and 160 (95%) farms, respectively, in the province of Saskatchewan, Canada. Only the 148 dairy farms sampled at both sampling periods were included in the analysis. A mixed effects logistic regression was used to determine whether differences between sampling periods were associated with herd size and sample characteristics (cow group contributing to environmental sample, type of housing and location).

Results: In S1 and S2, 55 and 34%, respectively, of farms had at least 1 MAP-positive environmental sample. Correcting for sensitivity of environmental sampling, the estimated true prevalence in S1 and S2 was 79 and 48%, respectively. Herds with > 200 cows were more often MAP-positive than herds with < 51 cows in both S1 and S2. Herds that were MAP-negative in S1 with a herd size 51-100 or 101-150 were more likely stay MAP-negative, whereas MAP-positive herds with > 200 cows stayed more frequently MAP-positive. For farms with at least 1 positive sample in S1, each additional positive sample decreased the odds of testing negative in S2. All environmental samples regardless of type, had decreased odds of testing positive in S2, with the largest decrease in environmental samples collected from areas containing dry cows.

Conclusion: Environmental sampling was a cost-effective method to monitor prevalence, as well as assess on-farm changes.

Key words: Johne's disease, environmental sampling, herd size, Saskatchewan

Consumer perception in relation to beef certification in Belo Horizonte

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ABSTRACT

Objective: Brazil has today a position of great importance in the international meat market, which is due to many factors ranging from natural conditions, available land, favorable climate, labor and genetics. To occupy this position in the market, the various chain links, Government, Rural Producers, and Slaughterhouse Refrigerators had to adopt different procedures to ensure the safety of meat from the farm to the consumer's table. Among the requirements for international trade is the traceability and certification of our products. Although rural producers, slaughterhouses, merchants, and international buyers well know traceability, which is already the subject of countless studies evaluating their approval, difficulties, and cost of implementation, little is known about the knowledge and interest of Brazilian consumers regarding traceability and certification.

Materials and methods: In this work, a questionnaire was used to verify, from the consumer point of view of Belo Horizonte, the importance of the use of traceability in Brazil and certification of marketed products, providing new information for producers and the refrigeration industry to plan strategies focused on the consumer market, as well as for the government to establish public policies more directed to the interest of the population.

Results: The results showed that the levels of consumer knowledge about the production, traceability and certification systems are not associated with the social extract of which it takes part. No significant differences between the various extracts were identified, however the frequency of consumption of the different types of meat was influenced by consumer knowledge about production, traceability and certification systems.

Conclusion: Associations were identified between the frequency of consumption of the different types of meat and the knowledge about the production methods, knowledge about the control of residues of hormones and antibiotics, and the certification and traceability of beef.

Key words: Traceability, consumer, meat, quality

The influence of case submission routes on animal rabies detection rate: case of lower northeastern Thailand, 2016-2018

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ABSTRACT

Objective: The present study thus aimed to explore the influence of case submission routes on animal rabies detection rate

Materials and methods: We gathered data on 2,791 animals submitted during 2016-2018 at Veterinary research and development center (lower northeastern region), Surin, Thailand. Two potential risk factors were analyzed including routes of sample submission (owners or veterinary officers) and animal species examined (dog, cat, cattle, buffalo and other livestock). The adjusted odds ratio was calculated with a multivariate logistic regression. Results: Our result revealed that rabies virus was 1.93 times (95% CI: 1.28 – 2.92) more likely to be recovered in animal owner submitted samples. The highest rabies detection rate was found in cattle (54.32%). Focusing on cattle samples submitted by their owners, the rate was 6.86 times higher (95% CI: 3.88 – 12.14) compared to other animals. Geographically, Surin province possessed the highest owner submission rate at 17.86 times (95% CI: 11.59 – 27.52) compared to other provinces

Conclusion: we primarily observed that sample submission routes did affect the rabies detection rate especially in cattle. Further elaborated studies are required to exclude possible confounding factors and establish a more concrete summary.

Key words: cattle, logistic regression, lower northeastern Thailand, Rabies, submission route

Investigation on the possible effect of the temperature on a Testudinid Herpesvirus 3 (TeHV3) outbreak

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ABSTRACT

Objective: The effect of the temperature in poikilotherm animals have been demonstrated for several infections. No specific information concerning these aspects is available for TeHVs. For this reason a time-stratified case-crossover study was carried out in a TeHV3outbreak occurred in a breeding consisting of 314 chelonians to assess possible effects of the environmental temperature on the infection.

Materials and methods: The definition of case was tortoises showing clinical signs and positive for the presence of TeHV DNA by PCR. Conditional logistic regression model was used to calculate odds ratio and 95% confidence intervals at lag 3, 4, 5 and 6 days before the event, estimated as possible incubation period. Meteorological data on temperature and humidity of the considered period were collected. An environmental temperature of 10°C was assumed as non-optimal for tortoises. P-values ≤0.05 was considered statistically significant. The analyses were performed using Stata software 11.2.

Results: The confirmed cases were 12. No significant impact of the environmental temperature variables on TeHV3 infection was found. However, an interesting p=0.085 was obtained with temperature range 9-11°C recorded 5 days before the onset of the clinical cases; the trend of the p-values for the group of the 6 days was nearer to significant results in all the three different temperatures analyzed.

Conclusion: The small sample size was most likely a limiting factor that reduced the power of analysis. A lag time higher than 6 days also should be further investigated; this hypothesis is supported also by the results of the epidemic curve that found a range of 5-10 days as incubation period for TeHV3. Further studies including a larger number of observations are needed to better understand the relationship between TeHV-associated disease and environmental conditions. The statistical analysis used could represent an initial model to implement and to build upon.

Key words: Testudinid Herpesvirus 3 (TeHV3), tortoises, time-stratified case-crossover study, temperature.

A system dynamics model of necrotic enteritis in broilers

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ABSTRACT

Objectives: Poultry production is an important food animal production system globally and especially in the United States. Necrotic enteritis is the most recognized enteric disease afflicting global broiler production. The transmission and progression of the disease under different predisposing factors have been studied extensively; however, the dynamic relationships between necrotic enteritis and these predisposing factors are not fully illustrated by current studies. Therefore, our objective was to review and identify these dynamic interactions via conceptual susceptible-infected-removed (SIR) models of necrotic enteritis and avian coccidiosis developed within a system dynamics model.

Materials and methods: Our hypothesis was that a system dynamics model can be used to better understand the interrelationship of predisposing factors and necrotic enteritis. The system dynamics model was designed to investigate the associations between predisposing factors, including interventions, in the case of necrotic enteritis. This model can help determine the most efficacious and cost-effective interventions to promote broiler health, welfare, and productivity.

Results: Within the model, we estimated the incidence of clinical and subclinical necrotic enteritis and coccidiosis in one or more grow-out periods. The mean weight gains of broilers not affected by necrotic enteritis, as well as clinically and subclinically affected with necrotic enteritis, were estimated in one or more grow-out cycles. The system dynamics model will be used to investigate the effect of modifying certain predisposing factors of concern by changing management practices. With the adjustment of these factors, the dynamic relationship between disease incidence and growth performance can be measured in the model. Moreover, the application of the system dynamics model is expected to reveal the leverage points in management practices, which will make disease control more effective for the industry.

Key words: Broiler production, system dynamics model, necrotic enteritis, coccidiosis

Characterizing transmission of Mycobacterium bovis in a multi-host system

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ABSTRACT

Objective: In Ireland in 1954, approximately 80% of the cattle herds were infected with *Mycobacterium bovis* (*M. bovis*), causative agent for tuberculosis in cattle. A control/eradication programme for *M. bovis* infection, largely based on test and removal of infected cattle, commenced that year in the country. This programme proved to be very successful, achieving a reduction of >95% of the cattle incidence in less than 10 years. Despite this early achievement, tuberculosis incidence in cattle has remained relatively stable at a low level since. Subsequent to the discovery of a second host for *M. bovis* (badgers, *Meles meles*), temporary target badger removal was added to an enlarged list of control options that primarily focused on reducing cattle to cattle transmission. The objectives of this research were two-folded, firstly, we aimed to quantify inter and intra-species transmission parameters for the *M. bovis* cattle and badger system in Ireland, as the quantitative role of each of the species in total transmission was unknown. Secondly, we aim to answer the question of whether or not Bacillus Calmette-Guerin (BCG) badger vaccination, if added to current controls, could help in achieving eradication of the infection not only from badgers, but from the system.

Materials and methods: For that purpose, general algorithms that allow estimations of the Reproduction Ratio (R) and the Next Generation Matrix (NGM) in any multi-host system, from data easily collected at the endemic equilibrium, were developed. Basic data such as prevalence and number of cattle herds and badgers, were entered in these algorithms to conclude that for almost all plausible transmission scenarios, BCG vaccination of badgers in addition to current controls could successfully achieve eradication of *M. bovis* infection in the system.

Key words: *Mycobacterium bovis*, badgers, cattle, basic reproduction ratio, next generation matrix

Overview of the Animal Disease Spread Model: A tool for simulating highly contagious disease outbreaks

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ABSTRACT

Objective: Simulation models used for epidemic preparedness of highly infectious diseases are important tools to evaluate competitive hypothesis of the factors associated with disease spread, surveillance and control strategies.

Materials and methods: The Animal Disease Spread Model (ADSM: https://github.com/NAVADMC/ADSM/releases/latest) is a stochastic, spatial, state-transition simulation model designed to simulate the between-herd spread and control of highly contagious animal diseases. Based on the logic of the North American Animal Disease Spread Model (NAADSM), ADSM features an upgraded user interface, expanded database, and enhanced capabilities and features while keeping the disease transmission and control mechanisms of the previous model.

Results: One unique feature of ADSM allows users to create re-useable parameter blocks that can be assigned to one or more species groupings, thereby decreasing the complexity and time for representing animal production management systems in the model. In addition to simulating disease spread, ADSM can be used for evaluating economic questions related to government costs of outbreak scenarios. For comparing the large volume of model outputs within a single scenario, summaries can be examined with spatial and graphical visualizations that are automatically generated within the application. Additionally, for comparisons across multiple scenarios, analytical visualizations of the simulated outbreaks metrics have been packaged for distribution and can be run using the open source R program (R Core Team 2018).

Conclusion: Developing simulation models that are freely available for download, such as ADSM, provide tools to better understand disease transmission and evaluate different control measures of highly infectious diseases, as well as provide a venue to educate the new generation of disease modelers.

Key words: Simulation, modeling, analytical tools, economics, ADSM

Epidemiological applications for the control of bovine tuberculosis in the state of Bahia, Brazil

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ABSTRACT

Objective: This work was carried out in Bahia - Brazil (2008 - 2010) in 3 stages: first a cross - sectional study with the purpose of estimating the prevalence and risk factors; second - spatial characterization to quantify the distribution of the disease; third - risk analysis to introduce the disease.

Materials and methods: The state was divided into four regions and a total of 18,810 adult cattle and 1,350 farms were sampled. The *Cuzick and Edwards test* and spatial scan statistic were used to identify spatial groupings of BTB. In the risk analysis was quantified the probability of introducing the disease in free BTB in southern Bahia.

Results: The results showed a herd prevalence of BTB of 0.3% (95% CI: 0% - 0.88% region 3) and 0.6% (95% CI: 0 - 1.49% region 4); a animal prevalence ($\geq$24 months) of 0.03% (95% CI: 0 - 0.09% region 3) and 0.04% (95% CI: 0 - 0,11% region 4). The risk factors were: Type of property of milk and larger herds. No significant evidence (P <0.05) of cluster was detected, possibly due to the low prevalence of the disease. These results suggest that BTB has a low prevalence in Bahia and homogeneous distribution, not recommending regionalization actions. In the risk analysis, the annual risk of introduction of BTB-infected animals into freehold properties in the South of Bahia through the movement of live cattle is very low; with an average risk of less than 0.001133 for both regions. Unofficial movements accounted for about 90% of this risk, indicating the importance of acquiring animals with negative results.

Conclusion: This study allowed to understanding of the epidemiology of BTB in Bahia. The control strategies for the disease in the state should include vigilance directed at milk properties and inhibition of illegal movements.

Key words: Bovine tuberculosis, prevalence, spatial analysis, risk analysis

Mathematical Model on Foot-and-Mouth Disease Transmission under the Regular Vaccination Strategy

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ABSTRACT

Objectives: Mathematical models on FMD transmission were developed in two stages: at the levels of within and between farms with current regular species-specific vaccination program of Korea.

Materials and Methods: Within-farm transmission model was based on SLIR (Susceptible, Latently infected, Infectious, and resistant - generating antibody) scheme, but status was expanded into eight compartments according to manifestation of clinical signs, antibody, and partial culling. Between-farm transmission was determined by the frequency of contacts through vehicles and factors on farm environment.

Results: Clinically infected pigs, newly added per day, predicted by within-farm transmission model were compared to the real outbreak data on a farm with 16,000 animals. The inter-quartile range of model prediction with 1,000 iterations included the real outbreak data. Daily or final numbers of infected animals in a farm were twice higher in a herd of immunity 50% compared to 90%. With between-farm transmission model, 14 out of 16 outbreak farms during the epidemic in February 2017 were correctly predicted.

Conclusion: These models proved potentials to predict FMD transmission pattern under regular vaccination policy, and this would help to develop detailed action plans of FMD control programs.

Predictive modelling of ovine haemonchosis risk based on the effects of climate on the free-living stage of *Haemonchus controtus* in the United Kingdom

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ABSTRACT

Haemonchus contortus (*H. contortus*) is responsible for substantial global production losses in small ruminants. The losses may be exacerbated by climate change and the widespread resistance to anthelmintic. Development of integrated-sustainable parasite control requires adequate knowledge of how climate drives the population dynamics of *H. contortus*. A simple model based on climate that is able to predict future challenges and risk resulting from *H. contortus* could greatly contribute to sustainable control. The effects of climate on the transmission potential of *H. contortus* is generally appreciated but its uptake in creating predictive models for strategic exploration of climate change effects and decision support systems is yet to be tested.

We used the basic reproduction rate (Q_0): a model system of instantaneous parameters that is run on climatic data to understand the effects of changes in climate on the population dynamics of the free-living stages, and to predict host infection with *H. contortus*. Q_0 was extended within geographic information system to consider spatial variation in haemonchosis risk and seasonality. In this study, we aimed to (I) analyse and predict the effect(s) that changes in climate will have on *H. contortus* infection pressure across the UK.

The Q_0-based risk maps display the capability of the Q_0 as a spatio-temporal predictor of haemonchosis risk across different geo-climatic zones. These risk maps have potential as spatial platforms for decision support systems, in support of integrated-sustainable control of *H. contortus*.

Key words: Basic reproduction rate, *Haemonchus contortus*, risk maps, climate, epidemiology

Session C: Health policy and capacity building

Sanitary status against bovine viral diarrhea and infectious bovine rhinotracheitis and biosecurity measures applied in dairy farms in Catalonia and Galicia

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ABSTRACT

Objective: Bovine Viral Diarrhea (BVD) and Infectious Bovine Rhinotracheitis (IBR) are diseases of paramount importance to the livestock industry and animal health authorities in Catalonia and Galicia because of animal health and economic consequences. Series of epidemiologic and sociologic studies are underway to measure the burden of and biosecurity measures in place to prevent and control BVD and IBR in dairy farms. The objective of this study was to measure the frequency of cattle farms with evidence of exposure to BVD or IBR and biosecurity measures applied in study farms.

Materials and methods: A convenience sample of 34 and 44 cattle farms in Catalonia and Galicia were included. Within each study farm, bulk tank milk samples and blood serum samples from a sample of cattle were tested for detection of BVD and IBR antibodies (Abs) by using an ELISA test. A structured questionnaire was used to collect data relevant to biosecurity measures on each study farm.

Results: Overall, 17/34 (50%) and 8/44 (18%) farms tested positive to BVD Abs in Catalonia and Galicia. In addition, 21 (63%) and 1 (3%) farms tested positive to IBR Abs, respectively. In Catalonia, 12/34 (35%) farms were classified as open herds, 10 (30%) herds had monitoring program for detection of BVD and IBR Abs, and 12 (35%) had a perimetral fence. In Galicia, 11/44 (7%) were open herds, 7 had monitoring program for BDV and IBR Abs, and 2 (4%) had perimetral fence. Protective clothing and boots are provide only in 13% of farms in Catalonia and none in Galicia. External transportation vehicles were used by all study farms in Galicia and 21/44 (48%) in Catalonia.

Conclusion: Overall, preliminary results revealed that the burden of exposure to BVD and IBR is higher in study farms in Catalonia than in Galicia.

The history of in vivo tuberculin testing in bovines: Tuberculosis a "One Health" concern

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ABSTRACT

Tuberculosis (TB) is over 3 million years old, thrives in multiple species and is distributed worldwide with zoonotic transmission happening in both directions between animals and humans. *M. bovis* in milk caused a significant number of deaths, from extra-pulmonary TB, particularly in children under 5 years old. Pasteurization effectively mitigated this risk and fewer young children were lost to TB during the 20thC. Koch developed tuberculin in 1890 and the first tests to detect TB infected animals were quickly advanced. Bovine TB (bTB) control/eradication programmes followed in the late 19thC/early 20thC. Scientists collaborated on the development of tuberculin tests, to refining and optimising the production and standardisation of tuberculin and to determining test sensitivity and specificity using various methodologies and injection sites. The WHO, OIE and EU set legal standards for tuberculin production, potency assay performance and intradermal tests for bovines. Now, those using tuberculin tests for bTB control/eradication programmes rarely, see TB as a disease. Notwithstanding the launch of the first-ever roadmap to combat zoonotic TB, many wonder if bTB is a problem; is there a better way of dealing with bTB; might alternative skin test sites make the test 'better' and easier to perform; are all tuberculins used for testing equally good; why haven't alternative 'better' tests been developed? This review was prompted by these types of questions. We focus on succinctly summarising the literature from the late 19thC to date to show why TB, particularly zoonotic TB, is an important 'One Health' concern; why reduction of zoonotic TB is necessary to save lives and secure livelihoods which is too important to await future possible novel diagnostic development assays for livestock. Thus, for the considerable future the tuberculin skin test will likely remain the screening test of choice for farmed livestock.

Key words: Bovine tuberculosis, zoonotic tuberculosis, tuberculin test

Comparison of alternative meat inspection regimes for outdoor-raised finishing pigs – considering the cost of error

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ABSTRACT

Objective: Denmark has been free from bovine tuberculosis (bovTB) for more than 30 years, but is obliged by trade agreements to undertake traditional meat inspection (TMI) of outdoor pigs to detect bovTB. To identify whether visual only inspection (VOI) should replace TMI of outdoor finishing pigs, cost of error, i.e. probability of overlooking infection and associated economic costs, was estimated and compared with surveillance costs.

Materials and methods: A scenario tree model was set up to assess the ability of detecting bovTB in an infected herd (HSe) calculated for three within-herd prevalences, WHP (1%, 5% and 10%), for four different surveillance scenarios (TMI and VOI with/without serology, respectively). HSe was calculated for six consecutive 4-week periods until predicted bovTB detection (considered high-risk periods HRP). 1-HSe was probability of missing all positives by each HRP. Next, probability of spread of infection and number of infected animals moved were calculated for each HRP. Costs caused by overlooking bovTB were calculated. Finally, average annual costs were calculated assuming one incursion of bovTB in 1, 10 or 30 years. Input parameters were based on slaughterhouse statistics, literature and expert opinion.

Results: HSe increased by high-risk period and within-herd prevalence. Assuming WHP=5%, HSe reached median 90% by 2nd HRP for TMI, whereas for VOI this would happen after 6th HRP. Serology had limited impact on HSe. Probability of spread increased with number of animals moved and WHP. Hence, the higher the probability of infection, the higher the probability of detection and spread. TMI resulted in the lowest average annual cost, if one annual incursion of bovTB was expected. When assuming one introduction in 10 or 30 years, VOI resulted in lowest annual costs.
Conclusion: Given the low expected probability of introduction, it may be more cost-effective to test imported high-risk animals instead of using TMI as surveillance on all outdoor pigs.

Key words: Surveillance, *Mycobacterium bovis*, meat inspection, cost of error, pigs

Assessment of the shrimp disease management behaviors of Vietnamese farmers using Vietnamese Good Aquacultural Practices

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ABSTRACT

Objectives: Shrimp aquaculture is a key national economic sector in Vietnam. Owing to pressing issues such as food safety, disease outbreaks, and environmental pollution, Vietnamese Good Aquacultural Practices (VietGAP) were regulated and mandatorily implemented in Vietnam as a sustainable aquaculture solution. However, despite their potential benefits and the efforts made by the government, adoption of VietGAP in shrimp aquaculture is still very infrequent. Therefore, this study was conducted to identify critical factors affecting the shrimp disease management behaviors of farmers using VietGAP, and thereby provide proper policy implications for VietGAP development.

Materials and methods: A total of 160 smallholder farmers were selected from 4 communes in Tam Giang lagoon. Four dependent variables were assessed, including whether farmers regularly monitored shrimp health indicators ("monitor" behavior), reported suspected cases of diseases to the governmental authority ("report"), disposed dead shrimps harmlessly ("dispose"), and used chlorine according to instructions ("chlorine"). These variables were used to comprehensively assess the disease management behaviors of farmers. A binary logistic regression model was carried out to clarify the effect of various independent variables on these behaviors.

Results: Approximately 40% of farmers performed one or more improper disease management behavior. Results of analyses demonstrated that credit accessibility had a significant positive effect on the "monitor" behavior. Farmers who received more support from other farmers were also more likely to adopt the "monitor", "report", and "chlorine" behaviors. On the other hand, high stocking density resulted in less adoption of these behaviors. Disease area and frequency had significantly negative effects on "report" and "chlorine" behaviors by farmers.

Conclusion: Adopting VietGAP is an important step towards adopting organic production in aquaculture. Therefore, to meet general VietGAP standards gradually, the relevant governmental authority should control appropriate stocking rates, improve access to credit, improve the knowledge among farmers for effective disease management, and establish penalties for improper behaviors.

Key words: Disease management, behavior, small-scale shrimp farmers, Vietnamese good aquacultural practices

The impact of farmers' attitudes and behaviours for the success of a high biosecurity compartmentalisation scheme in Taiwan's broiler industry

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ABSTRACT

Objectives: The aims of this research are to understand broiler farmers' opinions, attitudes, and behaviours concerning on-farm biosecurity programmes and for this knowledge to be used to assist in the establishment of high biosecurity compartments in Taiwan.

Materials and methods: A mixed-method research approach was used involved three phases. In the exploratory qualitative phase, face-to-face interviews with 25 farmers explored the influence of socio-economic conditions on famers' management and attitudes. In the confirmatory phase, categorical principal components analysis and a two-stage cluster analysis were utilized. The third phase applied targeted strategies as scenarios for the advocacy of on-farm biosecurity.

Results: In the exploratory qualitative phase, the influence of socio-economic conditions on famers' management and attitudes was revealed, such as: (1) there was some misunderstanding in relation to the effectiveness of biosecurity; (2) farmers lacked trust in the government; (3) farmers believed that researchers rarely provided solutions to practical problems; (4) farmers complained about the impracticality of the implementation of current regulations for farm biosecurity requirements. In the confirmatory phase, two types of clusters were identified (data from 303 broiler farmers): attitude (based on 15 variables) and behaviour clusters (characterised by 30 variables). Findings suggested it is essential to apply appropriate and specified behavioural change theories to reduce the mismatch of farmers' attitudes towards biosecurity. The third phase identified risk factors for the introduction and within-farm spread of the avian influenza virus and provided an example to help identify compartment candidate farms. Secondly, relevant targeted strategies were planned for farms surrounding compartment candidate farms.

Conclusion: Farmers' attitudes and behaviours towards disease prevention need to be considered as key drivers of farmers' biosecurity practices. Knowledge generated by behavioural change theories needs to be considered when developing strategies aimed at improving on-farm biosecurity. The scientific evidence generated can be used to inform the development of standard operating procedures for biosecurity in broiler compartments with Taiwan and other countries in the region with similar broiler production systems.

Key words: Behavioural change, biosecurity, broiler, compartmentalisation, risk factors

Short-term socioeconomic impacts due to Foot and Mouth Disease in a dairy farm in West Azerbaijan province of Iran in 2018

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ABSTRACT

Objective: The impact of Foot and Mouth Disease (FMD) consists of direct losses (reduction in production, treatment costs, and changes in herd structure) and indirect losses (control measures, management by livestock owner, denied access to markets, use of suboptimal breeds). In addition, there is often some sort of social impact on the affected livelihoods that will vary between production systems and societies. The objective of this study was to estimate direct and indirect losses of FMD in a dairy herd based on an outbreak of FMD on a dairy farm in Naghade district, West Azerbaijan province, Iran.

Materials and methods: Data were collected based on a structured questionnaire and complemented with data recorded by the farmer during the clinical phase of FMD.

Results: Of the 130 heads of cattle, 23 showed (18%) clinical signs of FMD including 18 heifers (13-24 months) (11.5%), 2 bulls (1.5%) and 1 calf (0-12 months) (0.7%) of which 3 heifers died. The estimated losses due to these mortalities were 3,333$. The overall losses to milk production and weight loss were estimated to be 730$ and 1,149$, respectively. Additional expenses were with treatment (987$), extra labor (711$), emergency vaccination (111$), sampling and diagnosis costs (89$), feed losses (72$) and the cost of buying additional equipment to control the disease (133$). Due to the FMD outbreak, the farmer lost the opportunity to sell livestock at appropriate time. As a result, the total estimated direct loss due to FMD accrued to 7,316$ in a 30 days period of disease.
On a personal level, the farmer indicated to have suffered from mental illness, family problems and frustration with his work.

Discussion: Additional investigations into direct and indirect losses due to FMD are currently underway and will be incorporated at a later stage of this study.

Key words: Socioeconomic, impact, FMD

Animal disease surveillance system: can it be optimised with contact rate?

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ABSTRACT

A surveillance system is usually designed by establishing the numbers of herds or individual animals needed in a survey to observe a disease to remain below a given prevalence level, with some predefined confidence. Finnish active cattle surveillance system functions at herd level: bulk milk samples from dairy herds and individual blood samples from suckler-cow herds are taken.

Our dairy farms have typically a low in-degree but a high out-degree. When sampled by present system we are focusing on farms that deliver animals mostly on finishing farms. Our aim was to see whether it was possible to develop a surveillance system that would focus on the high in-degree end of the dairy farms, to sample farms that receive animals from multiple farms.

Development of a contact-based approach requires the stability of the network structure. Cattle trading networks in 2014 and 2015 revealed a good stability among trading partners of cattle farms. On average 91% of the farms selling, and 86% of those buying were the same. In addition, the numbers of contact farms correlated strongly between the years (in-degree r=0.971, and out-degree r=0.796). These results indicate that a sampling plan can be based on the contact information from the previous year.

By using the number of samples in present dairy cow surveillance (< 1000 samples), it is possible to sample farms that represent 70% of ingoing contacts in a year in dairy farm population. Similarly, an additional 150 sampled suckler-cow farms would capture 70% of the ingoing contacts in this subpopulation. This would lead to a more efficient surveillance system to detect diseases that spread within the dairy and suckler-cow populations, and provide more indirect information of the farms outside the sampling frame.

Key words: Surveillance system, contact network, optimisation, cattle production

Surveillance system of contagious animal diseases of cattle in Finland – effects of inclusion by farm size and low renewal rate in years 2014-2015

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ABSTRACT

The most of the12000 cattle farms in Finland in 2014-2015, were dairy farms (>60%). Suckler-cow farms formed a distinct minority (15%). The Finnish cattle surveillance system focuses on these two subgroups of the cattle production sector.

The dairy farm surveillance consisted of taking bulk milk samples from farms experiencing reproductive disorders and having over 15 calvings per year. Suckler-cow farms were monitored through blood samples drawn at slaughter. The inclusion into the surveillance depends on the size of the farms in both subgroups. The renewal rates (sampling from the same farms each year) of the target populations tend to be 30-40% in dairy, and 50-60% in suckler-cow farms.

Size-based sampling obviously favors larger farms and introduces a bias. Farms having more numerous outgoing contacts tend to be sampled more frequently than others, whereas the proportions of the ingoing contacts of the sampled farms equals the proportions of the sampled farms out of the total farm population. Considering the animal trade network the importance of the renewal rates in both subgroups is emphasized. The unsampled dairy farms are not connected efficiently with the sampled farms whose trade partners mostly remain unchanged between years. This leads to a limited ability of the surveillance system to detect disease outbreaks outside of the sampling frame. Updating or providing supplementary data from one year to the next is not optimal, and additional information from farms delivering animals to sampled farms remains largely the same between years.

Key words: Surveillance system, contact network, cattle production

Understanding the importance of record keeping to assess profitability and enhance financial literacy of selected smallholder pig raisers in San Simon, Pampanga, Philippines

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ABSTRACT

Objective: Smallholders are important contributors to pork production in the Philippines. In 2015, a series of semi-structured interviews was conducted to estimate the gross margin per litter and per batch (batch of piglets bought after weaning) of fattener for farmers in San Simon, Pampanga, Philippines. Due to a lack of record keeping, the data gathered were very approximate. This study aimed to (i) demonstrate to farmers the importance of record keeping to assess profitability, and (ii) improve farmer's financial literacy.

Materials and methods: A participatory record keeping workshop was conducted among eight farmers (male=4; female=4) to develop a simple record keeping system to understand profits made through their business. Farmers also identified buddies in their barangays (villages) to share their learnings from the workshop. The production cost and income were based in litters (n=16) and batches of pigs (n=7). Feed cost was the main outlay in pig production which comprised 87% of the overall production cost. Examples of other input costs were: boar service, medication, vaccination, castration, electricity, water and gasoline. Total income per litter or batch was also recorded. Calculations of production cost and total income were conducted using Microsoft Excel®.

Results: The gross margin (excluding labor) per litter ranges from ₱1,417.00 to ₱21,547.00 with a median of ₱8,038. For every batch of fatteners, the gross margin ranges from -₱12,400.00 to ₱42,517.00 with a median of ₱2,594. A follow-on workshop for record keeping was conducted which enabled eight farmers (including some of the buddies of initial participants) to understand which part of the production cycle can be improved and to compute their profit.

Conclusion: In the future, a third record keeping workshop will be held to further enhance farmers' financial understanding. Results from these next steps will help provide recommendations for the wider pig raising community.

Key words: Profitability, record keeping, smallholder

Willingness to pay for preparatory on-farm disposal capacity for commercial poultry farms

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ABSTRACT

Objectives: Biosecurity practices can limit introduction and spread of foreign animal diseases. United States commercial poultry farms typically follow a series of biosecurity practices as outlined by government and industry standards, but ultimately implantation decisions are left to the discretion of the producers. This leads to tradeoffs between adoption and risks associated with non-adoption such as on-farm infection, movement restrictions on or off-farm, and market impacts. Additionally, restricted movement for premises in the control area can cause financial and logistical difficulties associated with carcass disposal of normal mortality. This work aims to estimate the willingness to pay (WTP) for disposal capacity to address movement restriction on premises not-infected but included in a control area. These estimates can provide industry and policy makers tools to better create policy and cost structures to incentivize adoption and pre-planning while continuing to encourage disease reporting.

Materials and methods: Using survey responses from a poultry producer online survey which asked about specific biosecurity practices currently used, disease occurrence expectations, and biosecurity adoption, a one-and-one-half bound econometric model will be estimated to determine producer WTP for on farm disposal capacity and factors that contribute to that value. Follow-up questions in the survey will be used to determine how policies could promote adoption in respondents.

Results: Producers make decisions accounting for short and long-term profitability while weighing any production risks. It has been shown that this can lead to underinvestment in valuable biosecurity practices due to producer perceptions surrounding disease incidence risk, cost of adoption, or expected payoff among other heterogeneous producer specific factors.

Conclusion: This work provides industry and policy makers an understanding of how much a U.S. commercial poultry producers' willingness to invest in disposal capacity and how on-farm differences may influence their decision to adopt.

The farmer factor: A qualitative investigation of farmer disease response behaviour and its implications for passive surveillance

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ABSTRACT

Objectives: Effective passive surveillance depends on those in regular contact with livestock to report unusual or important disease signs to animal health authorities or veterinarians. Farmers' observations are a rich source of passive surveillance data, if they are captured by a surveillance system. In Australia as in many countries, veterinary contact by farmers is infrequent, limiting the sensitivity of passive surveillance. This study aimed to understand why Australian sheep farmers chose not to contact veterinarians when their animals showed signs of disease.

Materials and methods: We used established qualitative methods to investigate farmers' decision-making process when facing unusual endemic disease situations. Data were collected during three focus group discussions with sheep farmers in Victoria, Australia. Transcripts of those discussions were analysed using a modified grounded theory approach.

Results: We present a preliminary theory of Australian sheep farmers' disease response behaviour (see Figure). Within the contextual identity of 'being a farmer', when 'dealing with the problem', the farmer must recognise action is needed, and then determine what that action will be. The farmers reported self-assessment to determine whether their experience was sufficient act independently, or whether advice was needed. Veterinarians played a small but important role as potential advisors.

Conclusion: Self-reliance in Australian farmers' responses to endemic diseases has not received sufficient previous attention. Rather than being seen as a barrier to effective passive surveillance, farmers' self-reliance needs to be acknowledged when designing novel surveillance approaches.

Key words: Grounded theory, qualitative, farmer behaviour, disease reporting, surveillance

Gaps in the paraveterinary systems: Case study from Cambodia

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ABSTRACT

Objectives: Nearly 80% of Cambodians live in rural areas and practice subsistence agriculture, with livestock increasingly important for their livelihoods. However, the national veterinary services are dependent on the paraveterinary service provided by Village Animal Health Workers (VAHWs). VAHWs are usually livestock owners selected for basic training in animal health and potentially have an important role in disease control, although their contribution to the national disease surveillance systems is uncertain and deserves investigation.

Materials and Methods: A closed-ended questionnaire was developed by project staff from the 'Village based biosecurity disease risk management in Cambodia' project, a collaboration of the Cambodian General Directorate of Animal Health and Production and the University of Sydney, funded by the Australian Centre for International Agricultural Research. It was translated to Khmer and administered in face-to-face interviews by Cambodian project staff. A total of 80 participants were chosen by systematic random selection from a population 546 VAHWS in two provinces (Takeo and Tbong Khmum).

Results: Results identified 45% of VAHWs had contact with district veterinary services staff every six months, and 24% only had annual contact. Awareness of the frequency of FMD outbreaks within the area serviced by the interviewee was low, with 69% stating they were unaware of how frequently outbreaks were occurring.

Conclusion: Rapid communication is essential for an effective emergency disease response and management of transboundary and emerging infectious diseases. VAHWs have the potential to provide health advice to smallholder farmers and should be capable of delivering disease outbreak information in a timely manner. These findings indicate there is inadequate communication between VAHWs and district veterinary services. Improving regular communication may help address these deficits, although other incentives may be required if the VAHWs are expected to be providing prompt feedback to enable local passive surveillance to contribute to an emergency disease response capability.

Key Words: Village Animal Health Worker, communication, surveillance, Foot-and-Mouth disease

Risk communication methodology for bovine leukemia virus infection

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ABSTRACT

Objective: The objective of this study was to clarify an appropriate method of risk communication when EBL cases were identified in somewhere.

Materials and methods: It was tried to estimate the mechanism of farmers' psychological aspects, evade action, and risk information. In the analysis of farmers' psychological aspect, negative emotion, disease anxiety, support to farmer who had disease, association for disease, knowledge, and rational thinking were categorized by factor analysis. And, the relationship between psychological aspects, evade action, and information disclosure intention was estimated by structural equation model (SEM).

Results: Based on the results, 20 % of farmers had experience on the occurrence of EBL infected cow, and the evade action was seen for 67 % of them. And its action was linked to the information disclosure intention strongly. However, when the farmer has excessive awareness to the risk of EBL infected cow, it might be the cause of harmful rumor. On the other hand, the evade action ratio of farmer who had no-experience was relatively low, the preventive measure was also reluctant. Therefore, they might not have enough knowledge for EBL infected risk. Moreover, knowledge and rational thinking had a negative effect on the evade action and positive effect on the information disclosure intention. Other factors categorized to intuition type had shown opposite trend.

Conclusion: Risk perception through experience and rational thinking lead to information disclosure and avoidance of harmful rumors. Moreover, the difference from mechanism of consumer's harmful rumor is that the support for farmers with infected animals also effect the evade action. There is a specific thinking that while wanting to support as a same profession, the farmer do not want to bring in risks to own farm.

Key words: Bovine leukemia virus infection, evade action, Japan, psychological aspect, risk communication

The contribution of veterinarians in preventing and managing disease among smallholder livestock producers in Australia

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ABSTRACT

Objective: This cross-sectional study aimed to investigate the contribution of veterinarians in managing disease among smallholder livestock producers in Australia, from the perspectives of both, veterinarians and the smallholders with whom they work.

Materials and methods: A series of self-administered electronic questionnaires and focus group discussions were completed. Questionnaire data was analysed descriptively and logistic regression analysis was used to identify potential drivers of practices. Qualitative data was analysed using thematic content analysis.

Results: A total of 1,140 and 91 usable responses were obtained for smallholders and veterinarians, respectively. In addition, 28 smallholders participated in three focus group discussions. With regards to veterinary involvement, on-farm visits were the most frequent interaction type, with emergencies the most frequently activity. Smallholders represented a mean of 19.2% of the veterinary business. Contact with a veterinarian in the past year was more frequent (75%; P<0.05) for dairy goat and alpaca smallholders, than for cattle, sheep and pig smallholders (36.5%); with a significant proportion of cattle, sheep and pig smallholders (17-28%) having never contacted a veterinarian. A challenge for a more frequent used was the involved costs. However, most respondents indicated that they would contact a private veterinarian if they saw unusual signs of disease. Over 95% of veterinarians provided some level of biosecurity and zoonotic disease advice to smallholders. Interestingly, biosecurity knowledge was positively associated with frequency of veterinary contact among smallholders. Although veterinarians provide advice and support to smallholders, only 14.5% considered themselves to be highly influential on smallholder practices. Confidence in investigating disease differed by livestock species, with lower confidence reported in pigs, poultry and alpaca.

Conclusion: This study provides an insight into the way in which veterinarians engage with smallholders and highlights the importance of providing both groups with the tools necessary to manage the livestock to which are exposed.

Key words: Veterinarian, biosecurity, smallholders, disease investigation

Combining ensemble modelling and social relationships for sustainable rural poultry surveillance in developing countries

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ABSTRACT

Objective: The livestock sector contributes significantly to the food security and economy of developing countries. Optimum production potential for the rural poultry sector is hindered by infectious poultry diseases that cause high mortalities. Establishing a full-fledged active disease surveillance system in developing countries requires resources which are either inadequate or non-existent.

Materials and methods: Within this context, we have trialled an ensemble model integrating a hazard analysis, social network and market chain analysis with a risk assessment (Fig. 1) within 4 Pacific Island countries (PICTs) (Solomon Islands, Papua New Guinea, Vanuatu, Fiji) and 1 African country (Zambia) that has enabled more cost-effective targeted surveillance. This model has been coupled to community driven poultry clubs (PCs) in Zambia to produce a low-cost sustainable syndromic surveillance reporting system using rural poultry farmers.

Results: This paper combines 7 years (2010-2018) of data collection and analysis comprising 2 in-depth literature reviews, 6 disease prioritization, 4 market chain analysis workshops and surveys of 50 regional and national experts, 86 animal health workers and 491 poultry farmers in the PICTs and 459 farmers, 138 traders and 82 service providers in Zambia, and it facilitated 12 poultry farmer group discussions and 48 PC meetings. Eight refereed scientific publications describe these individual components in more detail.

Conclusion: The study concluded that combining ensemble modelling with PCs can be used as a community-based platform involving rural poultry farmers in disease surveillance that is targeted, low-cost and sustainable while at the same time allowing capacity building, disease risk communication and improvement of livelihoods of rural communities.

Key words: Sustainable rural poultry surveillance, developing countries

Can change in animal behavior patterns be used for animal health surveillance?

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ABSTRACT

Objective: Syndromic Surveillance (SyS) detects disease epidemics by identifying changes in human behaviors that are associated with disease. SyS is also used in animal health to monitor many health related metrics including changes in human behavior (for example the behavior of a veterinarian choosing to submit necropsy samples to a diagnostic laboratory). However there have been few published examples where direct monitoring of animal behavior has been used to identify animal disease epidemics. Astute farm managers can identify animal behavior changes in response to disease, suggesting that changing animal behavior could have value for identifying disease epidemics. Recent technological advances have made data available that could be used to monitor individual animal movements that potentially could be used to identify behavioral changes associated with disease. The purpose of this study was to explore the value of monitoring animal movements for animal health surveillance.

Materials and methods: A custom designed system was developed to for monitoring of movements of laying hens in a commercial production environment. Data visualization tools were developed to identify daily movement patterns in hens over the production period, time series clustering methods were used to identify daily movement patterns that were similar within and between hens, and metrics such as sample entropy were used to identify changes in movement patterns that could be associated with disease or other events.

Results: Individual hens demonstrated unique movement patterns that were different between hens, but consistent within hens over the short term (weeks). These patterns changed gradually within hens and across groups of hens over the production cycle. Sudden pattern changes were detected in response to external stimuli.

Conclusion: Monitoring of hen movement patterns has potential for detecting changes in behavior patterns associated with disease, and should be further explored as a method for surveillance.

Key words: Animal behavior, animal movement, surveillance, complexity, precision livestock farming.

Economic losses due to hybrid heavy hens diseases and their impact on egg production economics

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ABSTRACT

Objectives: The aim of this study is to analyze the effects of economic losses due to diseases of hybrid heavy hens in intensive poultry production and their impact on economic production of hatching eggs.

Material and methods: The study was conducted at a poultry farms in northern Croatia, where chickens are hatched and then moved and kept at a production barn from the age of 23 weeks until the end of the production cycle at the age of 56 weeks or 32 weeks of laying. In the study, the flocks were followed during the breeding phase (23 weeks) and the laying phase (33 weeks). The analysis of economic losses and costs included the technological results of each phase, the average age of dead poultry, food consumption, mortality rate, egg production as well as farm's operational dana, planned and achieved results. Damages were estimated using differential equations and a detailed analysis.

Results: The total costs due to diseases during the breeding phase and in the production of hatching eggs amounted to U.S. $ 33,413.55 and U.S. $ 251,695.25, respectively. The most common causes of death in the breeding phase were cachexia (23.56 %), necrosis of the femoral head (7.97 %) and arthritis (10.51 %). In the production of hatching eggs, the most important causes of death of hens were reproductive organs diseases (4.87 %), Marek's disease (5.04%) and costs due to liver disease (2.02 %).

Conclusion: Since the poultry production has the significant role in the agricultural and food production sectors, it is of great importance to know the effect of poultry diseases on the poultry industry and their impact on the country's economy. This study contributes to better understanding of the economic losses due to hybrid heavy hens diseases and their impact on economic production of hatching eggs.

Key words: diseases, economic losses, hybrid heavy hens, poultry production

What is One Health surveillance?

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ABSTRACT

Objective: The One Health (OH) approach is being promoted for complex health challenges at the interfaces of humans, animals and the ecosystems constituting their environment. This article explores the consequences this approach has for surveillance.

Material & Methods: In an iterative consultation process, the EU COST Action "Network for Evaluation of One Health (NEOH)" identified important characteristics of the OH approach and illustrated the linkages to the health policy cycle. Population health surveillance has been defined as an activity which produces information that is used to make decisions about health. We will discuss the implications of OH as characterized by NEOH, for surveillance.

Results: The systems approach used in OH and the understanding of a population as being embedded in a complex adaptive system provides a new perspective for surveillance. First, complex adaptive systems demonstrate emerging properties at different levels of the organisational hierarchy, which can be used to assess the integrity of the system up to the level of observation. Modelling system dynamics considers more nodes in a system and moves representation beyond the biomedical aspects to better embody cultural and intangible elements. Finally, the transdisciplinary approach used in OH emphasises that the goals of surveillance as well as the methods of surveillance should be generated in a participatory process that includes tacit knowledge and provides socio-ecological imbedding.

Conclusion: The practice of OH surveillance shifts from traditional one domain surveillance that observes disease presence and absence to monitoring health indicators. The systemic approach provides a more holistic representation of the dynamics at hand. Finally, warranting citizen participation throughout the policy cycle defines new roles for surveillance, for transparency, accountability, collective decision making and ties it deeper into a continuous process of self-reflection in a public learning organisation.

Key words: OH surveillance, policy cycle, wicked problems, integrated approach, transdisciplinary

African swine fever still on the move – epidemiological evaluation of control measures in Latvian wild boar

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ABSTRACT

Objective(s): Considering available data, it seems that in countries where African swine fever (ASF) emerged within the wild boar population, the implemented control measures failed so far in eradicating the disease. Even controlling the spread within the wild boar population appeared impossible. We aimed to improve the understanding of the epidemiology of ASF in wild boar and analysed the effect of implemented control measures on the course of the disease.

Materials and methods: A comprehensive statistical analysis of available surveillance data in wild boar was performed. The temporal development of prevalences (virus detection and serology) was analyzed. The effect of implemented control measures was analyzed determining an appropriate control period and comparing the defined target figures statistically.

Results: Within the study period of 41 months, no significant increase or decrease of the prevalences was found in the study area. Although different measures had been implemented over time to control the epidemic in wild boar, no clear effect on its course was evident. Conversely, the extent of the infection appeared rather unaffected of the different implemented measures.

Conclusions: To control an established ASF infection within a wild boar population, the currently implemented measures need to be revised. It is open, whether efficient options for control exist if the disease is widespread.

Key words: African swine fever, control measures, epidemiology, Latvia, wild boar

"It's a real job, putting food on plates": A qualitative study of retention of UK farm animal veterinarians

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ABSTRACT

Objective: Private veterinarians are an integral part of national veterinary services. Retention, rather than recruitment, has been identified as the key issue for maintaining adequate numbers of suitably trained and experienced vets to deliver the services required. Retention is a complex issue, intrinsically linked to veterinarians' career decisions. The study aimed to explore how veterinarians' experiences, attitudes and perceptions of UK farm animal practice have influenced their career choices.

Materials and methods: The data consisted of free-text responses to an online survey exploring the reasons behind respondents' decisions to remain in or leave farm animal work, and semi-structured interviews with veterinary employers. Thematic analysis was conducted to identify the main themes around veterinarians' decisions to remain in or leave farm practice.

Results: Among veterinarians who had remained in farm practice, intrinsic enjoyment of their work and satisfaction with their role were the primary drivers behind their decision. Vets who had left farm practice cited mainly extrinsic factors relating to their employment, such as pay, hours and working conditions. The importance of a supportive working environment, sufficient exposure to farm cases, and a sense of competence were consistent themes across both groups. Employers described the challenges of staff retention in rural practice and the strategies used to retain veterinarians.

Conclusion: The results build on a previous quantitative analysis of factors associated with retention and demonstrate the complexity of individuals' career decisions, while identifying common themes from the experiences of current and former farm animal veterinarians in the UK. The findings have practical implications for employers and professional organisations attempting to improve retention of farm veterinarians. Retention will become even more important in the future, with increasing marketization and provision of public services by private companies, and uncertainty about the supply of overseas veterinarians in the UK after Brexit.

Key words: Farm, retention, qualitative, workforce, veterinarians

A 12-step aquatic animal health surveillance guideline to build and evaluate surveillance competencies

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ABSTRACT

Objective: The importance of aquatic animal diseases have been highlighted in several key references and they continue to gain recognition as one of the most challenging sustainability issues which needs to be addressed in this fastest-growing food producing sector. Animal diseases in general are one of the most important factors restraining cost-effective and sustainable animal production, product quality and marketability including export. There are many actions and approaches to understand disease patterns in populations and enable successful containment, however vast majority are developed and intended for terrestrial animal diseases. During the last few years, requests to the Food and Agriculture Organization of the United Nations (FAO) for technical assistance on the design and implementation of surveillance programs for aquatic diseases have increased. A number of technical publications specifically for aquatic animals elaborated on the principles of surveillance, sampling, survey types, survey design and planning. The purpose of this paper is to present simple but comprehensive tool for creating and evaluation of aquatic animal disease surveillance developed through collaborative effort of the FAO and several developing countries in Europe and Africa.

Materials and methods: The tool represents a 12-step aquatic animal health surveillance guideline that can be used as starting points to build surveillance competency or to evaluate existing surveillance measures/programs. The guidelines are in the form of a checklist that includes practical step-by-step design and requirements for implementing aquatic animal disease surveillance for non-specialists (i.e. those with limited formal education on epidemiology).

Results: The surveillance checklist was drawn from information and other technical elements contained in major aquatic animal disease surveillance references. The paper also reports summary of the outputs obtained using the 12 point surveillance guidelines in pilot testing in 5 Western Balkan countries (for VHS in trout) and 8 South Africa Development Community countries (for EUS in multiple fish species).

Key words: Aquatic animal health, disease surveillance, FAO, check list

One health challenges: Highly pathogenic avian influenza outbreak response

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ABSTRACT

Objective: As primary responders to an animal health emergency, much of the responsibility of considering aspects of one health in the control of an animal disease outbreak rests on state veterinary services. This study explores the response to an outbreak of highly pathogenic avian influenza in the Western Cape Province of South Africa in 2017. We record to what extent aspects of a one health response were considered as well as what barriers exist to an effective response.

Materials and methods: Veterinary Services officials whose work was affected by the outbreak were interviewed and their experiences recorded.

Results: Utilisation of existing government networks resulted in the involvement of agencies covering several important aspects of a one health response, including human health surveillance, environmental considerations regarding the disposing of infected material, social relief, animal welfare and media communication. However, the delay in response for some of these aspects was a challenge. Issues identified included the lack of a streamlined communication strategy both within and from veterinary services. While a contingency plan for outbreak response exists, it is not widely available or updated. No psychological support for those affected by the outbreak was provided. Adequate collection of data or facilitation thereof during the outbreak was lacking. As a result, useful analyses of the outbreak could not be performed to their full potential.

Conclusion: Although many aspects of a one-health approach were adequately considered, there is room for improvement to increase the efficacy of outbreak response. Recording and evaluation of actions is an important part of outbreak response. This should facilitate the production of widely-used contingency plans for improved outbreak response in the future.
Key words: One health, avian influenza, contingency planning

An observatory of gastrointestinal and pulmonary parasites in grazing livestock, as a tool to empower farmers and allow adaptation to a climate changing world

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ABSTRACT

Objective: A four-year project was recently funded by FIA (Agricultural Innovation Foundation) in Chile. The project (PYT-2018-0125) was granted to Vetwork SpA, a Chilean Company focused on informatic and veterinary sciences solutions and the University of Chile and its veterinary School. The objective is to combine first-hand information on parasitic infestation in multiple farms while recording weather information in local weather stations. Added to this, surveys will be conducted through the study to record management conditions.

Materials and methods: Fourteen independent farms will be enrolled in the study, seven from each of two agro-ecological areas in the Araucanía regions, in southern Chile. From these, surveys will be taken, and fecal samples will be gathered on a regular base, during the whole 4 years of the study. Eggs or oocysts or cysts counts (McMaster), or egg detection (Flukefinder®) will provide the information on parasites burden at animal and pasture levels. Weather information like UV radiation, moisture, rainfall, etc. will be collected also regularly, based on an ongoing weather stations records. On a yearly basis the collected information will be summarized an aggregated to produce descriptive statistics and a model, which will allow to establish which are the relevant factors behind the increase in parasitic activity in grazing livestock in the area. During the final year of the project, a web-based platform will allow farmers and veterinary practitioners to learn on which specific time of the year there is an increased risk for which specific parasitic infestation. This will allow farmers and veterinary staff to implement precise and timely actions to reduce losses, while understanding the effect of climate change in Chile and the region

Key words: Gastrointestinal parasites, climate change, precision farming, livestock, Chile

Development of a local risk map for African Swine Fever in Germany

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ABSTRACT

Objective: We develop a local risk map for veterinary authorities to estimate the risk of entry of ASF virus and the risk of exposure of domestic pigs and wild boar, taking into account local peculiarities.

Material and methods: Available data is first used to establish geographic layers for potential risk factors. This includes information on vegetation, season, temperature and the number of wild boar reported in the hunting bag. In addition, anthropogenic factors like settlements, pig holdings, roads, rest areas along motorways and traffic data are included. Veterinary authorities may add local knowledge like information on the presence of seasonal workers from ASF-endemic areas or on hunting tourism to areas where ASF has occurred, hot spots for illegal waste disposal or areas of outstanding wild boar abundance.

Results: We developed a risk map for Lower Saxony, Germany, using a grid of 3 km x 3 km. Each geographical layer presents the data in a categorized manner (presence of motorways in binary form, vegetation classes, etc.). The final risk for each grid cell is calculated in an additive fashion from the risks of the individual geographical layers. This will be complemented by weighing each layer individually.

Conclusion: The tool will provide risk managers with information on critical areas to increase the chance of early detection of ASF and to use resources effectively for both prevention and control if ASF is introduced. This tool can be extended to other wildlife diseases like avian influenza, classical swine fever, Hantavirus infections.

Key words: African swine fever, risk assessment, vegetation, map

Bovine-Herpesvirus 1 - Infection in cattle in North Rhine-Westphalia, Germany, during several phases of a control programme

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ABSTRACT

Objective: The aim of the current study was to develop classification criteria for the BoHV-1 herd status based on the diagnostic results.

Material and Methods: In the German federal state North Rhine-Westphalia, the national database for animal identification (HI-Tier) is used for recording diagnostic data on BoHV-1 in cattle. Data from 01.01.2010 until 31.12.2015 were selected, providing very good data quality due to the fact that compensation for diagnostic tests was tied to data entry in HI-Tier. The status of the farm is not recorded in the database, only the results of the diagnostic tests of individual animals or bulk milk testing. Within the study, classification criteria were developed to assess the farm status semi-automatically. Cohen's Kappa was used to assess the agreement of categorisation between two researchers.

Results: The farm status of BoHV-1 was categorised into nine different levels. One level was free of BoHV-1, one unknown, and seven sublevels were chosen for positive farms, depending on the results of bulk milk testing and gB and gE testing of individual animals. Furthermore, the phase of the control programme and the progress of the herd status were classified.

Conclusion: According to the developed criteria, it was possible to categorize the majority of farms automatically. The developed system will provide opportunities to compare the progress within the eradication programme between production types and regions.

Key words: BoHV 1, cattle, control programme, IBR

Poultry backyard production farming in Chile: contribution to food security in a high-middle income country threatened by animal diseases

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ABSTRACT

Objectives: Despite the importance of backyard poultry systems (BPS), there are no precedents of their contribution to the economy, food security and animal and zoonotic disease risk in of rural households in Chile. This study aims to characterize the poultry-rearing BPS in central Chile by assessing their constraints to biosecurity and animal diseases, and their contribution to the food security of these households.

Materials and Methods: A cross-sectional study was conducted at 384 BPS in three regions in Chile. A conceptual framework, describing inputs and outputs of these productive systems was developed, and a gross margin analysis (GMA) per household was performed to assess profitability of the system.

Results: BPS in central Chile are epidemiologically vulnerable to animal diseases due to lack in biosecurity measures such as absence of confinement, veterinary assistance and incorrect mortality handling. Annual gross margin indicates that 62% of the BPS had a positive balance from production. Distance to closest market and per capita income were factors associated to poultry value to farmers and predictors of poultry consumption were: older owners, higher transportation price to closest market, larger amount of poultry, and women as responsible of rearing birds. On the other hand, higher per capita income and bigger household size predicted reduction in consumption.

Conclusion: Backyard poultry production in central Chile contribute to food security, household economy and gender roles. However, due to deficiencies in biosecurity and the risk of the introduction of priority diseases in commercial farms, they are vulnerable to the adverse effects, like high mortality/culling. Thus, to face these threats, educational programs on biosecurity together with improved and comprehensive disease management policies that considers the food security of affected vulnerable populations, are needed

Key words: Influenza, economy, surveillance, risk

Assessing the risk of countryside access during an outbreak of foot-and-mouth disease

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ABSTRACT

Objective: During FMD outbreaks, management of countryside access is a particular challenge. FMDV can survive in the environment and countryside access risks movement of FMDV to uninfected areas via environmental contamination and via fomites such as people, vehicles and non susceptible animals. At the same time, there is an economic and societal impact of restricting access to recreational activities in the countryside. This was illustrated in 2001 in UK, when the effective closure of the countryside contributed to substantial economic losses to tourism and the rural economy.

Materials and methods: We assessed the risks of onward FMDV transmission as a consequence of allowing continued countryside access for a range of recreational activities, including hiking, climbing, canoeing, equestrian activities and holding countryside events. Risk pathways were developed for each activity, likelihoods were assessed for each step of the release and exposure pathways based on available relevant literature, and risk levels assessed on the basis of likelihoods and potential consequences, for activities in different FMD control zones.

Results: For most activities, risks outside the Protection Zone (which extends at least 3km around infected premises) were assessed as low or very low, as long as mitigation measures such as biosecurity were adhered to. Activities in the PZ, where there is an increased risk of undetected local transmission or environmental contamination, were assessed to be medium risk or above. Activities involving horses or susceptible wildlife, such as deer stalking, presented an increased risk in all zones. Uncertainty was high due to the lack of relevant literature on several parameters.

Conclusion: Risk levels were reviewed by the UK FMD National Experts Group and published online. Use of these risk assessments for decision-making in an outbreak situation was recently tested in a national FMD exercise.

Key words: Foot and mouth disease, rural access, risk assessment, policy

Factors associated with improved uptake of Johnes Disease control activities on Australian dairy farms: Regulatory insights from evolving control strategies.

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ABSTRACT

Objective: Johnes Disease (JD), caused by *Mycobacterium avium ssp. paratuberculosis* (MAP), impacts dairy industries globally. Australia, Canada, and Ireland have low cow prevalence with varying herd prevalence and have recently reviewed control activities owing to frustration with previous control programs and changing industry dynamics. Control objectives are similar, but drivers and execution vary. JD remains a notifiable disease in Australia, although farms certify low-risk status through a voluntary producer-centric, risk assessment-based program as part of an integrated biosecurity plan. We aim to identify characteristics of producers participating in JD control, satisfaction with control programs, and compare JD control activities in Australia, Canada, and Ireland to inform current and future control policy.

Materials and methods: Reviewed literature (2000 – 2018) using online research databases and key words covering epidemiology and economics associated with control and regulatory affairs, and JD vaccines in Australia, Canada, and Ireland. Comparison of tabulated results identified gaps to be addressed by future research. The latter has commenced and includes a questionnaire capturing JD control knowledge, attitudes, and practices plus demographics from 400 Australian dairy farms, veterinarians, industry, and state government. Choice variable analysis will identify strategy choice and associated demographics. Bayesian and scenario analysis will investigate likelihood of choosing options plus perceived benefits and barriers.

Results: Aside from country-specific differences, major review findings reveal control strategies using vaccination are lacking, suggesting opportunities for improved efficiencies of regulatory oversight. Preliminary evidence indicates positive returns from instituting control but requires 5-10 years to benefit the whole industry. Our analysis will clarify choice of and attitudes to control, demographics of participants, perceived benefits and sustainability barriers, and effective policy. Lessons for moving forward will be concluded.

Conclusion: Evolution and varied success of JD control in different countries indicates high likelihood of positive returns for long-term programs, but short-term challenges to adoption and sustainability. Canada and Ireland's JD regulatory policies may benefit from Australian experience with JD control.

Key words: Johne's disease, control, policy, participation

Semi-commercial modes of operation among village chicken producers may favor the release of HPAI-H5N1 to Indonesian villages

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ABSTRACT

Objective: Indonesia frequently reports Highly Pathogenic Avian Influenza H5N1 (HPAI-H5N1) events among village poultry. We conducted a data-driven exploration and modeling simulation to identify village chicken productive landscapes that favor the release of HPAI-H5N1 through trading activities.

Materials and methods: We analyzed survey data on 191 village chicken producers from Java, Indonesia using hierarchical clustering analysis. Clusters identified were used to inform a demographic model that simulates population dynamics of village chickens and allows estimation of trading events associated to outputs and inputs of the system. We estimated a presumed frequency of trading events linking villages with potential sources of HPAI-H5N1 in village scenarios with variable village chicken productive landscape. Multiple realizations of each village scenario were performed to produce distributions of trading event frequency. Finally, we estimated a *village release score* that represents the risk of HPAI-H5N1 release associated to the different village chicken productive landscapes evaluated.

Results: Three clusters with different farming practice, bird replacement source, and main produce traded beyond the village (F-exact: P < 0.001) were identified and named 'non-specialists', 'bird-specialists', and 'egg-specialists'. Overall, egg-specialists engage in the largest number of trading events per week, with a median of 13 per 1000 chickens; bird-specialists and non-specialists engage in median 7 per 1000, and 4 per 1000 chickens weekly trading events, respectively. Increasing presence of bird-specialist and egg-specialists in village scenarios raised the *village release score*, although egg-specialists are significantly riskier in terms of HPAI-H5N1 release.

Conclusion: A shift from subsistence to semi-commercial modes of operation among village chicken producers may lead to increased risk of HPAI-H5N1 release in villages, and egg-specialist may be key facilitators of HPAI-H5N1 incursions to these settings. Our results suggest that characterizing village chicken producers may help to quickly assess the risk of HPAI-H5N1 release to villages.

Key words: Modeling, dynamics, release, risk

A GIS framework for evaluation of spatial factors that affect the quarantine station selection

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ABSTRACT

Objective: The General Administration of Quality Supervision, Inspection and Quarantine of China (AQSIQ), is responsible for the identification of quarantine station. With a view to improve the framework for the evaluation of the quarantine station performance, AQSIQ, together with the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe), has developed a specific system based on a webGIS tool and a data analysis component. The present paper presents the technical solutions adopted for the system development and the results obtained.

Materials and methods: The webGIS tool is based on a PostGreSQL version 9.1 (with the spatial extension POSTGIS 2.0) as database server, GeoServer 2.4.4 as application server and PHP 5.3 as developing language. Javascripts with AJAX technology and OpenLayers 2.12 is used for the webGIS application. OpenStreetMap, showed through RESTful API version 0.6, is used as base map. The data analysis component, is based on a protocol founded on the Simple Additive Weighted method (SAW) combined with the Analytical Hierarchical Process (AHP). The Expert Choice software was used for the AHP exercise.

Results: A specific protocol, based on the webGIS functionalities, was developed. The protocol allows the local AQSIQ functionaries to georeference and characterised the relevant spatial features surrounding the quarantine stations. At central level, a dedicated GIS project automatically acquires the spatial information and calculates the spatial index of the quarantine station performance under evaluation.

Conclusion: The proposed system designed to support import-export veterinary inspection and quarantine activities was a breakthrough in terms of functionality and decision-making, since it redeployed functional priorities and lead to a revision of AQSIQ conventional approaches.

Establishing a serum bank of confirmed cysticercosis positive and negative samples

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ABSTRACT

Objective: This project aims to collect a bank of confirmed cysticercosis positive and negative samples from pigs that will be used for future diagnostic test validation

Materials and methods: We have recruited twelve slaughterhouses from two counties (Kakamega and Busia) with the help of County Directors of Veterinary Services. We will purchase, at market rate, 10 pigs from 12 different slaughterhouses. Sampling will be conducted over 5 months and no more than two pigs will be purchased from one slaughterhouse per month. This will avoid destabilizing the pork market as a result of our research activities. The selected pigs will undergo the normal slaughtering procedure at the slaughterhouse, enhanced by the study team to ensure appropriate ethical standards are upheld. Ante mortem lingual palpation will be carried out, while blood collection will be performed post mortem. The age, sex and origin of the animal will be recorded, and a very detailed carcass dissection (including major organs) performed, with tissue containing cysts being sampled for further molecular diagnosis.

Results: A bank with confirmed cysticercosis positive and negative samples will be established. The results will be in open access and hope this will expedient validation of better diagnostics kits to aid quicker and more accurate diagnosis of the disease.

Key words: Cysticercosis, *T.solium,* diagnostic test

Two approaches for assessing the coverage of vaccination against rabies and anthrax and assessing effectiveness of the campaigns in Georgia

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ABSTRACT

Objectives: Anthrax and rabies are two major endemic zoonotic diseases in Georgia. All prophylactic vaccination of animals were suspended from 2007 to 2012 which led to increase cases of anthrax and rabies in animals and humans. Vaccination of animals was reintroduced in 2012 and two different approaches have been to assess the effectiveness of vaccination coverage for rabies and anthrax in 2013-2017.

Materials and methods: Private veterinarians were contracted by the NFA to deliver the vaccination. Vaccination of large, small ruminants and horses for anthrax was risk based. Vaccination of owned dogs and cats for rabies was blanket coverage. Monitoring the over both vaccination campaign was conducted by state veterinarians from regional and central officies of the NFA. Anthrax and rabies vaccinaton coverage was evaluated through confirmation of vaccination status of 3% randomly selected animals. No serological survey on vaccinated animals was conducted due to the lack of available reliable serological test. In addition rabies vaccination coverage of dogs and cats was assessed by registering the whole population of dogs and cats in randomly selected villages. A post vaccination serological survey was conducted in dogs.

Results: In total 4 129 018 animals were vaccinated for anthrax and 1 138 613 dogs/cats for rabies from 2013-2017. As a result animal anthrax cases was decreased by 62.5% in 2017 (15 cases) as compared with 2013 (40 cases). Rabies cases decreased by 65.5% in 2017 (40 cases) compared with 2013 (116 cases). Vaccination status of all animals were confirmed by the owners. Vaccination coverage of dogs in randomly selected villages proved to be 69% and immune response of vaccinated dogs was 89% in 2017.

Conclusion: Control of anthrax and rabies is feasible through the vaccination campaigns therefore the NFA plans to strenghen surveillance of vaccination for anthrax and rabies including the use of epidemiological tools to ensure effective vaccination coverage.

Key words: Anthrax, Rabies, Zoonotic, vaccination, coverage

Comparing apples with apples: A simplified method for assessing animal health surveillance intensity at the regional level

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ABSTRACT

Objective: A major concern for animal health authorities managing surveillance programs is whether the number of surveillance reports submitted by administrative regions is sufficient, given the size of their respective livestock populations. We developed a simplified methodology to allow comparison of the number of surveillance reports by administrative region.

Materials and methods: Passive surveillance data from the National Sheep Health Monitoring Project in Australia for the period January-December 2016 provided counts of sheep enterprises investigated for ovine Johne's disease (OJD) by state. The expected number of OJD investigations for each state was obtained by dividing the total number of OJD investigations by the total number of sheep enterprises across all states and multiplying that value by the number of sheep enterprises in each respective state. The actual number of investigations per state was then divided by the expected number to return a standardised investigation ratio (SIR).

Results: In 2016 a total of 4907 sheep enterprises were investigated for OJD across Australia. New South Wales, a state with a relatively large number of sheep enterprises, had the highest expected number of investigations but the lowest SIR (0.13, 95% CI 0.12 to 0.16). In South Australia the number of OJD investigation was 4.1 (95% CI 3.9 to 4.2) times that expected, given the size of the South Australian sheep enterprise count.

Conclusion: This study demonstrates the use of indirect adjustment as means for comparing surveillance intensity across administrative regions. The method is suitable for relative comparison only. Determination of what constitutes an appropriate expected surveillance investigation count for each region will depend on specific diseases of interest for a given jurisdiction.

Key words: Surveillance intensity, passive surveillance, methodology, evaluation, Australia

Foot and Mouth Disease (FMD) survey of newly graduated veterinarians and their opinion towards vaccination

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ABSTRACT

Objective: Uruguay is free from FMD with vaccination since 2003. However, before the outbreaks occurred on 2000-2001 the country was free without vaccination, thus, the idea of stopping vaccination has raised in recent years, and that could help opening new exportation markets and reduce the national FMD budget. Our objective was to determine the perception about FMD on veterinarians entering the only Veterinary School (VS) in Uruguay after 2002.

Materials and methods: In 2016, we conducted a survey of the last 100 veterinarians to register as livestock veterinarians. The survey contained demographic information questions, opinion regarding national resource allocation for specific livestock diseases, and FMD-related questions. We estimated odds ratios and 95% confidence intervals (CI) between suspending vaccination opinion (yes & no) and other FMD-related questions.

Results: The response rate was 62% with one exclusion due to entering VS in 1999. Median year of entering VS was 2007, and median graduation was 2014. Veterinarians reported that the country should allocate more resources towards bovine brucellosis (28%), tick-borne diseases (22%), FMD (7.1%), and tuberculosis (7.1%). Forty-percent reported that Uruguay is prepared in case of an FMD outbreak and 65% thinks that veterinarians are qualified to identify an FMD case in the field. Eighty-six-percent reported that more resources are needed for surveillance and prevention, 67% reported that FMD is an ancient disease, and 79% thinks that the risk of re-introduction is at least moderate (versus low risk). When asked about suspending vaccination, 24% was in favor and 76% were against it. None of the odds ratios between the opinion of suspending vaccination and other FMD questions were significant (95 % CI's included 1)

Conclusion: This survey provided unique information about FMD perception on the recently graduated veterinarians and their opinion towards vaccination. This preliminary data was used on a larger survey being implemented in the current year.

Key words: Foot and Mouth Disease, FMD, vaccination, veterinarians, survey

Factors influencing the competitiveness of smallholder pig farmers in the Northern Cape province of South Africa

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ABSTRACT

Objective: Pork is one of the most important sources of relatively cheap protein in South Africa. Looking at the factors influencing the competitiveness of smallholder pig farmers in South Africa is therefore important in order for one to maximise the positive factors and minimise the negative or put countermeasures for the negative factors influencing competitiveness. In general, there is high demand for pig meat in South Africa as evidenced by the high dependency on imported pork products over the years. Therefore improving the competitiveness of the smallholder pig producers will go a long way in improving the socioeconomic conditions and food security in South Africa's rural communities. The research's main objective was to identify smallholder pig producers' perception of the important and critical factors that drive and influence their competitiveness in South Africa. This is important to elucidate and understand why the smallholder pig producer sector has remained relatively less competitive than commercial pork production sector of the pig industry.

Materials and methods: A carefully designed and structured questionnaire aligned to the Porter methodology framework was developed and completed by smallholder pig producers in order to identify the perception of the critical factors that drive and influence their competitiveness. A correlation coefficient analysis was carried out in order to interpret the underlying perceptions of the producers. The different business environments (macro-, micro- and meso-environments) were used to group the factors as was done by Will (2004) and Roduner (2005).

Results: The significant macro, micro and meso-environment factors that have an impact on the competitiveness of smallholder pig producers in the Northern Cape Province were identified.

Key words: Competitiveness, smallholder pig farmers, South Africa

Assessment of the value of PCR assays in oral fluid Samples for detection of African Swine Fever, Classical Swine Fever, and Foot-and-Mouth Disease in U.S. Swine

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ABSTRACT

Objectives: Sampling and testing oral fluids (OF) offers a convenient, unobtrusive mechanism for evaluating the health status of swine, especially grower and finisher swine. This assessment evaluates the potential testing of OF samples with real-time reverse-transcriptase polymerase chain reaction (rRT-PCR) to detect ASF, CSF, or FMD for surveillance during a disease outbreak, for general active surveillance, and for early detection in a disease-free setting.

Materials & Methods: We used a series of logical arguments, informed assumptions, and a range of parameter values from literature and industry practices to examine the cost and value of information provided by OF sampling and rRT-PCR testing for the swine foreign animal disease surveillance objectives outlined above.

Results: Based on the evaluation, OF testing demonstrated value for all three diseases and objectives. The greatest value was in an outbreak scenario, where using OF would minimize disruption of animal and farm activities, reduce sample sizes by 23%-40%, and decrease resource requirements relative to current individual animal sampling plans. For an early detection system, sampling every 3 days met the designed prevalence detection threshold with 0.95 probability, but was quite costly. Substituting OF sampling for tonsil sampling, which is currently used for CSF surveillance in the US could contribute to laboratory preparedness, and would result in a 0.95 probability of detection at 0.062%-0.094% prevalence among animals annually.

Conclusion: Implementation of OF testing for ASF, CSF, or FMD surveillance is not yet possible due to several limitations and information gaps. The gaps include validation of PCR diagnostic protocols and kits for ASF, CSF, and FMD on swine OF samples, minimal information on test performance in a field setting, detection windows with low virulence strains of some foreign animal disease viruses, and the need for confirmatory testing protocol development.

Keywords: Oral fluids, swine, African Swine Fever, Classical Swine Fever, Foot-and-Mouth Disease

Buzz in the pits: Production events and herding behavior in livestock future markets

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ABSTRACT

Objectives: Livestock futures market traders use currently available information to set price expectations at set intervals in the future (future contracts). Traders may take positions (buying or selling) today based on uncertain or unconfirmed information that are expected to impact production, trade, or consumer acceptance in the future. Livestock futures contract prices could serve as an immediate measure of expected market impact from production events. The objective of this study was to explore the implied volatility, persistency and rationality in futures market contract prices due to trader reactions to disease or disaster information that affected livestock production expectations.

Materials and methods: Hourly futures prices, trade volumes, and number of trades were obtained from 2006 to 2017 for live cattle, feeder cattle, and lean hog futures. Production events considered were major disease or food safety related events for United States livestock markets. Production event dates were used to create event windows, which helped determine unexpected trading behavior (herding or momentum trading). Data were analyzed using econometric models to determine if herding behavior affected the longevity and magnitude of price reactions. The presence of herding behavior could cause a greater magnitude or more persistent reaction than would otherwise be expected.

Results: Preliminary results of a single rumor of foot-and-mouth disease (FMD) in the United States indicated futures contract price volatility and herding behavior, which increased the magnitude of price effects and indicated the presence of momentum trading. Traders responded initially to the news by driving the market price sharply down but even after the FMD rumor proved to be false, markets continued to trade down due to herding behavior. Livestock futures contract price movement in reaction to a disease or disaster provided insight into the dynamics of trader response to uncertain information and emphasized the importance of communication in disease or disaster response.

Key words: Economic impact, futures markets, livestock production, information uncertainty

Does rapid response to the risk of tail biting in fattening pigs pay?

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ABSTRACT

Objective: Tail biting in pigs is a multifactorial animal health disorder and also an animal welfare issue. Tail biting can arise as a consequence of different factors such as inadequate provision of enrichment and rooting materials to the pigs, intensive production environment, inappropriate housing conditions, along with other emerging health problems in the pigs or changes occurring in the rearing environment. The aim of this study is to examine economic benefits of early response to control tail biting in fattening pigs.

Materials and methods: The emergence of tail biting on a fattening pig farm is modelled by a dynamic optimization model. The data used in the modelling originate from a test farm in Finland. Besides tail biting itself, the model takes into account the effect of secondary disorders related to tail biting (locomotory disorders in particular) and how arrival of new information regarding the risk of tail biting may influence response to the problem.

Results: The results suggest that once tail biting occurs in the pen, the situation can quickly escalate and several pigs can be bitten within a relatively short time period. The results suggest that there is a positive economic return on farmers' preparedness to respond to tail biting should it occur in the pen and measures applied temporarily after the first biting incident. By contrast, preventive measures which are applied constantly throughout the fattening period can have a lower profitability.

Conclusion: The results suggest that rapid response to tail biting outbreak is economically profitable.

Key words: Tail biting, pig, prevention, dynamic optimisation

Giving weight to non-economic factors in animal health decision-making

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ABSTRACT

Making animal health decisions is a complex process that involves integrating information on disease prevalence, risk factors, diagnostic tests, and treatments to identify the optimal management strategy for an individual farm. As veterinarians and researchers, we have a tendency to focus on the net economic value of interventions as the primary outcome when making the case for farmers to adopt a particular management strategy. However, there is growing evidence that other factors such as available labour resources, competing priorities, long-term farm business goals, animal welfare considerations, and social pressures can have an equally if not more important role in making the decision. As part of a new research programme to build the business case for bovine viral diarrhoea virus (BVD) eradication in New Zealand, we are conducting a series of qualitative and quantitative studies to better understand what motivates farmers to voluntarily adopt BVD prevention and management strategies. This includes (1) a Facebook advertising campaign to compare the efficacy of three different themed messages (economic, welfare, and social) in motivating farmers to click on a survey link, (2) semi-structured interviews with farmers across New Zealand to collect information on why they may or may not have already chosen to implement BVD management strategies, and (3) a national cross-sectional survey asking for farmer and veterinary opinions towards adopting a voluntary versus mandatory national eradication programme. Data from these studies is being used to generate new metrics beyond strict cost-benefits to decide which approaches to BVD eradication are optimal for individual farms as well as the New Zealand cattle industry.

Key words: Disease control, modelling, economics, dairy cattle, beef cattle

Development and application of joint risk assessment toolkits for zoonoses at human and animal interface

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ABSTRACT

A first collaborative step in decreasing zoonotic disease risks is to have a good understanding of where and why risks exist, which can be brought about through national level risk assessment based on existing information. Such information can be shared and risks assessed jointly by national animal and human health sectors, and other stakeholders. However, for such a joint risk assessment (JRA) to proceed efficiently, the sectors must agree on a standard process, guided by best practices, and have joint tools. Historically animal and human health sectors have had different approaches in conducting risk assessments. Although the principles remain similar, the processes are diverse. The FAO, OIE, and WHO have taken steps in developing standard tools and processes for conducting national JRA using zoonotic influenza as a model. The JRA tools combine the animal health and human health sector approaches and technical expertise. The JRA tools describe systems and technical processes, elements required to apply the JRA tools in case of emergency, elements required to have a sustainable national JRA system, and elements that may enhance the success of a JRA. The JRA tools were piloted in Indonesia based on zoonotic influenza (LPAI and HPAI), rabies and leptospirosis. In Indonesia, the JRA approach was appreciated as a platform to improve evidence-based decision making for risk management and communication messages. In addition, the JRA process improves multi-sectoral coordination and information sharing, and steps are taken to adopt the JRA processes into country context and existing national mechanisms.

The monetary burden of cysticercosis in Mexico

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ABSTRACT

Objectives: *Taenia solium* cysticercosis is a public health and agricultural problem in many low and middle-income countries where health education, sanitation, pig management practices, and meat inspection infrastructure are insufficient. Despite cysticercosis affecting both human health and animal productivity, few studies have been conducted to evaluate the monetary burden of cysticercosis. The objective of this study was to estimate the costs associated with cysticercosis in humans and pigs in Mexico.

Materials and methods: The monetary burden of human cysticercosis was estimated based on costs incurred by living with and treating epilepsy and severe chronic headaches associated with neurocysticercosis (NCC). The estimated cost of porcine cysticercosis took into consideration losses due to the reduction in the price of cysticercosis-infected animals. Epidemiologic and economic data were obtained from the published literature, government reports, and setting-specific questionnaires. Latin hypercube sampling methods were used to sample the distributions of uncertain parameters and to estimate 95% credible regions (95% CRs).

Results: A preliminary year 2012 monetary burden of NCC was estimated at U.S. $234,397,284 (95% CR U.S.$129,456,344 – U.S.$368,743,098), with U.S.$521 (95% CR: U.S.$344 – U.S.$760) lost per patient. Up to an additional 16 million U.S. dollars was estimated to be lost due to porcine cysticercosis.

Conclusion: This is a first study to estimate the monetary burden of cysticercosis in Mexico. The methodology developed here can be applied to estimate the monetary burden of cysticercosis in other regions in order to better prioritize disease control initiatives.

Key words: Cysticercosis, economics, Mexico, neglected tropical diseases

The cost of bovine respiratory disease in US beef calves prior to weaning

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ABSTRACT

Objective: To estimate the direct economic cost of bovine respiratory disease (BRD) in US beef calves prior to weaning.

Materials and methods: A stochastic simulation model was conducted using computer spreadsheet add-in software. Input data were obtained from USDA, peer-reviewed papers, and a survey of BRD treatment and labor costs by beef cow-calf producers. Results were reported by a median point estimate with 90% credible interval.

Results: Between 2011 and 2015 the estimate of the median total economic cost of BRD in pre-weaned beef calves was $165 million (129–246), of which the costs due to death, medical treatment, and weight loss were $126 million (92–200), $25 million (20–32), and $15 million (9–25), respectively. The median costs associated with death due to BRD in calves < 3 weeks and ≥ 3 weeks of age were $44 million (29–72) and $84 million (57–138), respectively. Death loss in calves prior to weaning was the largest cost component (76%). Total cost of BRD was most sensitive to death in calves ≥ 3 weeks of age.

Conclusion: This model estimated the total and component costs of BRD in US beef calves prior to weaning due to deaths, reduced performance, medicine, and labor to treat sick calves. Death loss was the most influential part of the total cost of BRD in beef calves prior to weaning.

Key words: bovine respiratory disease, pre-weaned calves, economics, stochastic simulation

Beef and sheep producers' perceptions of disease reporting and the impact of emergency animal disease outbreaks in Australia

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ABSTRACT

Objective: Vulnerability of Australian beef and sheep industries to exposure to and spread of an emergency animal disease was investigated in a cross-sectional study, as part of a project to improve animal health surveillance. This study investigates producers' perceptions around outbreak severity and likelihood, and efficacy of reporting to prevent disease spread.

Materials and methods: Data were gathered using a survey distributed electronically through government and industry groups, and analysed descriptively. Logistic regression analysis was used to identify differences between producers.

Results: Responses were obtained from 234 beef and 194 sheep producers. The majority of producers (91% beef; 86% sheep) agreed that reporting unusual signs of disease is efficient for preventing animal disease spread. Approximately 45% and 30% of beef and sheep producers expressed moderate to extreme confidence in identifying foot-and-mouth disease (FMD) in their animals and a similar proportion identified themselves as very/extremely concerned about this disease. In addition, FMD was identified, unprompted, by 56 beef producers (from 384 responses) and 20 sheep producers (from 302 responses), as one of the top three diseases of concern. Most beef (93%) and sheep (89%) producers reported the likelihood of FMD occurring on their property as a little likely/not likely at all. However, most (97% beef; 91% sheep) also believed that an outbreak on their property would be very/extremely serious.

Conclusion: In line with the Australian situation in relation to FMD, which has not been in the country since 1872, producers perceive a low likelihood but high impact of an FMD outbreak occurring in their properties. Producers consider reporting as crucial for preventing disease spread, however their level of reporting of animal health events and their confidence in identifying clinical signs of FMD could be improved. A better understanding of the drivers of these practices and perceptions could strengthen Australia's preparedness for this disease.

Key words: Response efficacy, disease reporting, emergency animal diseases, risk perception

Factors influencing farmer group participation in integrated surveillance and production systems: The case of cattle farmers in Indonesia

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ABSTRACT

Objective: The integration of animal health information systems at the national level has greatly enhanced disease surveillance and monitoring capabilities. The adoption of such technology by those at every level, from farmer up to high level government, is advantageous in capturing relevant data. New technologies, however, frequently encounter difficulties in their uptake at the farmer level. This work presents a case study evaluating the extension of the Indonesian Animal Health and Production Information System (iSIKHNAS) to cattle farmer groups in East Kalimantan, Indonesia.

Materials and methods: ThreeiSIKHNAS two-day training courses were conducted in November 2017 in Sepaku, Babulu and Penajam subdistricts with a total of 54 cattle farmers in East Kalimantan province. Eight different types of field reports were demonstrated on the first day, followed by one field day where participants practiced reporting to the system using text message. A follow-up trip was conducted two months after the initial training to evaluate iSIKHNAS uptake and determine the challenges faced by farmers in adopting this system.

Results: The uptake of iSIKHNAS varied by district. Overall, 35% of the trained farmers submitted one or more reports. There was a significant difference between subdistricts, with farmers from Sepaku much more active at reporting. Several factors that may have limited uptake of the system were identified. These included technical difficulties, a lack of technical support from agricultural livestock officers, communication issues within farmer groups, difficulties to change existing reporting practices, and a lack of perceived benefits.

Conclusion: This work highlights several issues associated with the successful uptake of animal health information systems by farmers in developing countries. Addressing the limitations identified above will increase reporting and facilitate a more sustainable and beneficial system.

Key words: Disease surveillance, farmer group, reporting, information system

Using animal health economics to improve companion animal care

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ABSTRACT

Animal health economics (AHE) has been used in veterinary medicine for many decades to help farmers make better decisions around livestock management. AHE is based on the principle that owners have limited resources to invest in animal health care and provides a framework for comparing the relative costs and benefits of different interventions. Although financial limitations are also important in companion animal medicine, there has been little research to date determining whether the same AHE principles can be used to improve individual patient care. In this article, we provide a basic overview of AHE for veterinarians and highlight several key areas where AHE can be potentially be applied to companion animal medicine including preventative care, chronic disease management, animal welfare, public health, shelter medicine, and national companion animal health policy. We then discuss some of the unique challenges in companion AHE particularly around developing a strong evidence base to support economic models, link between companion animal care recommendations and practice finances, getting small animal veterinarians to adopt a population medicine mind set, legalities of managing diseases with public health implications, assigning an economic value to the human-animal bond, and the political sensitivities attached to many companion animal health issues. To progress companion AHE as new discipline, the methodologies need to reflect the different role of companion animals in society and conduct more research to determine whether presenting clinical scenarios in an economic framework is effective in motivating owner behavioural change.

Key words: Animal health economics; dogs; cats; decision-making; welfare

Preliminary study of *Dirofilaria imitis* in dogs and their impact on human health in Istria County, Croatia

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ABSTRACT

Objectives: The aim of the study is to determine the seroprevalence of *D. immitis* in healthy dog population in Istria County and to evaluate age, keeping (indoors or outdoors) and use (pets, watchdogs, hunting dogs or truffle dogs) as risk factors.

Material and methods: The samples were taken from 134 healthy dogs in the Istrian County tested by SNAP* 4Dx* Plus screening test and modified Knott test. Risk factors (breed, age, sex, keeping, housing, moving, feeding, communication with other dogs, use (pet, hunting dog, truffle dog) were analysed. The prevalence ratio and odds ratio were used to calculate the risk and statistical significances (level of 95%) among groups tested using Chi Square Test and Regression Analysis.

Results: Out of 134 healthy dogs examined, antigen for *D. immitis* was found in 16 (11.94 %, CI 95 % 6.45-17.43 %). In dogs tested both by SNAP* 4Dx* Plus and modified Knott test, microfilria (modified Knott test) was found in 51.72 % (CI 95 % 33. 82- 70.19 %) while antigen for *D. immitis* (SNAP* 4Dx* Plus test) was confirmed in 20.69 % (CI 95 % 6.18 % do 35.72 %) of dogs. This implies that *D. immitis* was present in 40% of the modified Knott test positive dogs. Dogs kept outdoors were infected twice as much as indoor pets. The most significant differences were found between truffle dogs and other hunting dogs (OR = 12.37, P = 0.0046).

Conclusion: This preliminary study shows the potential risk of exposure to *D. immitis* in the Istrian County. The results of this study can help better understand risk factors and support risk-mitigation strategies to prevent and control *D. immitis*.

Keywords: *D. immitis*, prevalence, risk factor analysis

Retrospective study of human rabies exposure and associated risk factors in Istria County, Croatia

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ABSTRACT

Objectives: There is a limited number of studies examining risk factors associated with human rabies in Croatia. The aim of this study was to assess human rabies exposure and associated risk factors in Istria County.

Material and methods: A retrospective cross-sectional study was based on 1656 post-exposure patients reported at the Institute of Public Health of Istria County. The data set comprised patient data (gender, age, profession, post exposure prophylaxis) and animal data (species, breed, vaccination status, owner, keeping status, contact exposure (location, number, type and site of injuries). The significances (level of 95%) among groups were tested using Chi Square Test and Regression Analysis.

Results: The age and sex specific distribution showed that the majority of cases of human rabies exposure were in people above 50 years of age (40.22%) and among males (62.48%) and after contact with dogs (78.92%) and cats (15.82%). In 92 cases of other contacts, the highest number of contacts was with fox (17.39%), horse (13.04%), squirrel (8.70%), rat (8.70%) and badger (5.43%). Owners were known in 75.72% of contacts, while in 24.27% of cases contact animals were not under owner control and in 17.75% of cases the own animals were involved. Most injuries were bites (86.23%) and scratches (46%).The vaccination rate in dogs ranged from 50% to 75.41% and in cats from 2.04% to 5.71%.In 84.54% of cases wounds were treated locally. The rabies vaccine was used in 14.67% of patients.

Conclusion: A significant number of human rabies exposure cases in Istria county was reported. The results provide valuable information about risk factors associated with human rabies exposure which is of great importance for public health and can be implemented in educational programs as well as in other preventive strategies.

Key words: Human rabies exposure, risk factors, animals

Make health surveillance great again: How to ensure stakeholders' commitment in the reporting systems?

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ABSTRACT

Objectives: Early detection and control of animal diseases through efficient surveillance system is critical to control animal diseases and prevent emerging pandemic threats. Despite the recent global efforts, health surveillance system effectiveness remains limited especially in low and middle-income countries. Within the past ten years the French Agricultural Research Centre for International Development (CIRAD) and his partners have designed innovative evaluation tools to better understand local constraints impairing animal health surveillance performances. This paper presents a comparative analysis of the constraints observed in developed and developing countries and implication for animal health surveillance improvement.

Material and methods: Participatory epidemiology approaches were combined with modeling and econometrics techniques (e.g. discrete choice experiment) to generate information on the animal health disease surveillance process, acceptability, non-monetary costs and benefits; these methods were applied in 8 case-studies between South-east Asia and Europe. We used qualitative comparative analysis to describe the set of factors that would impact health surveillance system performances.

Results: All the studies used common evaluation tools based on participatory approaches, although the object of evaluation varied. North and South countries shared common constraints (socio-cultural and economical) on local actors' reporting decision. However, the origin and the responses to these constraints would differ from one setting to the other, linked to specific socio-cultural practices rather than the level of economic development of the country. The constraints were linked to the type and level of structuration of the livestock sector concerned.

Conclusion: This work highlight the importance of local constraints not only linked to sanitary and epidemiological issues but also to sociological, cultural and economical aspects, which impaired engagement of the actors in the system process. Such data are critical to better inform decision-making and ensuring efficacy of innovative or improved surveillance methods.

Key words: Health surveillance, evaluation, engagement, socio-economic factors

Poultry farm distribution models along a gradient of intensification in Nigeria, Thailand, Argentina and Belgium

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ABSTRACT

Objective: Over the last decades, animal production has intensified rapidly in transition economies to meet the demand of animal products, and this comes with significant environmental, health and social impacts. To assess these impacts, detailed maps of livestock distribution have been developed by downscaling census data at the pixel level (10 km or 1 km), providing estimates of animal numbers per pixel. However, in many epidemiological applications, the distribution and size of the farms are better suited for modelling disease transmission or assessing local impact than the number of animals per pixel. We aimed to build farm distribution models for commercial farms, predicting both locations and the number of chickens per farms, in Nigeria, Thailand, Argentina and Belgium. These countries are at different stages of the intensification process, with very different ecological, demographic and socio-economic conditions.

Materials and methods: The spatial distribution of commercial chicken farms was investigated as a pattern of discrete objects using point-pattern simulations models, more particularly using Log-Gaussian Cox Processes models with spatial predictors. These models were evaluated in their capacity to reproduce the correct level of spatial clustering and the most likely location of the clusters. In a second stage of the prediction, we modelled the farm sizes for the predicted farm spatial patterns using Generalized Linear models.

Results: Using two goodness-of-fit indices, we found that both the level of clustering and the location of clusters could be simulated with reasonable accuracy. In a second stage of the prediction, we modelled the farm sizes for the predicted farm spatial patterns using Generalized Linear models. Finally, a comparative analysis gives an overview of how the factors influencing the distribution of farms and their size may vary at different levels of intensification.

Conclusion: This will be particularly useful to project how farm distribution could evolve in the future in low and middle-income countries where intensification of poultry production still occurs, with several applications in the epidemiology of diseases such as avian influenza or Newcastle disease.

Key words: Agricultural intensification, farm distribution model, livestock production systems, point pattern analysis

Epidemiological surveillance network in poultry in France

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ABSTRACT

Since 1988, the epidemiological surveillance network in poultry, managed by the Epidemiological and Welfare Poultry and Rabbit Unit of Anses Ploufragan, supervise epidemiological evolution of avian diseases in France. This network collects the diagnoses voluntary transmitted by the veterinarians and laboratories members of the network. The objectives of the network are to follow the epidemiological trends of the poultry diseases in France and to detect emerging diseases. Since the beginning 2018, a new web platform has been developed to optimize the management of the network. For data transmission, members input diagnosis on the platform or download their data files, whatever the avian production type (turkeys, chickens, layers, guinea fowls, ducks, geeses, games). An application has been developed in RStudio to exploit anonymously the entire database of the network. Members can thus realize space-time research on the database from 1988 to 2018: graph show the monthly and annual data evolution of the diseases and maps allows having a departmental diseases location. Request can be made according to 5 criteria: diseases, pathogens, avian species and stage, date. Each year, more than 20 000 data are collected in 10 different poultry productions. The access to the platform is only reserved to the members of the network. A network charter gives right and duties for each actor to respect confidentiality and anonymity. A committee, with 12 members and the managers, approves the network rules and gives agreement to diffuse data. This epidemiological surveillance network in poultry in France is a tool helping to control poultry diseases, to improve the poultry sanitary situation and to detect the emergence of poultry diseases linked to animal or human health risks.

Key words: Surveillance, network poultry

A risk assessment tool for evaluating biosecurity on aquaculture farms

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ABSTRACT

Objective: Biosecurity consists in the implementation of measures to reduce the risk of introduction and spread of disease agents. At farm level, it plays a central role in disease prevention. To evaluate the level of biosecurity of a farm, several scoring system were developed for land- based farms animals. Until now, such approaches are limited for aquaculture production system. This project aims to build a risk based scoring tool to evaluate and manage biosecurity in freshwater trout farms in France.

Materials and methods: An analytical framework was designed where biosecurity were divided into two parts, external and internal biosecurity. External biosecurity relates to the prevention of pathogens entering and includes items like situation of the farm on the river, fish introduction, visitors and material movements, transport. Internal biosecurity relates to the spread of pathogens within the farm and is linked with animal husbandry practices, disease management, cleaning and disinfecting process. The lack of published data is the main constraint to the application of risk analysis in aquatic animal health. In such cases, reliable information can be obtained from knowledgeable experts using systematic and standardised methods for eliciting their knowledge. This method was applied and an expert knowledge elicitation was conducted among a group of 12 French specialists (fish farmers, scientists, veterinarians, technicians) in order to weight and rank each item.

Results: External biosecurity seems to be the stronger element compare to the internal biosecurity. The location of the farm on the river and the introduction of new animals weight heavily. This scoring tool was then validated, using data collected during field visits on aquaculture sites in order to test its robustness.

Conclusion: Such a tool would be can be used as an aid to evaluate biosecurity level in fish farms and to set priorities in order to prevent the introduction and the spread of infections between farms.

Key words: Biosecurity, aquaculture, fish, risk ranking, score

Models of two communities on factors affect pet owners'decision for rabies vaccination and population control

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ABSTRACT

Objective: Recently in Thailand, the incidents of rabies cases are still found in either animals or human, so rabies-free nation is certainly in need. Thailand has yet no regulation of pet registration or pet census, the increasing number of pets including strayed animals affected the epidemic of rabies. Pet's lovers from each community shares various cultures, habits, believes and attitudes. For a successful eradication of rabies, different approaches are needed and attitude of people from each community toward pets' rabies vaccination and population control has to be considered.

Materials and methods: This study used questionnaires and direct interview to collect data from pet owners in 2 small communities, Sam Khwai Pheuk subdistrict, Nakhon Pathom province (A) and Si-Chang district, Chonburi province (B).

Results: Rabies vaccination has been done in 78.99% of pets in A, compared to 53.25% in B. For birth controls, in A and B were 58.73% and 59.17%, respectively. For hormonal contraception, the results revealed that 91.88% of the owners in A used this method while only 31.40% of owner in B exploited. For female surgical neutering, 62.79% of pet owners in B preferred this compared to 4.06% in A. The study also showed that education level, source of pets and indoor/outdoor raising significantly affected the owners' decision to get their pets vaccinated from both communities, while the owners' occupation and knowledge on rabies significantly affected the owners' decision to get their pets vaccinated only in A. For pet population control, the education level had an effect in A significantly, while, for B, the source of pet had a significant effect. Different factors affected the concerns for pet population control and rabies vaccination of owners in different areas. In Sam Khwai Pheuk area, most owners exhibited low concern on the importance of pet population control and rabies vaccination despite an easy approach to veterinary services. In contrast, the owners in Si-Chang showed more concerned on those but lacked of the services.

Conclusion: The proper future plan protocol on rabies control management and population control in pet, which are important features for the sustainable rabies free area, has to be flexibly adapted due to diverse attitudes and factors in different areas.

Key words: Owner, attitude, contraception, neutering, rabies

Will Japanese encephalitis virus be introduced to North America?: A risk assessment

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ABSTRACT

Objective: The objective of this study was to investigate the risk of introduction of the Japanese encephalitis virus (JEV) into the United States (US) by means of a risk assessment (qualitative and quantitative).

Materials and methods: In the qualitative assessment we estimated the risk of introduction, transmission, and establishment of JEV, following a framework for the risk assessment of emerging vector-borne diseases. In the quantitative assessment we built a stochastic model to quantify the probability of introduction of at least one infected mosquito per year via aircrafts and cargo ships (pathways identified as likely in the qualitative analysis) from JEV-affected countries in Asia (including areas in the Russian Far East) and Northern Australia, into the US. In the quantitative risk assessment, we predicted a very high risk (0.95 median probability; 95% CI=0.80-0.99) of at least one infected mosquito being introduced in the US (the highest risk being attributed to the Mediterranean California ecoregion) each year via aircrafts from Asia, with Taiwan and Eastern China representing the regions of highest risk.

Results: The risk of introduction of at least one infected mosquito in cargo ships was deemed negligible. In the qualitative risk assessment, and given a hypothetical JEV introduction, we estimated a variable probability of transmission, ranging from low to very high, depending on specific vector and host parameters. The probability of establishment, however, was considered negligible, thus, even if entry is possible, circumstances for JEV to spread from vector to host given the conditions of introduction, are remote.

Conclusion: The conclusions drawn from this study are important for targeting mitigation strategies directed towards the most likely entry pathways of JEV and to support future interventions for JEV prevention and control, as well as other vector-borne diseases, in the US and other countries.

Keywords: Risk assessment, Japanese encephalitis, Japanese encephalitis virus

Implementation of a web-based information system for the automatic management of data on shellfish monitoring in the Venice Lagoon – Italy

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ABSTRACT

Objective: in order to establish and manage monitoring plans on the shellfish production chain, collaboration between public authorities and laboratories is essential, as the implementation of suitable protocols for data communication. For the management of official controls in the Venice Lagoon, an information system (Shellfish-IS) has been developed, involving both the Local Public Health Units (LPHUs) and the Official Laboratories, located at the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe). The system is now fully functional and it meets the requirements the European Union food safety legislation. The aim of this paper is to describe the web-based system and the data flow management.

Materials and Methods: Shellfish-IS is completely web developed. The Web Server used for data flows is Apache 2.2 (Apache © Software Foundation). The laboratory information system (IZILab) is client-server program based on web services technology, designed according to the HTTP / SOAP / XML standard. The databases are built on Oracle and Firebird 2.1 platforms.

Results: the system was developed to standardize both processes and terminology in use and to define harmonized information flows for the whole region. Interoperability with IZILAB ensures data exchange and information sharing in the veterinary administration. The information system has been in force from January 2016. To date 5,378 collected samples have been automatically recorded into the laboratory information system. The dematerialization has reduced costs and enhanced official data quality and availability.

Conclusion: the implementation of a regional data bank (RDB) of aquatic animal farms since 1994, which included geographical data of any classified production areas, has laid the foundation for the Shellfish-IS development. This new project has intended to optimize the way of communication between LPHUs and IZSVe, using IT solution applicable at field level. The current information system is going to be gradually applied to other regional sampling plans.

Seroprevalence of *Anaplasma marginale* in cattle, Kentucky USA

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ABSTRACT

Objective: To determine the seroprevalence of and factors associated with bovine anaplasmosis (BA) in Kentucky (KY).

Materials and methods: Data were obtained from an active slaughter survey (n = 232) performed between May and July 2013 as well as from reviewing The University of Kentucky Veterinary Diagnostic Laboratory (UKVDL) records of specimens submitted for BA testing from 2002-2012 (n = 2,573).

Results: With competitive ELISA, the apparent prevalence of BA in KY was 10.78% (95% CI: 7.41-15.42%) and 11.58% (95% CI: 10.31-12.98%) for the slaughter survey and laboratory records, respectively. Whereas the estimated true prevalence was 9.44% (95% CI: 5.65-14.48%) and 10.3% (95% CI: 8.92-11.8%), respectively. From the laboratory records, factors associated with positive BA results were age, breed, whether specimens were submitted singularly or as a group, year and quarter of the year the specimens were submitted. The odds of the outcome were 5 times as high when cattle were adults (vs juvenile) and almost 4 times as high when specimens were submitted singularly (vs group). In comparison to Holstein breed, the odds of the outcome were 3.5 and 2.5 times higher in Angus and mixed breeds, respectively. The odds of a diagnosis of BA varied in an undulating pattern by year of sample submission. When compared to 2011, the odds of a diagnosis of BA was approximately 3 times as high in 2005, 2008, and 2009 and approximately 5 times as high in 2004, 2006, and 2012. In comparison to the duration from January to March, the odds of the outcome were almost 20 times as high from July to September but 10 times as high from October to December durations. Counties with specimen submissions for BA testing had a significantly greater cattle population and number of cattle farms than counties without specimen submissions.

Conclusion: Future prevention and control measures for BA should target these factors and should be weighted more on counties with higher cattle population. Furthermore, current records from the UKVDL appear sufficient for the surveillance of BA in KY.

Key words: *Anaplasma marginale*, Anaplasmosis, cattle, Kentucky, prevalence

The use of systematic review methodology in evaluating the impact of surgical sterilisation in canine rabies control programs: benefits and challenges

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ABSTRACT

Rabies vaccination programs are complex interventions and are often aligned with surgical sterilisation programs which have different objectives of stabilising dog populations and improving animal health and welfare. Official guidelines promote vaccination-only programs but in practice many organisations are also performing sterilisation. This study used systematic review methodology to investigate the role of sterilisation in rabies control interventions. This was done by comparing the outcomes of vaccination and sterilisation programs with those using vaccination-only. Outcomes measured were dog bites (including confirmed or suspected rabid); doses of post-exposure prophylaxis administered; numbers of dog and/or human rabies cases; dog population turnover or other demographic changes; health and welfare of dogs; human behaviour changes. A systematic search of three electronic databases (CAB Abstracts, Medline and Global Health) and grey literature was performed. Twelve studies describing vaccination-only programs and six studies describing vaccination and sterilisation programs met the inclusion criteria from the peer-reviewed literature. Grey literature is still being screened. Included studies will be synthesised, appraised and theories identified that explain relationships between the context in which the program is carried out, the mechanisms by which it works and the outcomes produced. A 'realist synthesis' will be used in order to allow for the influence of context and the way in which interventions were carried out. The use of evidence syntheses has come from an increased interest in evidence-based practice across sectors. Systematic reviews attempt to provide an objective summary which can be more reliably used to draw conclusions, by using transparent and replicable methods. However there are challenges associated with applying this methodology to more complex health interventions.

Key words: Canine, rabies, sterilisation, vaccination, systematic review

Ensuring preparedness of national Caribbean veterinary services for Highly Pathogenic Avian Influenza - the essential contribution of the Caribbean Animal Health Network (CaribVET)

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ABSTRACT

Objective: Following the highly pathogenic avian influenza (HPAI) outbreak in North America (2015), CaribVET has implemented a regional HPAI preparedness plan to minimise the risk of HPAI introduction through migratory birds and/or through live poultry imports.

Materials and methods: CaribVET structured its plan around five key components: Biosecurity, Diagnostic capacity and Laboratory surveillance, Risk-Mapping and Risk-based surveillance, Emergency Preparedness and Risk Communications. All projects and funding sources available through CaribVET partners were used to implement the plan at regional and national levels, and to support overall coordination. The CaribVET Coordination Unit supervised the capacity building, knowledge transfer and cooperation and the plan was evaluated by USDA experts.

Results: The total cost was 850,000 USD. Within 2 years, the network developed and distributed materials focused on raising awareness of the disease, improving biosecurity practices and providing control and prevention guidelines, The network validated rapid diagnostic tests, trained laboratory technicians, organized Avian Influenza (AI) laboratory Proficiency Testing and coordinated a series of regional and national workshops (biosecurity, contingency planning, GIS, diagnostics), resulting in significant strengthening of the tools available in the Region to respond to HPAI.

Conclusion: With its continued efforts to promote coordinated actions across the Caribbean region, the network was able to leverage regional projects and funding to rapidly address the evolving threat posed by HPAI. These efforts were made available to the entire Caribbean region, resulting in a high level of impact for the time and energy invested. The network provided a strong and essential platform for this work, despite limited funds.

Key words: Preparedness, capacity development, Avian Influenza

How to implement a national livestock identification and traceability system for free (almost)

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ABSTRACT

Livestock identification and traceability system underpin disease control, quality assurance and trading requirements in many countries. Traditional approaches, involving the establishment of powerful data management and communication systems, and the purchase, application and maintenance of unique individual identifiers, are expensive and complex.

In 2016, Indonesia launched a program to improve cattle productivity and reproductive performance (SIWAB). Artificial insemination formed a cornerstone of the program, and requires accurate individual identification and recording of reproductive events. Instead of using the traditional approach, Indonesia chose to leverage the existing integrated animal health and production information system (iSIKHNAS) for data management, and adopted an innovative two-step individual identification approach.

The two-stage unique individual animal identification system depends on first uniquely identifying the animal owner. Within iSIKHNAS, flexible unique identifiers are used (the person's mobile phone number, driver's license or existing local identification). The second stage involves unique identification of animals within the owners herd, again using flexible identification. For larger herds, this may be ear tag number, but for small herds may be simply based on the animal's name. This approach eliminates the need for nationally unique tags or chips. The iSIKHNAS information system was designed to continuously expand to meet changing needs. This allowed a new module to be quickly added recording owners, animals, births, deaths, and change of ownership. Such registration data is integrated into the same system used to record reproductive data and movement permits. The Indonesian government plans to progressively increase the use of numbered identification tags, which can be mixed with, and eventually replaced, current informal identifiers.

This approach has allowed identification and traceability of over 4 million cattle, at almost no cost over the existing budget for iSIKHNAS and the SIWAB program. The limitations and challenges of the approach are discussed.

Key words: Animal identification, information system, traceability

Regionally integrated animal health surveillance systems

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ABSTRACT

Animal health information is required at different levels to support different activities. At the global level, the World Animal Health Organisation's (OIE) World Animal Health Information System (WAHIS) provides periodic official information on national disease status and alerts of outbreaks of listed disease, to support trade and risk analysis.

At the national level, much more detailed and timely information is required for a wide variety of purposes, including prioritisation of investment in animal health programs, monitoring and evaluating existing programs for disease control and eradication, early detection of emerging or exotic diseases, demonstration of freedom for trade purposes, case finding for eradication programs, veterinary public health, and so on. In between these two levels, regional information systems have been developed to meet the specific needs of regional country groupings. Often the main motivations are improved regional cooperation on disease control programs for endemic diseases of common interest, and secure sharing of early warning reports of emerging or exotic disease outbreaks to allow rapid response prior to official confirmation and notification to OIE. This is based on a recognition of the need for rapid response, but a desire to balance this with the negative consequences of trade restrictions as a result of OIE notification.

This paper uses examples of regional systems to examine their functionality and effectiveness. It focuses particularly on the essential role of national surveillance and information systems to provide timely and accurate data for regional systems, and the potential opportunities of regional integration of national and regional animal health information systems. This approach could provide resource-poor countries with powerful secure data capture, management and analysis tools for their own national information systems, using shared regional infrastructure. The relationships between national, regional and global systems are examined, along with issues of data security and control of sovereign data.

Key words: Surveillance, information system, data sharing, region

Decision support tools and multi-criteria decision analysis to support state and national-level decisions during an emergency response: application to foot-and-mouth disease in the United States

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ABSTRACT

Objectives: In the U.S., determining optimal disease response strategies is a complex situation involving multiple, and often competing objectives and priorities with trade-offs based on state and national-level response capacities and the interests of the agriculture sectors involved. We developed a set of interactive tools and applied multi-criteria decision analysis (MCDA) to support national and state-level emergency response activities. We illustrated the application of these tools to evaluate disease control decisions using simulated foot-and-mouth disease (FMD) outbreaks in the U.S.

Materials and methods: We utilized the U.S. national FMD model developed within InterSpread Plus, a spatial, stochastic disease spread model framework. FMD scenarios were created to evaluate alternative vaccination strategies with varying vaccine distribution capacities and vaccine dose availability. Interactive dashboards were designed using Tableau Software to compare scenario results. MCDA methods were incorporated that allow the objectives and priorities across the multiple perspectives of state and national-level decision-makers to determine optimal control strategies. Criteria are based on preferences of decision-makers during model development and through tabletop and functional FMD exercises of their emergency response plans.

Results: The dashboards provided a platform to evaluate disease response strategies and capacity needs in an interactive fashion. Specific to FMD, the dashboards demonstrated that vaccination can reduce the occurrence of longer/larger outbreaks as compared to a depopulation strategy only, but a program's overall effectiveness depends on vaccine distribution capacity, speed, and strategy. Incorporating MCDA into these tools enables decision-makers to dynamically explore the trade-offs of decisions based on their specific disease control objectives and priorities at different time points during an outbreak.

Conclusion: Interactive dashboards are effective tools to incorporate disease modeling into emergency response activities. MCDA allows the complexity of differing objectives and priorities across multiple stakeholders to be included when determining optimal control strategies, similar to how real-world decisions will be made during a disease outbreak.

Key words: Disease modeling, decision making, multi-criteria decision analysis, disease response, foot-and-mouth disease

Risk-based approaches to managing food safety in South Africa: A review with reference to Listeriosis outbreak in South Africa

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ABSTRACT

Objectives: To present a review of Risk-Based Approaches to Managing Food Safety in South Africa with reference to Listeriosis outbreak in South Africa.

Materials and methods: A desk review of national regulations and national and international standards was conducted to determine gaps in risk based approaches to the control of food safety hazards and factors that resulted in Listeriosis outbreak in South Africa.

Results: Government authorities and Industry have a joined role to play in ensuring the safety of food that is consumed by the public. The on-going Listeriosis outbreak, in South Africa, the largest recorded in the world, that has resulted in about 183 deaths and 948 confirmed clinical cases, (http://www.nicd.ac.za/wp-content/uploads/2018/03/Listeria-Sitrep-03Mar2018.pdf) has put risk-based approaches to food safety prevention and control in the spotlight. This has shown that the impact of microbiological contamination in products can be potentially huge, particularly in terms of risk to public health, if food safety control measures are not strictly adhered to. The implementation of effective food safety management systems (FSMS) using Hazard Analysis and Critical Control Point (HACCP) system has become very pertinent worldwide. While Government authorities have the responsibility of monitoring and ensuring compliance in the control of food safety in-line with national regulations, industry equally has the responsibility of complying with their certified FSMSs. These FSMSs, require food manufactures to satisfy the requirements of risk-based food safety prevention and control. Government authorities and Food Manufacturers need to have an in-depth understanding of using HACCP, TACCP and VACCP tools, and have a sufficient competencies to be able to effectively control and prevent food hazards in the food value chain. This paper reviews the role that government authorities and food manufacturers each play in ensuring production of safe food for human consumption in South Africa. Gaps in the South African food legislation and weaknesses in the food industry that have led to the current unprecedented Listeriosis outbreak are reviewed.

Conclusion: Both industry and government have a joint responsibility to prevent and control foodborne disease outbreaks in South Africa. Adherence to risk based practices to prevention and control of food pathogens can prevent or minimise the impact of food borne disease outbreaks in South Africa

Key words: Food Safety, HACCP, TACCP, VACCP, Listeria

The equine influenza outbreak in Pakistan 2016: Seroprevalence and Geo-Temporal epidemiology of a large propagating outbreak

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ABSTRACT

Objective: Khyber Pakhtunkhwa (KPK) province of Pakistan experienced an extensive epidemic of equine influenza (EI) in October 2015 in equine population. EI is among the OIE or WHO notifiable, contagious equine respiratory diseases. It is considered as an emerging infectious disease of equine in Pakistan. Due to lack of awareness and interest of all the equine industry stakeholders no vaccination against EI is performed, also the information regarding the epidemiology and occurrence of EI is lacking in Pakistan.

Materials and methods: A cross sectional survey was conducted. Here, we attempted to determine the seroprevalence, investigating the EI outbreak 2015-16, and describing the demographic and management risk factors associated with seroprevalence of EIV.

Results: Using ELISA kit and HI as serological methods for diagnosis, we found a 24.13% (168/696) overall seroprevalence, where the seroprevalence for H3N8 was 14.51% (101/696), for H7N7 6.03% (42/696), and 3.59% (25/696) as mixed infections, suggesting EIV current and active circulation in equine population of Pakistan. Statistical analysis suggested predicting variables including "local equine density per 2 KM", "equines workings in ponds and rivers", and "geography of the equine" were significantly (P<0.05) associated with seroprevalence of EIV.

Conclusion: Our findings of the EIV occurrence in equine population in Pakistan, suggests an under-diagnosis of this virus in Pakistan and warrant additional investigation and continuous surveillance at the molecular level to identify circulating strains for control and prevention of future outbreaks.

Key words: Equine, Influenza, seroprevalence, epidemic and Epidemiology

Rabies and animal bites incidence in IR of Iran during 2007-2016

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ABSTRACT

Objectives: Rabies is an endemic disease in Iran and infects human, domestic and wild animals. This study was conducted to estimate the incidence rabies and animal bites in IR of Iran.

Materials and Methods: In this descriptive study, the data of animal and human rabies reported by the Ministry of Agriculture and the Pasteur Institute of Iran were used.

Results: A total of 3,991 positive animal rabies were recorded which included dog (49.43%), cow (33.35%), sheep (7.14%), wild animals (5.06%), equidae (2.68%), goat (1.27%), cat (0.65%), and camel (0.42%). There was a downward trend in animal cases, so that the number of animal rabies was reached from 1,448 animals in 2007 to 286 animals in 2016. A total of 54 cases of human rabies was recorded in the past 10 years and there was no predictable and uniformity in its occurrence. On the other hand, the incidence of animal bites has risen from 185 per 100,000 people in 2007 to 212 per 100,000 people in 2016 (Fig. 1).

Conclusion: The highest incidence of rabies was occurred in dogs and cows, and by increasing the number of rabies in dogs, the rabies-induced economic loss was increased in ruminants in each region, and subsequently human rabies was increased. On the other hand, given the high incidence of animal bites, it is recommended to take effective control measures, such as training the vulnerable groups, strengthening the surveillance system, and immunization of the animal owners.

Key words: Rabies, epidemiology, animal bites, Iran

Prioritisation of livestock diseases susceptible to be affected by climate change in New Zealand

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ABSTRACT

Objectives: Changes to climate have resulted in the changes in the distribution of animal's disease (e.g. West Nile in North America and bluetongue in Europe) and there is growing evidence that this trend will continue for other diseases. The resources to mitigate the risk of climate change on animal disease are limited and policy makers, farmers and veterinarians need to decided how best to allocate resources. Often, a cost-benefit framework would be used to rank the diseases but many of the criteria that need to be considered cannot be monetarised (e.g. animal welfare). The objective of this study is to use multi-criteria decision analysis (MCDA) to develop a transparent and robust framework to determine priorities for the allocation of resources to mitigate the risk of climate change on animal diseases in New Zealand.

Materials and methods: We established a list of sheep and cattle diseases endemic in New Zealand during a stakeholder workshop. The list was crosschecked with the undergraduate veterinary curriculum for completeness. A systematic literature review of each disease was performed to investigate evidence of sensitivity to extreme weather events, rainfall and temperature. MCDA will be applied to identify a set of criteria that can be used to rank and prioritise the diseases by importance, during a second stakeholder workshop involving representatives from farming groups, sheep, beef and dairy cattle industries, veterinarians and government. The workshop is planned in August 2018.

Results: Forty-one diseases, infectious agents or adverse health events affecting sheep and cattle in NZ have been identified. The systematic review identified *Haemonchus contortus,* salmonellosis and liver fluke as those returning the largest number of results, and *Brucella ovis*, ergotism and bovine digital dermatitis with the lowest number of results.

Conclusion: Combining systematic review and MCDA provides a robust methodology to prioritise livestock diseases and enhance preparedness.

Key words: Climate change, prioritisation, livestock health

The Use of GIS in animal disease response. A distance-learning course

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ABSTRACT

Objective: A distance-learning course entitled "The Use of GIS in animal disease response" has been produced and published on the web. The present paper aims to present the development process and technologies used to implement the course.

Materials and methods: Course material development process was essentially developed in six stages: preplanning (preparing and finalising the syllabus of the course, defining the curriculum committee), planning (i.e. definition of objectives, target audience, course length), authoring (i.e. manuscript authoring, referee the manuscript), production (i.e. proof reading, video recording, corrections), post-production (i.e. video editing, adding illustration) and publishing (i.e. organisation of the course web page, creation of user profile). For the video recording a specific set was organised with a bluescreen wall, RayD8 Lastolite lights, Sennheiser microphones and Canon Legria HD cams. The software Shutterstock was used to produce the illustrations and Camtasia studio 8 for the screencast. Adobe After effects were used for the animation effects. The videos were uploaded in the Vimeo video-sharing website and Moodle 3.1 was the course management system application.

Results: The course is freely available at the https://www.izsvenezie.com/online-training-course-gis-oie/ and it has been structured in 4 sessions of 44 video-lectures for a total of 10 hours of videos. The course is organised in a theoretical lecture followed by a practical usage in the QGIS software. 27 tests and 3 invigilated assessments are also included. A forum with a facilitator is also available to students.

Conclusion: The proposed online course is aimed at providing an empirical approach for the implementation of a GIS project to capture, manage and analyse spatial data related to disease events. The course integrates several different tools and resources in order to provide the required flexibility and the freedom of self-directed learning without compromising the student's time organisation.

Economic evaluation of the eradication program for bovine viral diarrhea in the Swiss dairy sector

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ABSTRACT

Objective: The mandatory eradication program for Bovine Virus Diarrhoea (BVD) in Switzerland has been ongoing since 2008, and is focused on detection and elimination of persistently infected animals. Detection was initially based on antigen testing of the entire cattle population, followed by antigen testing of all new born calves until 2012. Since then, bulk milk testing (dairy herds) and blood sample serology (beef herds) have been used for the surveillance of disease-free herds. The aim of this study was to conduct an economic evaluation of the BVD eradication program in the Swiss dairy sector.

Materials and methods: The situation before the start of the program (herd-level prevalence: 20%) served as a baseline. Production models for three dairy farm types were used to estimate gross margins as well as net production losses and expenditures caused by BVD. The total economic benefit was estimated as the difference in disease costs between the baseline scenario and the implemented eradication program and was compared to the total eradication costs in a benefit-cost analysis. Data on the disease impact of BVD were obtained empirically in a retrospective epidemiological case-control study in Swiss dairy herds. Other production and economic parameters were based on benchmarking data and published agricultural statistics. The economic model consisted of a stochastic simulation and was conducted for a time period of 14 years (2008-2021).

Results: The estimated annual financial losses in BVD virus infected dairy herds were CHF 85-89 per dairy cow and CHF 1337-2535 for an average farm. The median net present value (NPV) obtained was CHF 44.9 million (90% central range: 13.4m to 69.4m) and the break-even point has been reached in 2015.

Conclusion: Overall, these outcomes demonstrate that the Swiss BVD eradication program results in a net benefit for the dairy sector. These finding are relevant for planning similar BVD control programs in other countries.

Key words: Cost-benefit analysis, gross margin, dairy cattle, control program

Socioeconomic impacts of working horses in urban and peri-urban areas of the Cape Flats, Cape Town, South Africa

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ABSTRACT

Objective: In the Cape Flats townships, Cape Town, South Africa, there are in excess of 250 working horses, known as 'cart horses' in the community. They serve the community with scrap metal collection and transportation, garden refuse removal, human transport and the general selling of goods.

Materials and methods: A questionnaire was undertaken to understand the social and economic impacts the use of a horse and cart in the Cape Flats has on individual owners and/or drivers, their households and the surrounding community. Welfare impacts on the horse itself were also considered. An understanding was also obtained on the spatial extent to which the cart horses work and how that relates back to the impact on the horse and participant of the survey. A mixture of classical quantitative questions combined with qualitative participatory technique questions were used to gain a well-rounded response.

Results: A total of 100 participants took part in the questionnaire, who worked with 163 horses between them. The majority (89%) identified the working horse income as their primary source of income. Over and above the participants, an additional 716 other people were supported financially through income generated by the working horses, where the mean number of children supported was 2.9 (95% CI: ± 0.42) per interviewed participant. Scrap metal transportation was the most common function of the working horse and season (winter), pregnancy and shoeing were important factors negatively impacting on their ability to work. It was demonstrated that the cart horse industry was impactful on not only those who worked in the industry, but also the surrounding residents either through their work or through supporting others with their income.

Conclusion: This study reveals the concepts of 'One Health' and 'Health in Social-Ecological Systems' in action as horse and human health and welfare within the Cape Flats are so closely intertwined.

Key words: Socioeconomic, working horse, welfare, community

Integrating livestock keeper and biomedical knowledge of sheep and goat disease in the pastoralist Afar Region of Ethiopia: implications for peste des petits ruminants disease surveillance

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ABSTRACT

Objective: Livestock disease control can contribute to the resilience of pastoralist systems, but data are limited to meaningfully inform control strategies. This study aimed to explore pastoralist concepts of small ruminant disease in Afar Region, Ethiopia, and the implications for disease surveillance.

Materials and methods: Over 18 months, qualitative and quantitative methods were applied in two villages; initial semi-structured group interviews, visits in different seasons to 40 households for informal interview, observation and clinical examination, and weekly flock questionnaires to record mortality and morbidity. Thematic analysis was applied to qualitative data and descriptive analysis to quantitative data.

Results: Afar concepts of disease were primarily naturalistic. Disease occurrence was associated with malnutrition and adverse weather, and disease spread with contact during grazing, watering and migration. Disease occurrence varied by season, with most syndromes increasing in frequency during the dry season. Names for disease syndromes were related to the main clinical sign or body part affected. A range of traditional and/or bio-medical treatments were applied. Disease was prevented by cleaning enclosures, migration to access good forage and minerals, and vaccination. The main disease syndromes were mild to severe respiratory syndromes, diarrhoea, pox, lameness, skin diseases and abortion. Some disease terms were applied consistently across the region, and some were more localised. Some terms were applied variably, and some syndromes had more than one term. Several terms were used for PPR-like disease, depending on the predominant clinical sign. This complexity demonstrates the importance of characterizing local disease terms and the associated clinical syndromes in each community. For PPR surveillance, a range of local terms should be considered as suspected PPR cases in need of further investigation.

Conclusion: In conclusion, the application of mixed methods generated rich information on local disease terminology and occurrence that has been applied to the development of PPR surveillance in pastoralist areas of Ethiopia.

Key words: Pastoralism, animal health, peste des petits ruminants, mixed methods

Importance of post-vaccination sero-surveillance for evaluating efficacy of vaccination programs against endemic diseases of livestock in developing countries

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ABSTRACT

Objective: Here we describe how post-vaccination sero-monitoring combined with consultation of different stakeholders has been useful to generate evidence on bottlenecks of vaccination campaigns and generate evidence to engage government decision makers in Mali.

Materials and methods: We evaluated the routine annual vaccination programs implemented by the Government of Mali against Contagious Bovine Pleuropneumonia (CBPP) in cattle and Peste des Petits Ruminants (PPR) in small ruminants in selected communes of Mopti and Sikasso regions in 2016. Questionnaires were administered to farmers to get information about their production systems, and serum samples were collected before and after vaccination from randomly selected 1500 cattle and 1500 small ruminants. Focus group discussions with farmers and key informant interviews with staff from veterinary services were carried to get knowledge about the constraints to effective vaccination programs. C-ELISA was used to measure the level of sero-conversion of animal following vaccination.

Results: Results showed an overall serological prevalence rate of 14.93% before vaccination and only an increase to 22.93% post-vaccination for CBPP; and 54.73% before vaccination versus 65.07% post-vaccination for PPR. Key constraints to effective vaccination programs include: low capacities of private veterinarians to secure adequate quantity of vaccines during vaccination campaigns, inadequate infrastructures and lack of equipment for transportation and maintenance of the cold chain. To achieve herd immunity for both diseases, an estimated coverage of 80% of animals should be achieved. Therefore, herd immunity cannot be achieved with the current vaccination programs strategies.

Conclusion: To improve vaccination programs, there is need for more participation of all stakeholders, and close engagement of government agents with other actors such as private sector to ensure that their investment in vaccination campaigns results in the expected returns, p.e. having effective protection against target diseases.

Key words: Sero-monitoring, vaccination, livestock, CBPP, PPR, Mali

Stakeholder engagement to increase vaccination coverage against endemic livestock diseases in Mali

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ABSTRACT

Objective: In Mali, annual vaccination campaigns follow a public-private partnership model with private veterinarians carrying out most of the vaccination, supported and overseen by the veterinary services. However, there are persistent challenges in achieving adequate vaccination coverage. A major constraint hindering proper implementation of vaccination programs is the low-involvement of producers and other key stakeholders in the process of planning, implementation, monitoring and evaluation of vaccination campaigns. The main challenge of the veterinary services remain on how to improve vaccination coverage in order to reduce livestock mortality.

Materials and methods: In the framework of the Feed the Future Mali Livestock Scaling Technology Program (2015-2019) which aim at improving productivity of cattle and small ruminants through upscaling of technologies in targeted communes of Mopti, Timbuktu and Sikasso regions, we established an integrated participatory approach through Multi-stakeholder Innovation Platforms (IP) to identify and address institutional, technical and social challenges at several levels of the livestock vaccine supply chain.

Results: IPs were established in 2016 in 31 target communes with the following stakeholders: producers, traders, transporters, butchers, women's cooperatives, local promoters of small livestock feed enterprises, milk processors, private veterinarians, public and private input and service providers, local NGOs, microfinance institutions and local leaders. IPs are facilitated by the project partners on ground in respective regions and overseen by experts from the program. The issue of how to increase vaccination coverage was among the top constraints to be tackled by most IPs. IP members meet periodically to discuss issues and take action.

Conclusion: Preliminary results show that IPs has been useful in improving linkages among livestock value chain actors, and improving knowlege of communities about the benefit of vaccination. It has also contributed to the reinforcement the relations of trust between producers, animal health professionals, and government actors. Actions taken thanks to IPs are more accurate estimation of animal population to be vaccinated for better planning to avoid vaccine shortage and improved participation of farmers to vaccination. In our experience, IPs proved a useful mean of enhancement of participation to vaccination, impact of which still needs to be evaluation.

Key words: Livestock, vaccination, innovation platforms, Mali

Estimating the sensitivity of the Canadian bovine tuberculosis surveillance system in farmed/captive cervids

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ABSTRACT

Objectives: Bovine tuberculosis is a zoonotic disease of economic importance. In Canada, the national bovine tuberculosis eradication program in farmed/captive cervids mostly relies on active and passive surveillance. Surveillance activities include: routine post-mortem inspection at slaughterhouses, export testing and on-farm testing associated with movement permits. Although on-farm testing serves as a useful surveillance function, it has the drawback of being time-consuming and can pose animal welfare issues. Therefore, there is a need to evaluate the sensitivity of the current bovine tuberculosis surveillance system to determine whether on-farm testing needs to be pursed. Therefore, the objective of the study was to estimate the sensitivity of bovine tuberculosis surveillance system in Canadian slaughterhouses and at exportation in the Canadian farmed/captive cervids population.

Methodology: We developed a scenario tree model (STM) estimating the surveillance sensitivity for the two surveillance components from 2011 to 2016. Data on the farmed/captive cervid population and number of cervids inspected and tested at export were collected using a questionnaire and governmental sources. A systematic review was undertaken to estimate the different probabilities of infection and of detection to be included in the STM model and their distribution. A stochastic approach was used for model estimation.

Results: Results will be presented and discussed.

Keywords: Bovine tuberculosis, surveillance, cervids, sensitivity, scenario tree model

Delivery of animal health services in extensive livestock systems in Kenya

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ABSTRACT

Objective: Control of livestock diseases in extensive livestock systems in many developing countries is constrained by poor animal health service delivery. The objective of this study was to evaluate new approaches that can improve the delivery of animal health services in three counties practicing pastoral livestock production in Northern Kenya.

Materials and methods: The first approach involved partnership between the public sector and a private animal health service provider in the delivery of vaccines and curative animal health services. The second approach was a regular mobile veterinary service by a private animal health service provider through areas of high animal concentrations such as livestock markets and watering points to provide all services including extension services. The analysis included the viability and sustainability of the services.

Results: Results indicate that both approaches are economically viable and can greatly improve the delivery of animal health services under pastoral settings. Viability of the first approach depends on the willingness of the parties to collaborate and share some resources such as transport. In the second approach, profitability of the business depends of a balance between the length of route travelled and the volume of business.

Conclusion: Unplanned subsidies by government and non-governmental organisations and a lack of commercial orientation of livestock keepers were the main constraints.

Key words: Delivery, animal health, pastoral, livestock, Kenya

Probabilistic risk assessment of Hepatitis E in pork products

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ABSTRACT

Objective: The epidemiology of Hepatitis E virus (HEV) in pigs is complex and still characterized by fundamental lack of knowledge in the host-pathogen interaction. The overall aim of this work was to increase the understanding of the factors driving the spread of HEV in pig herds and assess the risk posed by pork products to human exposure to HEV by means of probabilistic modelling.

Materials and methods: A comprehensive "farm-to-fork" stochastic model informed by available data and expert opinions was implemented to simulate the fate of HEV along the pork-food chain considering different organs of food safety interest. Sensitivity analysis on the model outputs was performed to identify, by means of tornado charts, the most influential inputs and the factors preventing accurate estimation of the risk of exposure to inform research priorities.

Results: Model results highlight the need of carefully considering farm-level mitigation strategies potentially shifting the peak of viraemic pigs towards the end of the production cycle. Furthermore, while adequate time-temperature cooking combinations play a critical role in preventing human infection, persistence of HEV in liver and gallbladder of recovered animals, the level of HEV contamination on the hide and the amount of residual blood after slaughter were identified as the most influential factors for human exposure to HEV via consumption of pork products.

Key words: Risk analysis, stochastic modelling, pigs, Host-Interaction dynamics, contamination

Engaging animal infectious diseases surveillance systems in interconnection: lessons from a participatory workshop

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ABSTRACT

Objective: The epidemiological surveillance of animal diseases may relies on several systems or components that are sometimes implemented in an independent way or even do not easily communicate between each other. This lack of coordination may impair the efficiency of the surveillance and increase the global costs. Such a situation is experienced regarding the French surveillance system of equine infectious diseases. An evaluation team, including epidemiologists and the surveillance system's managers, assessed the system and recommended a better connexion between existing components. Our objective was, in the line of these recommendations, to identify and prioritize ways of interconnection by eliciting an interdisciplinary panel of stakeholders involved in equine healthcare and/or equine industry.

Materials and methods: We organized a one-day participative workshop gathering thirty persons: public authorities, animal health institutes and laboratories, professionals (horse owners' and veterinarians' representatives) and epidemiologists.

Results: Through individual, plenary and group sessions, and using mind maps, the stakeholders identified 18 recommendations regarding three topics: objectives and governance; laboratory, surveillance tools and procedures; data management, data analysis and communication. The panel estimated the expected benefits of each recommendation and their levels of feasibility, acceptability and priority, using a scoring guide and a grid specially designed for the workshop. The main recommendations were the collective definition of detailed surveillance objectives, the creation of a common steering committee, the centralisation of surveillance data and harmonizing information distribution.

Conclusions: The workshop allowed involving numerous actors and beneficiaries of the surveillance. Their complementarity and the favourable atmosphere created contributed to achieve workshop's goals. Gathering such stakeholders probably lead to an evaluation of recommendations accurate and more comprehensive than individual elicitations. The discussions and joint assessment allowed a better collective trust in the recommendations. This approach requires minimal time and financial resources. Collegial political decisions must follow such workshop in order to materialize the recommendations, eventually after complementary economic and/or social evaluations.

Key words: surveillance, interconnexion, integrated surveillance, participatory workshop, horses

One for all: a generic risk framework for all pathways of disease introduction

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ABSTRACT

To improve the rapid identification of exotic infectious diseases expanding into new areas it is necessary to determine the potential hotspots for disease incursion and subsequent infection of native species. We provide a generic framework for quantitative risk assessments of disease introduction that can identify hotspots for initial infection. It can be adopted across multiple spatial scales, for any pathogen, type of disease transmission or location. The framework incorporates the risk of initial infection in a previously uninfected location for multiple pathways of introduction, both registered movement (e.g. trade) and unregistered movement (e.g. daily movements of wild animals). We discuss the steps of the framework and the sources of data employed to compute each step.

We present results for applying the generic framework to one case study, African swine fever (ASF). We focus on the risk of initial infection in current disease-free areas within Europe for two introduction pathways – trade in live pigs and movement of wild boar. We use TRACES trade data and pig density to estimate the risk from pig trade and wild boar habitat suitability maps to model both home range movement and dispersal of wild boar. We consider the potential spread of ASF to new regions of Poland given the current disease situation in this country, and highlight specific areas as potential hotspots of disease incursion along Germany's border. We compare this to the risk to all countries in Europe currently disease-free.

Our generic framework enables comparisons in risk across diseases and pathways, providing horizon scanning functionality. It also allows for targeted surveillance at specific locations or specific pathways of disease introduction. This saves money and resources required for surveillance but, more importantly, it reduces the time to discovery of an emerging disease, and therefore allows disease eradication or management strategies to be more effective.

Key words: Spatial risk assessment, generic framework, African swine fever, disease hotspots

Surveillance of antibody titres protective to rabies on postvaccination dogs in Tungka village of Limapuluh Kota district, West Sumatera province, Indonesia, 2017

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ABSTRACT

Background: Rabies is an important zoonosis for public health because it results in death for the sufferer. Rabies is caused by a virus from the genus Lyssavirus that is transmitted to humans through animal bites such as dogs, cats and monkeys. The survey aimed to determine the prevalence of Rabies antibody protection during 12 months (1 year) on postvaccination dogs and the relationship between Rabies antibody titres on dog by maintenance management.

Materials and methods: The survey conducted in May 2017 in Tungka Village of Lima Puluh Kota District. Data of vaccination was taken from Livestock and Animal Health Services of Lima Puluh Kota District. Total 40 dogs were selected using simple random sampling proportionally from 275 dogs that had been vaccinated in May 2016. Interviews through questionnaires were conducted on the owners. Questionnaire data were collected and analyzed univariat and bivariate with chi-square ($\chi2$) and odds ratio (OR).

Results: Survey results indicate that the prevalence of Rabies-protective antibody during 12 months (1 year) in dogs is 35%. Risk factors that affect antibody titres are dogs located in the Village, dogs that act as hunting dogs and maintenance (Dogs that are caged and tied up). Based on the results of the survey has been conducted communications, information and education (KIE) to the owner of the dog who became a sample examination of antibody titers.

Conclusion: Antibody titres protective during 12 months on postvaccination dogs is low so it must be done repetition of Rabies vaccination.

Key words: Rabies, prevalence, risk factors, antibody titres, postvaccination

Avian Influenza Surveillance in Poultry Collecting Facilities and Poultry Slaughterhouses in Subang, Indonesia

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ABSTRACT

Objective: The aim of this study was to conduct a surveillance of avian influenza in poultry collecting facilities/ poultry slaughterhouses (PCFs/PSHs) in Cipunagara Subdistrict, Subang District, West Java Province during April until June 2010 and November 2010 until January 2011.

Materials and methods: The sampling unit was a poultry consignment, that was a batch of birds arriving on the same transport vehicle (i.e. truck, car or motorcycle). Ten tracheal swabs samples were taken from consignments with less than 50 birds whereas 15 samples were taken from consignments with 50 birds or more. In addition, 15 environmental swabs were taken from the PCF/PSH whenever a poultry consignment was sampled. Information regarding general PCF/PSH characteristics and poultry type, size, origin and transportation method were collected using structured questionnaire. Swab samples were analyzed with a M-PCR and a H5 PCR.

Results: There were six PCFs/PSHs in Cipunagara. The 2625 tracheal swabs which were combined into 525 pooled samples. Nine pooled of four consignments sample tested positive with the M-PCR indicating the presence of Influenza A genetic material but subsequently tested negative for the presence of H5 antigen. The 900 samples collected from the PCF/PSH environment and transport equipment were combined into 180 pooled samples of which five pooled samples of five consignments tested positive for Influenza A but all tested negative in the H5 PCR. Most consignments which came into Cipunagara were from other subdistricts in Subang District and the neighboring Indramayu District.

Conclusion: The surveillance could not demonstrate the presence of HPAI virus in incoming poultry consignments or in selected areas of the PCF environment.

Key words: Avian infulenza, poultry collecting facilities, poultry slaughterhouses

Developing wildlife health surveillance in Cambodia

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ABSTRACT

Objectives: Wildlife health surveillance is essential to the early detection and response to emerging health threats and an integral part of International Health Regulation core capacities. In Cambodia, we developed a surveillance network to detect wildlife morbidity and mortality events as indicators of emerging health threats. After a 3 years pilot, we provide a baseline evaluation of the network's performances.

Materials and methods: The network development was based on field and laboratory resources from the public health, animal health and environmental sectors. The network was primarily structured around protected areas and rescue centers. Forest rangers, conservation organization and rescue center staff were trained to report morbidity/mortality cases, and submit carcasses for necropsy or samples. The Wildlife Conservation Society (WCS), the National Animal Health and Production Research Institute (NAHPRI) and Institut Pasteur du Cambodge (IPC) coordinated the reception of specimen, necropsies, the management of sample and data, and laboratory testing. The Surveillance Network Analysis Tool (SNAT) was used to establish a baseline of the network's performances.

Results: By the end of the pilot phase, 186 field personnel were trained, covering 18 protected areas and two rescue centers in Cambodia. Over 210 cases of sick, dead or rescued wildlife and 5 mass mortality events were investigated, demonstrating the effectiveness of the network at detecting and responding to health threats. The SNAT evaluation is pointing to fair scores for representativeness, flexibility and simplicity, while stability and rapidity scored lower due to the pilot nature of this implementation. Policy development toward a national-level multi-ministerial strategy for wildlife health surveillance is expected to improve the acceptability and stability of the network.

Conclusion: Linking government and non-government partners in the conservation and health sectors allowed the rapid establishment of effective surveillance mechanisms while taking important steps toward the development of cross-sectorial policy tools.

Key words: Wildlife, health, network, surveillance, evaluation

Upward trend for the Indonesian Animal Health Information System, from 2016 to 2017

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ABSTRACT

Objective: Indonesia's animal health information system, "iSIKHNAS", was established in 2012. We described the number of users and amount of data captured and managed between 2016 and 2017.

Materials and methods: We extracted data on users and messages received from the 2016 to 2017 Users Performa Report and Monitoring Report. We epidemiologically analyzed it using descriptive analysis.

Results: iSIKHNAS has been implemented in all (34) provinces. The number of users increased two times from 5,065 to 10,726. The highest proportion of users was recorded in Jawa Timur Province from 11% (554/5,065) to 17% (1,850/10,726) and Jawa Tengah Province from 10% (520/5,065) to 10% (1,064/10,726). In 2016, registering as more than one type of users was done by 56% (2,830/5,065) users compared with 51% (5,470/10,726) in 2017. The number of messages increased 19 times from 704,994 messages in 2016 to 13,480,082 messages in 2017. The message traffic per day increased from 1,931 messages in 2016 to 36,932 messages in 2017. The least active months were June and December. The proportion of error messages avoided by the system was 7% (49,600 messages) in 2016 and 17% (2,157,371 messages) in 2017.

Conclusion: There was an increasing trend of users and data managed by the iSIKHNAS system between 2016 and 2017. These findings can be used as a basis for investigating the users increase motivations and the error messages in order to improve the system. The iSIKHNAS system seems able to accommodate the needs in order to monitor and evaluate users and messages reported.

Key words: iSIKHNAS, information system, user, message

GREASE a research network in partnership for a better management of emerging risks in South-East Asia

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ABSTRACT

Global changes in Southeast Asia (such as increasing urbanization and population densities, intensification of trade and farming systems, drastic land use changes and biodiversity erosion) are affecting the drivers of health risks emergence. Therefore, building bridges among Health, Environment and Agriculture sectors is one of the main challenges that SEA countries have to face, in the framework of a "One health/Ecohealth" approach. It calls for a better integration between animal health and public health, social and environmental sciences, and agriculture to address complex and emerging health issues. Nevertheless, such integrative approach cannot be achieved spontaneously with the relevant stakeholders, and implies methodological guidelines for cross-sectorial and interdisciplinary collaborations.

GREASE is a regional network that supports research activities for a better Management of Emerging Epidemic Risks in Southeast Asia. It responds to the challenge of emerging transboundary animal infections and zoonotic diseases by producing a theoretical and operational framework, in line with the OH approach. GREASE provides scientific and institutional support to facilitate interactions between various stakeholders including: scientists from SEA and worldwide, decision-makers and local actors.

This research network and its activities were initiated end of 2009 and formalised between the seven core members in May 21012: Kasetsart University in Thailand, the National Institute for Veterinary Research in Vietnam, the National University of Laos in Laos, the National Veterinary Research Institute in Cambodia, Central Mindanao University in the Philippines, Gadjah Mada University in **Indonesia** and CIRAD. More than 20 associated partners are also participating in the network for the implementation of projects and training.

The network has been set up around 4 objectives: understanding interdependence between epidemiological and socio-economic dynamics in veterinary public health issues; understanding the interactions between biodiversity and health; improving epidemiological data sharing at the animal/human public health interface; Evaluating and reducing animal and zoonotic diseases' impact.

Key words: Research Network, One Health, Health risk management, participatory approaches, Ecohealth

A cross sectional study and blood biochemical profile of anestrus on beef cattle in Grobogan district, Central Java, 2013

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ABSTRACT

Objective: Anestrus is caused by multifactorial problem and that can lead to low productivity and reproductivity, so that effort to prevention and control anestrus. The objectives of this study were to determinethe prevalence, factors associated withanestrus and blood biochemical profile in anestrus beef cattle.

Materials and methods: This study used a cross-sectional design, conducted on 228 beef cattles in five sub-district. Simple random sampling was done at the level of sub-district and village, and the farms as the smallest units taken as a cluster. Anestrus cows examination conducted by rectal examination and risk factors were taken with the questionnaire. Analysis of the data include: univariate, bivariate and the odds ratio, multivariate logistic regression, selected at random were used to analyze the blood biochemical profile.

Results: The results showed that the prevalence of anestrus in beef cattle at livestock and farm level, respectively 18.4% and 19.2%. Risk factor that had association to increase the incidence of anestrus in cattle are a lactation level, retained placenta, dystocia, feed straw, and postpartum estrus, whereas risk factor which hadassociation to increase the incidence of anestrus at farm level arethe experience raising livestock was less of two years and a dirty cage conditions. Blood biochemical analysis showed that the calcium level in beef cattle which suffer anestrus were significantly lower than fertile cows, whereas the levels of glucose, total protein, cholesterol and phosphorus were not significantly different.

Conclusion: The results of this study can be concluded that anestrus in beef cattle is caused by multifactor, and blood biochemical profile in anestrus beef cattle were lower than fertile cows.

Key words: anestrus, prevalence, risk factors, Grobogan district, blood biochemical

Innovative strategy for the coordination of regional health networks: the contribution of Project, Quality and Multi Project Management - the example of CaribVET

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ABSTRACT

Objective: The Caribbean Animal Health network (CaribVET) is a result-oriented and scientifically driven participatory regional animal health network. It is recognized by the CARICOM Secretariat and official veterinary services (VS) in the Caribbean and garners the efforts of 47 VS, universities, research institutes and regional/international organizations in health and agriculture. The Coordination Unit (CU) ensures that epidemiological surveillance, capacity building and research projects implemented by various CaribVET partners do not duplicate, are complementary and address regional priorities. With its recent development, CaribVET management methods evolved from basic project management (PM) to advanced PM using quality (QM) and multi-project management (MPM) principles. To study the evolution of the CaribVET management and promote powerful methods for the effective coordination of other regional networks, allowing easier management of animal health projects portfolio at the Regional scale.

Materials and methods: QM principles derived from ISO 17025 standards (for diagnostic laboratories) are used to: ensure traceability of members, manage quality documents and design a quality policy for the network. ISO 10006:2003 standards for PM, and MPM principles are used to standardize and share tools/methods (SWOT, PDCA, …) and templates (ToDoLists, Event Reports…) developed by the CaribVET Secretariat and tailored to the Caribbean context to ease coordination overall. Moreover, several online tools (Caribvet-event.com, directories, regional planning) were developed.

Results: Drawing on few human resources, numerous positive externalities were generated: enhanced structuration of the network, harmonized mechanisms, synergistic collaborations, better time management, increased participation in CaribVET management (25 persons from 16 organizations), continuous improvement. This collective effort lead to more efficient resource allocation allowing CaribVET to quickly address Avian Influenza threat.

Conclusion: This experience may be of interest for cost-effective coordination of multiple regional research and development projects to address highly complex emerging health issues worldwide, such as antimicrobial resistance.

Key words: Management, economics, health network, CaribVET

Quantitative assessment of the probability of introducing bovine Brucellosis into Scotland and Wales by imported cattle

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ABSTRACT

Objective: A stochastic model was used to estimate the quarterly probability (PIntro) of introducing bovine Brucellosis into Scottish and Welsh cattle herds, by at least one imported cattle (carrier of Brucella abortus). Sixteen surveillance periods (Q-1-2013 to Q-4-2016) were considered.

Materials and methods: Inputs for the model came from: literature, legislation and data analysis. Countries exporting cattle to Scotland and Wales were divided into Officially Brucellosis Free (OBF), Non-Officially Brucellosis Free (Non-OBF), and in Validation (during the five transition years between Non-OBF and OBF status). Moreover, the local cattle population was divided into several strata according to sector (dairy or beef) and testing scheme used. The stratum of herds not tested at the official laboratories was also considered. Thus, the model related the probability of disease introduction to the testing coverage in the local surveillance components (representing also the Scottish and Welsh population strata).

Results: In Scotland, the quarterly median PIntro ranged from 0.4% to 1.5%. The overall median (of the 16 quarterly medians) PIntro was 0.9%. Considering 2016 only, the overall median was 0.644% (median of 5th p. = 0.137%; median of 95th p. = 2.025%). Therefore, under the current situation, on average, at least one introduction could be expected (approximated) each ≈ 39 years (12; 182). In Wales, the quarterly median PIntro ranged from 0.3% to 1.6%. The overall median PIntro was 0.9%. Considering 2016, the overall median was 0.420% (median of 5th p. = 0.038%; median of 95th p. =1.809%). Therefore, under the current situation, on average, at least one introduction could be expected each ≈ 60 years (14; 658).

Conclusion: The model could be used to assess PIntro in the future if official Brucellosis status changes for trading partners; and to assess the relative risk of disease introduction in the different population strata, when evaluating the national surveillance system (accompanying abstract).

Key words: Bovine brucellosis, imported cattle, quantitative assessment, PIntro

Pork value chains in Rwanda: national value chain structure as a means of understanding cysticercosis risk in the pig sector

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ABSTRACT

Introduction: We present the results of a study to map pig value chains in Rwanda. Rwanda has a population of approximately 1.6 million pigs, largely in small-holder production. In some regions, 80% of households are estimated to keep pigs, with 1-4 pigs per household. Pig production is increasing rapidly to meet rising demand in urban and rural areas, and for export to neighbouring countries. Our aim was to produce the first systematic mapping of this value chain, with a view to understanding cysticercosis risk.

Material and Methods: Focus group discussions and key informant interviews were undertaken in all 5 provinces, focussing on identifying available infrastructure related to pig value chains, namely location of farms, availability of pig markets, slaughterhouses, pork processing factories, transport routes. In addition, the interviews gathered data on source of inputs, flow of pigs and pig products, seasonality, routes/geographical mapping as well as relationships between actors involved in the flow of pigs and derived products.

Results: Findings revealed existence of both informal and formal value chains, with significant informal trade between farmers and brokers, without involvement of state governance structures. The study highlights the volume of pork supplied by the two different systems in urban and rural areas. Pig slaughtering is carried out in formal and informal settings; the former through slaughter slabs and the latter characterized by slaughtering in farm settings that lack adequate infrastructure to ensure pork safety. Interestingly, both informal and formal market and slaughtering systems intersect, implying crossover of risk of infectious disease transmission to humans.

Conclusion: This is the first study to formally map pig value chains at a national scale in Rwanda. Our results demonstrate flows of pigs and pork supplying urban and rural settings, and highlight associated risks in terms of infectious diseases transmission.

Key words: Pig, Rwanda, value chain, governance, cysticercosis

Entomological surveillance of vectors of Bluetongue virus in Croatia

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ABSTRACT

Objectives: Bluetongue disease was reported in sheep in Croatian Mediterranean region (Dubrovnik-Neretva County) for the first time in 2001. Since then *Culicoides* has been regularly monitored. *The aim of this study is to analyze vectors and to assess the vector distribution and* seasonal abundance as factors in predicting disease incidence and spread.

Material and methods: Samples were collected at 26 sites in nine Croatian counties, with special focus on the population of vectors in the Mediterranean region. Vector abundance was determined by light traps on selected farms. *Culicoides* species were morphologically identified. The *distribution and* seasonal abundance of *Culicoides* were also analysed.

Results: 46.709 adult insects of the *Culicoides* genus were identified, out of which 40.21 % belonged to the Obsoletus group and 51.50 % to the Pulicaris group. Female adults predominated in both groups. The highest rate of nulliparous (more than 70 %) and the lowest rate of gravid females (les than 1 %) was recorded in both groups. Out of all vector risk areas, the highest number of both vectors was found in the Mediterranean region. In summer, significantly higher number of vectors of the Obsoletus group (9.16 %, CI 95 % 6.72-11.68 % per sample) than of the Pulicaris group (3.66 %, CI 95 %, 1.90 - 5.43 % per sample) was found, while in autmn Pulicaris vector was dominant (39.72 %, CI 95 %, 29.64–49.90 % per sample). *Culicoides immicola* was not identified at any study sites.

Conclusion: In Croatia, bluetongue virus can be transmitted by multiple *Culicoides* vectors, belonging to the Obsoletus group and the Pulicaris group. Significant differences in seasonal abudance were found. The results can serve as input data for creating a national targeted surveillance program taking into consideration both spatial and temporal distribution of vectors.

Key words: *Culicoides*, age granding, distribution, seasonal abundance, Croatia,

Costs estimation of Human Salmonellosis outbreaks associated to animal products consumption in Brazil, 2008/2016

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ABSTRACT

Objective: This study had as objective to estimate the costs of human salmonellosis outbreaks carried by animal products, notified to Health Ministry of Brazil, occurred from January 2008 to December 2016.

Materials and methods: A partial budget model with stochastic modeling was used to estimate the costs of human salmonellosis outbreaks carried expressly by animal products. The costs were estimated on absence days of work and on hospital treatment expenses. Infected people were categorized according to illness severity: people who felt ill and stayed at home; people who got sick and received ambulatory care; people who got sick and needed hospitalization and people who got severely sick needing intensive care treatment. Probabilistic models were created to estimate costs for each category using @ Risk® (version 5.7, Palisade Corporation©, 2015).

Results: The total average cost was estimated at US$ 1,132,368.05. The variable of greatest impact was the average hospitalization ($R^2 = 0{,}90$), followed by average of absence days of work due hospitalization ($R^2 = 0{,}38$) and average of absence days of work per outpatient case ($R^2 = 0{,}22$).

Conclusion: The model definition to estimate salmonellosis outbreaks costs, associated with animal origin products consumption, helps to show not only the financial impact of the disease in Brazil, but also allows a better visualization of the problem magnitude, improving the assertiveness of health surveillance programs.

Key words: Costs simulation, Salmonellosis, zoonosis, Brazil

International collaboration to change animal health policy, and control animal diseases

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ABSTRACT

Veterinary services need to design, develop, and execute animal health policies that are science based, economically feasible, and politically accepted. The combination of these three factors make the job of the veterinary services complex, and this increases when two countries try to find collaboration approaches.

In 1993, the U.S./Mexico binational committee for bovine tuberculosis was created to address concerns over cattle being exported to the U.S. The committee was composed of livestock producers, regulatory officials, and research scientists from both countries. Mexico and the U.S. have signed a 2013-2018 Joint Strategic Plan for Collaboration on Bovine Tuberculosis. The results of this work has allowed for a reduction of bTB cases exported to the U.S., and an average of 1 million head of cattle exported.

In 1994 USDA signed a cooperative agreement with Panama to build a sterile fly production plant to eradicate New World Screwworm (NWS) from Panama, and the maintenance of a permanent barrier. The permanent international collaboration that the USDA has stablished with Panama was an instrumental tool to fight NWS in Florida with fast and efficient results.

In 2001 the USDA worked together with Bolivia investing 4 million USD to implement an FMD program focused in high risk areas. There have been no FMD outbreaks in Bolivia since 2007, and Bolivia is planning to be able to lift FMD vaccination by 2019. These significant achievements show the power of policies applied to control of diseases in conjunction with close collaboration with producers, and international organizations.

The relation between the policy making process has to accompany what is economically and scientifically sound, accompanied by a long term strategy. This process needs being accompanied by the collaboration of official veterinary services, academia, producers, stakeholders, and international organizations to observe proper results in the long term.

Key words: Bilateral agreement, animal health, policy, erradication

Progressive control Pathway for Foot-and-Mouth principles into practice in Southeast Asia

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ABSTRACT

Objective: The occurrence and impact of endemic Foot-and-Mouth Disease (FMD) in Southeast Asia (SEA) is impairing income of livestock owners and trade opportunities with China. The progressive control pathway for FMD control (PCP-FMD) was adopted as component 1 of the global strategy for FMD control, launched in Bangkok, Thailand (2012). Under the South-East Asia and China Food and Mouth Disease (SEACFMD) Roadmap 2016-2020, application of PCP is enhanced. Support was given to veterinary services of Cambodia, Lao PDR and Myanmar to apply PCP principles into feasible, effective and stakeholder-supported risk-based strategy plans (RBSP) for FMD control.

Material and methods: Through online webinars, in-country workshops and regional meetings, OIE-SRR-SEA with the help of Animal Health Works provided expertise on risk-based FMD control in endemic situations and facilitated the process of developing a risk-based strategy plan by each of the national FMD committees. This process included risk- analysis along value chains of livestock products, identification, consultation and engagement of stakeholders, identification of risk hotspots for FMDvirus transmission and impact, definition of objectives, tactics and activities and establishing a mechanism for monitoring and evaluation.

Results: Each of the countries developed its own RBSP. Country-specific elements to progressive control of FMD will be presented.

Conclusion: Progressive control of FMD is possible through small steps addressing a risk-based approach. It requires a mind-shift for veterinary services as well as stakeholders in thinking about disease control.

Key words: Progressive control pathway, risk-based strategy plan, FMD control, value-chain analysis

Assessment of the potential economic impact of MRSA to the Australian pig industry

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ABSTRACT

Objectives: Livestock-associated MRSA ST398 is reported to represent an additional burden and cost to MRSA infections in some countries. However, the impact of the newly emerged CA-MRSA strains, such as ST93 in piggery workers is uncertain. Recently, a high prevalence of ST93 carriage has been identified in pigs and humans on a pig enterprise, and reported this strain as an occupational health risk for the first time. The current study aims to estimate the potential economic impact due to MRSA carriage and infection among piggery workers in the Australian pig industry

Materials and methods: A risk assessment approach was used based on scenario trees and a Monte Carlo simulation model. Three different situational scenarios were considered depending on strain carriage in piggery workers, these being: Scenario 1) ST93 MRSA carriage only; Scenario 2) ST398 MRSA carriage only; and Scenario 3) A combination of ST398 and ST93 carriage (4:21 ratio).

Results: Scenario 1 resulted in the highest number of infections, with a median of 830 (5%-95%, 477-1316), and hospitalisations (median = 262, 106-539), costing the industry a median of AU$4m (1.74-7.92) per year. Scenario 2 resulted in the lowest rate of infections (68, 18-153) with a median of only two people requiring hospitalisation and a median cost of $15,206 (2,250-5,657). In Scenario 3, a median of 710 (409-1119) people are estimated to be infected per year, resulting in a median of 220 (89-453) hospitalisations and costing the industry a median of $3.36m (1.47-6.66). The majority of infections (¬median = 697, 401-1105) in Scenario-3 were associated with ST93.

Conclusion: The predicted outputs of this study show that emerging new CA-MRSA strains within the pig industry, using ST93 as an example, have the potential to cause substantial disruption to pork production, with a high number of infections in workers and resultant marked economic loss.

Key words: LA-MRSA, CA-MRSA, ST398, ST93, antibiotic resistance

Risk mitigation for Influenza A (H7N9) spread outside of China through informal poultry trade

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ABSTRACT

Objective: Influenza A (H7N9) was firstly emerged in China in March 2013, and five seasonal epidemic waves of H7N9 have been observed. No human cases have been reported so far beside of China. FAO and FAO China pay serious and cautious attention and actions the border areas with high level of risk and focus on chicken value chain. Yunnan province is surrounded by Sichuan, Guizhou and Guangxi provinces with H7N9 human cases reported in the current wave. Meanwhile, Southern part of Yunnan province shares borders with Viet Nam, and informal trade of spent hens from China to Viet Nam have been noticed. In order to know the pattern of informal trade of spent hens, and to further identify the potential risk pathways for the risk mitigation plan, we interviewed the key informants in border area, and assessed the risk of the informal way regarding the release of avian influenza (AI) viruses.

Materials and methods: We selected Hekou border country in Yunnan province for pilot study. Methods on open group discussion with county level veterinary staff have been used to collect relevant information. The snowball survey method was also used to identify key informants and structured questionnaires have been given for the information collection.

Results: We found that approximately 0.3 million spent hens per year were moved across Hekou port via boat to Vietnam in recent years, much less compared to 1 million volume per year in 2013. Economic-oriented (3 to 4 yuan/kg price difference) and consumer preference drive cross-border poultry movement. We also used the information on organization of informal trade to qualitatively evaluate the risk of release of AI viruses.

Conclusion: Continue conducting value chain studies (in collaboration with Viet Nam) to better understand the situation of cross-border movements of poultry and identify the potential risk pathways. A risk mitigation plan has been proposed on legally organizing trade with safer poultry sources and better biosecurity practices.

Key words: Value Chain; Risk; Influenza A (H7N9); Poultry Trade

Animal health needs for small-scale farms and urban agriculture in the Western United States

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ABSTRACT

Objective: With the increase in small-scale and backyard livestock and poultry farming in urban and peri-urban settings in the Western United States, there is a need to evaluate how much urban veterinary practices mainly focusing on companion animal medicine are exposed to production species. We also seek to understand how prepared they are to assume this new role both in terms of serving a new customer base with different needs and in terms of their role in public health.

Methods: A survey was conducted amongst urban and peri-urban veterinary practices in California, Oregon, Washington and Colorado. Questions focused around 4 main themes: frequency of contact with livestock, knowledge in livestock medicine, perception of the role of veterinary medicine in food safety and zoonotic disease control, and continuing veterinary medicine education. Data were analyzed through basic descriptive approaches and multivariate logistic regression.

Results: A total of 880 surveys were completed, of which 728 (86.4%) were companion animal practices and 701 (85.6%) were in urban or peri-urban settings. Almost 700 (76%) respondents reported an increasing trend in the presence of urban and peri-urban livestock in their area. Some 601 (69.5%) reported receiving questions relating to livestock more than once a month, but few respondents felt proficient in answering such questions (e.g. 83, 9.6% for poultry and 131, 15.2% for cattle). About 400 (57.1%) participants showed interest in participating in continuing veterinary medicine education (CVME) programs focusing on poultry and 300 (42.0%) on other species.

Conclusion: Results of this survey provide information on the knowledge level of urban and peri-urban practices in livestock and poultry medicine. This helps in understanding how the needs of small scale farmers in these environments will be met. The main outcome of this survey is to understand how to develop and format educational programs for both veterinary students and practitioners who seek continuing education.

Evaluation for action – Enhancing animal disease surveillance capacity in West, Central and East Africa

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ABSTRACT

Objective: The devastating outbreak of Ebola in 2014 was a wake-up call for West African countries to improve capacity to detect pathogens in both humans and animals. Unfortunately, the animal sector has long lagged behind its public health counterpart in disease surveillance capabilities. To fill this gap, African countries in phase 1 of the Global Health Security Agenda (GHSA) requested a tool to evaluate and improve animal disease surveillance systems. The Food and Agriculture Organization of the United Nations (FAO) developed the Surveillance Evaluation Tool (SET) to provide national veterinary services with a standardized, comprehensive and repeatable evaluation strategy to identify animal disease surveillance gaps and develop specific, realistic and time-bound recommendations for improvement.

Materials and methods: SET was created in 2017 from the Oasis toolkit (ANSES) and consists of a comprehensive method of assessment focusing on 7 major themes, divided into 19 categories and 90 indicators. In-country SET evaluation missions last 10-12 days each and include a strong field component, where evaluators meet with stakeholders and gather information at all levels of the surveillance system. The data is analyzed using SET, and outputs are produced in graphs to easily identify strengths and weaknesses of the system. From this, the team develops specific and locally-relevant recommendations in the form of a prioritized action plan for implementation.

Results: By end of April 2018, SET was used to evaluate 13 national animal disease surveillance systems in West, Central and East Africa. As a next step, a tracking strategy to follow-up on recommendations and their implementation at country level will be developed.

Conclusion: SET allows national veterinary services to identify a stepwise approach to build animal disease surveillance capacity. Implementation of the toolkit at a regional level can identify patterns between countries and help focus funding efforts to build surveillance capacity at a regional level.

Key words: Capacity building, animal diseases, zoonoses, evaluation

An overview of animal health and communication constraints in smallholder farming systems of Machakos County, Kenya

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ABSTRACT

Objective: This study was designed a study to 1) identify existing animal health constraints in rural smallholder systems of Machakos, Kenya, and 2) analyze practices related to sharing of animal health information in these areas.

Materials and methods: Data were collected using both focus group discussions (number of groups =3) and one-on-one questionnaire interviews (n=172), and analyzed using both descriptive and thematic approaches.

Results: Pneumonia was not only the most frequently reported problem (62%) but was also the disease most feared (33%) by farmers. Rabies, Newcastle disease and East coast fever were scored high during the focus group meetings. Sharing of animal health information is constrained by a number of factors including bad roads, poor mobile network coverage and bad relationships between farmers and the health providers. Farmers often delay reporting the problems they observe on their farms, for several reasons e.g. tendency to first try local herbal formulations, for cases that occur at night, and when animal health providers are not available at the time when the farmer needs them.

Conclusion: This study has provided useful baseline data that can then used to 1) design a village-based animal disease reporting system which is currently lacking in the surveyed villages, and 2) support the county government's efforts to manage animal diseases and zoonoses through better reporting, for improved health, nutrition and livelihoods.

Key words: Animal health; disease reporting; surveillance systems

Detection of swine influenza virus infection in a high-risk pig population in North Sumatera, Indonesia

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ABSTRACT

Objective: Swine influenza viruses (SIV) are important both as a potential public health concern and due to the economic loss to pig farmers. Swine play an important role in the ecology of influenza A viruses. Increased surveillance in swine is therefore important to detect and characterize influenza viruses in pigs, which co-circulate with avian and human influenza viruses so that re-assortment events can be rapidly identified. The study was aimed to detect SIV infection in high-risk pig populations and to identify risk factor associated with SIV presence in North Sumatera.

Materials and methods: A study was conducted in the March-November 2017 period in 196 high-risk pig farms in five districts in North Sumatera, where high poultry populations are found in close contact with pig and human populations. Nasopharyngeal swab samples were collected and pooled for qRT-PCR Influenza A testing; blood sera were collected for swine influenza virus ELISA serological testing.

Results: Results showed that 5% (19 / 374 pooled swab samples) were positive for Influenza A viruses and 13% (85 out of 663 sera) were seropositive for swine influenza. Farms that were sampled in October-November 2017 were found to have a higher rate of seropositivity and influenza Avirus detection than during other months of this study. These months were colder and experienced higher rainfall, probably increasing influenza A virus transmission. The October-November period also exhibited greater pig movement and farms having higher numbers of finisher pigs due to expected higher year-end demand for pork.

Conclusion: Further risk factor analysis will expand on these findings, and molecular characterization will be performed on PCR-positive influenza type A samples to explore the possibility of virus re-assortment between avian and human influenza viruses in the target areas. This initial finding allows better targeting of surveillance for influenza viruses in high-risk pig populations at swine-poultry-human population interfaces.

Key words: Detection, high-risk population, influenza viruses, swine influenza, pig farms

Infectious bovine rhinotracheitis: results of the Italian National Surveillance Plan

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ABSTRACT

Objective: The objective of this manuscript was to describe the two-year results of the first national surveillance plan to control and eradicate Infectious Bovine Rhinotracheitis (IBR) in autochthonous beef cattle breeds in Italy.

Materials and methods: Herds registered with the National Herd Book for Italian beef cattle breeds (Chianina Marchigiana, Maremmana, Podolica and Romagnola) voluntarily submitted to commercial ELISA gE serologic testing for BoHV-1 antibodies. Herds were characterized as seropositive if any cow, older than 12 months, tested positive. Monetary incentives are used to encourage breeders to achieve the annual seroprevalence ranges stated in the plan.

Results: In the 2015, 820 of the 5,144 herds recorded in the National Herd Book were included in the national surveillance plan and 455 of these were identified as IBR-seropositive. In the 2016, 718 of 5,201 herds and 319 were IBR-seropositive. A herd seroprevalence was 55% (CI95%: 52–59) in 2015, in 2016 54% (CI95%: 51-58); in 2015 animal seroprevalence was 32% (CI95%: 31–33) and in 2016 30% (CI95%: 29-31). The Podolica breed showed the highest seroprevalence and the Maremmana breed the lowest seroprevalence.

Conclusion: This is the first national surveillance plan for BoHV-1 in Italy. Voluntary eradication schemes were considerate not be sufficiently robust to eradicate BoHV-1 but it can be the basis to know the prevalence of the infection. The seroprevalence values found showed the need to stop the inevitable severe economic losses due to the infection.

Keywords: IBR, Italy, autochthonous cattle breeds, surveillance plan

Situation of priority diseases in South Sulawesi based on integrated National Animal Health Information System of Indonesia (iSIKHNAS) during 2015-2017

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ABSTRACT

Objective : Rabies, Anthrax, Brucellosis, Avian Influenza and Classical Swine Fever are five priority and major diseases in South Sulawesi Province, Indonesia. In 2013, Integrated National Animal Health Information System of Indonesia (iSIKHNAS) was launched and South Sulawesi Province as the choice of pilot project of this system. Five among six of priority diseases above were listed in iSIKHNAS classified as zoonotic disease, moreover have economic impact. Real-time based of animal health report in iSIKHNAS from local field officer and farmer need to be analyzed as communicable and useful information for every stake holder. The aim of this study was to describe the dynamic of five priority diseases in South Sulawesi based on iSIKHNAS database.

Material and methods : Syndrom priority reports of South Sulawesi from year 2015 – 2017 derived from iSIKHNAS database were evaluated and analyze excel software. Each disease syndrom were analyze using QGIS software to create disease mapping.

Results : There were 844 priority sindrom reports (364 reports in 2015; 430 reports in 2016 and 50 reports in 2017), and 1,07% (nine) reports were not response by veterinary officer. Rabies syndrom were the highest report followed by Brucellosis syndrom, Avian Influenza syndrom and Anthrax, there were no CSF reports during 2015 – 2017.

Conclusion: These findings could be useful to evaluate the effectiveness and sustainability of the system in South Sulawesi and to support effective decision-making to control and mitigation effort of diseases and for emergency response.

Key words: iSIKHNAS, priority diseases, south sulawesi

Livestock diseases in the highlands of Ethiopia: Participatory epidemiology and gender perspectives

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ABSTRACT

Objective: Infectious diseases are a key constraint in livestock production in Ethiopia. This study aimed to understand livestock producers' perception on their importance. Participatory tools were used to identify and rank livestock species, major livestock diseases and their epidemiological patterns in smallholder systems.

Materials and methods: The study covered four states, 23 districts, and two *kebeles* (smallest administrative unit) in each district. To capture views of women and men, separate focus group discussions (FGD) were conducted. Data collected through proportional piling were used in multinomial logistic regression analysis.

Results: Taking sheep as reference, men prioritized the importance of cattle as 1.73 times higher ($P<0.0001$). Sheep were more important ($P<0.05$-0.01) than goats, equines and poultry. Cattle were also the most important species for women, but contrary to men, goat and poultry were as important as sheep. Only 12 out of 29 identified cattle diseases were mentioned by at least 10% of FGDs in their list of five most important diseases. FGD groups allocated similar scores ($P = 0.111$) for Anthrax, FMD, Black leg and Bovine Pasteurellosis compared to the reference disease Lumpy skin disease. The scorings provided by women and men FGDs were similar. Reasons for scoring included suddenness of death, zoonosis risks, animal age groups and species affected, frequency of occurrence, rate of transmission in herds, curability and inefficient vaccination. Seasonality and agro-ecology were also factors associated with disease occurrence. Men and women are more involved in activities related to disease transmission compared to other family members. Severe impacts of diseases include loss of livelihood, displacement and infection with zoonoses, with women more affected.

Conclusion: In conclusion, participatory tools allowed to understand disease priorities of and their perceived epidemiology in smallholder systems. The perceptions and priorities of men and women are very similar and both need to be involved in designing health management interventions.

Key words: Diseases, Ethiopia, epidemiology, gender, smallholders

Risk assessment on highly pathogenic avian influenza using machine learning method for poultry farms in Korea

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ABSTRACT

Objectives: Outbreaks of highly pathogenic avian influenza (HPAI) are confirmed in poultry farms of Korea for almost every winter season during the last 15 years. This study presents a big data based HPAI risk assessment model developed aiming to minimize damage from HPAI.

Materials and Methods: Poultry livestock related vehicles were traced to address the risk of HPAI if vehicles visit (an) outbreak farm(s) during 21 days previous to be confirmed HPAI. A machine learning method was implemented to find relationship between the movement records of vehicles and HPAI outbreaks on farms. Graphic user interface was accompanied for easy use of the model.

Results: The machine learning model was converged to three hidden layers and 10 nodes per layer. Hyperbolic tangent was the activation function. Sensitivity and positive predictive value were estimated to be 90.2% and 51.4%, respectively.

Conclusion: Risk was assessed for poultry farms and communicated to local governments to implement pre-emptive control measures during the epidemics of HPAI in 2016/2017 and 2017/2018 winters. The first big data based risk assessment model on HPAI provided guidelines of risk management of poultry farms and wild birds.

Information and communication technology for animal diseases control in the Republic of Korea

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ABSTRACT

Objectives: This study presents how information and communication technology (ICT) was to be applied to control animal diseases in Korea.

Materials and methods: Four items of ICT have been adopted one by one, to enhance ability of responding animal diseases including highly pathogenic avian influenza and foot-and-mouth diseases. These were global positioning system (GPS) based vehicles tracking system, E-visitors' book, positioning with cellphone signaling, and expressway record. Whole processes from collection to analysis of data were performed with informed consent of persons concerned.

Results: The first two items, vehicles tracking system and E-visitors' book were for positioning visitors, meanwhile cellphone signaling and expressway record were to trace farmers' movement. Combination of vehicle tracking system and E-visitors' book, could collect approximately 30% of visitors records on farms. However, most of residents and neighbors coming and going were not recorded. Cellphone signaling and expressway record were helpful to investigate farmers' behaviors in details but without exact positioning.

Conclusion: ICT items were proved to be complementary tools for epidemiological investigation. Some supported verbal statement, and others induced further action of response.

Syndromic surveillance system for early detection of rabies cases in Bali Province, 2017

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ABSTRACT

Objective: The purpose of this study was to provide an overview of syndrome report compared to rabies incidence during 2017 confirmed by laboratory result, and the dog vaccination and FAT positive case.

Materials and methods: Data that were used in this study were from the syndrome report data from i-SIKHNAS (reports of animal bite cases suspected of rabies), data on the result of brain samples and blood serums testing were from Disease Investigation Centre (DIC) Bali, rabies vaccination coverage and dog population data were from Bali Provincial Livestock Services. All Data were analyzed descriptively and location distribution of syndrome report presented through Quantum GIS.

Results: Surveillance syndromes results obtained that 658 syndromes have reported from 9 districts in 2017, and 92 positive FAT spreads in 7 districts/cities. Average of vaccination coverage in all districts in 2017 was 83.71 % (77%-90%). All syndromic reports from i-SIKHNAS were important source of information for follow-up action using integrated bite case management (IBCM) response.

Conclusion: Syndromic surveillance was intensively used in early detecting suspect of rabies cases in Bali, however not all cases reports has been followed or linked with the laboratory testing. Vaccination program with coverage vaccination more than 70% has succeed to decrease number of rabies cases more than 50% base on 2016-2017. The coverage vaccination more than 70% very impotent to archived with following higher hard immunity.

Key words: Syndromic surveillance, rabies, vaccination coverage

Moving sheep towards improved surveillance design – a case of resistance

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ABSTRACT

Objective: The design of surveillance activities is often a compromise between science, feasibility and available resources. This study aimed to inform the design and interpretation of ovine slaughter-house based surveillance activities, by the analysis of data generated through the reporting of sheep movements and use of electronic identification devices (EID). The outputs were then applied to an existing survey for antimicrobial resistance (AMR) in faecal samples from sheep slaughtered in Scotland.

Materials and methods: Available sheep movement data from a statutory database (ScotEID) for the years 2015-1017 were used to describe the population of Scottish sheep slaughtered annually, where they were slaughtered, their immediate origin and how this changed over time. The AMR survey consisted of 40 samples collected in one week per month, for one year, from one Scottish abattoir from June 2017. One E. coli isolate per sheep sampled was tested using EUCAST methodology and interpretative criteria, plus PCR, against a selection of antibiotics, including some regarded as critically important for human treatment. The distribution of these samples was compared to a number of denominator populations from the abattoir catchment to the Scottish slaughter sheep population.

Results: Despite a number of data limitations, the Scottish slaughter sheep population, the sheep slaughtered in Scotland population and the abattoir catchment areas and throughputs could be described in time and space. There are differences between the populations. The ovine population sampled for AMR was similar to the abattoir catchment area; however, there were parts of the other populations that it did not reach. Interpretation of the results of the sensitivity testing will need to account for these biases. In addition, it may be worth exploring the feasibility and cost:benefit of alternative sampling strategies.

Conclusion: Analysis of sheep movement data can help to optimize ovine surveillance activities conducted in Scottish abattoirs.

Key words: surveillance, design, slaughter-house, ovine, AMR, animal movements

Trade in live animals and animal products: Exploring global trends over a 20-year period using social network analysis

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ABSTRACT

Objective: Trade networks facilitate and accelerate the spread of infectious diseases. To inform policy and ensure preparedness, it is essential to understand their structure and properties. This study analyses the temporal changes in global trade networks of live animals and animal products from 1997 to 2016.

Materials and methods: Data for selected commodities were retrieved from the United Nations International Trade Statistics Database. Weighted directed networks were created for each commodity and year aggregating all trade flows between two countries within one year into single links. Network properties and centrality measures were determined and compared over time to identify trends or changes.

Results: Global trade in meat of all livestock species increased steadily and was particularly high for poultry, while countries undergoing economic development showed rising demand for beef. Trade in live animals followed a similar pattern. All networks consisted of only one weakly connected giant component with a few central countries accounting for most of the volume of trade. Others maintained fewer and weaker trade relationships. Over time, the number and density of trade links increased steadily, while the clustering coefficient varied from year to year. High trading volumes were not always correlated with large numbers of trading partners.

Conclusion: Trade in live animals and animal products is increasing in line with the demands of a growing human population. The trend towards high connectedness in livestock and meat trade promotes the spread of infectious diseases and resistant pathogens, which requires new approaches to transboundary disease control and risk-based surveillance.

Key words: Trade flows, social network analysis, food safety, transboundary animal diseases, globalization

Evaluating freedom of chronic wasting disease in wild reindeer populations accounting for differential sensitivity during the course of infection

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ABSTRACT

Objective: In 2016, chronic wasting disease (CWD) was detected in Norwegian wild reindeer, being the first detection of CWD in Europe. CWD was detected in a reindeer population of approximately 2100 reindeers with limited functional connectivity to other reindeer populations. A decision to cull the entire population was made in 2017 and the last animal was culled 2nd of April 2018. After a period of at least five year fallowing, the area should be repopulated from one of two adjacent populations consisting of approximately 450 animals or 10,000 animals. Before repopulation, these populations must be documented free at a sufficient level.

Materials and methods: A simulation model for surveillance based on stochastic simulation of scenario trees was developed. Input to the model was population size, number of tested animals and tissue sampled in 2016 and 2017 and various scenarios for testing regimes in the following years, diagnostic sensitivity and design prevalence. The sensitivity was varied based on infectious stage and sampled tissue and the design prevalence was increased annually based on assumed R0. Introduction risk was based on expert opinion. The model was used as a tool to enlighten uncertainties in time needed to document freedom from disease by using various scenarios.

Results: A sufficient number of samples from small populations to document freedom of disease could be difficult to achieve within the fallowing period of five years while still having animals for repopulation.

Conclusion: The model could be used to aid in predicting the number of years and samples required to reach a sufficient level of freedom from disease in adjacent populations before repopulation. The model also enlightened uncertainties in input parameters and was used to explain stakeholders the time costs involved when aiming for being precautious.

Key words: Chronic wasting disease, reindeer, Norway, simulation model, freedom of disease

Characterisation of One Health surveillance based on a systematic literature review and an expert-opinion elicitation

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ABSTRACT

Objective: The One Health (OH) concept promotes transition from traditional sectoral to inter-sectoral and multi-disciplinary management of health issues at the human-animal-interface. The approach is used increasingly for different initiatives, including surveillance. Nevertheless, confusion and uncertainty regarding practical application and consequences are persisting. We believe that a conceptual framework is missing to (i) define and characterize OH surveillance, (ii) describe and implement appropriate modalities of inter-sectoral and multi-disciplinary collaboration. Based on a systematic literature review of existing OH surveillance systems and an expert-opinion elicitation, we proposed several models of inter-sectoral collaborations as well as a conceptual framework to guide implementation of OH surveillance approach.

Materials and methods: A systematic literature review of existing OH surveillance systems was conducted using the Prisma guidelines to define the organisation and operations of such systems, as well as the collaborative modalities in place. Based on the SRL's results, we conducted an expert-opinion elicitation to refine and validate our findings.

Results: This study led to the identification of (i) various modalities of collaborations at the different steps of the surveillance process, that are mainly influenced by the surveillance objective; (ii) three main models for inter-sectoral collaborations, that are mainly influenced by the surveillance context.

Conclusion: This study underlined that collaborations taking place in a OH surveillance system exist at different scales with various degrees. A rigorous framework must be considered at the policy, institutional an operational level to ensure the effective operations of the collaborations. There is not a single model for OH surveillance and collaborations need to be tailored to the surveillance context and objective.

Key words: One Health, surveillance, collaborations

Backyard poultry and small-scale livestock production in the Western United States: a risk factor analysis

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ABSTRACT

Objective: The growing consumer interest in local food production and sustainability, and increased preference for fresh, local and organic products in the last years has been linked to an increase the number of small-scale farms, community supported agriculture and farmer's markets in the Western US. This increasing popularity of small-scale farms and urban agriculture has led to a growth of production of livestock animals in urban and peri-urban areas. One of the recognized challenges faced by small-scale livestock producers is the lack of access to technical information and veterinary oversight. This might create an increased risk of occurrence of zoonotic and emergent diseases, drug or chemical residues and foodborne pathogens in the food chain.

Materials and methods: A survey was conducted amongst small scale farmers in 4 states of the Western United States (California, Oregon, Washington and Colorado). Questions focused around four main themes: demographics, access to veterinary care, animal health and husbandry practices, perception and knowledge. Data were analyzed through basic descriptive approaches and multivariate logistic regression.

Results: A total of 474 surveys were completed. The majority of farms produced poultry (407, 87.9%) and were in rural areas (328, 74.9%). About 300 (66.7%) respondents had access to a veterinarian that treated livestock. Owning Birds (OR=0.07, 95%CI=0.01 to 0.52) and being located in an urban (OR=0.21, 95%CI=0.07 to 0.62) or peri-urban (OR=0.35, 95%CI=0.14 to 0.87) environment were associated with lower odds of having access to a vet that treats production animals.

Conclusion: Results from this survey provide a valuable insight into the needs of small-scale livestock and backyard poultry farmers in terms of knowledge and access to animal health and management and food safety. This will guide new approaches to risk-based surveillance and the opportunity to build outreach and educational programs for farmers.

The transmission of some mosquito-borne flaviviruses in urban cities in Vietnam

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ABSTRACT

Objectives: With rapid progress of urbanization, it is likely that we will see increased diseases transmission in cities, and more vector-borne viruses may adapt to these circumstances. Vietnam is a country where mosquito-borne diseases are common. There are, however, few studies exploring the urban transmission of mosquito-borne flaviviruses in Vietnam. Our objective was to explore the transmission of some mosquito-borne flaviviruses in urban cities in Vietnam.

Materials and methods: We reviewed the scientific research/ report which contained key words "flaviviruses in urban Vietnam", "dengue virus in urban Vietnam", "japan encephalitis virus (JEV) in urban Vietnam", "Zika virus in urban Vietnam" from Google Scholar.

Results: Our review findings show that urban epidemiology of JEV has mainly been studied in South Vietnam where JE is endemic. The entomological surveys conducted in a southern city, namely Can Tho, have found many potential vectors for JEV, including vectors PCR positive for the virus. Dengue outbreaks usually occur in three to five-year cycles in Vietnam with the circulation of all four serotypes. Those dengue cases were concentrated in big cities with huge population and high density such as Ha Noi city, Da Nang city or Ho Chi Minh city. In April 2016, there were two autochthonous Zika virus cases in women from Nha Trang city and Ho Chi Minh city. After that, 1,215 samples collected from people with Zika virus symptoms from 32 provinces in Viet Nam were tested. No other cases of Zika virus infection have yet been identified till now. We present a framework for the epidemiology of mosquito-borne flaviviruses in regards to urbanization and other anthropogenic changes.

Conclusion: Dengue and Japan Encephalitis are the most common mosquito-borne flaviviruses in Vietnam with occasional epidemics. Urban transmission is mostly studied for Dengue, but much less so for JEV, which has been considered rural previously. Zika virus is less active but still a major concern, and not much is known about the epidemiology, particularly in regards to urbanization.

Key words: Mosquito-borne flaviviruses, urban transmission, urban city, Vietnam

Getting rid of property codes solves the modifiable areal unit problem

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ABSTRACT

Objective: The need to accurately describe land areas led to cartographic systems of describing parcels, which were catalogued, and titles provided to owners. Over longer time periods than the average eradication campaign, these parcels were split-up, aggregated, merged and dissolved, leading to confusion over which code referenced which parcel of land at any time - the modifiable areal unit problem (MAUP). This has potentially serious implications for disease managers, particularly for diseases which may persist in the environment, and for those required to certify property freedom from disease. Reliance on instruments such as temporary property codes makes it almost impossible to find instances of disease on non-agricultural land (roadsides, urban areas, wilderness areas) when data systems are based on a code. We describe how we overcame this problem.

Materials and methods: To overcome the MAUP in managing property disease status, we took advantage of modern database technology to build an animal health information system (AHIS) from the ground up using primary geometry of each premise for all location-based searching – property disease status, previous animal health reports and investigation records. Every record stores a geometry corresponding to the area of interest for the disease (by default the legally registered boundary, but for each investigation able to be adjusted).

Results: The jurisdiction now has an AHIS which allows searching to be done by property code, street address or map location, and returns any premise that has ever intersected with the geometry of interest, or within a suitable distance from the point of interest. This also allows for proactive warning of problems on surrounding premises.

Conclusion: Code based identifiers for spatial units have their uses in a short-term situation, but managing land by treating the spatial boundary as an inherent part of the disease record, rather than 'additional' information provides a robust, long-term solution.

Key words: Surveillance, information system, property identification code, geography, maup

Isolation and Characterization of H9N2 Influenza Virus from the first reported H9N2 outbreaks in chicken layer farms in South Sulawesi, Indonesia

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ABSTRACT

Objective: The first Indonesian outbreaks of low pathogenic avian influenza (LPAI) H9N2 subtype were reported in chicken layer farms in Sidrap District, South Sulawesi, in December 2016. Infected chickens showed severe respiratory signs including sneezing, coughing, gasping, nasal discharge, head swelling, and decreased feed consumption. The disease caused up to 5% mortality in laying birds and a drop in egg production of up to 80%. Hemorrhage and congestion on visceral and reproductive organs were observed during post mortem examination. To understand H9N2 influenza virus circulation in domestic poultry, isolation and characterization of the H9N2 influenza virus was carried out from the first reported H9N2 outbreaks in chicken layer farms in South Sulawesi, Indonesia.

Materials and methods: Samples were collected from layer chickens on 15 affected farms and tested by real time RT PCR, virus isolation, and histopathology. PCR testing showed 11 out of 15 samples positive for Influenza A and H9N2 subtype virus. Virus isolation in embryonated chicken eggs caused embryo death with multifocal hemorrhages. Sequencing was performed from the positive isolates.

Results: Three viruses were successfully isolated and sequenced for the hemagglutinin (HA) and neuraminidase (NA) genes. Genetic sequencing showed that the viruses isolated had 98% HA nucleic acid sequence identity to A/muscovy duck/Quang Ninh/11/2013 (H9N2). Phylogenetic analysis revealed that the virus isolates (A/Chicken/Sidrap/07161511-1/2016, A/Chicken/Sidrap/07161511-61/2016, and A/Chicken/Sidrap/07170094-44OA/2017) clustered distinctly to other viruses within the Y280-H9N2 lineage. The HA cleavage site showed the monobasic pattern of RSSR (aa 335 – 338) indicating that these isolates are LPAI viruses.

Conclusion: This is the first report of outbreaks of LPAI H9N2 virus in Indonesia. This finding provides valuable information on the circulation of H9N2 viruses in domestic poultry and informs the updated and amended government policy to control and manage avian influenza viruses in Indonesian poultry, focusing on increased on-farm biosecurity and flock vaccination.

Key words: Avian influenza, low pathogenic, H9N2 subtype, virus characterization

Livestock markets classification for guiding targeted interventions along the livestock supply chain in Cameroon

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ABSTRACT

Objective: Livestock markets can have key roles in epidemic outbreaks and are common hotspots for the dispersal of multiple infectious diseases and in multiple settings. In Cameroon, livestock trade occurs predominantly via an established and consistent system of livestock markets. The objective of this study was to improve the understanding of the risks associated with livestock trade through live animal markets in the country, and inform the design of targeted interventions at livestock markets.

Materials and methods: In the current study, official transaction records for a 12-month period were collected while a questionnaire-based survey was conducted in 62 livestock markets across Central and Southern Cameroon.

Results: The structure of the livestock markets system was characterized using information readily available at these markets. Based on trade volume, markets centrality in the trading network, cattle price and the intensity of stakeholder attendance, four main classes of livestock markets were identified. Although species of traded livestock, husbandry and management practices were variable between market classes, and despite an evident hierarchical structure of the system there was no clear variation in terms of the predominant diseases reported affecting the traded animals in the different market classes This relatively limited pool of infectious diseases reported as priorities between market classes, highlights homogenous disease risks along the livestock market chain. However, the variable management practices (e.g. traded species, husbandry practices and transhumance habits) highlight diverse potential risks for disease dissemination between market classes.

Conclusion: Making use of readily available commercial information at livestock markets, this study describes a relatively rapid approach for livestock market classification. Simultaneously, this study identifies priorities for guiding targeted surveillance, communication and control interventions in Cameroon, aiming at mitigating the risks for diseases dissemination associated with current management practices at livestock markets.

Key words: Cameroon, markets, categorization, infectious diseases, surveillance

Quantitative risk assessment for bovine tuberculosis in White rhinoceri intended for export from the Kruger National Park, South Africa

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ABSTRACT

Objectives: Given the recent detection of *Mycobacterium bovis* in White rhinoceri (*Ceratotherium simum simum*) in the Kruger National Park (KNP) and the limited diagnostic tools and epidemiological knowledge available for this species:
Develop an interactive stochastic simulation model to assess the risk of exporting tuberculosis through white rhinoceri translocated from the KNP.
Assess the ethical, logistical and risk implications of various quarantine and diagnostic testing scenarios.

Materials and methods: A prevalence probability distribution was based on opportunistic necropsy data from rhino carcasses. Probability distributions of test characteristics were based on very limited validation data from two interferon gamma-based tests, still under development, which was supplemented by data from field animals where ante and post mortem samples were available. The risk of exporting a tuberculosis infected white rhino undetected was quantified through simulation of various test and quarantine cohort scenarios. The total number of animals to be exported, quarantine cohort sizes, the number of tests used simultaneously and the number of rounds of consecutive testing was made adjustable through an interactive interface to ensure informed discussion between animal health and conservation decision makers.

Results: Risk estimates based on currently available prevalence and diagnostic test characteristics was lowest when three consecutive rounds of testing, six weeks apart, with both available diagnostic tests were performed on cohorts of two animals. The risk of an infected animal being exported undetected under this scenario was less than 1%.

Conclusion: It is crucial for the conservation of KNP rhinoceri that some animals be translocated to safe locations. In order to do this responsibly, without potentially spreading bovine tuberculosis from an endemically infected area, we propose that risk estimates for consideration by decision makers can be obtained through stochastic simulation of limited available data.

Key words: *Mycobacterium bovis*, White rhinoceros, risk analysis, stochastic simulation

Optimisation of national monitoring systems incorporating risk analysis, mapping and animal movement

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ABSTRACT

Objective: There is a need to assist national veterinary services who works in data-scarce environments, in developing operational disease surveillance programmes on the field. Here, we expand the OIE and the French Agency for Food, Environmental and Occupational Health & Safety (ANSES) qualitative risk analysis methods, by integrating spatial data, animal movement information, as well experts' knowledge. The framework includes data collection and mapping, resulting in risk maps of disease occurrence. These are being used to reinforce risk-based disease surveillance activities.

Materials and methods: The risk question and potential spatial risk factors for disease introduction and spread are identified based on a collective discussion with the relevant veterinary services, and a literature review. Existing spatial data are collated and additional necessary data are collected on the field by the veterinary services, such as national and transboundary livestock movements. Maps of the risk of introduction and the risk of spread are obtained by combining the risk factor maps, based on experts' knowledge, and classified in four risk categories "negligible", "low", "high", "very high". In parallel, the surveillance activities conducted are reviewed, revised if necessary and designed to be reinforced in higher risk areas.

Results: The framework was implemented for different diseases (FMD, RVF, PPR, HPAI) in Maghreb, Sahelian countries and the Caribbean. When compared to notified outbreak data, for example FMD in Tunisia, more 75% of the outbreaks were located in "high" or "very high" risk strata.

Conclusion: This approach can be routinely used in by veterinary services, in a data-scarce environment to design risk-based surveillance programs in the field. The method should be applied further in various contexts (islands, regional), countries and diseases, with different datasets from one country to another. The proposed framework is an iterative process that should be updated as new data becomes available and reinforce national capacity building.

Key words: Qualitative risk assessment, spatial data, mobility animal, operational framework

Development of GIS capacities in animal health in the Caribbean, application to the Avian Influenza risk mapping – the essential contribution of CaribVET

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ABSTRACT

Objective: The Caribbean poultry industry is the most rapidly growing subsector, under high risk for the introduction of Highly Pathogenic Avian Influenza (HPAI) following the US HPAI epizootics. To optimize regional surveillance for HPAI, the Caribbean Animal Health Network (CaribVET), a collaborative participatory network, has set up a capacity building program on risk mapping and risk-based surveillance in a context where the collection of georeferenced data, the management and analysis is sometimes poorly developed and insufficient for spatial epidemiological studies. The aim of the program is to strengthen the capacities in the Caribbean national veterinary services (VS) with tools and methodology which could alleviate the lack of manpower, competence, databases and fill in geographic detail.

Materials and methods: A "training/action" program including an initial train-the-trainer program (basic GIS, risk mapping principles), development of self-learning materials (GIS bulletins, forum, closed Facebook page), and advanced workshops on HPAI qualitative risk mapping and optimization of national monitoring systems was implemented in 12 countries. Participants applied the integrated method of Squarzoni et al. that incorporates qualitative risk analysis, mapping and animal movements, using their own datasets to do a spatial risk assessment of HPAI virus introduction, establishment and spread.

Results: Areas at risk of HPAI introduction and/or occurrence have been identified and risk-based surveillance protocols have been developed in 12 Caribbean countries. Updating of source data for risk factors is ongoing and the group is monitored and followed-up by the CaribVET coordination unit to ensure objectives are met and results are validated by an expert CIRAD team.

Conclusion: Participants have gained proficiency in developing risk maps and the countries are able to use GIS for their surveillance programs. Another main benefit is the optimized collection and systematic organization of homogenous data collection and topographic integrity necessary to improve regional diseases surveillance in the Caribbean.

Key words: GIS, CaribVET, Preparedness, Capacity building, HPAI

The increasing role of entrepreneurial skills in the veterinary private sector: the case of Slovenia

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ABSTRACT

Objective: Economics of animal health aims to offer veterinarians tools and methods to facilitate decision-making. In this context, we are faced with three different aspects of economics: the determination of the economic viability of preventive and control measures for individual animal diseases, entrepreneurship in veterinary activities and disease control policies, where the consequences of animal diseases are to be placed in the broader context of all related industries. Veterinary companies and practicing veterinarians are more or less involved in all levels of economics of animal health. However, due to the viability of the companies and provision of their own income, entrepreneurial role is the most prominent. The question arises: is it worthwhile to have a company in charge of providing veterinary services in Slovenia?

Materials and methods: We prepared a detailed operation analysis of the veterinary companies in Slovenia and a simple analysis of the veterinary market from 2008 to 2016. Publicly available data were obtained from the Statistical Office of the Republic of Slovenia, the commercial business directory Bizi.si, the application Erar for displaying the use of public money in the Republic of Slovenia and the Reports on the Condition in Agriculture published by Agricultural Institute of Slovenia.

Results: Despite the gradual reduction of the revenues from the state budget, the veterinary market in Slovenia is slowly growing. The trend of setting up new companies is also evident. The average annual growth rate of the number of companies is considerably higher than the average annual growth rate of the number of employees. In addition, the average total revenue per company is decreasing.

Conclusion: For practicing veterinarians, knowing what is happening on the market, the positioning of one's own business and the business of competition is important for the precise formation of goals and strategies that will enable the successful operation of the company.

Key words: Economics of animal health, business of veterinary companies

Evidence-based veterinary capacity development using Epidemiology Mapping Tool

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ABSTRACT

Epidemiology capacity strengthening programs often focus on improving capacity of individuals, subsequently fall short in adequately leading to more effective prevention, detection, and response to animal and public health threats. Epidemiology capacity improvement is multi-dimensional, requires strengthening individual and institutional capacity, as well as enabling environment based on evidence of prioritized needs and gaps, especially in a resource-constraint environment. Therefore, there was a need for a tool to provide objective assessment of epidemiology capacity at all dimensions. The Epidemiology Mapping Tool (EMT) development was initiated in 2013, encompassing assessment of individual and institutional capacity, for both structural and functional capacity to implement epidemiological practices, and at national, subnational and local levels. The EMT is built on and in complementarity to other existing tools and international standards. Following initial piloting of the EMT in 2014 and 2015, an extensive review process was conducted. The current EMT has a core tool which serves as the main assessment guide, supported by 5 additional supplemental tools: HR, Surveillance Planning, Surveillance Evaluation, Disease Investigation, and Training Tool. The core tool comprised of a total of 3 main themes (institutional, epidemiology workforce, and applications of epidemiology capacity), and 9 technical areas. A total of 38 main indicators were developed. The tool uses a scale of 1-4 to determine the EMT score. The process to apply the EMT was also set up, emphasizing roles of an assessment team led by national experts, with support from external experts. The EMT was tested in Bhutan in 2017, when the experience of applying the tool was also documented.

The EMT is the only tool that provide detailed assessment of technical and functional capacity, encompassing individuals, organizations, and enabling environment, and at national and subnational levels. Results of EMT assessment can support evidence-based and strategic capacity development programs for veterinary epidemiology.

Building veterinary epidemiology capacity in West and Central Africa through a training workshop, a process evaluation based on the Kirkpatrick model

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ABSTRACT

Objective: The World Health Organization (WHO) defines capacity building as "development of knowledge, skills, commitment, structures, systems and leadership to enable effective health promotion". A workshop building competences in veterinary epidemiology was conducted in December 2017. The objective was to assess which epidemiological skills had improved due to the intervention.

Materials and methods: The training intervention provided knowledge based learning, practical application and analytical skills. By teaching key skills in categories, Principles of Epidemiology, Data Collection, Laboratory Interpretation and Data Analysis. Existing studies provided case material forming higher level learning.
Methods for evaluating capacity building interventions were examined, the Kirkpatrick Four-Level *Training Evaluation Model* helps trainers to *measure* the effectiveness of their training objectively was used. The levels include immediate response to training applicability, change in learning outcomes, change in individual and organizational practices. Data were collected through pre workshop survey, interactive class survey, post workshop surveys and follow-up surveys 6 months later, descriptive and univariate analysis were performed.

Results: 47 delegates from 14 countries participated, 43% working in national bodies. A total of 42 participants completed the post-workshop survey. Participants gave a mean satisfaction score of 4.1 / 5 (sd = 0.65). Before and after workshop percentage change in learning outcomes were measured. Data analysis 20% (sd =20%) and data collection 20% (sd = 10%) showed the greatest improvement.

Conclusion: The Kirkpatrick model is a useful framework to evaluate the workshop efficacy. Further training in veterinary epidemiological competencies in West and Central Africa are warranted.

Key words: Capacity building, veterinary epidemiology, process evaluation, Kirkpatrick model

Using ontologies to create open source smartphone-based differential disease diagnosis and reporting tools for animals in rural settings

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ABSTRACT

Objective: Smartphone-based tools are increasingly being used to aid in disease diagnosis and the reporting of animal health events, particularly in rural regions with limited resources. However, there is a need to maximise the value of the expertise embedded in and data captured by such tools, as well as to minimise the costs of applying these to new contexts. Use an ontology-assisted approach to create a flexible framework in which novel species and diseases can easily be integrated into mobile diagnostic platforms, as well as support language localisation and automated aggregation/analyses of animal disease reports.

Materials and methods: The Animal Health Surveillance Ontological (AHSO) framework, which supports disease recording and passive surveillance, was used to adapt a diagnostic tool designed for cattle to also cover sheep, goats, camels and equids. The expanded smartphone-based tool is currently being trialled in four regions of Ethiopia.

Results: Our research provides a clear demonstration of how AHSO can support more flexible tool design and multi-language implementation. The additional value in terms of data reporting and use will only be able to be fully evaluated after a significant quantity of data has been collected, as is expected by the end of the first year of this field trial. Both the AHSO framework and the core code, or APIs, to support such diagnostic tools are available via an open source (GitHub) repository.

Conclusion: Modern informatics approaches, including those supported by the Sematic Web, can be utilised to significantly improve the efficiency of mobile tool design. In addition, the provision of open source ontologies such as AHSO can greatly enhance the value derived from such tools by supporting interoperable code and data that can be transparently processed and readily shared.

Key words: Differential disease diagnosis, disease reporting, mobile platforms, ontology, passive surveillance

Control of refrigeration temperature at retail stores for food safety

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ABSTRACT

Objectives: The objectives of this project were to i) study the compliance of the storage temperature for food products at retail stores and their associations with the store characteristics, and ii) learn about the in-house-control management of temperature.

Materials and methods: Inspections were carried out in 62 retail stores randomly selected from two regions of Finland during 2015-2016. Selection of stores was stratified by municipalities, store chain, and size. Official food control inspectors visited the stores using temperature data loggers to measure the temperature of the food products. Stores with non-compliances were reinspected within a few weeks for corrective actions. The temperatures were measured for approx. 48 h. A total of 161 food products were included in the study, 72 fresh vegetables, and 89 processed fishes (e.g. gravad or cold smoked fish).

Results: During the first inspection 45% of stores did not meet the temperature requirements. Temperature violations were detected in 30% of fishes and 40% of vegetables at the first inspection. No associations between non-compliance and store chain (P > 0.05) or size of the store (P > 0.05) were found. Temperature violations of food products were most common in refrigeration equipments without door (p < 0.05). All retail stores complied with the storage temperature requirements at the end of the study.

Conclusion: The in-house-control management of temperature was greatly improved in all stores as result of the project. Food business operators should actively monitor the temperature of the easily perishable food products, e.g. by improving their practices.

Key words: Temperature, retail store, ready-to-eat products, food safety

Economic aspects of the control of pancreas disease in Norwegian salmonid aquaculture

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ABSTRACT

Objectives: The Norwegian salmonid production is affected by disease outbreaks that impacts both production volumes and trade volumes. One of the major diseases is pancreas disease (PD), which results in increased mortality, lower growth rates and reduced fillet quality. The causal agent, salmonid alphavirus (SAV), is an OIE-listed agent and its presence may thereby affect international trade patterns from affected areas. The aim of this study was to estimate the cost of PD outbreaks due to SAV subtype 2 and investigate whether control strategies such as stamping-out, vaccination and the use of large smolts are economically justifiable.

Materials and methods: A range of data sources were used in this study, including nationally available register data, expert opinion elucidation through questionnaires and interviews with production managers. A variety of regression models were used.

Results: There are significant costs associated with PD outbreaks, however the magnitude of losses are very sensitive to fluctuations in the salmon price and management adaptations such as the ability to prolong the production period. Control strategies such as stamping-out, vaccination and the use of large smolts can be justifiable, with the break-even points varying depending on the assumptions used.

Conclusion: While it is clear that PD causes significant economic losses on affected farms, and that the different control measures may be economically justifiable with the defined scenarios, there are important caveats. Both the estimated cost of disease and the effect of the control measures are highly dependent on the input data and the assumptions that are used in the models. It is therefore essential that such assumptions are clearly communicated to those who may be utilizing the results, from competent authorities to farm managers. Finally, the associated impact of the general lack of incentives for the control of PD in Norway will be discussed during the presentation.

Are classical approaches to disease surveillance still relevant? People, technology and the pursuit of the surveillance 'holy grail'

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ABSTRACT

Objective: To describe the opportunities that people-centered approaches and modern technology provide for disease surveillance.

Materials and methods: Based on a paper submitted recently to Preventive Veterinary Medicine and with examples of the large-scale application of these technologies and approaches in Indonesia and Chile, this presentation will highlight the realities and impacts of real-time surveillance with near complete coverage.

Results: In a perfect world, disease surveillance would yield unbiased real-time information with complete coverage of the diseases and populations of interest. In reality (until recently), the high costs of data collection and management have necessitated sampling, and surveillance objectives are often constrained by a paucity of data. This has long been a problem; its origins dating back to the pre-digital age when the collection and management of health data was laborious and expensive. In response, a substantial part of 'modern' epidemiology is concerned with sampling methods and statistical inference based on analysis of data derived from a sample. But are the premises that underpin classical approaches to surveillance still true? Are the approaches still relevant? Advances in technology and the social sciences have the potential to fundamentally change the paradigm and approaches on which the majority of surveillance programs are based.

Conclusion: Cloud computing and other types of information and communications technology allow flexible integration of data sources, real-time data collection in the field and secure, inexpensive management of vast amounts of data. A people-centred approach puts the focus on providing benefit to all actors in the surveillance system and overcoming impediments to their willingness and ability to participate. The implications for disease surveillance—and epidemiology more broadly—are profound.

Key words: Surveillance, epidemiology, information systems, cloud computing, people-centred

Strengthening national sharing of surveillance data for the good of all

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ABSTRACT

Objective: Every country has obligations and objectives relating to surveillance for animal diseases. These typically include support for trade (through justifiable claims of disease status), early detection of incursions and control of priority endemic diseases. Many of these objectives require a comprehensive and complete national 'picture' of animal health and rely on the sharing, integration and analysis of data from multiple sources.

Materials and methods: This paper explores the needs for integration of surveillance data from numerous stakeholder groups, the real and perceived risks associated with data sharing, and practical ways to overcome existing impediments.

Results: Maximising the benefits of data integration while managing the risks (both real and perceived) of data sharing is a challenge for many countries. Key impediments include lack of clarity about national surveillance objectives and information needs; lack of perceived benefit by data providers; lack of technology; concern about security and privacy of the data; expectations of higher costs; and fear of a loss of control over the use and interpretation of the data. These factors impede data sharing and the utility of national animal health information systems.

Conclusion: Implementing this change is not purely a technical challenge. Change is required across a spectrum including legislation and data-sharing policies, information system design, data management, technology, and stakeholder engagement. Most importantly, leadership and an understanding of factors influencing stakeholder perceptions are key to effective change management. Addressing these challenges has the potential to provide enormous benefit to stakeholders at all levels of the animal health system: from national policy-makers to field veterinarians and farmers.

Key words: Surveillance, information systems, data sharing, integration, national

Entry risk analysis of West Nile Virus to China

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ABSTRACT

Objective: The aim of the study is to analysis the entry risk of West Nile Virus (WNV) from other countries to China and identify the most likely risk pathway.

Materials and methods: Through OIE/FAO disease database searching, systematic review and meta-analysis, existing data/information on WNV will be collected and analysis. Risk pathways of WNV will be built via scenario tree and the pathway poses the highest risk to China will be identified via risk analysis. For the purpose of providing a scientific risk control strategy to the Chinese government, Critical Control Points (CCP) of the risk pathway will be identified via sensitivity analysis. An applicable controlling strategy will be proposed to the Chinese government for minimising the WNV risk to China.

Results: West Nile Virus is the widest spreading arbovirus which causes West Nile fever, West Nile meningitis, and West Nile encephalitis. The mosquito, as its vector, transmits the virus between the infected and the healthy susceptible birds. Human and horses can be infected by the WNV via infected mosquito bites, so human and horses are the occasional hosts and also the dead end hosts.

Conclusion: Current outbreak data indicated that WNV are widely spreading in population living in Africa, Europe, America and Latin America. However, so far only two human cases were report in China. The Chinese Ministry of Science and Technology funded a national research project to Zhejiang Agricultural and Forestry University (China) to identifying the risk pathway of this exotic virus and to suggest a scientific control strategy (Grant No. 2017YFD0501806).

Key words: West Nile Virus (WNV), entry risk analysis, risk pathway, China

Quality control of purified protein derivative tuberculins: Essential for effective bovine tuberculosis control and eradication programmes

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ABSTRACT

Introduction: Bovine tuberculosis (bTB) control relies tuberculin PPD (Purified Protein Derivative) for diagnosis in-vivio. This study set out to determine the relative potency and specificity of commercially available PPDs and to demonstrate the impact of potency variation on bTB eradication by comparing the field performance of the SICTT and SIT using different potencies of a single bovine PPD.

Materials and methods: Bovine and avian PPD potency was estimated using guinea pig assays (European Pharmacopeia). Excepting three bovine PPDs specially formulated for the study, all PPDs were from commercially available batches purchased on the market.

One avian and 3 bovine PPDs (high, normal/control, and low potency) were administered intradermally in the mid-third of the neck to each of 2,102 cattle, including 48 previously identified test positive (reactor). A trial and control reactor-status were assigned based on the SICTT and the SIT (Single Intradermal test – cervical).

Results:
Guinea pig bioassays showed the majority of bPPDs did not meet the minimum dose at 0.1ml of 1mg/ml and <50% of the aPPDs achieved the minimum 2,000 I.U. per dose. SICTT and SIT showed the proportion of 'all-positive' animals significantly different for the 3 potencies of tuberculin (p<0.001), with high potency yielding the highest and low potency the lowest proportion of positives.

Conclusion: Low potency PPDb failed to detect 20% of animals with multiple visible TB lesions; 11% of visible lesion animals did not show a positive bovine response, passed the SIT and, if tested singly in an undetected TB infected herd, been eligible for export certification. Bovine PPDs assayed with even lower potency had been sourced on the market. PPD purchasers need independent quality checks of manufacturers potency claims.

Key words: Tuberculosis, bovine tuberculosis, tuberculin, PPD, potency

Compulsory inoculation against porcine reproductive and respiratory syndrome: Evaluation of cost, coverage and compliance

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ABSTARCT

Objective: The retrospective study aimed to evaluate the cost, coverage and influencing factors of self-paid PRRS vaccinations in swine farms located in Liaoning province in the north-eastern part of China from January to August, 2015.

Materials and methods: Field investigation and questionnaire which comprised 22 closed, semi-closed and open questions had been used in 737 randomly selected farms. Univariable and multivariable logistic regression analyses were used to determine significant associations between compulsory inoculation and farmer's perceptions and practices based on questionnaire data.

Results: The government spent 21636840 Chinese Yuan on compulsory inoculation of PRRS vaccines in 2015. In August 2015, the herd level vaccination rate of the PRRS vaccine in Liaoning province was 96.49% (95%CI, 94.49%-98.49%), the government compulsory vaccination rate was 87.94% (95%CI, 84.94%-90.94%). 79.44%(95%CI, 77.44%-81.44%) farmers approved PRRS compulsory inoculation policy. 82.31%(95%CI, 80.31%-84.31%) of respondents were not willing to pay the market price for PRRS vaccines. We use ArcGIS to draw a spatial distribution map. The main reason of using self-paid vaccination were higher quality (51.47%), brand (23.53%) and vaccine strain (16.18%). Vaccine price had no significant effect on the compulsory inoculation. However, univariable and multivariable logistic regression analyses showed that self-paid vaccination in three aspects of antibody level, immunity failure and growth after immunization were not superior to government vaccines. Those farms with 400-2500 slaughter per year, non-breeding swine farm and single species farms were more likely to use compulsory inoculation PRRS vaccines. We built an identification model of the farms not complying with compulsory vaccinations. For this regression model, the area under the ROC curve was 87.7%.

Conclusion: Interventions targeting psychosocial factors, such as making the vaccine evaluation information known to the public, building confidence of domestic brands and providing compulsory vaccine selection of different vaccine strains, could also be effective on increasing the uptake of compulsory vaccinations.

Key words: Compulsory inoculation, PRRS, Cost, Coverage, self-paid vaccination

The benefit of competency development for Government Veterinary Service Officer in Klaten district for avian influenza disease handling in Indonesia

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ABSTRACT

Objective: Competency development is a transformation to empower individual, organization, and community in producing changes or expected benefit from the program, to make an impact for the end beneficiary. This research analyzes the benefits obtained by the farmers from local government Veterinary Service Officer (VSO) competency development as performed by FAO Emergency Centre for Transboundary Animal Diseases (EC-TAD) Indonesia. Activities were carried out in cooperation with Directorate General of Livestock and Animal Health Services on control and prevention of Highly Pathogenic Avian Influenza in commercial poultry farms at Klaten district, Central Java province, Indonesia.

Materials and methods: This primary data is based on direct observation and in-depth interview with to 4 VSOs and 16 commercial poultry farmers in Klaten District, while for the secondary data from Poultry Veterinary Health Programme of FAO ECTAD Indonesia.

Results: Analysis shows that the establishment of harmonious communications between VSOs and farmers lead to increased need for technical assistance from trained government VSOs. Farmers also wanted to report any problem in their farm and to share their farm production data. Moreover, this program has increased farmers knowledge on technical aspect through the farmers training program and technical assistance on farm and could resulted in healthier animal with optimum farm productivity. The total economic benefit realized by the farmer by implementing the intervention in biosecurity, vaccination and farm management was IDR 1,076 per hen per cycle. This benefit was attained with farmer investments of IDR 28 per hen per cycle.

Conclusion: By FAO ECTAD Indonesia's programme to develop the competency of VSOs in Klaten district has enhanced the capacity of the Government of Indonesia and partners to control highly pathogenic avian influenza disease. This program is very well implemented and could be a pilot for other animal health services activities that involve farmer actively with participatory approach.

Key words: competency development, veterinary service officer, poultry farmers, avian influenza

Session D: One health (animal–human–environment interface)

Epidemiology of ophidian accidents in southern Columbia

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ABSTRACT

Objective: In Colombia, more than 4,000 ophidian accidents occur per year with a lethal rate that can reach 0.6% and sequelae left in 6% of survivors. Ophidian accidents in Colombia are a public health problem that has its greatest impact on rural areas, where a deficit of knowledge in physicians regarding the diagnosis and treatment of snake bites has been observed, as well as an inappropriate management of the antivenoms. A better knowledge of snake bite epidemiology may help health authorities to better understand therapeutic requirements, especially concerning antivenoms, in order to improve the treatment. The aim of this research was to acquire knowledge about the ophidian accident epidemiology in a southern region of Colombia.

Materials and methods: Data from cases reported to the Nariño Health Institute from 2015 to 2016 were analyzed.

Results: Out of 204 cases reported, epidemiological information of 127 victims was obtained. *Bothrops*, *Crotalus*, and *Micrurus* genuses were responsible for 46, 3 and 2% of the accidents, respectively. Men (75%) and patients between 10 and 30 years-old (27%) were the most common victims. The main bite sites were hand (44%), foot (32%) and leg (23%). Farm workers were bitten more frequently (53%). The accidents often occurred during work (55%) and when people were walking in open fields (20 %). Use of tourniquet, squeezing, and suction of the bite site were the initial practices in 34% of the patients, in 31% of the cases medicinal plants and traditional healing prayers were used and 35% of victims did not receive initial attention . Antivenom was applied in 96 patients, but only in 36 the recommended protocol was completed.

Conclusion: The delay in the administration of antivenom is of vital importance in southern Colombia, since the geographic conditions severely limit the distribution and availability of the antivenoms in rural areas. Consequently, some communities rely initially on alternative therapies for treatment.

Key words: Antivenom, bothrops, crotalus, micrurus, ophidian accident

Dog overpopulation and diagnosis of intestinal parasites on Santa Cruz Island, Galapagos

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ABSTRACT

Objective: Dog overpopulation and diseases are hazards to native island species and humans on the Galapagos. The main objective of the study reported here was to estimate the observed human:dog ratio on Santa Cruz Island, Galapagos in September 2016. In addition, dog demographic data were used to model the expected annual dog population growth in the next 10 years. A secondary objective was to measure the burden of dogs infected with intestinal parasites.

Materials and methods: The observed human:dog ratio was 964:202 (or 4.77:1), which extrapolates to 3290 dogs; an increase of 31% in the dog population on Santa Cruz from 2014 to 2016.

Results: Study results show that current spay-neuter efforts (about 300 dogs per year; 60% females, 40% males) are not enough to keep the population stable (i.e., current baseline of 3290 dogs). The frequency of dogs infected with *Ancylostoma* spp., an intestinal parasite in dogs that can cause cutaneous larval migrans in humans, was 18/44 or 41% (95% CI = 27%, 55%).

Conclusion: These results provide the most complete assessment of the dog overpopulation on the Galapagos to date.

The monitoring of beta-agonist residue in cattle of Chiang Mai municipal slaughter house during June – August 2017

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ABSTRACT

Objectives: Uses of beta-agonists have been approved in the case for bronchodilatation in horses and calves in countries; however, using of beta-agonist in food animal production in Thailand is illegal. The monitoring of beta-agonist residue in cattle slaughter house is a conventional way to upgrade the standard of food quality.

Materials and methods: We conducted purposive sampling during June-September 2017 in cattle slaughter house of Chiang Mai municipality. We interviewed merchants with structure questionnaire. Urine samples were tested with rapid test kit for beta-agonist. We analyzed the data with Epi-info 7 and Qgis (v2.18).

Results: One hundred urine samples from slaughtered cattle were collected for beta-agonists residue. Dairy cattle were from Chaiprakarn (7), Maeon (42) and Sankumpang districts (17). Eight beef cattle were from Maesareang district and twenty-four were from Sankumpang. From all 100 samples, 17 were beta-agonist positive, eight positives (33.33%) were beef cattle (Sanpatong), while 9 positive dairy cattle were from Maeon (14.29%), Sankumpang (11.76%) and Chaiprakarn district (14.29%). In those positive samples, livestock market cattle had greater 3.7 times chance found in each beta-agonist than dairy cattle from farm (OR: 3.72, CI = 1.24-11.15) and beef cattle had not significantly greater 2 times chance found each beta-agonist than dairy cattle.

Conclusion: This study stated that illegal beta-agonist still used in food production animal for gaining weight and lean muscle. The intensive surveillance and long-run monitoring will be useful to contribute food safety strategy for human health.

Key words: Monitoring, cattle, beta-agonists, beef slaughterhouse, Chiang Mai municipality, Thailand

Modernizing the antimicrobial residue monitoring programs for pig meat – the balance between flexibility and harmonization

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ABSTRACT

Objective: Consumers perceive chemical residues in meat as unwanted, and trade restrictions may arise due to detection of such residues in imported meat. One key question is how to balance flexibility and harmonization of residue monitoring while assuring free trade and consumer confidence.

Materials and methods: To address this, we reviewed Danish, Dutch and Swiss monitoring programs for antimicrobial residues in pig meat using the recently developed RISKSUR design tool.

Results: The results identified variation regarding the number of surveillance components, reactions to suspect samples and positive findings, preventive activities, diagnostic method, sample matrix, use of targeted/risk-based approaches, and sampling frequency. The structure and aims of pig production are different in the three countries and, therefore, the surveillance objectives differ. Denmark and the Netherlands have a large export of pig meat for which monitoring data documenting compliance with legislation are perceived as useful, whereas Switzerland only trades with the European Union.

Conclusion: It is recommended that future legislation should set standards to ensure a basic level of monitoring enabling a comparison of results. This should be possible within the European Union, but more challenging world-wide, among others because maximum residue levels (MRL) are varying greatly for some antimicrobials between the different regions in the world. Still, at least handling of carcasses with residues above MRL should be harmonized. Risk-based sampling should be encouraged, and results from risk-based and random sampling should be reported separately. Harmonization is unnecessary for the number of surveillance components (but a private component is recommended, implying abattoir's own check), prevention, diagnostic method, and way of sampling – under the assumption that the diagnostic method and sampling matrix combination have sufficient validity. Finally, it was concluded that the role of residue monitoring is primarily to verify the effect of actions taken earlier in the supply chain - implying compliance with withdrawal times after treatment.

Key words: Antimicrobials, residues, EU legislation, risk-based, surveillance

Complexity of factors influencing the success of on-farm biosecurity and animal disease prevention and control

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ABSTRACT

Objective: This research aims to reveal that farmers' on-farm biosecurity decision-making process can be influenced by complex factors and further develop a systematical understanding of the drivers associated with individual farmers' biosecurity attitudes and behaviours.

Materials and methods/ Results: A content analysis of 25 face-to-face interviews was used to develop a social ecological model to explain the complexity of social factors influencing on-farm biosecurity practices. Using categorical principal components analysis and a two-stage cluster analysis, survey data from 303 broiler farmers showed a significant proportion of farmers who have attitudes inconsistent with relevant behaviours was revealed. Farmers recognising the importance of biosecurity measures without translating their knowledge into the relevant biosecurity actions may do so because of a lack of farm resources while farmers who do not have a better attitude towards the importance of biosecurity but still adopt desirable biosecurity behaviours may do so due to the forced compliance behaviour at the farm level. A systematic approach was used to identify underlying drivers resulting in the attitude-behaviour inconsistency. Based on the drivers, six key factors were identified for the improvement of on-farm biosecurity in global livestock production systems.

Conclusion: These findings suggest a lack of effective policy implementation as a result of the government placing most effort on providing knowledge and the enforcement of a policy. The novelty of this research lies in its wider relevance to Taiwan's poultry production industry as it identifies the shortcomings of focusing primarily on epidemiological risk factors, as tends to be the case in many animal disease control activities.

Key words: Cognitive inconsistency, biosecurity, cluster analysis, social ecological model, systematic review

Situation analysis of rabies control policy in Thailand; towards achievement of disease elimination

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ABSTRACT

Objective: The number of rabies outbreaks in humans and animals in Thailand declined during in the past decades. Despite this apparent success, rabid cases in human and animal populations have been increasing since 2016 and rabid animals have been emerged and spreading out in different areas of Thailand. To achieve the WHO benchmark for disease elimination, strategies and policy for rabies control in Thailand need to be evaluated to identify gaps and develop a rationale for improving its effectiveness. To evaluate the status of rabies control measures in humans and animals from 2012 to 2017 in Thailand.

Materials and methods: Initially, a systematic review to review of the scientific literature will be conducted. We will also seek to retrieve reports, documents and surveillance data released by stakeholders such as the Ministry of Public Health and the Bureau of Disease Control and Veterinary Service. Subsequently, a semi-structure questionnaire will be developed to collect additional information from key individuals about the current situation of rabies control. It will be applied by face-to-face interviews and focus group discussions. Qualitative analysis will be performed to identify key factors influencing the effectiveness of rabies control in both humans and animals.

Results: Findings will be presented at the conference and include at-risk population demographics, case incidence in space and time, and the effectiveness of various features of national rabies control. It will also describe collaborative interactions between stakeholders at all critical levels of government for rabies elimination. Further study: Findings of the first study phase will be used to evaluate the cost-effectiveness of various elements of rabies control interventions to inform public policy about the most cost effective strategy for eliminating rabies in Thailand up to 2030.

Key words: Rabies, control policy, situation analysis, Thailand

Prevalence and antimicrobial resistance (AMR) profile of non-typhoidal *Salmonella* (NTS) in pigs in Kenya and Malawi

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ABSTRACT

Objectives: Non-typhoidal *Salmonella* has a huge global disease burden in humans and AMR strains are commonly found. This study investigates whether pigs act as a potential source of transmission of NTS to humans in sub-Saharan Africa. The aim of this work was to determine and compare prevalence, strains and diversity of NTS in pig samples collected at post mortem from 3 slaughter house sites; 2 rural (Busia, Kenya and the Chikwawa Valley, Malawi) and 1 urban (Nairobi, Kenya), and to compare the AMR profile of NTS detected.

Materials and Methods: Faecal and mesenteric lymph node samples were collected from pigs at slaughter (Busia=267, Nairobi=306 and Chikwawa Valley=65). Microbiological and molecular analyses were performed and 259 isolates were submitted for whole genome sequencing (WGS) with the aim to confirm the serovar and sequence type of any NTS detected, as well as the presence of AMR determinants, and so determine whether zoonotic transmission of NTS is a possibility from pigs slaughtered at the study sites.

Results: A variety of zoonotic serovars of NTS were detected in faecal and mesenteric lymph nodes of pigs at each site. Currently WGS is complete from 39 isolates from Busia and 22 isolates from Nairobi. One isolate of *Salmonella* Typhimurium ST313 was identified in the mesenteric lymph node of a pig and 6 isolates of *Salmonella* Typhimurium ST19 were detected in pigs at slaughter in Nairobi. Two multi-drug resistant (MDR) isolates (resistant to 3 or more classes of antibiotics) were detected in pigs slaughtered in Busia. 10% of NTS isolates from Busia (CI 4-24%) and 14% from Nairobi (CI 5-3%) were resistant to 1-2 antimicrobials. A range of different antimicrobial susceptibility phenotypes were present, including resistance to the third-generation cephalosporin ceftazidime (1.6%, CI 0.3-8.7%) and the fluoroquinolone ciprofloxacin (3.3%, CI 0.9-11.2%).

Conclusion: This study shows that pigs at slaughter in all study sites carry a variety of NTS serovars including MDR phenotypes. There is the potential for zoonotic transmission of NTS between pigs and humans in Kenya and Malawi and the transfer of AMR determinants between these species should be considered.

Key words: Salmonella, Kenya, Malawi, pigs, AMR

The role of rabies preparedness cadres (Kasira) on rabies control program in Indonesia: A community-based approach

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ABSTRACT

Objective: The aim of this study was to involving and empowering communities in rabies control and eradication programs in Sukabumi District through the establishment of the rabies cadres called Rabies Preparedness Cadres (in Bahasa: Kasira="Kader Siaga Rabies").

Materials and methods: The program was begun with the establishment of rabies caders institution, the development of Standard Operational Procedure (SOP) related rabies and training of trainers on rabies cadres (Kasira). Kasira training materials included The introduction of rabies, The first aid for dog-bite cases, The dog handling and vaccination, The communication techniques, The cases reporting and introduction of SOP related rabies. Kasira's task were to educate community about rabies, assist in the implementation of mass rabies vaccination programs conducted by the local government, conduct first aid and reporting when there were dog bite cases, and assist local health workers in investigating rabies cases and rabies control programs.

Results: Kasira was a volunteer persons who consisting of local village communities namely integrated health cadres, hunters representatives, village officials, village territorial advisor (army) and village security advisor (police). The first three were the most important in the handling of rabies and giving the education to the villagers. The results of the evaluation showes that Kasira could increase people's knowledge on rabies, bite cases were quickly handled and reported, and helped the government in the dog registration process and mass vaccination program, so the coverage of vaccination increased.

Conclusion: Since its establishment, KASIRA had helped a lot in rabies control programs and campaign. This community-based approach was expected to overcome obstacles to rabies control especially in terms of vaccination coverage, first handling of dog bite cases and delays in case reporting.
Key words: Community-based approach, rabies, rabies preparedness cadres

Macrolides, probiotics, and the pen environment: effects on *Enterococcus faecium* diversity and antimicrobial resistance in U.S. feeder cattle

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ABSTRACT

Objective: Enterococci are used by the National Antimicrobial Resistance Monitoring System to track antibiotic resistance among Gram-positive bacteria due to their abundance in both food animals and meat. In the U.S. cattle industry, macrolides are used to prevent liver abscesses which cause significant economic losses. Previous studies have suggested that both the pen environment and feeding tylosin expand the prevalence of multidrug resistance among enterococci; in particular, to erythromycin. This has led to increased research into alternative feed supplements and improved stewardship practices.

Materials and methods: In two replicates (n=96 finisher cattle each) of a randomized controlled trial, we measured the impact of a probiotic and an altered pen environment on antimicrobial resistance among fecal *Enterococcus* spp. in cattle fed tylosin. Diluted fecal samples were spiral-plated on m-*Enterococcus* agar, and agar supplemented with tetracycline and erythromycin at CLSI breakpoints. Two colonies from each plain and erythromycin-supplemented agars were typed using MALDI-TOF. MICs for *E. faecium* and *E. hirae* were obtained. *E. faecium* was sequenced on the MiSeq platform. Bioinformatics data yielded sequence types (ST), phylogenetics, resistance genes, and plasmid types.

Results: Tetracycline-resistant CFU counts increased as the trial progressed. Erythromycin resistance increased to day 84, then decreased to day 112 following tylosin withdrawal. The same trends were seen with MICs among individual isolates. The probiotic *Enterococcus faecium* sequence type was ST296. ST240 and ST296 appeared most frequently; ST296 did not appear at day 0. Prevalence of *erm*B encoding high level macrolide resistance was maximized on day 84. ST240 was associated with *erm*B and *tet*(M); all ST240 isolates contained *tet*(M). ST296 did not carry *erm*B or *tet*(M); however, all *E. faecium* harbored *msr*C encoding reduced macrolide susceptibility.

Conclusion: Supplementation with an *Enterococcus* and *Saccharomyces*-based probiotic had a sparing effect on erythromycin resistance.

Key words: Antimicrobial resistance, feeder cattle, tylosin, probiotics, *Enterococcus*

Temporal patterns and predictors of antimicrobial resistance of canine *Staphylococcus* isolated from a diagnostic laboratory in Kentucky, USA

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ABSTRACT

Objective: The objective of this study was to investigate temporal patterns and predictors of antimicrobial resistance among *Staphylococcus* spp. isolated from canine samples submitted to the University of Kentucky Veterinary Diagnostic Laboratory (UKVDL) between 1993 and 2009.

Materials and methods: Retrospective data of 4,971 *Staphylococcus* isolates assessed for antimicrobial susceptibility using the disk diffusion method at the UKVDL between 1993 and 2009 were included in the study. Temporal trends were assessed for each antimicrobial using the Cochran-Armitage trend test. Logistic regression models were used to investigate predictors of antimicrobial resistance (AMR) and multidrug resistance (MDR).

Results: The overall percentage of AMR and MDR were 64.2% and 18.8%, respectively. The highest levels of AMR were seen in *S. aureus* (70.7%; 265/375), CoNS (66.4%; 602/907), and SIG (64.7%; 2192/3387). The lowest levels of AMR were observed in *S. hyicus* (44.1%; 128/290) and *S. schleiferi* subsp. *coagulans* (33.3%; 4/12). Overall, AMR showed a significant (p=0.011) decreasing temporal trend while no significant (p=0.062) temporal trend was observed for MDR. Significant temporal trends (both increasing and decreasing) were observed among 11 of the 16 antimicrobials covering 6 of the 9 drug classes assessed. Thus, significant increasing temporal trends in resistance were observed to β-lactams (p<0.001) (oxacillin, amoxicillin-clavulanate, and cephalothin), aminoglycosides (p<0.001) (gentamicin, and neomycin), lincosamide (p=0.003), and enrofloxacin (p<0.001). In contrast, sulfonamides (p<0.001) (sulfadiazin) and tetracyclines (p=0.008) both showed significant decreasing temporal trends in AMR. *Staphylococcus* spp., geographic region, and sample source were significant predictors of both AMR and MDR.

Conclusion: The high levels of AMR to a number of antimicrobial agents and the increasing temporal trends are concerning. Therefore, continued monitoring of AMR among *Staphylococcus* spp. is warranted. Future studies will need to identify local factors responsible for the observed geographic differences in risk of both AMR and MDR.

Key words: *Staphylococcus aureus*; antimicrobial resistance; multi-drug resistance; temporal patterns; predictors

Developing rapid diagnostics for use in livestock to combat antimicrobial resistance: An innovation systems approach

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ABSTRACT

Objective: Rapid diagnostics have potential to address the challenge of antimicrobial resistance (AMR) in humans and animals. However, successful development and application of novel diagnostic tools requires both scientific innovation and understanding of relevant social, political and economic factors, including regulation. The Diagnostic Innovation and Livestock (DIAL) project aims to facilitate the development of novel, rapid diagnostic tests to rationalise antimicrobial use in livestock in the UK and Tanzania.

Materials and methods: This is an interdisciplinary investigation bringing together social, veterinary and innovation sciences. Using an innovation systems approach, researchers at the University of Edinburgh aim to identify barriers and enablers to diagnostic innovation, assess the regulatory support required and understand potential markets for rapid AMR diagnostics in farmed animals. The research is based on a series of semi-structured interviews and workshops with diagnostic developers, regulators and laboratories. Qualitative data analysis is utilising the Strategic Planning for Advanced Technology Innovation Systems (STRATIS) framework, an established approach which has been applied previously to innovation in human healthcare and life sciences.

Results: Data collection and analysis are proceeding simultaneously, as is common in qualitative research, ensuring that initial findings, including the structure of value chains and the regulatory landscape for innovative diagnostics, will be newly available to share with the research community at ISVEE.

Conclusion: The study will produce practical recommendations for industry, research and policy audiences to support the development of livestock diagnostics to combat AMR, and demonstrate the value and future potential of approaches from innovation studies for One Health research.

Key words: Diagnostics, AMR, livestock, innovation, qualitative

Antimicrobial resistance of mastitis agents in dairy farms in Bosnia and Herzegovina: A base line study

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ABSTRACT

Objective: Mastitis in dairy farming is the most expensive disease. On the other hand antimicrobial resistance (AMR) of bacteria is identified globally as the most important public health treat, projecting to be leading cause of death in the near future. Increased rate and proportions of resistant bacteria among human pathogens emphasize need to investigate this phenomena among animal pathogens since many are zoonotic.

Materials and methods: Study conducted on registered dairy farms in the Canton Sarajevo (Bosnia and Herzegovina (BiH)) aimed to establish prevalence of mastitis, identify causing agents and investigate antimicrobial resistance. Lactating animals (n_a=1214) in all farms were tested using California Mastitis Test (CMT) during November 2017. From CMT positive animals pooled milk samples from all quarters were taken.

Results: Overall prevalence of mastitis based on CMT results was 9,9 %, while 19 out of 180 dairy farms had at least one mastitis case. Farm level mastitis prevalence was higher among larger farms (> 50 animals) while within farm prevalence was higher among small family farms. Microbiological investigation resulted in 49,2 % of cultured samples identified as coagulase positive staphylococci (including *S.aureus*), 2,5 % as *E.coli*, 0,8% as enterococci, 13,3 % as mixed infection and 34,2 % of samples showed no growth. Using disk diffusion test 95 isolates were investigated for AMR, where high proportion of isolates resistant to tetracycline is observed, while resistance to other antimicrobials was established for only few.

Conclusion: Even though established prevalence figures are moderate compared to reported mastitis prevalence in dairy farms from other countries, there is still room for improvement especially in small family farms where zoohygiene conditions are less adequate. Giving that BiH is developing country where oversight on antimicrobial use in farm animals is less comprehensive, additional investigation should be done in future to establish trends in AMR in mastitis causing agents in dairy farms.

Key words: Mastitis, dairy, antimicrobial resistance, Bosna and Herzegovina

The red fox as sentinels for the occurrence of antimicrobial resistance in the environment

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ABSTRACT

Objective: Antimicrobial resistance (AMR) is one of the major global public health challenges. The objective of this study was to assess the suitability of the wild red fox as sentinels for assessing the occurrence of antimicrobial resistance in the environment. Further on, we aimed at assessing if the human density might play a role for the occurrence of AMR in the environment.

Materials and methods: In total, 528 red foxes have been sampled during the hunting season. A subset of samples (n=387) were subjected to selective culturing to detect E. coli resistant to 3. generation cephalosporins, quinolones, carbapenems and colistin, and enterococci resistant to vancomycin. Additionally, one E. coli isolate from each sample was tested to a panel of substances using broth microdilution method and Sensititre™ TREK plates.
The samples (subset) were categorised according to the human population density areas resulting in 108 (20.5%), 328 (62.1%) and 92 (17.4%) from areas with low, medium and high population density, respectively.

Results: In total, 92.3% of the *E.coli* isolates were susceptible to all antimicrobials included in the test panel. However, the occurrence of AMR differed significantly between the medium and high population density areas with 4.7% and 15.2% resistant to at least one antimicrobial substance, respectively. Both quinolone resistant *E. coli* and *E. coli* resistant to 3. generation cephalosporins detected by selective screening were uncommon in the low population density areas, whereas these resistance forms were more abundant in areas with medium and high population density.

Conclusions: Our study indicates that the occurrence of AMR in the Norwegian environment is low, and that the red fox can serve as sentinels to assess the occurrence of AMR in the environment. Not surprisingly, our results indicate that human density plays a role in the dissemination of AMR in the nature.

Key words: Fox, antimicrobial resistance, environment

Evaluation of the live monitoring programme for radioactive ^{137}Cs in Norwegian sheep

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ABSTRACT

Objectives: Describe the variation of the ^{137}Cs concentration in sheep and determine how the sample size affects the determination of the correct median concentration for a flock.

Material and methods: All results from live monitoring of ^{137}Cs in sheep 2010-2015, 1598 flocks, were collected retrospectively. Data consisted of median, maximum and minimum values (Bq/kg) and flock size. In addition, data from eleven flocks where all animals were sampled were collected and used in a simulation model in R. Different sample sizes from each flock were simulated to obtain estimates of the median concentrations.

Results: There was large variation between years, geographical regions, flocks and within flocks. Sampling of 20-30 animals per flock gives a higher probability of estimating the correct median compared to ten animals.

Conclusion: There is large variation of median concentration values. The reason for this could be annual variation in weather that affects the availability of plants and fungi ingested by the sheep. By increasing the sample size to 20-30 animals per flock, there will be an even better confidence to sustain the high level of food safety.

Key words: Sheep, food safety, radioactive contamination

Seasonal *Shiga toxin-producing Escherichia coli* (STEC) prevalence and concentration on hides and feces of cull dairy cattle at commercial processing plants in the United States

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ABSTRACT

Objective: Cull dairy cattle are mainly processed into ground meat, which represents one of the main sources of STEC-7 (O157, O26, O45, O103, O111 O121, and O145) infection in humans in North America. Thus, understanding prevalence and concentration of STEC-7 in peri-harvest cull dairy, and their seasonality patterns, will allow us to identify better post-harvest control practices. The objective of the study was to determine the prevalence and concentration of STEC-7 serogroups, and their associated virulence genes, on hide-on carcass surface and rectal fecal samples from cull dairy cattle in processing plants in United States (US), in summer and spring months.

Materials and methods: Two cull dairy processing plants in Pennsylvania and one in California were sampled as they are located in the east and southwest catchment areas where most US dairies are concentrated. During each season, we collected 60 hide-on samples and 60 rectal fecal samples from each plant. Hide-on samples were collected from an area of 35 cm X 60 cm from the brisket to the umbilicus of the carcass, before any interventions were applied, using Speci-Sponges®. Fecal samples, from the same animals, were obtained by swabbing the mucosal surface of the recto-anal junction using a sterile cotton-tipped applicator. Samples were tested using a spiral plating method for quantification and an immunomagnetic separation method followed by plating on selective media for detection of STEC-7, followed by chemical and molecular confirmation of isolates.

Results: On hide-on samples, O157 was the most prevalent STEC serogroup whereas non-O157 serogroups were more prevalent in fecal samples. Predominant non-O157 serogroups were O103 on both hide-on and fecal samples, followed by O111 on fecal samples.

Conclusions: This study provides evidence that STEC-7 are prevalent on hides and feces of cull dairy cattle at peri-harvest in the Northeast and Southwest regions of the US.

Key words: Food Safety; STEC-7, peri-harvest, cull dairy, cattle

Production animal antimicrobial use in New Zealand

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ABSTRACT

Objective: There are few data available in New Zealand describing antimicrobial use (AMU) in production animals. This paper reports on a pilot project to assess and analyse all production AMU data from six clinics across New Zealand.

Materials and methods: This project was co-funded by NZVA and XLVets New Zealand. Data were gathered for all farm clients serviced by participating businesses during 2016. Antimicrobial sales data (proxy for AMU) was classified according to route of treatment, class, and active. Total biomass was calculated for each farm. Data were then combined to calculate mg active/kg PCU.

Results: Data were gathered for 1462 dairy farms and 707 other (general) farms representing 623,430 dairy cows, 27,399 beef cattle, 706,035 sheep and 12,107 deer.

Dairy Mean PCU was 8.54mg/kg (range by clinic: 4.72 to 11.91), 56.3% of AMU (by weight of active) was injectable, followed by intramammary: dry cow (33.4%) and lactating cow (8.9%). The majority of actives used were Penicillin (77.6%), Macrolides (9.04%) and Cephalosporins (5.1%), General farms Mean PCU was 0.57mg/kg (range by clinic: 0.32 to 0.94). Fifty nine percent of AMU was oral, followed by injectable (39.2%). The majority of actives used were Tetracyclines (66.0%), Penicillin (19.2%) and Sulphonamides (7.1%).

Conclusions: These data confirm that the use of antimicrobials amongst production animals in New Zealand is very small, and that routes of administration and actives vary between dairy and red meat sectors. The data also confirm that the use of (3rd generation) cephalosporins and macrolides is very low amongst general farms and low amongst dairy farms. Fluoroquinolone use is virtually negligible across all species.

Key words: Antimicrobial use

Expert opinion on livestock antimicrobial usage indications and patterns in Denmark, Portugal and Switzerland

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ABSTRACT

Objective: Reduction of antimicrobial use (AMU) in livestock production requires interventions that target areas where antimicrobials are frequently used. To ascertain the measures with the largest feasibility and impact, detailed knowledge about the temporal patterns and indications of use of specific antimicrobial substances is needed. On a European level, no comprehensive data on AMU patterns are available. Therefore, expert opinion is a valuable alternative to estimate and compare AMU patterns across countries. This study aimed at describing the usage patterns of specific antimicrobials throughout a standardized production cycle of the main livestock sectors (broilers, swine, dairy cattle and veal/fattening calves), and comparing them across three countries from Northern, Central and Southern Europe (Denmark, Portugal and Switzerland).

Materials and methods: Veterinary experts (n=67) replied to a questionnaire focusing on the time-periods in the production cycle when different antimicrobial products are administered, and the respective indications for treatment. This expert opinion study provides new insights into the time-periods during which specific antimicrobial substances are used in different livestock sectors. For several antimicrobials, between- and within-country variation was detected with respect to the temporal distributions of treatments and indications for use. These differences were also observed for several critically important antimicrobials, which is a matter of concern. Moreover, licensed antimicrobial substances also differed between countries. To present the results interactively, a web-application using the R package "Shiny" was developed.

Results: The results can inform decision-making with the aim to foster antimicrobial prudent use in the veterinary setting and, therefore, protect Public Health from the threat of antimicrobial resistance. Specifically, it is recommended to establish and promote treatment guidelines, invest in the prevention of diseases in critical moments of the production cycle and target undifferentiated AMU. Finally, differences between countries should be further investigated to better understand the factors influencing AMU patterns.

Key words: Antimicrobial use, livestock, antimicrobial resistance, international comparison, treatment indications

A risk profiling approach to investigate food safety risks within the red meat industry in Australia

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ABSTRACT

Objective: To inform research priorities and support market access, a semi-quantitative risk profiling exercise was conducted to investigate the food safety risks posed by red meat products in Australia.

Materials and methods: Initially, a hazard characterization was conducted - via a review of literature and data on foodborne outbreaks, pathogen surveillance and product recalls, and an expert elicitation process with 15 food safety experts - to identify the Product:Process:Hazard combinations to be considered. The expert elicitation estimated the likelihood of contamination of these combinations. Likelihood ratings were then combined with hazard severity ratings to qualitatively estimate the relative risk posed by each combination. Combinations with a moderate to high risk were included in the semi-quantitative risk profiling using Risk Ranger v2 (http://www.foodsafetycentre.com.au/riskranger.php), which uses eleven criteria describing the hazard severity, population susceptibility, consumption patterns and probability of the product containing an infectious dose. The outcome is a risk ranking (RR); RR ranges from 0 (no risk) to 100 (every member of the population eats a meal that contains a lethal dose of the hazard every day).

Results: STEC *E.coli* O157 (RR 35-39) and *Salmonella* spp. (RR 33-37) in undercooked hamburgers and *Listeria monocytogenes* in ready-to-eat products (RR 35-38) resulted in the highest risk, with this risk being moderate. The model predicted 11-32 annual cases due to STEC *E.coli* O157 and 28-90 due to *Salmonella* spp. under different undercooking scenarios. Fifteen cases were estimated due to *Listeria monocytogenes*. The process identified *Toxoplasma gondii* in undercooked lamb as high risk among pregnant women (RR 49), with a prediction of 142 annual congenital infections.

Conclusion: This study provides a risk profiling for the red meat industry in Australia, which, considering the available information, suggests red meat products do not pose a high food safety risk.

Key words: Risk profiling, food safety, red meat industry, Australia

Participatory planning for community-based control of bovine brucellosis in Tanzania

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ABSTRACT

Objectives: Brucellosis is one of the most prevalent zoonoses in the world. Since 2015, a series of socio-epidemiological studies have been conducted in Tanzania by the authors. This study was conducted to understand the view of communities on the preferred control option of brucellosis in the study areas.

Materials and methods: Four participatory rural appraisals were conducted with the agro-pastoralists who participated in the cattle surveillance in 2016, in the four villages in Mvomero District, Tanzania. Prior to the appraisals, results of risk factor analyses for bovine brucellosis, and willingness-to-pay study for different levels of vaccination were returned, and characteristics of the disease in animals and humans were explained. The survey team answered to the questions related with brucellosis by the participants, and qualitative data on the culture and belief on the risky behaviours associated with human infection were collected. Finally, participants were encouraged to discuss about sustainable and community-based voluntary control of brucellosis.

Results: Risky behaviours such as drinking raw cattle blood and milk were common particularly among Maasai tribe, and they believed that raw cattle blood provides strong energy. One village preferred to talk without research team about disease control. All the villages came to the same conclusion of continuous conduct of calf vaccination paid by themselves. A Maasai leader mentioned that adults cannot stop risky behaviours, but education can change behaviour of young generation. Technical supports from both medical and veterinary authorities were perceived to be important.

Conclusion: Provision of evidence-based information on brucellosis was confirmed to raise motivation of community-based control of brucellosis among cattle keepers. One Health brucellosis control among medicine, veterinary medicine, and education may be a key to success.

Key words: Brucellosis, participatory rural appraisal, vaccination, willingless-to-pay, Tanzania

Development of a national collaborative Veterinary Antimicrobial Stewardship Online Program

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ABSTRACT

Objectives: An online Veterinary Antimicrobial Stewardship (AMS) training program was developed with the aim of assisting veterinarians to reduce and rationalise their use of antimicrobial agents in clinical practice and address the spread of antimicrobial resistance. This was a collaborative project, from all eight Australian and New Zealand Veterinary Schools and funded by the Department of Agriculture and Water Resources.

Materials and Methods: An expert panel was created, consisting of academics in veterinary microbiology, pharmacology, epidemiology, public health and clinical practice. This panel developed resources that were integrated within an interactive online system (B Online Learning Systems) allowing scenario-centered learning for veterinarians across all areas of practice. Modules included: 1) Antimicrobial resistance as a societal problem; 2) How does antimicrobial resistance develop?; 3) How do antibiotics work and what is their relative importance?; 4) Biosecurity and infection control in veterinary clinical practice – how do we stop transmission?; 5) What evidence supports the diagnosis of a bacterial infection?; 6) Drug selection and regimen – which drug is best for the patient and society?; and 7) Implementing an antimicrobial stewardship program in your practice Results: The training program has a release date of June, 2018 and uptake and impact of the program will be evaluated after its release. Active collaboration between academics across all Veterinary schools in Australia and New Zealand, resulting in development of post-graduate teaching material in an area that requires marked veterinary engagement, represents a unique outcome in and of itself.

Conclusions: The capacity to provide consistency within teaching of critical concepts to veterinarians in practice is a model that could be expanded to other areas. The provision of a learner-centred, clinically focused resource available to graduates provides the necessary tools and processes for practitioners to instigate marked practical and cultural change in veterinary use of antimicrobial agents.

Key words: Antimicrobial stewardship, Education, Antimicrobial resistance

One health approach to control avian influenza; experience from Iran

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ABSTRACT

On 31 January 2018, unexpected high mortality was reported in wild birds of Boujagh national park, Gilan province; north of Iran. Following epidemiological investigations, on 4 February, Iran veterinary national reference laboratory confirmed the presence of highly pathogenic avian influenza virus, H5N6 subtype in the collected samples from sick and dead birds. The area in vicinity to Caspian Sea, is hosting millions of migratory birds annually, to spend their wintering season. It was the first occurrence of H5N6 outbreak in Iran. Shortly after the confirmation, Iranian veterinary organization, Iranian department of environment and ministry of health were prompted to implement control measures to prevent further spreading of outbreak. Active surveillance was implemented in Boujagh national park, neighboring villages and high risk areas to monitor any unexpected mortality in wild birds and backyard poultries. In order to minimum the risk of virus transmission to human, recreational visiting to Boujagh national park was prohibited. Daily collecting of dead birds was conducted by park rangers. All individuals exposed occupationally or in close contact with infected or potentially infected birds were vaccinated and monitored for 10 days. Control of transportation of live poultry, poultry products and/or any commodities that might potentially spread the virus was intensified inside the Gilan province. Disinfection points were established around the area and on the main roads for the vehicles of poultry related industries exiting the Gilan province. Fortunately, the outbreak was contained within Boujagh national park. The ongoing preventive measures will continue until the full control of outbreak. The intimate connection of avian influenza virus with wild and domestic birds and humans require multidisciplinary collaborative efforts to prevent disease outbreak. The one health approach which engages a wide range of sectors is found very helpful to mitigate the risk of infectious diseases especially when the resources are limited.

Key words: Avian Influenza, Iran, One health, surveillance

Brucellosis in northern Tanzania: insights into human disease prevalence, multi-species transmission processes and the design of sustainable interventions

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ABSTRACT

Objectives: Brucellosis, caused by multiple *Brucella* spp., is an important cause of human febrile illness in northern Tanzania. The objectives of this study were to determine the prevalence of disease in humans, identify the *Brucella* species present in different hosts and quantify the contributions of different animal host species in multi-species transmission.

Materials and methods: Outpatients presenting at Endulen Hospital in the Ngorongoro Conservation Area were enrolled. Individuals presenting from August 2016 to October 2017 with reported fever within the past 72 hours, or a tympanic temperature of ≥38.0°C were eligible and blood culture was performed. A *Brucella* genus-level qPCR detection assay was used to test vaginal swab samples from livestock sampled in pastoral areas of northern Tanzania. A latent process model based on serology data collected across northern Tanzania was used to reconstruct *Brucella* transmission dynamics.

Results: Eight patients with acute brucellosis were identified among 218 (3.7%) febrile study participants. Seven of eight *Brucella* isolates are typed as *B. melitensis* and one preliminarily typed as *B. abortus*. Swabs from 8 of 252 (3.2%) cattle, 5 of 216 (1.9%) sheep and 10 of 260 (3.9%) goats were qPCR positive for *Brucella* infection (including zoonotic and non-zoonotic species). One qPCR positive swab collected from a sheep was typed as *B. ovis*. Modelling results identify goats & sheep as the most likely source of human *Brucella* exposure in northern Tanzania.

Conclusion: These data reveal that *B. melitensis, B. abortus* and *B. ovis* are present in this northern Tanzania system. *B. melitensis* is the predominant zoonotic *Brucella* species causing acute human brucellosis and goats and sheep are the most likely source of these infections. Control strategy developments for this setting should include both *B. melitensis* and *B. abortus* control in goats, sheep and cattle.

Key words: Brucellosis, zoonoses, One Health, veterinary public health, livestock

The British *E. coli* O157 in Cattle Study (BECS): more than just prevalence estimates - implications for veterinary public health

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ABSTRACT

Objective: The British *E. coli* O157 in Cattle Study (BECS) was designed: to estimate E. coli O157 prevalence on British farms with cattle destined for the food chain; to allow, for the first time, contemporaneous comparison of *E. coli* O157 prevalence and strain composition between Scotland and England & Wales, and, to facilitate comparison over time within Scotland, following two previous Scottish cross-sectional surveys between 1998 and 2004.

Materials and methods: Across Scotland and England & Wales, 270 farms were visited between September 2014 and November 2015. Faecal pat samples were collected from the pasture/housing environment of the group of cattle closest to slaughter at the time of sampling, using established methodologies, and a questionnaire was completed by face-to-face interview.

Results: Farm-level prevalence within Scotland has not changed significantly across the three Scottish surveys; change has been seen at pat-level, with the highest prevalence reported from BECS. There is no significant difference in current prevalence estimates between Scotland and England & Wales, despite differences in some risk factors associated with the presence of *E. coli* O157 on-farm. The main difference is in the composition of the cattle strains, with greater strain diversity in isolates from England & Wales than from Scotland (p <0.05). The Scottish BECS isolates were dominated by the highly virulent phage type PT21/28 strain, which has persisted in Scottish cattle since the first survey in 1998.

Conclusion: It is possible that this strain difference in the cattle populations contributes to the difference seen in the rates of human clinical *E. coli* O157. This may have implications for measures to mitigate the public health risk.

Key words: E. coli O157, prevalence, cattle, zoonosis, risk mitigation

Quantitative assessment of the veterinary risk of using animal viruses in oncolytic therapy

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ABSTRACT

Objective: Some viruses infect and lyse cancer cells and therapy with these so-called oncolytic viruses is an alternative treatment for cancer patients. Application of human viruses is not always successful, and therefore animal viruses are also being investigated for their oncolytic capacity. Excretion of these viruses by patients may, however, result in release of virus into the environment and subsequent infection of livestock animals. This study aimed to estimate the probability that use of Seneca Valley virus (SVV) in oncolytic therapy would result in a disease outbreak in pigs in the Netherlands.

Materials and methods: A quantitative microbial risk assessment (QMRA) was performed to estimate the probability that excretion of SVV by patients would result in clinical disease at pig farms. The daily dose of SVV ingested by pigs via drinking water was calculated taking into account the excretion of SVV by patients in their faeces, inactivation of virus by sewage treatment, dilution of virus in river water, and inactivation of virus by treatment for drinking water production. Dose-response parameters estimated from animal experiments were used to estimate the probabilities for infection and clinical disease of pigs.

Results: The probability that discharge of SVV results in clinical disease at pig farms is very low. Even in the worst-case scenario of low inactivation by drinking water treatment and consumption of the contaminated water on a large farm, this probability is less than 10^{-8} with 95% certainty.

Conclusion: Use of animal viruses in oncolytic therapy might pose a risk to the livestock sector if these viruses are not present in the country yet. Hence, a risk assessment is warranted before admission of these viruses. Based on QMRA, we conclude that the risk of SVV is very low, despite high uncertainty for some input parameters.

Key words: Oncolytic virus, quantitative risk assessment, dose response, Seneca Valley virus, pigs

Prevalence of *Enterobacteriaceae* resistant to the third generation cephalosporin and Extended-Spectrum β-Lactamase producing *Enterobacteriaceae* among urban rats (*Rattus sp.*) in Reunion Island, 2017-2018

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ABSTRACT

Objective: In South-western Indian Ocean, Extended-Spectrum β-Lactamase producing *Enterobacteriaceae* (ESBL-E) represent a significant public and veterinary health burden. In Reunion, epidemiological situation regarding ESBL-E was unknown. The synanthropic lifestyle of urban rats make them likely to be in contact with antibiotic drugs, and multidrug resistant bacteria. They are zoonotic pathogens reservoirs and could be considered as bio-indicators of antibiotic environmental contamination. The aim of our study was to estimate the prevalence of *Enterobacteriaceae* resistant to third generation cephalosporin (ER3GC) and ESBL-E on urban rats of Reunion.

Materials and methods: From May to October 2017, 115 rats (*Rattus rattus* and *Rattus norvegicus*) were trapped in urban areas of Reunion. Bacteria of rat intestines were cultured on selective media and antimicrobial susceptibility assessed according to EUCAST standards.

Results: Prevalences observed were 7.0% [2.0%-12.0%] for ER3GC and 0.9 % [0.0%-2.9%] for ESBL-E in urban rats from Reunion in 2017-2018. In comparison with Guinea, West Africa, in 2015, ESBL-E prevalence observed was 20.7 % [7.5%-35.8%], and 16 % [6.2%-25.8%] in Reinfeld, Germany, in 2010.

Conclusion: ESBL-E prevalence in Reunion was significantly lower than data previously reported. It probably reflected limited environmental contamination by antimicrobial residues and multidrug resistant bacteria. We questioned the ability of rats to be «sponge » of environmental pathogens as proposed by other authors.

Key words: Rat, Reunion, antibiotic resistance, cephalosporine, extended-spectrum-beta-lactamase, Enterobacteriaceae

Cysticercus bovis in central Chile and its spatial association with watercourses and populated areas

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ABSTRACT

Objective: Bovine cysticercosis (*Cysticercus bovis*) is a zoonosis of economic and public health importance. This study evaluated 26,167 cattle slaughter records and 457 diagnosed cases of cysticercosis in two slaughterhouses. Information was collected by the official veterinary inspection services in 2010 in the Valparaíso region. Objective: The objective of this study was to identify the association of bovine cases with human settlements and water courses.

Material and methods: Of all the 457 cases, 424 were considered mild cysticercosis (92.78%) and 33 cases severe (7.22%). Of these records, 161 could not be used for further analyses, being animals from regions not included in the study or for lack of traceability.

Results: A group of 296 cattle belonging to 112 properties was obtained, of which 12 were found in the Coquimbo Region, 78 in the Valparaiso Region and 22 in the Metropolitan region. These farms were georeferenced. The distance to human settlements and watercourses was recorded, being considered, in both cases, all farms closer than 300m of these risk factors.

Conclusion: Of all 26,167 cattle slaughtered, cows were the ones that showed a higher *C. bovis* prevalence (2.38%), a statistically significant difference when compared with heifers, steers, bulls, heifers and calves (α=0.05). Also, there was a statistically higher proportion of cases in the summer months, in comparison to other seasons (α=0.05).

Key words: Cysticercosis, parasites, risk factors, Chile

The influence of weather on primary Middle East respiratory syndrome coronavirus (MERS-CoV) cases in Saudi Arabia

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ABSTRACT

Objective: Middle East respiratory syndrome coronavirus (MERS-CoV) is endemic in dromedary camels in the Arabian Peninsula, and zoonotic transmission to people is a sporadic event. In the absence of epidemiological data in the reservoir species, environmental patterns of zoonotic transmission may be approximated from primary human cases. This study aimed to identify acute environmental factors that increase the risk of primary MERS infections.

Materials and methods: A case-crossover design was used to measure associations between primary MERS cases and preceding weather conditions in Saudi Arabia using univariable conditional logistic regression. Cases with symptom onset between January 2015 and December 2017 were obtained from a publicly available list maintained by the World Health Organization. The complete primary case dataset (N =891) was reduced to approximate the cases most likely to be spillover transmission from camels (N = 448). Data from meteorological stations closest to the largest city in each province were used to calculate the daily mean, minimum, and maximum temperature ($^\circ$C), relative humidity (%), wind speed (m/s), and visibility (m).

Results: Low temperature (Odds Ratio = 1.27; 95% Confidence Interval = 1.04-1.56) and humidity (OR = 1.35; 95% CI = 1.10-1.65) were associated with increased cases 8-10 days later. High visibility was associated with increased cases 7 days later (OR = 1.26; 95% CI = 1.01- 1.57). Results suggest that primary MERS cases in Saudi Arabia are more likely to occur when conditions are particularly cold and dry. This is similar to seasonal patterns that have been described for other respiratory diseases in temperate climates. We hypothesized that low visibility would be positively associated with primary cases of MERS, however the opposite effect was seen in the analysis. This may reflect human behavioural changes in poor weather conditions. Zoonotic transmission of MERS-CoV may be linked to weather conditions, which has implications for veterinary public health.

Key words: Middle East respiratory syndrome, case-crossover, veterinary public health

Environmental parameters and estimation of bacterial contamination in sentinel oysters and estuarine water from Phang Nga area in southern Thailand

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ABSTRACT

Objective: This study was performed to characterize levels of indicator bacteria (*Escherichia coli*; EC), *Vibrio parahaemolyticus, Salmonella* and *Shigella* contamination from a shellfish growing area in Phang Nga Bay, southern Thailand.

Materials and methods: Pooled oyster meats (n=144) and estuarine water (n=96) were collected to quantify bacteriological concentrations from March, 2016 to February, 2017. Twelve cultivated oyster and eight estuarine water samples were collected each month to analyze the bacterial contamination levels. Instantaneous, 24-hour and 7-day average environmental parameters were recorded in order to test their association with levels of bacterial contamination.

Results: Prevalence and mean concentrations of EC were 93.1% and 4.6×10^3 MPN per gram oyster meat, and 78.1% and 2.2×10^2 MPN per 100 ml of estuarine water. Vibros was detected in 100% of samples. In contrast, *Shigella* and *Salmonella* were detected in 7.6% and 30.6% of pooled oyster samples, and 27.1% and 0% in 100 ml of estuarine water samples. The most predominant strain of *Salmonella* observed in pooled oyster meat was Paratyphi B. Temperature, relative humidity, 7-day average precipitation and the presence of *Salmonella* were associated with the concentration of EC in oyster meat. The raw data and log-transformed of the level of EC in oyster samples were analyzed in two contrasting regression models. However, the more valid predictions of MPN/g oyster were conducted using non-log transformed value of EC.

Conclusion: These findings could be used as a rapid warning system to predict levels of EC contamination prior to harvest oyster to reduce the risk of consuming contaminated oysters. Implementing monitoring programs for bacterial contamination and adequate thermal exposure during cooking of oysters would enhance the microbiological safety of these cultured shellfish.

Key words: *Escherichia coli*, estuarine water, fecal contamination oyster, and *Salmonella*

The effect of tylosin on antimicrobial resistance in beef cattle enteric bacteria: a systematic review

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ABSTRACT

Objective: Tylosin is a commonly used in-feed antimicrobial in beef cattle for disease treatment and prevention. However, macrolides are critically important antimicrobials in human medicine and their use in food animals could select for resistance in enteric bacteria, which can cause disease in humans. We conducted a systematic review to evaluate the enteric bacterial resistance in beef cattle associated with tylosin use.

Methods: We used the PICO (population, intervention, comparison, outcome) framework to characterize the research question. Search strategies and inclusion/exclusion criteria were created to identify published studies with four main factors: (1) primary research studies of the (2) use of tylosin in feedlot cattle that (3) measured phenotypic or genotypic resistance in (4) *Campylobacter* species, *Salmonella enterica*, *Enterococcus* species, or *Escherichia coli*. We searched for published manuscripts, dissertations, and conference proceedings in ten databases. Two reviewers independently screened the studies and a third reviewer resolved disagreements.

Results: We identified 587 studies across the ten databases; 306 were removed as duplicates and 256 were excluded during title and abstract screening. There was moderate inter-reviewer agreement (kappa=0.52). Of the 25 studies that progressed to full text review, 11 met all the inclusion criteria: one studied *Campylobacter* species, two studied *Salmonella enterica*, six studied *Enterococcus* species, and three studied *E. coli*. Five studies reported resistance from selective plating, seven reported minimum inhibitory concentrations, and eight reported resistance genes.

Conclusion: Relatively few studies have examined the effect feeding tylosin to beef cattle on the antimicrobial resistance in their enteric bacteria. A variety of methods were used to examine antimicrobial resistance, with most studies using two different methods. There is sufficient published data for a meta-analysis of *Enterococcus* species resistance associated with tylosin use.

Key words: Cattle, antimicrobial resistance, tylosin, systematic review

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The effect of tylosin and DFM supplementation on *Enterococcus* and antibiotic resistance determinants in the cattle feedyard environment and potential implications on human health

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ABSTRACT

Objective: Investigate the effects of tylosin, probiotics, and pen relocation on the presence and antibiotic resistance of *Enterococcus* and antimicrobial resistance determinants in the cattle feedyard environment.
Methods: Samples were taken on days 0, 84, and 119 from a study with 2x2x2 factorial design with tylosin, direct fed microbials (DFM), and change in feedlot pens as treatment groups. Samples were spiral plated onto m-*Enterococcus* agar and m-*Enterococcus* supplemented with antibiotics. Susceptibility testing by microbroth dilution was conducted on 326 MALDI-TOF confirmed *Enterococcus* isolates. WGS was conducted on select *E. faecium* isolates. Metagenomic sequencing was conducted on fresh samples for all days and dust from day 84 samples. TaqMan qPCR with *Enterococcus* specific and *E. faecium* specific primers were used to further investigate changes in *Enterococcus* populations.

Results: Colony counts on plain and antibiotic media from the environmental samples demonstrated similar trends to colony counts of cattle fecal samples processed in an alternate study; finding increased tetracycline and erythromycin resistance from day 0 to 84 and a subsequent decrease in resistance from day 84 to 119. Phenotypic resistance to erythromycin and tetracycline was detected in 75 and 82 *Enterococcus* isolates, respectively. Tetracycline resistance was confirmed in 11 sequenced isolates with the presence of *tet*(M) and/or *tet*(L). Erythromycin resistance was confirmed in 9 phenotypically resistant isolates by the presence of *erm*B. WGS further revealed a diverse group of sequence types including: ST240, ST540 ST22, and several previously undescribed. A variety of plasmid replicon types were detected, most prevalent being *rep*2, which was associated with *erm*B/*tet*(M). Analysis of qPCR and metagenomics data is ongoing.

Conclusion: By investigating the effect of treatments on bacteria and antibiotic resistance determinants in the feedyard environment, we can inform best management practices for combatting antibiotic resistance. Furthermore, we can assess the risk of feedyard dust on human health.

Evaluating the evolution and clonal expansion of *Salmonella enterica* serovar I 4,[5],12:i:- in swine and their environment

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ABSTRACT

Objectives: The Centers for Disease Control and Prevention has reported an increase in human foodborne illnesses related to MDR *Salmonella enterica* serovar I 4,[5],12:i:- largely associated with the consumption of contaminated pork. The cause of the rapid emergence of *Salmonella* I 4,[5],12:i:- is unknown. The overall objective of this study is to determine the virulence and antimicrobial resistance traits of *Salmonella* I 4,[5],12:i:- in order to understand the genetic mechanisms that have allowed the evolution and clonal expansion of *Salmonella* I 4,[5],12:i:- in swine and their environment.

Materials and methods: *Salmonella* I 4,[5],12:i:- and additional *Salmonella* serovars were isolated from head trim and cheek meat collected from a pork processing plant in the United States. Bacterial growth curves were determined using a BioScreen C under different concentrations of enrofloxacin, tetracycline, and ceftiofur. Growth curves were analyzed using a 4 parameter Gompertz-model in STATA®. Whole genome sequencing was performed on an Illumina MiSeq platform and Oxford Nanopore MinION. Resistance genes, plasmids, virulence genes, and point mutations were identified using the ResFinder, PlasmidFinder, VirulenceFinder, and PointFinder databases on the Center for Genomic Epidemiology website.

Results: Phenotypic and genotypic analyses confirmed all 47 *Salmonella* I 4,[5],12:i:- were MDR displaying the common ASSuT phenotype. At higher concentrations of enrofloxacin, *Salmonella* I 4,[5],12:i:- isolates with the *qnr*B gene had little to no growth and were significantly different compared to low concentrations. *Salmonella* I 4,[5],12:i:- with *tet* resistance genes performed well throughout the different tetracycline concentrations; however, there were significant differences in the curves between concentrations. Bacterial growth curve analyses in the presence of ceftiofur, SNP analyses, and MinION sequencing work is ongoing.

Conclusion: This study is important to determining the characteristics of *Salmonella* I 4,[5],12:i:- that have led to an increased prevalence in swine for preventing salmonellosis linked to swine and pork products.

Key words: Monophasic, *Salmonella*, resistance, fitness, growth curves

European Food Safety Authority Emerging Risks Identification Procedure

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ABSTRACT

Objective: The European Food Safety Authority's has established procedures for the identification of emerging risk in food and feed. The main objectives are: (i) to carry out activities aiming at identifying, assessing and disseminating information on emerging issues and ensure coordination with relevant networks and international organizations (ii) promote the identification of data sources and data collection and /or data generation in prioritized emerging issues and the (iii) evaluation of the collected information and identification of emerging risks.

Materials and methods: The presentation will describe the analysis carried out in 2017 - 2018 of the EFSA emerging risks procedure and recommendations provided by the expert group for further developments.

Results: The analysis considered the results obtained by EFSA and the methodologies in place. It was concluded that a systematic approach to the identification of emerging issues based on experts' networks is the major strength of the procedure but at present, it's mainly focused on single issues, over short to medium timescales, no consistent weighting or ranking is applied and clear governance of emerging risks follow up actions is missing. The analysis highlighted weaknesses with respect to data collection, analysis and integration. No methodology is in place to estimate the value of the procedure outputs in terms of avoided risk and a communication strategy that addresses the lack of data and knowledge uncertainty and addresses risk perception issues is urgently needed. Recommendations were given in three areas.

Conclusion: Further develop a food system based approach including the integration of social sciences to improve understanding of interactions and dynamics between actors and drivers and the development of horizon scanning protocols. Improve data processing pipelines to prepare big data analytics, implement a data validation system and develop data sharing agreements to explore mutual benefits. Revise the EFSA procedure for emerging risk identification to increase transparency and accountability.

Key words: Emerging risks, data, prioritization, communication

Quantified dynamics of antibiotic-susceptible and resistant *Salmonella enterica* among feedlot cattle treated with antibiotics

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ABSTRACT

Objective: The purpose of this study was to quantify the dynamics of *Salmonella* using both hydrolysis probe-based qPCR and colony counting (via a spiral-plating method). Additionally, we quantified antibiotic-resistant *Salmonella* by plating to agar containing antibiotics at CLSI breakpoint concentrations.

Materials and methods: Cattle were randomly assigned to 4 treatment groups; No-CCFA/No-CTC, No-CCFA/CTC, CCFA/No-CTC, and CCFA/CTC in 2 replicates consisting of 176 cattle. Fecal samples from Days 0, 4, 8, 14, 20, and 26 were quantified. Hydrolysis probe qPCR targeting the *invA* gene was performed on total community DNA for 1,040 samples in duplicate. Diluted fecal samples were spiral plated on plain Brilliant Green Agar (BGA) and BGA with ceftriaxone (4 μg/ml) or tetracycline (16 μg/ml). Effects of antibiotics on the rounded $\log_{10}$ quantity of *Salmonella* were analyzed via zero-inflated Poisson regression models since many qPCR runs yielded results below the limit-of-detection.

Kappa (agreement beyond chance) between the hydrolysis probe qPCR and the spiral-plating method was 0.5238. The *invA* gene copies decreased with CCFA treatment approximately 2 logs (on a $\log_{10}$ scale) and remained low following additional CTC treatment. The quantity of tetracycline or ceftriaxone-resistant *Salmonella* were approximately 4.0 $\log_{10}$ CFU / gram feces, however most of the samples were under detection limit.

Conclusion: The results of this study demonstrate that antibiotic use decreases the overall quantity of *Salmonella* in cattle feces; however, the quantity of resistant *Salmonella* tends to remain at a constant level throughout.

Key words: Antibiotic resistant *Salmonella*, feedlot cattle, quantification, hydrolysis probe qPCR, spiral plating

A monitoring system for veterinary antimicrobial consumption in pig farms in Japan

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ABSTRACT

Objective: Prudent use of antimicrobials for livestock is an important means to reduce the risk of antimicrobial resistance (AMR) coming from the livestock sector. Among livestock farms in Japan, pig farms use the largest amounts of antimicrobials. We constructed a farm monitoring system (PigINFO Bio) to evaluate the quality and quantity of different antimicrobials used for pig farms in Japan.

Materials and methods: The PigINFO Bio system was constructed as a collaborative research effort among the University of Tokyo (UT), the National Agriculture and Food Research Organization (NARO), and the Japanese Association of Swine Veterinarians (JASV). In 2016, JASV veterinarians collected annual data on the drugs (commercial names and quantity) prescribed to more than 100 pig farms. NARO converted the drug product names to antimicrobial names by using both a program they developed and a code list of antimicrobial products created by UT. The total amounts (g) of different antimicrobials were calculated for each of the participating farms and the standardized usage of antimicrobials (g/finishing pigs being shipped/year) was calculated. To compare the standardized usage of antimicrobials among participating farms, evaluation scores (A (lowest), B, C, D, E, F (highest)) were assigned according to the level of antimicrobial usage.

Results: Based on descriptive statistics, the most prevalent antimicrobial classes employed at the pig farms were tetracyclines, followed by penicillin, and macrolide. Ninety-five percent of antimicrobial drugs were administered orally. Detailed results from 2016 will be discussed in the presentation.

Conclusions: PigINFO Bio was a useful tool to evaluate the levels of antimicrobial usage. We plan to expand this system throughout the livestock sector to reduce the usage of antimicrobials and potential risk of AMR.

Key words: Antimicrobial, AMR, PigINFO Bio, benchmarking, Japan

Antimicrobials in livestock farming: reducing their use while limiting health and socioeconomic risks into low and middle-income countries

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ABSTRACT

Objectives: While there are numerous measures restricting the use of antimicrobials on livestock farms in industrialized countries, this is not the case in southern countries. On the contrary, their use has been boosted by the growing demand for animal protein and the boom in intensive livestock farming. One need to decipher the complexity and impacts on small farmers of the phenomenon of antimicrobial resistance and of the global strategies planned to fight it.

Material and methods: To address the complexity of these issues, we drew on data obtained by research teams in the South and the North, which reflect the diversity of agricultural contexts and livestock farming systems. This research focuses on the implementation of technical solutions, methodological approaches and innovative surveillance mechanisms in different areas.

Results: In both the North and the South, the major challenge is to implement policies enabling the reduction and rationalisation of antimicrobial use, through a set of actions and associated regulatory measures. However, it should be noted that the effective application of these policies is dependent on one key factor: minimising adverse health and socioeconomic impacts on the standard of living for farmers, especially in the most vulnerable regions.

Conclusion: We suggest lines of research aimed at reducing or rationalizing antimicrobial use, in the interests of people in the most vulnerable regions and through a 'One Health' approach calling for interdisciplinary efforts on subjects ranging from genes to the human society in its environment.

A comparison study of the antimicrobial prescription patterns in organic and conventional pig herds in Denmark

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ABSTRACT

Objective: The objective of the study was to look for differences in antimicrobial prescription patterns between organic and conventional pig herds.

Materials and methods: Data from the national database VetStat covering sales of veterinary prescription medicine for all pig herds in Denmark were extracted for the year 2016 Information regarding herd type and number of animals were extracted in the Danish Central Husbandry Register (CHR).

Results: In 2016, there were 122 organic pig herds recorded in CHR. This corresponds to nearly 2 % of the total number of herds recorded in CHR. The total number of antimicrobial prescription for organic herds in 2016 corresponded to 133 kg active compound, which is only 0.2 % of the total amount of active compound sold for use in the Danish pig production that year. Similar to conventional pig herds, gastro-intestinal indications also represent the most often used indication in organic pig herd. Compared with conventional pig production, a larger proportion was prescribed for respiratory indications in organic weaners and for arthropathy indications in organic finishers. According to Danish legislation, organic weaner and finisher pigs are only allowed to be treated once in their live span. If any medicine is left after a treatment course, it cannot be re-prescribed as in the conventional pig herds. The farmer has the obligation to return the rest of a medicine to the pharmacies for destruction. There are no official registration of the amount of returned medicine in Vetstat, why there may be a margin of error when reporting antimicrobial use in organic pig farms.

Conclusion: A project is now investigating this by evaluating actual usage data collected from the organic pig farmers. The next step will be to include meat inspection data to evaluate whether the prescription patterns can explain the lesions found at slaughter.

Key words: Pigs, organic farmning, register data, antimicrobial use, meat inspection

Whole-feedlot administration of direct-fed microbials to reduce fecal shedding of *Escherichia coli* O157:H7 in commercial feedlot cattle during period of high transmission

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ABSTRACT

Objective: Direct-fed microbials (DFM) are microorganisms fed to cattle that, via competitive exclusion, can inhibit the growth of harmful bacteria. The objective of the study was to compare fecal shedding of *Escherichia coli* O157:H7 in finishing cattle pens from commercial feedlots that do and do not feed a DFM.

Materials and methods: Twenty feedlots in Nebraska, USA, 10 that administered a DFM and 10 that did not, were enrolled. Cattle in DFM feedlots (BOV) received a *Lactobacillus animalis* LA51 and *Propionibacterium freudenreichii* FP24 10^9 CFU/g product (Bovamine Defend®, Chr. Hansen) from day 1 of finishing phase to harvest. Cattle in control feedlots (CON) did not receive <u>any</u> DFM. Twenty-two pen-floor fecal samples were collected from 3 pens in each feedlot, and each feedlot was sampled 3 times in summer 2017. Samples were subjected to cultural procedures for detection and quantification of *E. coli* O157.

Results: The association between DFM status and the within-pen prevalence of *E. coli* O157 significantly ($P < 0.05$) differed by sampling visit. During the second visit, when the prevalence of *E. coli* O157 was the highest across feedlots, pens from BOV feedlots had a lower prevalence of *E. coli* O157 than pens from CON feedlots (Figure 1). Only 0.5% of samples (6/1,320) were enumerable: 5 of the 6 samples belonged to pens from CON feedlots.

Conclusion: Whole feedlot administration of a DFM would be beneficial when implemented during periods of high transmission, for reducing the pathogen load of cattle entering slaughter plants.

Key-words: Food safety, Direct-fed Microbials, *E. coli* O157, feedlot Cattle
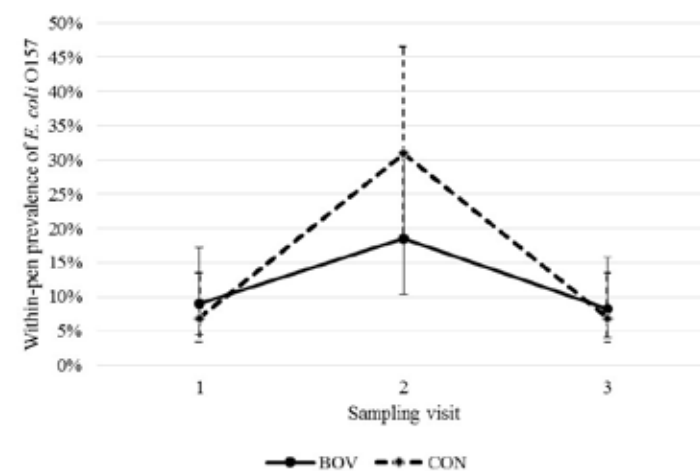
Figure 1. Within-pen prevalence of *E. coli* O157:H7 by DFM status and sampling visit

Note: BOV = DFM; CON = control (No DFM)
Error bars represent 95% Confidence intervals

Estimating antimicrobial usage in Scottish beef and dairy herds from veterinary sales data

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ABSTRACT

Objective: Our objective was to make use of sales data from a Scottish veterinary practice to estimate the quantities of antimicrobial sold and to relate these estimates to targets set by the Responsible Use of Medicines in Agriculture Alliance (RUMA) Task Force.

Materials and methods: Data were collected anonymously from the veterinary practice on the pharmaceutical products sold to 75 beef or dairy farms and linked anonymously to demographic data for the animals present on each farm. A sequence of filters was run in series and parallel to identify the sales records that related to sales of antimicrobial products. For each sale the total weight of antimicrobial active ingredient was estimated by dividing the sales price for each sale by the estimated unit price.

Results: Overall results were assessed as to whether they made sense, which they did: the herds designated as dairy were larger than those designated as beef; larger herds tended to purchase more antimicrobials than smaller herds; the amount of antimicrobial sold per kg of animal (Population Correction Unit) was greater in dairy herds than in beef herds. These observations are indicative of successful processing of the raw sales data. The results suggest that the dairy herds are, on average, below proposed total usage targets set by RUMA for the dairy sector, whereas the beef herds, on average, may require some management changes to achieve their sector targets.

Conclusions: it is possible to get apparently sensible approximations of antimicrobial usage data from veterinary sales data and these are useful in assessing the potential for achieving targets.

Key words: Beef, dairy, cattle, antimicrobial, resistance, usage, Scotland

Detection of *Brucella* spp. in milk from various livestock species raised under pastoral production systems in Isiolo and Marsabit counties, northern Kenya

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ABSTRACT

Objective: We investigated the presence of *Brucella* spp. in milk from various livestock species in pastoral households in Isiolo and Marsabit Counties, northern Kenya.

Materials and methods: A total of 622 milk samples were collected in a cross-sectional survey that involved 182 households. Up to 379 samples were collected directly from lactating animals (51 cattle, 7 sheep, 317 goats and 4 camels) while 179 samples were from milk pooled of cattle, sheep, goats, camels and mixed species in households. Questionnaire surveys were also done to determine milk consumption patterns in the target households.
All the samples were screened using real-time PCR (qPCR) for detection of *Brucella* spp. as well using *B. abortus* and *B. melitensis* specific assays. Cattle milk samples were also screened using a milk indirect ELISA kit to detect anti-LPS *Brucella* antibodies. Risk of human exposure was determined based on the prevalence estimates and whether or not milk was boiled before consumption.

Results: *Brucella spp.* DNA was detected in fifteen (n=15, 2.7%) samples and thirty-five antibody-positive cattle were detected (n=35, 37.6%). The prevalence of qPCR *Brucella* spp. was higher in Isiolo (4.7%, 95% CI: 2.5 – 7.9) than in Marsabit (0.7%, 95% CI: 0.1 – 2.5) (Chi²=8.7, p=0.003). qPCR positives were detected in 3.4% (14/418) of the goats sampled and in 1.1% (1/93) cattle. *B. abortus* was detected in 11 goats and *B. melitensis* in 3 goats and 1 cattle, suggesting cross-transmission of brucellosis in herds. The demonstration of *Brucella* spp. in milk and the consumption of raw milk demonstrates considerable risk of exposure.

Key words: *Brucella* spp., milk ELISA, Kenya, pastoral

Bayesian risk assessment model of human cryptosporidiosis cases following consumption of raw Eastern oysters (*Crassostrea virginica*) contaminated with *Cryptosporidium* oocysts in Prince Edward Island, Canada

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ABSTRACT

Objective: *Cryptosporidium* spp. have been associated with foodborne infectious disease outbreaks; however, it is unclear to what extent raw oyster consumption poses a risk to public health. Control of *Cryptosporidium* in shellfish harvest seawater in Canada is not mandatory. Risks of human infection and illness from exposure to oysters contaminated with *Cryptosporidium* oocysts were assessed in a Bayesian framework.

Materials and methods: Three data sets were used: counts of oocysts in oysters harvested in Approved, Restricted, and Prohibited zones; oocyst elimination rate from oysters exposed to oocysts in laboratory experiments; and oocyst infectivity (extracted from the literature to build a dose-response model). Eighteen scenarios were assessed according to number of oysters consumed in a single serving and different relay times.

Results: The median probabilities of infection and illness were zero for all scenarios. However, probabilities at the 95th percentiles were 75% (infection) and 39% (illness) for all scenarios with short relay time (≤30 days). These probabilities were reduced by 39% and 49% when extending the relay time to 60 days. The 14-day relay period established by Canadian authorities for harvesting in Restricted zones seems prudent to eliminate fecal coliforms but not *Cryptosporidium* oocysts, which can remain viable in the oyster for over a month. Extending relay periods of 14 and 21 days for oysters harvested in Restricted zones to 60 days will likely decrease the risk of illness, but these estimates were made from highly uncertain information. The highest risk was found for oysters that originated in Prohibited zones.

Conclusion: Our findings suggest that *Cryptosporidium* oocysts are a potential cause of foodborne infection when raw oysters are consumed in Prince Edward Island. We discuss data gaps and limitations of this work in order to identify future research that can be used to reduce the uncertainties in predicted risks.

Key words: *Cryptosporidium* spp., Eastern oyster, Bayesian, risk assessment, dose-response model

Prevalence and characterisation of Shiga toxin-producing Escherichia coli in sheep and goats from South Africa

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ABSTRACT

Objective: Shiga toxin producing Escherichia coli (STEC) are zoonotic foodborne pathogens that have been associated with mild to severe diarrhoea, haemorrhagic colitis and complications including the haemolytic uremic syndrome in humans. Ruminants are considered the main reservoir of STEC and Shiga toxins (stx1, stx2) are the major virulence factors of STEC. Additional virulence markers are intimin (eaeA) and enterohaemolysin (ehxA). The objective of this study was to investigate the occurrence and characterise STEC from the faeces of 81 sheep and 65 goats using culture and PCR. Further genetic characterisation was carried out on 35 and 37 STEC isolates that were recovered from goats and sheep respectively.

Materials and methods: STEC were recovered through enrichment on EC broth and culture and ChromAgar and Drigalski Agar. STEC were confirmed by multiplex PCR which targeted the *stx1, stx2, eaeA* and *hlyA* genes.

Results: PCR revealed that 54.1 % (44/81) of sheep and 66.1 % (43/65) of goats carried STEC. Among the 35 goat isolates, 37 % carried stx1 only, 32 % had stx2 only and 31 % were both stx1 and stx2 positive. Among the 37 sheep isolates, 46 % carried the stx1 only, 19 % were positive for stx2 only and 35 % harboured both stx1 and stx2 concurrently. Only sheep isolates carried the eaeA gene. The ehxA gene was present in 78 % and 86 % of sheep and goat isolates, respectively.

Conclusion: In conclusion, most STEC isolates carried stx1, stx2 and ehxA but lacked eaeA, a major STEC virulence factor in human disease. These findings are evidence that sheep and goats in South Africa are a reservoir of STEC. Further work on the characteristics and epidemiology of STEC is needed to elucidate the role played by STEC from goats and sheep in human disease.

Key words: Shiga toxin, E. coli, goats, sheep

Framework for the economic assessment of the antimicrobial use and resistance complex for the livestock sector in South East Asia

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ABSTRACT

Objectives: Antimicrobial resistance (AMR) is influenced by antimicrobial use (AMU) in the human and animal health sectors, exerting selection pressure on pathogen populations that encourage the development of resistance and exchange of resistance genes. The scale of AMR in South East Asia remains unknown, however, studies suggest that it is a major issue in both human and animal health.

Materials and methods: Structured farmer interviews and the collection of antimicrobial packaging were used to understand antimicrobial use in the poultry and pig sectors in Vietnam, Thailand and Indonesia. The research had a particular focus on understanding the economic costs and benefits of AMU on small-scale commercial farm and other market chain stakeholders.

Results: These case studies have provided baseline data on the quantity of antimicrobials used in livestock, antimicrobial classes used, economic drivers for use and perceptions of producers on AMR. For example, antimicrobial use was found to be high on commercial pig farms in Vietnam with frequent reported use of the World Health Organisation highest priority critically important antimicrobial classes and antimicrobials routinely used in combinations. Farmer awareness of what constituted an antimicrobial was poor and they perceived a low risk to human health from AMU in pigs. The study identified the importance of stakeholder support and institutional support at all levels of the market chain, particularly the integrator companies who contract directly with farmers, produce and market feed and provide technical and disease and production management support.

Conclusion: The case study results provide insight into AMU behaviours in pigs and chickens in South East Asia. These data may form the basis of further research to inform policy makers in supporting economically sustainable production systems, with minimum risk from AMU and which focus on food safety. The data collection framework is described and is available for use in other countries.

Key words: Antimicrobial resistance, South East Asia, pig and poultry sectors, economic analysis

Simultaneous human and animal symptom surveillance in Yao and Danamadji, Chad

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ABSTRACT

Objective: Chad faces, as many Sub-Saharan African countries major difficulties in providing adequate health services for rural populations. Community members live in close contact with their animals and are thus, under high risk of being infected with transmissible diseases. To improve the health of humans and animals in these populations, understanding the most common symptoms and their concurrent occurrence in humans and animals is crucial. The objective of this study is to estimate the frequency of symptom occurrences in humans and animals in Yao and Danamadji, Chad.

Materials and methods: Swiss and Chadian researchers visited villages and nomad camps selected by a randomized cluster sampling. Interviews were conducted using the KoBoCollect application and community members were asked – in addition to demographic information – about the perceived frequency of cough, diarrhea, skin problems, fever, weight loss, weakness, vertigo, pale mucosa, swollen joints, ulcer and abnormal behavior, that occurred among humans and animals in their households over the past 12 months and past cold, hot and rainy season.

Results: Eighty-nine interviews were conducted in total. Interviewees reported 1373 household members and 9013 animals. Over the past year, in humans fever was reported most frequently (720 times), whilst among animals it was cough (1912 times). Regional, seasonal and species related cluster analysis will be further conducted.

Conclusion: The resulted frequency of symptom occurrences in humans and animals in different seasons will be used as a baseline to estimate the sensitivity of a newly implemented One Health syndromic surveillance system in these regions.

Key words: Syndromic surveillance, interviews, Chad, animal-human transmission

Zoological Parks are underutilized insect surveillance opportunities

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ABSTRACT

Objective: Zoological parks contain a surprising diversity and abundance of pest insects and disease-vectors of human and animal diseases that are neither monitored nor controlled by commercial pest control operators. The objective of the study was to assess if zoos can be used as surveillance tools to quantify entomological risk to the surrounding community using a one health approach.

Materials and methods: Insects were collected day and night for 3 consecutive days, each month, for 8 months during spring, summer, and fall, using carbon dioxide baited Centers for Disease Control ultraviolet light traps and BG-sentinel traps, placed at the Sunset Zoo in Manhattan, Kansas (USA). A total of 22,652 mosquitoes and 8,399 female biting flies were collected representing 52 species and 6 families. Collections consisted of 20 mosquito (Culicidae) species, 21 biting midges (Ceratopogonidae: *Culicoides*), and 7 black fly (Simuliidae) species, among other blood-feeding species. These included 3 new state records of *Culicoides* and one of Simuliidae.

Results: The Sunset Zoo consists of 26 acres with 300 captive animals pertaining to more than 100 animal species, with the zoo insect fauna representing 37%, 72%, and 41% of the total mosquito, biting midge, and black fly diversity, respectively, of the state of Kansas. Many of the collected blood-feeding species are known disease vectors to mammals (e.g., *Dirofilaria* and Zika) and birds (e.g., *Haemoproteus* and West Nile) or cause considerable harm as pest insects at high abundance.

Conclusion: In conclusion most commercial pest control companies operating at zoos do not apply targeted species-specific control measures such as insect larval habitat removal. The diversity and abundance of biting insects provide a unique opportunity for disease vector surveillance, which through informing targeted interventions, can improve the health and welfare of animals and the larger community.

Evaluation of oral bait drop to access dogs for rabies vaccination in Goa, India

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ABSTRACT

Objectives: Rabies causes around 20,000 human deaths annually in India, predominantly through bites from rabies-infected dogs. To achieve elimination, WHO recommends annual vaccination of at least 70% of the dog population. India has a large population of free roaming dogs that cannot be readily restrained for vaccination which hampers attempts to achieve high vaccination coverage. This proof-of-principle study investigated the feasibility of accessing dogs using oral bait in different land types in Goa State.

Materials and methods: The study took place in February 2018 in Ponda Taluka, which was divided into 45 zones and stratified by land type. Four vaccination teams were trained in both Oral Bait Drop (OBD) and Catch Vaccinate Release (CVR) methods and randomly assigned working zones on each day. Teams that spent week one doing OBD switched to CVR on week two and visa-versa. OBD teams comprised of two people riding a two-wheel moped, while CVR teams comprised of seven people on a truck. Dogs that could be handled were vaccinated parenterally in both methods, whilst inaccessible dogs were given blister baits containing no vaccine (OBD) or caught and vaccinated parenterally (CVR). Mission Rabies App was used to record number of dogs accessed and total seen. Multivariable logistic regression was used to estimate the effect of each method on the proportion of sighted dogs accessed each day.

Results: Preliminary results show that a higher proportion of dogs can be accessed by OBD compared to CVR (OR 1.64, 95% CI 1.45-1.87), after correcting for team and land type. The average number of dogs vaccinated per person per day was 32 (95% CI 28-37) using OBD compared to 9 (95% CI 7-10) when using CVR.

Conclusion: A combined oral bait/parenteral vaccination approach may help boost vaccination coverage in areas where administration of parenteral vaccination is logistically challenging.

Roaming and social behavior of free roaming dogs

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ABSTRACT

Objective: Dogs and humans both benefit from a close relationship. However, this relationship can become detrimental, particularly in case of zoonotic disease transmission. For example, 99% of the human rabies cases are caused by dogs and around 60 000 people still die of rabies every year, especially in low-income countries in Asia and Africa. Often, recommendations for control strategies for canine diseases do not take into account the heterogeneity among dogs, which might be very influential for disease spread. The objective of this project is to identify factors influencing dog ecology parameters and investigate their influence on disease spread.

Materials and methods: We studied the behavior of dogs living in villages and nomadic camps in rural areas of Chad, one of the study sites on three continents. To collect data about dog's movements and contacts, we collared 107 dogs with Georeferenced Contact Sensors (GCS) associating a GPS and a contact sensor. In addition, we performed interviews to collect data on dog-related, human-related and environmental factors. We analyzed the home range (HR) of the sampled dogs and used social network analysis for the contact data.

Results: Preliminary results show that the core HR of the dogs varied from 0.2 to 1.7 ha. The number of proximity events recorded varied from 0 to 228 with an average of 29 events per day for dogs living in different households and from 37 to 2091 with an average of 766 events per day for dogs living in the same household.

Conclusions: The results of this study highlight the heterogeneity in terms of roaming and social behavior between dogs living in the same population. The study of the factors influencing their behavior would be of upmost importance for understanding the transmission dynamics of infectious diseases and for informing evidence-based policy-making.

Key words: Dog, ecology, rabies, network, GPS

Emergence, Prevalence and Diversity of Rodent Zoonotic Viruses in the United Kingdom

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ABSTRACT

Objectives: Rodents are the most abundant land mammal in the United Kingdom and can harbour a variety of pathogens, including zoonotic viruses that could be detrimental to human health. This study aimed to further understand the emergence, prevalence and diversity of these rodent zoonotic viruses.

Materials and Methods: Samples from brown rats (*Rattus norvegicus*, n=61), house mice (*Mus musculus*, n=110), wood mice (*Apodemus sylvaticus*, n=43), bank voles (*Myodes glareous*, n=56), field voles (*Microtus agrestis*, n=23), red squirrels (*Sciurus vulgaris*, n=21) and grey squirrels (*Sciurus carolinensis*, n=12) were collected from a range of locations around the UK which included pig farms, dairy farms, rural sites and urban dwellings. Using diagnostic PCR assays Hantaviruses, Lymphocytic choriomenigitis virus (LCMV) and Hepatitis E virus (HEV) were screened for in these rodents. Sanger sequencing and phylogenetic analysis performed.

Results: This study identified two species of Hantaviruses circulating in British rodents; Seoul virus (SEOV) in brown rats and Tatenale virus (TATV) in field voles. LCMV RNA as detected in the livers of 21 house mice, 2 brown rats, 1 wood mouse and 2 bank voles. For the first time in the UK, Hepatitis E viral RNA (rat HEV variant) was identified in 8 brown rats.

Conclusion: There is a diverse range of pathogens currently circulating in the British rodents. With some (SEOV and LCMV), circulation in wild rodent populations may pose a direct risk of zoonotic transmission to people. However, with others such TATV and rat HEV, the zoonotic potential is currently unknown and further study of these viruses is required. Co-infections with multiple viruses were also observed in rats. These findings could be used to increase understanding of transmission dynamics, viral biology and understand the risk to public health.

Regional approach to ending pandemics: South Asia One Health disease surveillance network

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ABSTRACT

The world is experiencing increasing events of emerging and re-emerging infectious diseases, and about 70% of emerging infectious diseases (EID) originated in animals. Furthermore, increasing incidence of antimicrobial resistance (AMR) has been recognized as a serious public health and animal health threat. The challenges of EIDs and AMR require a One Health approach that supports a holistic, multisectoral, coordinated and collaborative network, not only at a country level but at a regional level. Several regional disease surveillance networks have been established in Southeast Asia, East Africa, South East Europe, Southern Africa, and Middle East, and recently in South Asia. The purpose of establishing South Asia One Health Disease Surveillance Network are *inter alia*, to facilitate coordination and strengthening of regional capacities for disease surveillance, rapid outbreak detection and response to controlling zoonoses and pandemics at best at a country or regional levels, support development of effective disease surveillance systems, create a common platform for timely sharing of disease information, coordinate and organize training on disease surveillance, outbreak investigation and laboratory diagnoses, and facilitate cross-sectoral and cross-border collaboration to address issues related to transboundary and zoonotic diseases. This presentation will share the vision, purpose, opportunities and expected benefits of establishing this network through the support of ECTAD-FAO and Ending Pandemics of Skoll Foundation. The ultimate goal is to end future pandemic.

Stress and resilience among Canadian farmers: a mixed methods approach

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ABSTRACT

Objective: Farmers worldwide face disproportionately high rates of mental health issues and suicide compared to other occupations. A serious gap in knowledge exists regarding Canadian farmer mental health. The objectives of this study were to: (1) identify factors associated with mental health outcomes (stress, resilience, anxiety, depression, and burnout); and (2) characterize the lived experience of mental health among Canadian farmers and its impacts.

Materials and methods: This project uses a mixed-methods sequential explanatory design. For Objective 1, 2015-2016 data from a national survey of farmer mental health (Jones-Bitton et al.) were used to construct multivariable linear and logistic regression models of the mental health outcomes to explore relationships between demographic variables, lifestyle, self-rated health and mental health variables. For Objective 2, 75 semi-structured, in-depth qualitative interviews were conducted across all factions of agriculture, including all major farming commodities in Canada, and industry, veterinarians, and governmental representatives in agriculture. A thematic analysis of the data is underway.

Results: Pig farming was the only commodity significantly associated with higher levels of perceived stress. Other variables associated with this outcome included female gender, financial stress, and perceived lack of support from family and industry. As resilience increased, perceived stress significantly decreased. Additionally, there was a significant moderator effect of depression and anxiety. Increasing age, self-rated health, perceived support from friends, and lower depression scores were significantly associated with increased resilience scores. Preliminary themes associated with stress and resilience will be discussed.

Conclusion: These data provide a comprehensive understanding of mental health in Canadian farmers. They are also informing the development of culturally-appropriate and evidence-based resources to support farmers, and thus, Canadian agriculture and economy. Building on these results, stakeholder working group meetings with members of agricultural groups are being used to inform the co-development of an agriculture-specific mental health and wellness intervention.

Key words: Agriculture, epidemiology, mental health, mental health, risk factors, mixed methods research

Mapping out socio-economic drivers of antimicrobial usage in poultry farms in Vietnam: a combined Participatory Epidemiology and Q-methodology approach

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ABSTRACT

Objectives: In the Mekong Delta of Vietnam antimicrobials are widely used by poultry farmers to raise their flocks, however little is known about socio-economic drivers and farmers' perceptions on antimicrobial use (AMU). The study aims to identify these drivers and the socio-economic context for this behaviour.

Materials and methods: A total of 27 focus group interviews (Participatory Epidemiology) were conducted on 73 advisers (veterinarians, veterinary drug owners and community animal health workers (CAHWs) and 125 chicken/duck farmers in 5 districts of Dong Thap province. Through these interviews, 46 statements relevant to the subjects' attitudes towards AMU, including the antimicrobials' perceived reliability, practice, costs and impact on flock health, were developed. Those statements were then processed using Q-methodology on two structured populations: (1) Veterinarians, veterinary drug owners and CAHWs (Population 1) (n=26); and (2) Chicken and duck farmers (Population 2) (n=28). The participants were selected according to their work experience and education level. Results were analysed by principal component analysis and factor analysis.

Result: For each of the two populations three discourses were identified, representing 48-50% of the total variance. Consensus points for Population 1 were: (a) antimicrobials are always given as the first choice of treatment by farmers when the flock gets sick; (b) antimicrobials are preferentially given at the first week of chicken life to prevent disease; (c) AMU is more costly than the use of vaccines. Consensus points for Population 2 were: (a) Good quality drugs were perceived to have a relative higher price than low quality counterparts. (b) Controlling disease using antimicrobials is more costly than using other biosecurity methods.

Conclusion: The methodology presented here allowed obtaining meaningful insights into perceptions of the different stakeholders involved in prescription/usage of antimicrobials in poultry farming. This knowledge can contribute to improving the success of intervention strategies aimed at curbing indiscriminate use of antimicrobials in the region.

Key words: Antimicrobial use, Q-methodology, participatory epidemiology, farmers' perception

Risk perception and practices regarding the antibiotic use in pigs and poultry farms in Madagascar - A Q method approach

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ABSTRACT

Objective: Antimicrobial resistance (AMR) is a One Health issue that needs to be tackled worldwide. In order to implement effective communication strategies in Madagascar, practices and perception related to antimicrobial use at smallholder farms level (AMU) need to be better understood. Our study aims at identifying patterns of practices and perception of usage of antimicrobials or their alternatives amongst pigs/poultry farmers, and drug sellers in the province of Imerintsiatosika.

Materials and methods: We applied a semi-qualitative approach called Q methodology to explore subjectivity of individuals. Thirty breeders and 30 drug's sellers were chosen according to socio-demographic criteria. A Q-set of 40 statements for breeders and 46 for drug sellers about AMU, related risk and alternatives were produced from semi-structured interviews. We then asked our participants to rank these statements through 7 grade scales from -3 (totally disagree) to +3 (totally agree). These Q-sorting were finally analysed by factor analysis and principal component analysis.

Preliminary results: The semi-structured interviews show that preventive measures are a common practice in poultry farming but not for swine. The awareness about AMR and the link animal/human health is higher among veterinarians and technicians than other drug's sellers and breeders except for some well-educated farmers. In most of the case, economic concerns are prior to antibiotic resistance ones.

Expected results: A few factors representing clusters of similar viewpoints shared by a group of people will be obtained and consensus and distinguishing statements analysis will help to determine differences and similarities between discourses. Socio-demographic factors which influence the opinions will also be determined.

Conclusion: This study will contribute in devising suitable educational interventions for national stakeholders, tailored according to their earlier held knowledge, beliefs, capabilities and experience.

Key words: Antibiotic resistance, attitudes, drug sellers, participatory epidemiology

Investigating practices and attitudes of poultry and pig farmers and vet drug suppliers towards antibiotic usages and alternative practices in Nan Province, Thailand

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ABSTRACT

Objective: Although antimicrobial usages (AMU) in veterinary medicine have brought about numerous benefits to animal health worldwide, their overuse and misuse have led to antimicrobial resistance (AMR) which is currently one of the most serious threats to global health. These poor practices are still done for different purposes in animal husbandry in Thailand including treatment, prevention of diseases, or enhancement of animal production. To achieve a more rational use of antimicrobials among farmers, it is important to understand on one hand the practices of use and on the other attitudes of farmers and drug sellers regarding the risk of resistance along with their beliefs regarding alternative practices.

Materials and methods: The study was conducted using a qualitative approach, the Q methodology which was divided into five steps: (i) generation of opinion statements; (ii) selection of the opinion statements; (iii) selection of participants; (iv) sorting of statements by participants (Q sorting) and in-depth interview; and (v) statistical analysis using principle component analysis and factor analysis.

Results: Regarding the diversity of practices and attitudes towards antimicrobials uses among two distinct populations; farmers and veterinary drug suppliers were categorized into different discourses which were influenced by variables such as production type and geographic location (for farmers) or education level and role/ responsibility (for veterinary drug suppliers). Consensual points were identified through those discourses.

Conclusion: This study illustrated critical elements which influence farmers to use antimicrobials. Recommendations were generated for farmers to achieve a more rational use of antibiotics and in order to strengthen the health regulation to reduce inappropriate dispensing of antibiotics by suppliers. Moreover, some alternative practices and ethno-veterinary knowledge was identified as interesting to be promoted.

Key words: Q methodology, participatory epidemiology, antimicrobial resistance, livestock, qualitative analysis

Antimicrobial resistance in intensive poultry and milk production in South Africa: from historical data analysis to the monitoring of the use of antibiotics

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ABSTRACT

Objectives: The gross income generated by animal production industries in South Africa was estimated at R80.8 billion (US$6.86 billion) for 2012. The contribution from poultry meat was R30 billion with an addition of R8 million from eggs. The milk inductry contributed for R11 billion. These industries represent more than 50% of the contribution of animal products to the gross income. Regular diseases outbreaks impact negatively the growth and development of these livestock industries. The incidence of specific diseases within South Africa plays a decisive role in the selection of antimicrobials to be administered and judicious use of antimicrobials is paramount. Avian pathogenic *Escherichia coli* causes major losses in the poultry industry and became the predominant bacterial disease due to the increased intensive confinement housing. In addition *E.coli* infections are often secondary to viral disease. Standard practices currently employed in South Africa are to start prophylactic treatment to prevent secondary bacterial infection whenever a sanitary problem occurs in poultry. In commercial dairy herds, somatic cell count higher than 400 000 cells/ml leads also to the treatment of sub-clinical mastitis involving mainly *Stapylococcus aureus*.

Material and methods: Time series analysis on *E. coli* and *S. aureus* resistance over a perid of 10 years in relation with antibiotics use were performed Seasonal and geographical patterns were also highlighted for some specific antibiotics family using general linear mixed models.

Results: Various temporal trends have been highlighted according to the different antibiotics allowed us to better understand the farmers practices leading to these resistance. Seasonal and regional patterns may vary according to the antibiotics that could be related to climatic variation.

Conclusion: This better understanding of the trends and patterns of antimicrobial resistance in intensive farming in South Africa provided room for advising farmers practices on the monitoring of antibiotics but chalenged also research in terms of antimicrobial resistance drivers.

Nationwide prevalence of *E. coli* O157:H7 and shiga toxin producing *E. coli* (STEC) in Brazilian beef, 2015-2016

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ABSTRACT

Objective: A nationwide baseline survey was conducted in Brazil by the Federal Inspection Service, from the Ministry of Agriculture, Livestock and Food Supply (MAPA), to estimate the prevalence of *E. coli* O157:H7 and STEC (O26, O45, O103, O111, O121 and O145) in beef.

Materials and methods: The study was conducted from 2015 to 2016. The samples were collected in 82 abattoirs under Federal Inspection Service (SIF). The establishments were classified according to bovine slaughtered per day in: Small (S); Medium (M) and Large (L). The sampling involves collecting 60 thin slices from the external surface of beef tissues randomly selected, comprising at least 325 grams of beef trimmings. A total of 1.920 samples were analyzed in official laboratories (LANAGRO) using MLG 5 analytical method.

Results: The results obtained were one *E. coli* O157:H7 positive sample and five non-O157 STEC positive samples. The non-O157 STEC serotypes detected were O45, O26, O111, O103.

Conclusion: This information demonstrates the good quality and safety of the Brazilian beef and emphasizes the importance of the pathogen control programs to evaluate the dressing procedures and slaughter controls.

Innovation warning system approach for meat inspection in poultry slaughterhouses

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ABSTRACT

Objective: European Union recommends implementing alternative methods for meat inspection using risk analysis principles. To this aim, we proposed an innovative risk-based approach to poultry meat inspection based on a two-level warning system: information flow from observers to controllers.

Materials and methods: An experiment on a sample of slaughterhouses was carried out for one year in 2012-2013. All slaughtered flocks were controlled according to this warning system, and all data were continuously recorded (indicators, events, actions).

Results: The analysis included 2,505 flocks, representing more than 17 million poultry. Half of the flocks showed at least one of the indicators on alert. By task of meat inspection, the percentage of flocks on alert was divided as follow: around 20% of flocks were on alert after the food chain information analysis or during the *ante mortem* examination, and 28% of flocks were on alert during the *post mortem* examination. Among the flocks on alert, around 90% of alerts were detected by the observers, and well received by the controllers. Our results reveal opportunities for improvement: review of some warning criteria for a better understanding, communication optimisation between stakeholders, and enhanced feedback.

Conclusion: In conclusion, this warning system guarantees the achievement of sanitary meat inspection thanks to a system based on risk analysis, in which tasks are shared under the supervision of the controllers and skills and knowledge are optimised. The system is efficient thanks to its ability to detect alerts early, which is ensured by adapted warning criteria, and moreover it enables harmonised practices.

Key words: poultry, meat, sanitary inspection, alert system

Serotypes and antimicrobial resistance of *Salmonella* spp. isolated from the smallholder pig value chain in Hung Yen and Nghe An provinces, Vietnam

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ABSTRACT

Objective: To identify the frequency and distribution of serotypes and antimicrobial resistance (AMR) of *Salmonella* spp. isolated from the smallholder pig value chain in Hung Yen and Nghe An provinces, Vietnam.

Materials and methods: A total of 293 *Salmonella* spp. positive samples, isolated from pork and environment specimens, were analyzed for serotypes and AMR. *Salmonella* serotyping and antimicrobial susceptibility of *Salmonella* serotypes (against 12 drugs) were performed by using a micro-titer agglutination test following the Kauffmann-White scheme, and the agar diffusion assays followed the guidelines of the CLSI, respectively.

Results: Thirty *Salmonella* serotypes were identified from all sample types. The predominant serotypes were *S.* Typhimurium (37.2%), *S.* Derby (17.7%), *S.* London (10.6%) and *S.* Rissen (5.1%). *S.* Typhimurium found on pig carcass and in pork were 45.9% and 37.1%, respectively, while only *S.* Derby was found in all sample types along the pig value chain. Antimicrobial susceptibility test results indicated that 64.2% of the isolates were resistant to ampicillin, 60.8% were resistant to tetracycline, 60.1% were resistant to chloramphenicol, and 56.3% were resistant to trimethoprim. Low resistance to nitrofurantoin (7/293, 2.4%) and ceftriaxone (43/293, 14.7%) was observed. The proportion the isolates were resistant to three or more was 52.6%. Resistance to gentamycin (54.5%), piperacilin (53.0%) and ciprofloxacin (51.1%) by *S.* Typhimurium were 54.5%, 53.0%, and 51.1%, respectively.

Conclusion: Our findings underline the need for better hygiene practices along the smallholder pig value chain to reduce *Salmonella* contamination. The high level of *Salmonella* AMR also urges the proper use of antimicrobials and control programs of the spread of this resistant foodborne pathogen.

Key words: Salmonella, serotype, pork, antibiotic resistance, Vietnam

Freshwater aquaculture and dissemination of antibiotic resistance in watershed in Chile

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ABSTRACT

Objective: Point sources such as wastewater treatment plants, terrestrial agriculture, and aquaculture, release antibiotic resistance genes (ARG) to the aquatic ecosystem. However, results from a systematic review conducted by our team showed that increases of ARG in the natural environment associated with specific point sources have not been quantified, and emphasized the need for epidemiological study designs and analytical tools. Based on those results, the goal of this study was to evaluate the role of trout farms on the increase and dissemination of ARG in adjacent rivers.

Materials and methods: We collected river sediment samples upstream and downstream from 5 freshwater trout farms longitudinally in southern Chile. After DNA extraction, we used a microfluidic qPCR approach to quantify 48 ARG covering different mechanisms of resistance. We conducted surveys to obtain information about farm management practices including antibiotic use. Spatial data on relevant variables such as other point sources was gathered, and linear mixed models were used for the data analysis.

Results: A total of 97 samples were collected. Surveys revealed that florfenicol and oxytetracycline were the antibiotics of choice, and their amounts varied among the farms. Across all farms, we detected 42/48 ARG. Of those, the most abundant and significantly increased at downstream sites (expressed as: mean (95% CI) in log copies normalized to 16S) were: *intl1* 2.5 (1.85, 3.19), *qacG* 2.31 (1.66, 2.96), *sul1* 2.93 (2.14, 3.72), *strB* 2.2 (1.67, 2.73), *tetA* 2.12 (1.38, 2.88), and *tetC* 2.97 (2.33, 3.59). There was no significant difference across time points or between farms, but there was a trend of higher ARG levels in farms with higher antibiotic use.

Conclusion: This study combined careful study design, a cutting-edge molecular approach, and statistical methods to advance our understanding of how AMR disseminates in the natural environment from point sources, which can ultimately affect human, animal, and ecosystem health.

Key words: Antibiotic resistance genes, trout, Chile, point source, linear mixed model

Identifying opportunities to improve the effectiveness in rabies control in Thailand using geographical analysis

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ABSTRACT

Objective: A primary goal of our study was to generate rabies risk maps in Thailand which may inform program planning and provide opportunities to prioritize investments

Materials and methods: Upon a literature search to identify risk factors commonly associated with dog-mediated rabies, the presence of global and local spatial autocorrelation in the distribution of animal rabies was evaluated. Then, a multivariable logistic regression model was used to investigate the association between the number of animal rabies cases and available covariates at the sub-district level.

Results: Preliminary results suggest that the number of dog bites, the density of dog population (both owned and stray), the density of stray cat population, human population density, and the number of Buddhist temples were significantly associated with the number of animal rabies cases. Moreover, the regression residuals indicated statistically significant spatial dependence, and therefore a conditional autoregressive model was fit. Predicted risk of animal rabies varied largely by sub-district, with 2,859 (35%) sub-districts at high-risk (Figure 1).

Conclusion: Multiple significant risk factors were recognized. In subsequent steps, human rabies and post-exposure prophylaxis data will be incorporated to further characterize the risk of rabies and to allow an effective communication with stakeholders.

Key words: conditional autoregressive model, dog-mediated rabies, risk factors, risk maps
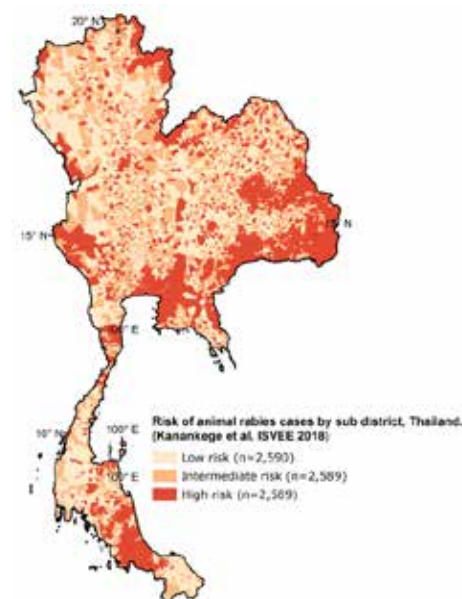
Figure 1. Map indicating the risk of animal rabies by sub-district in Thailand. High risk (estimated number of cases = between 2 to 7), Intermediate risk (estimated number of cases = 1), and Low risk (estimated number of cases <1). The number of sub-districts under each risk category are listed.

Ranking of consumer exposure to antibiotic resistance genes from retail meat

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ABSTRACT

Objective: Antimicrobial resistance genes are present in diverse ecosystems and can be transmitted across various pathways, including food. The relative importance for public health of each pathway is currently uncertain. Yet undisputedly, the cumulative exposure of consumers to bacteria and genes via food is substantial. Therefore, the relative contribution of this pathway deserves priority in terms of research efforts. Using data from a multi-European project, an exposure assessment was conducted for a range of animal-derived foods.

Materials and methods: The analysis is conducted based on PCR results for selected resistance genes in five retail meat categories. However, many information gaps are likely to be present regarding the impact of such exposure on public health outcomes. A stochastic model was developed in order to quantify the relative exposure to an ARG, tet(W), through food consumption. The model was implemented using data from nine European countries: Belgium (BE), Bulgaria (BG), Denmark (DK), France (FR), Germany (DE), Italy (IT), Poland (PL), Spain (SP), the Netherlands (NL). Prevalence and abundance of relevant genes were obtained from descriptive analysis of preliminary qPCR data. The food products sampled in the selected countries at retail were pork, chicken, turkey, veal and trout. These food products were assessed as sources of exposures.

Results: Exposure varied considerably between food sources and was also significantly influenced by consumption patterns. Highest exposures were recorded for poultry and pork.

Conclusion: This study tackled the need of quantifying the exposure to ARGs of the human population through food consumption. It ranked the relative human exposure to genes through several retail meat products in nine European countries. The health consequences of this exposure was not quantified and remains unknown. The qPCR methodology used in this study needs further development and standardisation. qPCR data could potentially serve as a safety indicator for food hygiene and could help to prioritise risk management practices in the production chain.

Key words: Food safety, risk assessment, molecular epidemiology

Patterns of antimicrobial usage reduction in French rabbit farms - a trajectory analysis

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ABSTRACT

Objectives : Since 2011, the French professional Rabbit Council has established a plan for reducing use of antimicrobials in rabbit-farming sector. Whereas over the last six years collective reference points have demonstrated the reduction of usage at the sector level, professional rabbit-farming stakeholders have still reported contrasted experiences at the farm level, from individual success to marked difficulties. Our study therefore aimed to analyse on-farm data on a longitudinal perspective, to determine temporal trends in usages at the farm level.

Materials and methods: Data on 167 farms, which antimicrobial usage over the period 2012-2015 in both mother and fattening rabbit successive batches, were compiled, represented and analysed. The indicator used is the Index of Frequency of Treatments with Antibiotics (IFTA), based on counts of actual number of treatment days reported to the rearing period length in days. A joint-variable trajectory analysis was performed to identify particular patterns, considering jointly IFTA values recorded in fattening and mother rabbits.

Results: Regarding antimicrobial usage trajectories, four classes of farms differing by the initial level of usage and the trends in usage over the study period were identified. Three classes exhibited a continuous decrease, more or less marked depending on the year, a fourth class representing ~20% of the farms considered, showed a slight increase of IFTA values during the last years, for both mothers and fattening rabbits.

Conclusion: Individual on-farm records of antimicrobial usages are valuable insights to assess variability between farms at a given time but also regarding antimicrobial usage reduction as a temporal process. Different patterns were identified, including in particular a sub-group of farms which experienced difficulties in reducing persistently antimicrobial usage.

Key words: Antimicrobial usage, trajectory, rabbits

Two risk models to assess the potential for resistance selection and residues transferred to soil due to oral antimicrobial treatments of pigs

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ABSTRACT

Objective: Oral antimicrobial (AM) treatments of pigs can lead to cross-contamination of non-medicated feed with AM residues, and spread of AM residues, or their active metabolites, via manure onto agriculturally used areas. These residues cause a public and animal health concern associated with the potential for selection and dissemination of resistance.

Materials and methods: To analyze these risks, we built a probabilistic model to show the effect of cross-contaminated pig feed on resistance selection, and a model to estimate the amount of AM residues that is transferred to soil via manure application.

Results: Based on the first model, indicatively, an average of 7.76% of sows, 4.23% of piglets and 2.8% of fatteners in Belgium have residues of doxycycline, due to consumption of feed with at least 1% carry-over. Doxycycline concentrations higher than 1 mg/L (corresponding to consumed feed with at least 1% carry-over) can select for resistant porcine commensal *E. coli in vitro* and *in vivo*. Based on the second model, at least 17.96% of the total amount of orally administered AM are present in manure readily applied onto land in a country where common AM are used. This percentage is reduced considering export and processing to around 10%. Considering both models, tetracyclines and especially doxycycline are of most interest because of their high use, association with resistance selection, low bioavalaibility and high stability in manure.

Conclusion: These results highlight that the use of oral group antimicrobials treatments, including AM medicated feed, should be reduced substantially, and can be used to draw recommendations regarding manure treatment and storage duration.

Key words: Antimicrobial residues, medicated feed, manure, pharmacokinetics, risk model

MRSA prevalence amongst commercial pig herds in Australia

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ABSTRACT

Objectives: Livestock-associated (LA) MRSA has been reported as an occupational health issue for piggery workers across the globe. However, the epidemiology and distribution of MRSA has not been investigated in the Australian pig industry. This cross-sectional study aimed to investigate the presence, prevalence and distribution of MRSA in commercial piggeries in Australia with a focus on identifying which sequence types are present. Materials and methods: Sixty nasal swabs from weaners and five environmental samples were collected from each of 26 farms. MRSA was isolated, and antibiotic susceptibility testing was performed against 12 different antibiotics. The presence of *mecA* and PVL genes were confirmed using RT-PCR.

Results: MRSA was identified in 53.9% of the study farms and ranged between 1.6% to 100% on infected farms. On average the prevalence of MRSA carriage in pigs on MRSA affected farms was 40.28% (95% CI 27.03-53.54). MRSA was found in 36.6% of the total environmental isolates. All MRSA positive isolates possessed *mecA*, were typed as ST398, and lacked the *lukF-lukS* genes encoding Panton-Valentine leukocidin. A high prevalence of resistance was observed for tetracycline (100%, CI 99.6-100), clindamycin (94.6%, CI 92.5-96.1), erythromycin (76.7%, CI 73.2-79.9), and amoxicillin-clavulanate (68.3%, CI 64.5-71.9). A lower prevalence was noted for resistance to chloramphenicol (30.5%, CI 27-34.3), ciprofloxacin (25.8%, CI 22.5-29.4), and Quinupristin-dalfopristin (17.2%, CI 14.5-20.4). Only 4.1% (CI 2.8-6.0) of isolates showed resistance to gentamycin and neomycin. Resistance to sulfamethoxazole-trimethoprim was only 1.6% (CI 0.9-3.0). All isolates were susceptible to linezolid.

Conclusion: This study found evidence of the widespread presence of LA-MRSA ST398 amongst commercial piggeries in Australia, as reported in other parts of the world. However, a lower proportion of resistance was noticed for most of the non-betalactam antibiotics tested in comparison with other study findings. No other MRSA strains were found in this study.

Key words: LA-MRSA, CA-MRSA, ST398, antibiotic resistance, Australia

Annual rabies vaccination of 89,000 dogs in urban and rural Malawi – WHO recommended 70% target can be reached

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ABSTRACT

Objective: Canine transmitted rabies is estimated to cause 59,000 human deaths annually. Sub Saharan Africa is disproportionally affected. WHO have set the goal of eliminating dog-mediated human rabies by 2030 through annual vaccination of at least 70% of the dog population. Designing campaigns that will achieve adequate vaccination coverage can be challenging with limited access to expertise and funding. This results in challenges in securing the support and funding to conduct large scale initiatives. This study aims to use data from pilot mass vaccination campaigns in Southern Malawi to estimate the operational requirements for successful vaccination campaigns.

Materials and methods: Data from a combination of door to door and static point vaccination campaigns along with post vaccination surveys in urban and rural Blantyre, Zomba and Chiradzulu districts were analysed. Survey data were used to assess vaccination coverage. A multivariable logistic regression model considered the effect of land cover, poverty, population density and distance to the nearest city on achievement of 70% vaccination coverage in each survey area.

Results: A total of 89,886 dogs were vaccinated in the three districts. Estimates of mean number of dogs vaccinated per hour per team in each region ranged from 22 to 36 during static point campaigns, and from 5 to 18 during door to door campaigns. The interquartile range of time of people visiting a static point was between 9:17 and 13:34. Post vaccination surveys showed that vaccination coverage was higher than 70% in all regions, except Chiradzulu district (65%). The regression model showed that increasing population density increased the odds of achieving optimal vaccination coverage, while the effect of population density decreased as distance to nearest city increased.

Conclusion: Results from this study in combination with dog population estimates can be used to inform planning of vaccination campaigns in Sub Saharan Africa.

The HyData Project: Building what we know about *Echinococcus granulosus* in the United Kingdom

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ABSTRACT

Objective: *Echinococcus granulosus* is a canine tapeworm of global importance for animal and human health. Infection with tapeworm larvae (hydatid disease) manifests as cystic lesions in the viscera, particularly the liver and lungs, of secondary host species including livestock and humans. Historically, several areas in the United Kingdom have been recognised as infection hotspots, but there is little data on current geographical distribution and impact of the parasite. The HyData project was set up to investigate *E.granulosus* in several important high-risk primary and secondary host species, including sheep and cattle at slaughter, hunting hounds, farm dogs and canid species in zoological collections.

Materials and methods: In canid species, a questionnaire and sampling protocol was developed to investigate feeding practices, anthelmintic use and risk factors for infection, and receive pooled faeces samples. Routine sampling of suspect hydatid and non-hydatid (control) lesions in abattoirs has also been implemented. Questionnaire data, microscopy, coproELISA and coproPCR aim to build a picture of *E.granulosus* distribution and identify associated risk factors for infection.

Results: Preliminary data showed that 84% (27/32) hunts fed raw meat products with 38% (12/32) reporting feeding raw viscera from cattle and sheep. All hunts used anthelmintics as part of a hound health programme although 44% did not use praziquantel-based anthelmintics. 38% (8/29) were positive for coproELISA on pooled faeces samples; supporting coproPCR work is ongoing. Data from 16 zoos housing 12 canid species revealed that 75% (43/57) of enclosures regularly received anthelmintics, but 67% (38/57) were not administered assuming dosages for domestic dogs could be directly extrapolated to other canid species). Faeces samples from 25% (14/57) enclosures contained helminth ova on microscopy; supporting coproPCR work is in progress.

Conclusion: This study will inform on the geographic distribution of *E.granulosus* in the UK and important information about potential risk factors for infection that will impact animal and human health.

Identification and understanding of social dimension regarding the antimicrobial usage in Thailand

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ABSTRACT

Background: Antimicrobial resistance (AMR) is a growing problem in human and veterinary medicine. AMR infections is estimated to infect over 10 million (1) mortalities annually by 2050. There is a need to identify, assess, monitor, and manage the antimicrobials usage (AMU) in the foods that comes from the farm level to the plate. However, communication gap between stakeholders, cultural differences, farming practices, seasonal variation of practices, population dynamics between countries etc. further aggravates the situation.

Materials and methods: This study was aimed at identifying the decision drivers for AMU among potential stakeholders at pig and duck farms in two districts of Thailand. Three different stakeholders were imposed in the study in each farm: farmer, consultant veterinarian for respective farm and the policy maker in academic field. Five different open questions were used for the farmer, while two main questions focusing on the deeper information were used for the consultant veterinarian and the policy maker. The data were analysed through summarized information and comparison of information between three stakeholders from the transcript of the interviews.

Results: The farmer justified the answers on decision drivers, socio-relationships, and reason of AMU. They perceived AMR as 'contamination' rather than a negative consequences of use of antimicrobials. The veterinarian and policy maker were not serious enough about the prescription choice or alternatives to the drugs and reducing the AMU. Yet, they govern the authority on AMU in animals. The results of the study also showed the relation of power between the consultant vet and the farmer.

Conclusion: Substantial information and communication gaps between the three stakeholders were observed regarding the AMU. The synergistic combination of different stakeholders is necessary to reduce the AMU from the farm level. This study has made the realization of importance of top-down relationship while implementing the national AMU strategic plan and recommend for controlled integrated studies in society, health care, and agriculture settings.

Key words: Antimicrobial usage, Antimicrobial resistance, pig farm, duck farm, stakeholders

One medicine – the interface between veterinary and human health

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ABSTRACT

One Health' is an emerging global key concept integrating human and animal populations through international research and policy. The complex relationships between the human and animal have resulted in a human-animal-environment interface since prehistorical times. The One Health Commission defines One Health stating that "One Health is the collaborative effort of multiple health science professions, together with their related disciplines and institutions—working locally, nationally, and globally—to attain optimal health for people, domestic animals, wildlife, plants, and our environment'. The people, animals, plants and the environment are so intrinsically linked that prevention of risks and the mitigation of effects of crises that originate at the interface between humans, animals and their environments can only improve health and well-being.

This paper gives indication for the widespread acceptance of 'One Health' due to the logical approach to combat zoonoses. The containment of pandemic threats like avian influenza, SARS etc. within months of outbreak are few examples of important zoonotic disease to name. There are several successful applications of One Health paradigm.

The paper begins with a brief overview of the human-animal interface. The paper continues with the socioeconomic and public health impact caused due to various zoonotic diseases such as Middle East Respiratory Syndrome, Influenza, Ebola virus etc. This is followed by the role of 'One Health' to deal the global problem by the global solution. The 'One Health' approach was successfully implemented in numerous projects around the world.

There are challenges to limit One Health implementation, while on the other side it gives a value of interdisciplinary collaboration for reducing threats in human-animal-environment interface.

Key words: Emerging infectious disease; One Health, viral zoonoses

What a tangled web we weave: rabies ecology at the human-livestock-wildlife interface in Punjab, India

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ABSTRACT

Objective: Describe an outbreak of rabies in bovines in a village in Punjab, India, and assess socio-economic indicators associated with affected farms and the level of knowledge about rabies prevention.

Materials and methods: A questionnaire was administered to farmers in Shadipur Momian, Punjab, India, in April 2016. Data about householders, rabies exposure, prevention and cases were collected. Rabies cases were ascertained by both passive and active surveillance. Clinical cases were defined as acute-onset, rapidly progressing illness culminating in death within 7 days, in which signs consistent with rabies-induced encephalitis were observed by a veterinarian. Confirmed cases were defined as a clinical case that was laboratory confirmed using fluorescent antibody testing of a brain sample.

Results: Two confirmed and 13 clinical rabies cases occurred in bovines in a three-week period in August and September, 2015. A clinical rabies case also occurred in a farmer in October, 2015, who did not receive post-exposure prophylaxis following a bite from a stray dog in July, 2015. Indicators of low socio-economic status – location within the village, large households and farming practices in which livestock were not kept in enclosures – were significantly associated with case-farms. Free-roaming, owned dogs were not vaccinated against rabies and many participants believed that traditional remedies prevented rabies.

Conclusion: This outbreak illustrates the inequitable burden of rabies, which would have had a proportionally greater impact on case-farm households due to their already low socio-economic status. As well as improved public education about rabies prevention in both humans and valuable livestock in rural India, we also suggest investigation of the importance of a 'rural-cycle' of canine-rabies transmission. Since the decline of India's vulture population, village carcass disposal areas might increasingly provide ample food to sustain a large stray dog population in which rabies is endemic.

Key words: Rabies, cattle, buffalo, Punjab, India

The enterotoxic activity of Sarcocystis fayeri actin depolymerizing factor (ADF)

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ABSTRACT

Objective: Genus *Sarcocystis* is a protozoa which has two-host life cycle. Herbivores are main intermediary hosts, and genus *Sarcocystis* forms sarcocysts in their muscle tissue. Sarcocystosis has been known as a problem of economic loss in cattle, but nowadays it also be known as a causative factor of food poisoning. Among them, *S. fayeri* is identified as a causative pathogen of food poisoning by eating raw horsemeat, but the pathogenic causing mechanism is not yet investigated in details.

Materials and methods: A protein of 15 kDa molecular mass from the cysts homogenates of *S. fayeri* was fractionated by gel filtration chromatography for a rabbit illeal loop test and intravenous administration in rabbits. To identify the protein, amino acid sequence was obtained by reversed phase high performance liquid chromatography (HPLC). Recombinant 15kDa protein was applied to cell stimulation to examine cytotoxity.

Results: 15kDa protein was identified as actin depolymerizing factor (ADF). Fractionated *S. fayeri* ADF showed a toxic possibility to rabbit. Recombinant *S. fayeri* ADF protein showed an enterotoxic activity in the rabbit illeal loop test with 200 μg injection into a loop. The stimulation of L929, RAW264, and Caco-2 cells by recombinant ADF protein did not decline each cell viability in a cytotoxicity test. However, the culture supernatant of RAW264 macrophage cells stimulated by the recombinant ADF declined the viability of L929 fibroblast.

Conclusion: In this study, we confirmed the enterotoxic activity of *S. fayeri* ADF in vivo test. And from the result of in vitro test, we suggest that *S. fayeri* ADF may be an indirect cytotoxic protein.

Key words: *Sarcocystis fayeri*, food poisoning, toxic protein, ADF, horsemeat

Evaluation of the food safety risk associated with hepatitis in broilers

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ABSTRACT

Objective: The objective of this study was to assess the potential human health risk associated with consumption of breast meat originating from chickens with the meat inspection code acute or chronical hepatitis.

Materials and methods: Breast meat from 100 chickens with the inspection code acute or chronical hepatitis were investigated for the number of bacteria present focusing on bacteria that could impose a risk for consumers. A similar investigation was conducted on breast meat originating from 83 approved chickens. Bacteriological analyses of liver were also conducted from 78 of the chickens (1 g of liver and swabs with < 1 g of liver material). For the statistical testing of bacteria presence or not in the condemned and approved chickens, a $\chi 2$-test was used.

Results: In the condemn chickens 72% were negative - and only 8% had bacteria counts >7 cfu/g. Similarly, in the approved chicken 72% were negative - and 9% had bacteria counts > 7 cfu/g. Hence there was no statistical difference between the "condemned" and the "approved" chicken's regarding presence (+/-) of bacteria. There was no agreement between the bacteria species isolated in breast meat- and in liver-samples from the condemned chickens. It cannot be excluded that some of the isolated bacteria was a result of contamination in the sampling process.

Conclusion: The conclusion based, on the findings from this study and on the European Food Safety Authorities Scientific Opinion on the public health hazards to be covered by inspection of meat (poultry), is that hepatitis seems to be a chicken disease problem – and not a food safety issue.

Key words: Meat inspection, food safety, hepatitis, microbiology

Integrating knowledge of the quantitative effect of antimicrobial usage on resistance with national register-based data at pig farm level to assess effect of usage alternations

V.D. Andersen*, F.M. Aarestrup, A.C. Birkegård, H. Vigre

ABSTRACT

To curb antimicrobial resistance (AMR) abundance in pigs requires knowledge of the quantitative relationship between antimicrobial usage (AMU) during rearing (lifetime-AMU) and AMR, and knowledge of the lifetime-AMU for the entire Danish population of batches at farm level. The latter was obtained given the national register on prescribed medicines for animals, VetStat. Results from observational studies of AMU and AMR in pig farms and VetStat data were integrated into a simulation model predicting the effect of interventions targeting AMU at farm level on the national level of AMR at slaughtering. Subsequently, the AMR level was predicted for finisher pig batches at farm level given their specific lifetime-AMU combined with knowledge of its effects on the AMR. Afterwards the AMR level of finisher pig farms was weighted by production size and summarized to constitute the national level. Simultaneously with the simulation of an AMR baseline, the effects on AMR of alternative lifetime-AMU can be predicted and hereafter compared to the baseline.

Several different scenarios of lifetime-AMU were simulated. When the peroral tetracycline usage of the 10% highest users was replaced with peroral macrolide usage, the tetracycline resistance was reduced by 1-2% and the macrolide and MLSb resistance increased by 5-8% at national level. When all tetracycline usage were ceased, the aminoglycoside, lincosamide and tetracycline resistance were reduced by 4-42%, 0-8% and 9-18%, respectively.

In the quantitative relationship between AMU and AMR studies comprehensive sampling were performed, whereas the explanatory variables foremost were generated from registers. The reason was that the overall project aimed at predicting the national AMR level. Therefore, only explanatory variables that could be obtained for all pig herds in Denmark were included in the model. Presently, the simulation model is static, but work is being carried out to predict a time-span AMR change, given a change in lifetime-AMU.

Using system effect modelling to evaluate food safety impact and barriers in low-income-countries: an example from urban Cambodia

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ABSTRACT

Objective: The study tested the applicability to low-and-middle income settings of a System Effects model developed for high-income countries. The objective is to better understand the damage caused by foodborne diseases, and barriers for consumers in accessing safer food.

Materials and methods: In January 2018, ten group sessions with 66 participants were held in Phnom Penh, Cambodia. Five were organized in low and five in middle income areas of the city. The participants, half of them women, were purposively recruited, of similar background but not knowing each other. Each group discussion consisted of two exercises that was completed by each participant individually. The first exercise mapped impacts to visually depict the complexity of peoples' experience of unsafe food including damage caused, flows of effects, and interconnections between them. In the second exercise, barriers to avoiding unsafe food were illustrated. Circumstances, incidents, pre-existing conditions that make it harder to get safe food were described.

Results: More than 600 consequence items of eating unsafe food were listed by all participants, with little variation between low and middle income groups as well as between men and women. While most concerned health and economic impact, women in the middle income group listed several social consequences. More than 250 items described barriers to accessing safe food, most dealing with lack of money, lack of accessibility as well as limitations to tell safe from unsafe food. The items were coded and grouped, adjacency matrices generated, impacts and barriers aggregated and the density of connections made between different impacts and barriers evaluated.

Conclusion: The findings can help to understand impact and components of resilience that could help inform food safety intervention design.

Source attribution of *Salmonella* in macadamia nuts to animal and environmental reservoirs: Queensland, Australia

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ABSTRACT

Objectives: In Australia, rates of human salmonellosis vary from state-to-state, and a high number of macadamia nuts in Queensland are contaminated with *Salmonella*. We hypothesize non-human sources in the surrounding and plantation environments contaminate macadamia nuts. A source attribution model based on serotypes was developed and applied to attribute *Salmonella*-positive macadamia nuts to animal or environmental source(s).

Material and methods: We applied and modified the Hald source attribution model to attribute macadamia nut *Salmonella* detects to specific animal and environmental sources based on *Salmonella* serotype. Sources included avian, compost-soil-biosolids, equine, companion animal, porcine, poultry, reptile, ruminant and wildlife based on data provided by Queensland Health.

Results: The model attributed 36% of all macadamia nut *Salmonella* detects to compost-soil-biosolids, suggesting transmission from an animal source to macadamia nuts through compost-soil-biosolids. Poultry and wildlife were the second and third most attributed sources, respectively.

Conclusion: Results indicate compost-soil-biosolids as the most likely source of macadamia nut *Salmonella* contamination suggesting a transmission route via poultry-, and wildlife-faeces. These findings will be used to inform and guide environmental and wildlife sampling and analysis in an ongoing macadamia nut-*Salmonella* and human salmonellosis source attribution project applying whole genome sequencing of isolates.

Key words: Salmonella, food safety, source attribution, macadamia nuts, Australia

Machine learning is a potentially innovative method for source attribution using next generation sequencing data: case of *Salmonella Typhimurium*

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ABSTRACT

Objectives: Being able to prevent the emergence and spread of foodborne diseases is important and improves public health. With the next generation sequencing technology, new and promising methods for source attribution models are available. Source attribution models quantify the number of cases of a specific illness to food sources and animal reservoirs. Here, we investigate the potential of machine learning to predict the source from which a given bacterial strain origins based on input derived from next generation sequencing (NGS) data in order to define a set of host associated features.

Materials and methods: Machine learning methods recognize patterns in large and complex datasets and use the gained knowledge to build models. The assumption is that the model learns the general properties (i.e. pattern of features) associated with bacteria isolated from the different animal sources. We selected different machine learning algorithms to predict sources for Danish *Salmonella* Typhimurium isolates sampled from broilers (n = 43), cattle (n = 2), ducks (n = 24), layers (n = 5), pigs (n = 223) and turkeys (n = 3).

Results: Preliminary findings using whole genome MLST as input features showed an accuracy of above 90 % for all six tested machine learning algorithms in the source prediction. Logit boost algorithm was the most accurate of the algorithms tested (accuracy: 97.7 %).

Conclusion: The method identifies a set of unique host associated features using sequence data that can be used as input to new mathematical models for source attribution. Results of such models can inform risk managers to identify and prioritize food safety interventions.

Key words: Food safety, *Salmonella* Typhimurium, machine learning, source attribution, epidemiology

Antimicrobial Resistance Surveillance in chicken and pig in Viet Nam

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ABSTRACT

Objective: To describe antimicrobial resistance (AMR) in *E. coli* and non-typhoidal *Salmonella* (NTS) collected from chicken and pig in Viet Nam.

Materials and methods: Viet Nam National Center for Veterinary Hygiene and Inspection No.1 (NCVHI No1), Department of Animal Health (DAH) conducted a pilot national surveillance in Hanoi City, Hai Phong, Quang Ninh, Long An and Ho Chi Minh City from September to December 2017. A total of fourteen pig and chicken slaughterhouses with the highest number of animal processed were selected. Two rectal swabs or two chicken droppings from 25 randomly selected chickens or pigs were collected from each slaughterhouse. Isolation, identification of *E. coli*, NTS and susceptibility testing using the disk diffusion assay were performed at NCVHI No1 according to the standard operation protocols (SOP) established by DAH in compliance with international standard. The Chi-Square test was used to determine the significance of the different resistance proportion between animal species.

Results: Overall resistance proportion of the *E. coli* and NTS to at least one of 20 tested antimicrobials were 97% (n=345) and 98% (n=64) respectively. The highest proportions of *E. coli* and NTS were resistance to tetracycline (94%, 81%), ampicillin (90%, 89%) and sulfamethoxazole (88%, 84%). Multi-resistance to two or more antimicrobials were observed in 96% and 97% of *E. coli* and NTS with the highest resistance up to 15 antimicrobials. The proportion of resistance *E. coli* collected from chickens was significantly higher than those collected from pigs (p<0.01) while NTS was not significantly difference.

Conclusion: We observed high level of antimicrobial resistance *E. coli* and NTS collected from chicken and pig in Viet Nam.

Key words: Antimicrobial resistance, surveillance, Salmonella, livestock

Ecologic and social factors on canine tungiasis in an endemic region, Brazil: longitudinal study

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ABSTRACT

Objective: To determine factors associated with the behavior of canine tungiasis in an endemic area.

Materials and methods: We performed quarterly prevalence surveys (n=8) during a period of two years in a tourist rural community, Juerana Village, Ilhéus/Bahia State/Brazil, where 31 dogs were inspected in all the surveys. The place had geo-environmental characteristics appropriate to the development of the *Tunga* spp., as well as underprivileged communities that shelter canine populations with low levels of restriction and sanitary management. There were 104 households (±370 inhabitants), mostly living in poor socioeconomic conditions. The entire animal body surface was thoroughly examined for the presence of embedded *Tunga* parasites.

Results: The longitudinal analysis indicate that canine tungiasis is highly prevalent in the area during all year. The period prevalence was 94% (29/31;95%CI=79.3%-98.2), with point ranging from 52%(August/2013) to 84%(November/2013-2014). There was a high persistence of infestation. Most of the dogs (16) remained infested during five continuous quarterly surveys or more. Only two dogs had no infestation during the eight surveys, both under the care of guardian A. The time series of infestation is associated with the dog owners in cases where there was more than one dog/household: 1.Infestation throughout the period (tutors B, C); 2.Without Infestation for the whole period (D); 3.Infested by 7 surveys (E, F); 4.for 6 surveys (G, F); 5.for 5 surveys (H). There was no difference in prevalence by sex or age (p <0.05).

Conclusion: The physical/biological environment favors infestation throughout the year. There is an association between the time series of the dog infestation and the perception of sanitary management of the dog owners. The dog owners perception of sanity explains the conditions of the ecological/social environment in which the dogs are inserted and the presentation form of tungiasis.

Key words: *Tunga penetrans*, dogs, epidemiology, Brazil, zoonosis

Modelling the introduction of *Varroa*-resistance into the Australian honeybee population

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ABSTRACT

Introduction: In Australia, honeybees (*A. mellifera*) are free of *Varroa destructor*, but it is widely expected that this devastating ectoparasitic may reach Australia in the future, as is the case in other countries. Breeding *Varroa*-resistant bees and spreading this genotype throughout the Australian honeybee population represents an attractive alternative to miticide use.

Materials and methods: We developed a simulation model of managed and feral honeybee colonies in eastern Australia based on a scenario where *V. destructor* was endemic. Within the model resistance to *V. destructor* was achieved by introducing Varroa Sensitive Hygienic (VSH) bees into the population. Using this approach, the level of resistance in half-sister female workers can range from zero to full resistance depending on the genetic makeup of queen and drone sires. For each year, using set genotype-dependent probabilities, we simulated the 900,000 colonies (either managed or feral) in eastern Australia, documenting on a yearly basis counts of colonies that survive, undergo supersedure (i.e. replace the existing queen), swarm, or die-off (from *Varroa*, starvation or other causes).

Results: To quickly distribute *Varroa* resistance into the managed honeybee population the role of queen breeders will be critical. After initial collapse of the agriculturally important feral honeybee population, repopulation by *Varroa*-resistant feral colonies to pre-*Varroa* levels can be expected within ten years.

Conclusion: Our model highlights several key deficiencies in our understanding of the epidemiology of *Varroa* such as the proportion of *Varroa*-resistant female workers needed in a colony to confer specific levels of resistance. Also shown is that the genetic makeup of the managed population will continue to be significantly different to the feral honeybee population. The information gaps identified by the model will inform the nature of future research activities.

Session E: Special section: our trend and future

An investigation of Foot-and-mouth disease outbreak in Siem Reap province, Cambodia from December 2016 to February 2017

L. Sileap*

ABSTRACT

Background: Foot-and-mouth disease (FMD) is an acute, highly contagious viral infection of domestic and wild cloven-hoofed animals. It is known to be endemic in Siem Reap province, with periodic outbreaks occurring in different geographical areas of the country.

Materials and methods: This study was conducted to investigate the presence of FMD virus in reported FMD suspected cases in cattle from the district veterinary in Siem Reap province. Epithelial samples and vesicular fluid were collected from cattle in FMD outbreak districts and then submitted to the National Animal Health and Production Research Institute to be tested by ELISA for sero-type of FMD virus (FMDV). Cattle owners were interviewed to determine the source of FMD outbreaks.

Results: Siem Reap province had FMD outbreaks in December 2016 to February 2017 that were found FMD virus sero-type A. It affected 7 districts in Siem Reap and caused sick young cattle (age less than 1 year) 729/5610(13.00%), sick adult cattle (age greater than 1 year) 668/8668 (7.71%), dead young cattle 29/5610 (0.52%) and dead adult cattle 38/8663 (0.44%). Also, 83.75% (67/80) of cattle household had no experience with FMD outbreaks and 16.25% (13/80) cattle household used to it. Plus, during the FMD outbreaks, it had trader visited the cattle household: neighboring village 37.50% (30/80), middleman 23.75% (19/80) and village animal health workers 22.50% (18/80). Anyway, 58.75% (47/80) household asked village animal health workers for treatment the sick cattle and 25.00% (20/80) household cured the sick cattle by itself.

Conclusion: Most cattle affected by FMD were seen on both young cattle and adult cattle. It caused high morbidity 1397/14273 (9.92%) but low mortality67/14273 (0.47%). The source of this outbreak possibly associated with traders visited such as middle man, village animal health workers, neighboring village and sometime, cross-border movements of cattle between village to village. It is important to do vaccination regularly for cattle and to avoid the cattle contact with other cattle in village.

Key words: Foot-and-mouth disease, cattle, investigation, outbreak, Siem Reap province, Serotype A

The overview of epidemiology education in Iran

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ABSTRACT

Epidemiology was recognized as an independent profession in Iran in 1951 during establishment of the Health Cooperation Organization, where an epidemiology unit took the responsibility to control the epidemics. The Malariology Institute was established in 1952 and concluded an agreement with WHO in 1953, entitled "the program to combat arthropods-induced diseases," part of which was the creation of a one-year epidemiology course. Subsequently, in 1975, the Master's Degree Program in Epidemiology began with the admission of 2 students which is currently reached 108 per year.

The "Epidemiology PhD" curriculum was launched in 2009 at medical universities, and currently, 19 PhD candidates are admitted annually. In addition, the veterinary epidemiology residency was established at the Faculty of Veterinary Medicine, University of Tehran, since 2004, and 3 PhD candidates are currently studying at the Department of Veterinary Epidemiology in this faculty annually.

Since the ultimate goal of veterinary epidemiology is same as the main purpose of veterinary science, namely, to promote public health and well-being as well as the productivity of animal capital, it is necessary for veterinarians to be familiar with the fundamentals and principles of epidemiology. In this regard, given the important role of veterinarians in the field of epidemiology to solve the problems of human and animal health, which importance was understood by senior managers of the Ministry of Science and the Ministry of Health, veterinarians can continue their study in epidemiology doctorate in medical sciences universities in Iran in addition to the Faculty of Veterinary Medicine (Table 1).

Key words: Education, epidemiology, veterinary, Iran

Knowledge, attitude and practice of Dealers regard to Foot and Mouth Disease (FMD) in North West and center of Iran in 2017

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ABSTRACT

Objectives: Domestic and wild animal movements are important factor in the spread of FMD and dealer have main role in animal trade and transport. Our aim was to study the level of knowledge, attitude and practice of dealers in distribution of FMD in Iran.

Methods and Materials: We performed a cross-sectional study on dealers of two provinces of Iran, 2017. In this study a questionnaire was designed to obtain the required data. A panel expert in the field of FMD evaluated the validity of the questionnaire.

Results: In this study 324 dealers by the median (range) of age and work experience 46.00 year (range: 24-83) and 240 month (range: 8-840) respectively were participated. 90% have other job addition to dealer. The mean knowledge of dealers regard to FMD was 42.40± 13.28. Dealers believed that: the most effective group in the control of FMD were veterinary officers, farmers, veterinarians and dealers respectively, all the farmers in the region (49.7%) are the most group who suffer from FMD outbreaks, Veterinarians and dealers are equally responsible for FMD occurrence and the main causes of failure in controlling and preventing of FMD is fault in vaccine (low efficient and coverage of vaccine), illegal animal trade and low knowledge. 89% of dealers didn't like to buy sick animals and 42.9% of dealers don't ask about history of the vaccination. Only 17.9% of dealers like to get animal transport license after buying animals. 13.2% of dealers said that they sell affected animals. 13.8% of dealers never wash their hands after contact with affected livestock. Most of the dealers immediately mix bought animal with their own animals.

Conclusion: This study showed that the level of knowledge and attitude in dealers was moderate but the practice was low.

Key words: FMD, dealers, knowledge, attitude, practice

Using geospatial methods to measure the risk of environmental persistence of avian influenza in South Carolina

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ABSTRACT

Objective: Avian influenza (AI) is a highly contagious virus affecting wild birds and domesticated poultry. In addition to exposure from wild birds, outbreaks in domestic poultry can be initiated and propagated by exposure to virus surviving in the environment near poultry operations. This study aimed to define areas of South Carolina at heightened risk for environmental presence of the AI virus using geospatial methods. Environmental covariates known to influence AI survival were determined based on published studies. Data on the distribution of these variables within South Carolina were downloaded from publicly available sources. All covariate layers were mapped at a 1-km resolution for ecological time periods (e.g. breeding, fall migration, winter, spring migration) and weighted based on their influence for virus survivability. Environmental suitability maps were created using these layers and ESRI ArcGIS 10.4 software with the Predictive Analysis tool.

Results: Geospatial model results were evaluated to assess the validity of suitability maps using USDA Wildlife Services Surveillance data. After classifying map values based on World Organization for Animal Health (OIE) risk assessment guidelines, < 1% of the 1-km geographic areas showed a high risk of AI persistence in the four time periods assessed. A higher number of geographic areas showed either moderate (1-2%) or low risk (17–19%), with a higher percentage of risk present in winter and spring migration. When farm density data were combined with AI suitability maps, there was a very low percentage of locations where moderate or high environmental risk co-located with low, moderate, or high farm density areas (0.001 – 0.120% of areas based on time period).

Conclusion: These results can be used to guide monitoring and surveillance activities, aid in biosecurity and emergency preparedness efforts, minimize transmission risk to domestic poultry, and support AI related outreach within South Carolina.

Key words: avian influenza, waterfowl, geospatial, risk map, validation

Assessment of veterinary communication on dairy farms

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ABSTRACT

Introduction: Herd veterinarians are, in addition to treatment of individual animals, increasingly expected to provide proficient whole-herd consultancy. To provide effective advice, competent communication is a very important skill for veterinary practitioners, as it affects clients' satisfaction and adherence to medical advice. Research from the companion animal context was crucial in informing veterinary education programs, whereas communication information from the farm animal environment is scarce. Therefore, the objective of this study was to determine veterinary communication during dairy herd health visits.

Materials and Methods: Fourteen Canadian dairy practitioners were equipped with action (GoPro®) cameras and recorded 3-7 farm visits each. The resulting 70 audio-video recordings were analyzed using the Roter Interaction Analysis System (RIAS). Intraclass-correlation coefficients were calculated to assess variation of communication patterns, and influence of study participants' demographics on communication was assessed. Additionally, relationship-centeredness of interactions was evaluated and compared among demographic groups.

Results: Communication patterns varied greatly among recordings of the same veterinarian on different farms. Nevertheless, most veterinary talk focused on farmer education and building a relationship through personal remarks, whereas especially open-ended questions (which motivate farmers' participation in the conversation and shared decision-making) were rare. When discussion revolved around health issues of an individual animal, veterinarians used less social talk, but focussed on medical information gathering. Veterinarians' age, gender and length of the veterinarian-farmer relationship had limited influence on communications; however, if the farmer and veterinarian were both male, the conversation was more relationship-centered. Communication of veterinarians with previous communication training was very similar to veterinarians without training.

Conclusion: Detailed description of veterinary communication patterns on dairy farms will contribute to establishing the importance of communication as a clinical skill and to identify unique aspects of veterinary on-farm communication, providing opportunities for improvement.

Key words: Veterinary communication, consultancy, herd health, dairy

The activities of the Japan society of veterinary epidemiology

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ABSTRACT

Objective: This paper describes the history of Japan Society of Veterinary Epidemiology (JSVE).

Materials and methods: Information on the history of JSVE was obtained from the previous editions of the Journal of Veterinary Epidemiology and questionnaire-based survey conducted for the members of the JSVE.

Results: In 1997, Japan became the first country in Asia to establish a scientific society specifically for veterinary epidemiology, called the Japan Society of Veterinary Epidemiology. This was formed following two previous organizations: the Japan Association of Veterinary Informatics (1987–1997) and Japan Association of Veterinary Statistics (1976–1987). The main yearly activities of the JSVE are publishing its academic journal (*Journal of Veterinary Epidemiology*) biannually, holding scientific conferences, and providing study sessions and seminars. The JSVE's research targets include a wide range of epidemiological topics, such as descriptive epidemiology, observational studies, animal health economics, risk analysis, simulation, and modeling. Over the last 20 years, the members of the JSVE have been actively working on animal health and public health issues, such as outbreaks of foot and mouth disease, bovine spongiform encephalitis, avian influenza, porcine epidemic diarrhea, and others. In doing so, they apply the knowledge and skills of veterinary epidemiology. These research activities will be detailed and discussed in the presentation. Recently, reporting has begun to focus on emerging topics such as epidemiology in small animals and wild animals and social epidemiology. The JSVE has more than 300 members, consisting of local governments (45%), universities (17%), private companies (9%), large animal clinics (8%), research institutes (7%), and others. There are also now more than 40 student members whom the society, in offering awards such as the Best Article Award and Best Presentation Award, encourages to actively publish both in journals and for conferences.

Conclusion: The JSVE's future plans are to strengthen veterinary epidemiology education both at the undergraduate and postgraduate levels, develop advanced training courses for professional veterinarians, and promote the *Journal of Veterinary Epidemiology*, hopefully obtaining impact factor. We also wish to promote international collaborations with veterinary epidemiologists, both in Asia and beyond this region.

Key words: History, education, veterinary epidemiology, Japan

Interhemispheric gene flow of influenza virus among wild birds in Chile

P. Jimenez-Bluhm*, J. Hicks, G. Boldt, V. Marambio, P. Galdames, N. Bravo-Vasquez, S. Schultz-Cherry, J. Bahl, C. Hamilton-West

ABSTRACT

Objectives: In the wake of the highly pathogenic H5Nx avian influenza viruses (AIV) outbreak in North America, surveillance data from South America remains sparse. There is little known about patterns of viral spread that could help quantify the risk wild bird viruses pose in South America, making pandemic preparedness cumbersome. Hence, the objective of this study is to understand viral spread in the region and between hemispheres.

Materials and methods: We have undertaken AIV surveillance in wild birds in parts of Central and Northern Chile since 2012. Here we analyze genomic data obtained in Chile, including 48 recently fully sequenced AIV samples. We use Bayesian analysis to test for viral migration and genetic reassortment.

Results: We observed that 35.2% (148/420) of the gene segments were closely related to North American viruses obtained from the Pacific (41.2%), Atlantic (27.7%), Mississippi (18.2%) and Central (12.8%) flyways, suggesting viral intercontinental gene flow between avian populations. Our results show gene segments could be traced back to viruses obtained in eleven U.S. states and one province of Canada. The three highest contributions from the North American gene pool circulating in Chile were identified as coming from California (22.3%), Alaska (17.6%) and New Jersey (16.9%). Most North American gene segments were associated with *Charadriiformes*, suggesting that the contribution of North American genes might preferentially occur through specific migratory flyways and host species.

Conclusion: Our studies show the diversity of origins of viruses circulating in Chile, through a novel dataset of South American-origin AIV samples. Through this research, we hope to be able to understand the viral spread and risk these viruses pose to humans and livestock, by developing informed predictive models for pandemic preparedness.

Evaluation of intervention strategies to prevent the transmission of influenza viruses from wild birds to domestic poultry in Backyard Production Systems in Chile

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ABSTRACT

Objectives: Little is known in South America about the circulation of influenza virus in backyard poultry populations, nor in wild birds. Backyard productive systems (BPS) frequently exhibit biosecurity deficiencies and could play a major role in the epidemiology of animal diseases and zoonosis. During the last years, our results of active surveillance have shown that there is a prevalence of 27% in BPS in central Chile. On the other hand, risk-based surveillance in wild birds identified a prevalence of 2.8% (rRT-PCR) and the highest diversity of influenza viruses described in South America so far. We have also found evidence that indicates spillover from wild birds into backyard poultry populations. The objective of this work was to identify the effect of interventions in order to reduce the risk to both, animal and human health.

Materials and Methods: A mathematical simulation model of HPAI outbreak at BPS level in central Chile was developed. This was done using the NAADSM software. Complementarily pilot interventions activities (improving health education, construction of chicken coops and feed delivery for the birds, to make sure that owners keep the birds confined) in BPS are being carried out in central Chile

Results: The model indicated that in a base scenario a median of 10,182 BPS would be infected and the outbreak would last 208 days. Improving biosecurity through confining birds and increased passive surveillance, would diminish this impact to a median of 3,811 affected BPS and 151 days. Pilot interventions have reduced the prevalence of influenza at BPS level from 27% (rRT-PCR) to 3%.

Conclusion: Improving biosecurity through education, confining birds and increased passive surveillance, can diminish this impact of HPAI outbreaks in BPS in central Chile

Key words: Influenza, backyard, model, biosecurity

What are the long-term future challenges and opportunities for animal health surveillance

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ABSTRACT

Objective: To use scenario planning methodologies to identify and explore long-term future challenges and opportunities for animal health surveillance.

Materials and methods: The scientific knowledge-base for animal health surveillance is evolving rapidly, with improving technologies and faster access to better data. In parallel, there is an increasing impetus for rapid translation of knowledge into transparent, robust, future-proofed evidence-based health policies which will have a beneficial impact for industry stakeholders. In this study, EPIC, the Scottish Government-funded Centre of Expertise on Animal Disease Outbreaks, explored the use of scenario planning as a participatory technique to increase stakeholder engagement in the process of long-term strategy development, focusing on the future of animal health surveillance in Scotland. Elements of the process included: identification of trends and key uncertainties, development of consistent and plausible scenario narratives, and use of these as decision tools.

Results: Scenario planning workshops created opportunities for scientists, industry stakeholders and policy-makers to participate in a dialogue about the importance and impact of different societal, economic, environmental, technological, legal and political drivers on the explicitly uncertain long-term future of animal health surveillance. Stakeholders identified opportunities and challenges in different potential future scenarios and used these to co-construct strategies with policymakers to improve future collection of animal health data and digital literacy and to help address potential gaps in veterinary and scientific research capacity relevant to rural areas.

Conclusion: Scenario planning offers a structured, robust approach to enable meaningful dialogue about the complexities and uncertainties inherent in evidence-based decision-making. It encourages some degree of social learning and development of partnerships between government and society. These relationships are important if stakeholders are to feel any ownership over animal health surveillance strategies and accept changes to future delivery systems.

Key words: surveillance, futures, scenario planning, uncertainty

Using secondary data to model livestock truck-borne fomite disease transfer potential

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ABSTRACT

Objectives: Contaminated fomites can play an important role in indirect disease spread between farms for diseases like foot-and-mouth disease (FMD). Feed and milk trucks with multi-stop routes can spread FMD virus by carrying contaminated mud and feces to down-route locations. This study examines disease spread implications of alternative approaches to developing and parameterizing indirect contacts in a spatial, stochastic FMD spread model.

Materials and methods: Contacts from feed and milk trucks are incorporated into the model either via farm-specific frequency contacts or directed routes of trucks between multiple farms. We used least-cost path modeling to develop synthetic routes for feed and milk trucks in Michigan and derived their contact probabilities to different farm types. Farm locations were simulated using data based on National Agricultural Statistics Service and actual feed mill and milk creamery locations. Resulting contacts were compared to national averages. A regional FMD model with parameterizations for frequency and directed movement contacts was used to evaluate disease spread.

Results: The modeled number of feed and milk truck contacts using Michigan-specific data were lower than national averages. Indirect contacts resulting in FMD infection were similar to slightly higher when feed and milk trucks were broken out separately from other indirect contacts. For areas in Michigan with more small dairies than the national average, the use of directed milk truck routes resulted in a greater number of indirect contacts that could have resulted in disease transmission. Directed routes resulted in a 34% increase in infected premises at the median and an increased risk of larger outbreaks.

Conclusion: Using directed routes to represent livestock truck movements significantly impacted simulated FMD spread in Michigan, particularly among small dairies. Further analysis of these parameters are needed regarding the sensitivity of disease spread to variations in directed routes. The relationship between directed routes and different control strategies should also be examined.

Key words: Least-cost path modeling, indirect disease spread, disease modeling, foot-and-mouth disease

Spatial risk-based prioritisation of FMD control zones in southern Lao PDR

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ABSTRACT

Objectives: FMD is endemic in Lao PDR. There is probably substantial under-reporting of outbreaks. Current vaccination activities are focussing on Savannakhet and Champasak Provinces, where little vaccination has been carried out and for which limited epidemiological data are available. The objectives of this study were to identify elevated risk areas for FMD outbreaks, and to optimise the effectiveness of vaccination by informing risk-based vaccination activities.

Materials and methods: A knowledge-based spatial risk assessment was conducted. Data sources included administrative geographical data, livestock census data, and FMD outbreak data for large ruminants from December 2010 to May 2015. Qualitative risk maps were developed in participatory workshops with Government animal health personnel to elicit knowledge of FMD. Subsequently, a weighted linear combination (WLC) was developed of prioritised risk layers; this was applied to generate a risk surface map and calculate an FMD risk score for each village.

Results: Outbreak reports reflected an attack rate of 6.00%, a mortality rate of 1.55% and a case fatality rate of 25.90%. Proximity to roads, outbreak areas and livestock density were included in the WLC. The results identified higher risk areas in central to north-western areas of Champasak and western areas of Savannakhet (Figure 1). Systematically varying WLC parameters did not significantly affect the outputs.

Conclusion: We demonstrate that a spatial risk-based approach can be applied to guide decision-making even when quantitative FMD epidemiological data are limited. However, there is no substitute for such data to validate the findings, also considering the existence of reporting biases.

Key words: Foot and mouth disease (FMD), risk assessment, spatial analysis, participatory appraisal, epidemiology
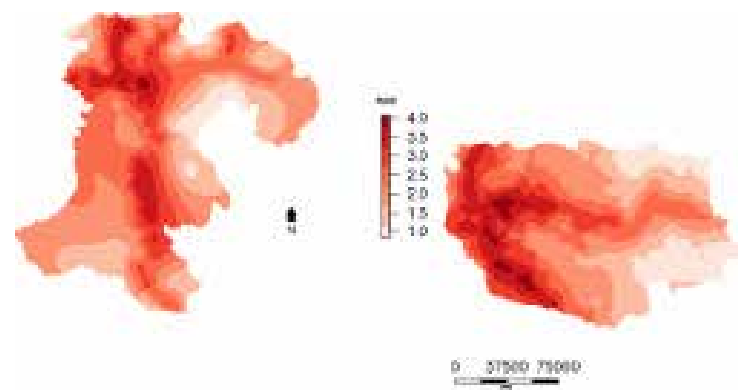
Figure 1. Interpolated surface maps of village ranking scores, obtained using a weighted linear combination of three criteria, showing the risk of FMD outbreaks in Champasak (left) and Savannakhet (right) Provinces, Lao PDR, for the period 2011-2015.

Matched case-control study of the influence of inland waters surrounding poultry farms on avian influenza outbreaks: 2004–2017 in Japan

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ABSTRACT

Objective: Wild birds play an important role in the global spread of avian influenza viruses. Inland waters where wild birds inhabit are believed to increase the risk of avian influenza outbreaks. To evaluate the risk of inland waters nearby poultry farms on highly pathogenic avian influenza (HPAI) outbreaks, matched case-control analyses were conducted for outbreaks in Japan from 2004 to 2017.

Materials and methods: At maximum four control farms were selected for each affected (case) farm. The distance between nearest inland waters and poultry houses was identified using Google Earth Pro. The distance was converted into a dichotomous variable by judging the presence of inland waters using the threshold value of distance, which was changed between 10 and 300 meters. The influence of inland waters was evaluated by Cochran-Mantel Haenzel chi-squared tests.

Results: The matched case-control analyses were conducted for five distinct periods from 2004 to 2017, i.e. 2004 (3 cases), 2007 (4 cases), 2010–2011 (23 cases), 2014–2015 (5 cases) and 2016–2017 (10 cases). None of the results from 2004 to 2011 outbreak periods showed significant differences (P values > 0.05). Conversely, for the 2014–2015 and 2016–2017 outbreak period, there were significant risk when neighboring inland waters were present within 20–25m and 25–105m from the farms, respectively.

Conclusion: The risk of inland waters surrounding poultry farms on HPAI outbreaks was significant in outbreaks after 2014. In 2011, the legal standards on biosecurity at farms were strengthened by requiring disinfection of vehicles/humans entering farms and covering poultry houses with netting. This would suggest that the risk of HPAI introduction into farms was mitigated after 2011 and the farms exposed to greater risk from nearby inland water had the outbreaks after 2014.

Key words: Avian influenza, matched case-control study, inland waters, Japan

Sero-epidemiological investigation of foot and mouth disease in cattle at the livestock-wildlife interface in Maasai Mara, Kenya

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ABSTRACT

Objective: Using foot and mouth disease (FMD) as a case study disease, we investigated the effects of varying levels of livestock-wildlife interactions on its transmission patterns in Maasai Mara ecosystem, Kenya.

Materials and methods: The study used a cross sectional study design with multi-stage cluster sampling framework to estimate FMD seroprevalence and the associated risk factors for exposure in pastoral cattle herds. We stratified the study area into three zones with varying levels of cattle-wildlife interactions. Five villages were selected purposively across these zones, two in zone 1 with intense cattle-wildlife interactions, another two in zone 2 with moderate cattle-wildlife interactions and one in zone 3 with low cattle-wildlife interactions. A total of 1170 cattle were randomly sampled from 390 herds and screened for FMD non-structural antibodies using a 3ABC blocking Elisa (PrioCHECK® FMDV NS, Prionics AG, Netherlands). A generalized linear mixed-effect model was used to analyze seroprevalence data and identify risk factors for exposure; herd ID was fitted as a random effect.

Results: This study revealed an overall individual-level seroprevalence of 81.2% (95% CI: 79.1 - 83.5). FMD seroprevalence differed significantly between zones ($\chi^2 = 88.96$, df = 2, p < 0.001). Cattle herds grazed in zone 1 and 2, respectively, had higher odds of FMD exposure (adjusted odds ratio (OR) = 3.16, 95% CI: 1.1 - 9.06, p= 0.03) and (OR = 1.75, 95% CI: 0.98 - 3.13, p=0.06), than those grazed in zone 3. FMD seropositivity was also significantly associated with animal sex (female), mixing of cattle herds at watering points, large cattle herd sizes, sharing of grazing areas between villages and non-vaccinated herds. The Intracluster Correlation Coefficient (ICC) among seropositive cattle in herds was estimated at 0.34 for the null model.

Conclusion: The study highlights important risk factors for FMD transmission and will help in the establishment of mitigative strategies.

Key words: Foot-and-mouth disease (FMD), livestock-wildlife interface, seroprevalence, risk factors, Kenya

Veterinary vs. medical curriculum in educating future public (one) health workers

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ABSTRACT

Questionnaire survey of professionals in public health sectors (animal and human) was conducted during 2016 in Bosnia and Herzegovina. Targeted respondents were medical and veterinary professionals working in public faculties, government bodies, institutes, primary health care as well as senior year medicine and veterinary students. Survey aim was to investigate self-assessed professional capacities in dealing with human or animal health issues and identify most priority training needs within the One Health (interdisciplinary) framework. Following groups of public health disciplines were considered:
- epidemiology, prevention and control of zoonoses,
- occupational health,
- hygiene and quality of food,
- health economics and
- public health management.
- Further on we compared responses of veterinary and medical graduates in order to identify similarities and discrepancies between resulting competencies from two curriculums in preparing them to work in interdisciplinary One Health setting.

Average respondent dealing with public health in Bosnia and Herzegovina (animal or human) most commonly deals with variety of tasks, most frequently in relation to food safety and epidemiological surveillance. Most respondents working on these tasks view their skills as adequate, but also recognize need for improvement. Our results show that less extensive training in public health disciplines during previous education (veterinary or medicine faculties) does not automatically translates to most currently required training needs. While there are differences in exposure to different disciplines during earlier formal education (i.e. physicians are less lacking training in occupational health, while veterinarians were more exposed to food hygiene and quality and economics training), as well as in perceived training needs (i.e. veterinarians seek more training in ecosystem health and health economics), the common areas where both professions identified gaps and need for self-improvement are epidemiological surveillance and risk analysis, public policy making, management and quality of official control programs and application of international standards.

Key words: Veterinary medicine, human medicine, One Health, self-assessed competencies

Mastitis mayhem: an on-farm exercise for integrating epidemiology into veterinary clinical education

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ABSTRACT

Managing the health of food animal populations requires veterinarians to have a solid foundation in epidemiology, economics, and data analysis. Although these skills have traditionally been taught using didactic lectures, there is increased interest in adopting more case-based approaches to help students better appreciate the clinical relevance. In 2016, Massey University removed its long standing fourth year epidemiology course from the curriculum and the content has now been integrated into other clinical courses. During the production medicine course, for example, the students now conduct a class investigation into mastitis in the university dairy herds. The students first work through self-directed tutorials to (1) compare herd performance against industry targets use data recorded in a commercial veterinary software, (2) estimate the economic benefits that could be achieved by reducing mastitis levels, (3) evaluate the performance of difference diagnostic tests for mastitis, (4) identify important risk factors for mastitis from the literature, and (5) plan a sampling strategy to estimate mastitis prevalence in the herd. The students then (6) visit the farm to collect individual milk samples, (7) perform bacteriology on the samples in the laboratory, and (8) record their microbiology and risk factor data into an appropriate spreadsheet. The class data is collated and the students then work through (9) cleaning errors in the dataset, (10) calculating and interpreting risk ratios, and (11) determining the clinical relevance and limitations of their findings. The exercise finishes with the students preparing a short letter to communicate their results and recommendations back to the farmer. Although we have not conducted a formal comparison of this teaching method against the previous lecture-based format, feedback from the students suggests that this is a valuable exercise for teaching them basic epidemiology and economics skills disguised in a practical clinical scenario they will encounter frequently in their careers.

Key words: Education, epidemiology, economics, veterinary student, case-based learning

Socioeconomic impacts of endemic foot-and-mouth disease in Laos and Myanmar

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ABSTRACT

Objective: Foot-and-mouth disease (FMD) is a highly infectious livestock disease currently endemic in South-East Asia including Lao PDR and Myanmar. FMD control in this region is challenging due to low awareness by farmers, frequent illegal animal movements, poor veterinary infrastructure and strict resource constraints. This survey-based study was conducted to understand the socioeconomic impacts of FMD in typical households in Lao PDR and Myanmar.

Materials and methods: Questionnaire interviews were conducted in 1,628 livestock-owning households of 291 selected villages in three provinces of Lao PDR (Champasak, Savannakhet, Xiengkhouang) and in two regions of Myanmar (Mandalay and Sagaing).

Results: More than half of the households typically reported at least one observation of clinical FMD between 2012 and 2016. Households with a recent occurrence of clinical FMD were associated with a lower income from rice (-26%), a lower calving rate (-30%) and/or a higher death rate (+125%) of large ruminants. In addition, households with a small draft cattle herd (5 or less cattle) where FMD had been observed had a higher sales rate (+23%) and a higher purchase rate (+63%) for draft cattle. The majority of households (>70%) with a history of clinical FMD spent USD 4 - 8 per animal on treatment of infected animals. In addition, a proportion of households (<17%) spent USD 11 on renting another animal, USD 1 on vaccination, or USD 572 per animal on buying replacement animals.

Conclusion: Our findings indicated that FMD would reduce net household income due to extra expenditure or reduced performance of livestock. The cost of vaccination was relatively low and was regarded as acceptable by farmers to mitigate the losses by FMD. The findings also suggested an enhanced trade of animals by occurrence of FMD, warranting a further study to investigate the impacts of FMD on trade.

Key words: Foot-and-mouth disease, Lao PDR, Myanmar, socioeconomic impact, livestock

Clinical rotation in population medicine

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ABSTRACT

Objective: Faculty at the Mississippi State University College of Veterinary Medicine recognized a need to provide veterinary students experience in population medicine. Although students were occasionally exposed to herd or population level medicine in other rotations, there was no experiential course dedicated to population medicine. Our objective was to create a new clinical rotation to encourage population level thinking.

Materials and methods: A required 3-week population medicine rotation was created for the third year of veterinary school. The problem-based clinical rotation includes onsite disease outbreak investigations and population-level consultations, taught by faculty with expertise in epidemiology, preventive medicine, internal medicine, shelter medicine, food animal medicine, poultry medicine, diagnostic medicine and food safety. There are 5 principles as learning objectives: 1) How the "system" affects animal health outcomes; 2) Critical thinking about causation; 3) Using diagnostic tests in population-based disease investigations; 4) Using data (evidence) to investigate/monitor population health; and 5) Implementing and communicating strategies for disease control and prevention. Students and faculty, investigate outbreaks of disease of impaired productivity in farms and shelters, prepare written recommendations post-visit, and demonstrate scientific literacy by preparing a Critically Appraised Topic (CAT) on a medical question of their choice. Fifty multiple choice questions are randomly selected from a question bank for pre- and post-test evaluation of learning.

Results: The rotation has been positively received by students. On the question "the laboratories and clinical experiences enhanced my learning," 83 students rated the course a mean 3.5 (stdev =0.6) on an ordinal scale of 1-4, low to high. On the same scale, students rated the course 3.4 (stdev 0.6) on the question "the rotation provided opportunities to improve my communication skills." Students demonstrate a mean 15 percentage point pre- to post-test gain in knowledge (n=163, $p < 0.0001$).

Conclusion: Students improved knowledge and communication skills in population medicine.

Key Words: Veterinary education, population medicine, clinical training

Public-Private Partnerships in animal health: what is the current picture?

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ABSTRACT

Objectives: Public-Private Partnerships (PPPs) are defined as a collaborative approach in which the public and private sector share resources, responsibilities and risks to achieve common objectives and mutual benefits in a sustainable manner. PPPs are identified as one key solution to reinforce Veterinary Services. However only limited information is available on the added value and enabling factors of PPPs in this sector. The aims of this study were to develop a typology of PPPs in the veterinary field and to identify key success factors and obstacles to their implementation.

Material and methods: A structured questionnaire was sent to all 181 OIE Member Countries and to 50 private contacts. 47 different variables characterizing the PPP initiatives were collected. Multiple correspondence analysis was combined with non metric multidimensional scaling and K-means clustering to establish a typology of PPPs and derive a set of simple rules to classify new instances of PPPs.

Results: 97 examples of PPPs were retrieved from 76 countries. Three clusters were identified separated by two main variables: the type of private partners and the type of interaction. Cluster 1 represented the classic type of PPPs, initiated and funded by the public sector, giving service delivery accreditation to mostly private veterinarians; cluster 2 included partnerships between producers' associations and public Veterinary Services, driven by trade interests; cluster 3 represented joint programs initiated and funded by private companies and initially driven by development objectives. Specific success factors and key obstacles affecting the performances and sustainability of these initiatives were identified for each cluster.

Conclusion: This study represents the first practical attempt to develop a meaningful typology for PPPs in the field of animal health, to identify fundamental obstacles currently inhibiting the development of PPPs, and informs ways to support national Veterinary Services to overcome these hurdles.

Key words: Public-Private Partnership, veterinary services, evaluation, animal health

Epidemiology of *Avian Influenza* in HPAI endemicity study in Purbalingga, Jawa, Tengah, 2017

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ABSTRACT

Objective: The purpose of this research is to identify frequency and distribution of AI cases in Indonesia through HPAI endemicity study.

Materials and methods: We selected Purbalingga district as the study area because it has representation of endemic situation in Indonesia. The methodology includes survey and sampling using active and passive surveillance. The active surveillance was conducted by taking pooled samples from birds in commercial poultry farms, nomadic ducks, and households owning chickens in selected villages; and sample collection from environment in live bird markets and poultry collectors. Passive surveillance was conducted by collecting sample from reported sick or dead poultry from community. All samples were tested in laboratory using Real-Time PCR (RT-PCR) Matrix and continued with H5 test for positive Matrix.

Results: Based on the Matrix test results, it shows that 18.9% (153/807 pools) were positive A-type Influenza. Of these, 29.7% (22/74 pools) was from live bird market, 24.6% (41/167 pools) poultry collector, 17.6% (13/74 pools) villages, 16.6% (55/332 pools) nomadic ducks, 14% (22/157) commercial poultry farms, and 0% (0/3 pools) from passive surveillance. Result of H5 test shows that 3.5% (28/807 pool) were confirmed H5 sub-type of AI. The percentage was identified 8.4% (14/167 pool) from poultry collectors, 8.1% (6/74 pool) live bird market, 2.1% (7/332 pool) nomadic ducks, 1.4% (1/74 pool) villages, and 0% from passive surveillance.

Conclusion: In conclusion, AI virus was mostly detected in poultry collectors and live bird market. It suggested that poultry collector and live bird market have highest risk of AI transmission. It is recommended that control measures should be focused in these enterprises.

Key words : Avian Influenza, endemic, highly pathogenic Avian Influenza, surveillance, Real-Time PCR .

What can we say from the death of layer chickens? Estimating within-flock HPAI (H5N2) dynamics using an Approximate Bayesian Computation framework

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ABSTRACT

Objective: In early 2015, outbreaks of H5N2 clade 2.3.4.4 highly pathogenic avian influenza (HPAI) were detected in commercial poultry in the upper Midwestern states of the United States. The unprecedented scope of the outbreak highlighted gaps in the epidemiological understanding of this novel HPAI in commercial flocks. In particular, it was unclear how the complex population structure present in caged layer operations may affect the spread of the virus within barns. In this study, we aim to infer the epidemiological characteristics of how this virus spread within barns of table egg layer operations during the outbreak.

Materials and methods: A stochastic, individual-based, Susceptible-Infectious-Recovered (SIR) model was fitted to bird mortality data recorded in six barns using Approximate Bayesian Computation employing sequential Monte Carlo (ABC-SMC) to infer epidemiological parameters. The model assumed that susceptible birds can be infected through both direct (structured, occurring only between birds within cages and between contiguous cages, consistent with a caged housing structure) and indirect contacts (homogeneous mixing process).

Results: The spread of H5N2 in table egg layer operations was characterised by a long infectious period (12.4 to 16.4 days). This is greater than what was reported for other subtypes. Posterior estimates of direct (β_w) and indirect (β_b) transmission rates varied from 8.42 to 10.2 and from 4.03 to 5.15 per infectious chicken per day, respectively. Although these estimates are based on a small number of barns, inferences highlight the importance of indirect/fomite transmission. For all barns, the model estimates that 16-to-17 days would, on average, elapse between a virus introduction and detection of clinical signs.

Conclusion: This work provides an improved understanding of how this novel HPAI virus may spread in caged layer operations, which can strengthen planning for surveillance and response activities.

Key words: Avian influenza, outbreak investigation, modelling, ABC-smc

Identification of research priorities of veterinary surgeons and horse owners with regard to the diagnosis and treatment of Pituitary Pars Intermedia Dysfunction (PPID) in horses and ponies

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ABSTRACT

Objectives: To identify the research priorities of veterinary surgeons and horse owners for pituitary pars intermedia dysfunction (PPID), the most prevalent endocrine disorder of older equids. To achieve this by adapting public and patient involvement methodology, widely used in human medicine to help inform research agendas, into an equine veterinary setting.

Materials and Methods: The James Lind Alliance (JLA) Priority Setting Partnership (PSP) Framework was adapted. Questions about the diagnosis, treatment and prognosis of PPID were gathered via an online survey targeting veterinary surgeons and horse owners with experience of the disease. Thematic analysis was used to form a longlist of unique indicative research questions (UIRQs). The evidence-base was searched to identify which UIRQs were 'uncertainties', defined by the JLA as a question which is not answered by a published clinically relevant up-to-date systematic review. In an interim prioritisation survey, questions were ranked by weighted scores creating a shortlist of 25 taken forward to the PSP workshop. During the PSP workshop participants prioritised and reached a consensus on the 10 most important research questions.

Results: 524 useable responses containing ≥1 question were received (n=485, 92.6% owners; n=39, 7.4% veterinary surgeons). After screening for relevance, 1,260 individual questions were included in the thematic analysis, resulting in 47 UIRQs. Interim prioritisation votes for the UIRQs were received from 360 respondents. The top 10 questions prioritised at the workshop focused on long-term prognosis, diagnostic accuracy, efficacy of pergolide, alternative treatment/management strategies and poor responders to treatment.

Conclusions: The response and quantity of questions generated indicates an extensive number of uncertainties regarding the diagnosis, treatment and prognosis of PPID. The top 10 research questions will help to direct future research into areas most important to the end users.

Key words: Pituitary pars intermedia dysfunction, horse, priorities, evidence-based veterinary medicine

Moving towards a One Health surveillance system for antibiotic resistance in Vietnam

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ABSTRACT

Objective: Following international recommendations, the Vietnamese government has issued an inter-ministerial surveillance strategy for antibiotic resistance (ABR) in line with the One Health (OH) concept. To appraise the feasibility of operationalizing this strategy within the national context, we aimed to explore the rationale behind the willingness of operational actors to embark or not in the collaborative strategy developed at the policy level, stressing out factors that may impede or enhance its implementation.

Materials and methods: We based our reasoning on an iterative stakeholder mapping and analysis, conducted in three distinct steps: (1) a description of the structure of the national surveillance strategy (literature review, key informant interviews); (2) an analysis of the key actors' position regarding the strategy (semi-structured interviews); (3) the identification of factors influencing the operationalization of the collaborative surveillance strategy.

Results: The mapping of the surveillance system, as well as the characterization of key actors regarding organizational and functional attributes underlined that inter-sectoral surveillance initiatives are occurring but that the organization of the national surveillance system remains highly silo-oriented. Based on actors' perspectives, we identified seven factors that may influence the implementation of the OH strategy at national level: the governance and operational framework, the divergence of institutional culture, the level of knowledge, technical capacities, allocation of resources, conflicting commercial interests and the international partners' influence.

Conclusion: The study suggests that the operationalization of the collaborative surveillance strategy requires the full adhesion of the actors and the provision of appropriate resources. Based on these findings, we propose a guidance framework together with recommendations to move towards a more suitable governance and operational model for OH surveillance of ABR in Vietnam.

Key words: One Health, surveillance, antibiotic resistance, influential factors, actors mapping

Epidemiology of Foot and Mouth Disease in an Endemic Setting

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ABSTRACT

Objective: Foot-and-mouth disease (FMD) is a highly contagious viral infection of cloven-hoofed animals. A study was conducted to investigate the disease's spatial and temporal occurrence, farmer knowledge and risk factors for the disease in an endemic area in Kenya.

Materials and methods: Semi-structured interviews were conducted on 220 smallholder farmers in Nakuru County, Kenya, selected using random spatial sampling. Data from the laboratory analysis of 171 samples was also obtained from the Kenya National FMD laboratory. The samples were self-submitted by community animal health workers and farmers as well as from outbreak response teams for the period 2010 – 2016 in the same area.

Results: The majority of respondents [207/220 (94.1%)] knew of FMD and 166/207 (80.2%) of the respondents could correctly identify the disease based on their knowledge of the clinical signs. FMD had occurred in 5.9% of the surveyed farms within the previous six months.

The use of a shared bull, the number of sheep owned and the number of additional cattle bought in the previous 12 months were associated with the farm experiencing a case of FMD in the previous six months. A spatial Bernoulli model revealed a single disease cluster (radius = 5.32 Km) in the northern part of the study area. In the retrospective study a total of 107/171 (69.3%) of the samples were positive for FMDV serotypes (A, O, SAT -1 and SAT-2) with simultaneous outbreaks occurring every year under study. There was weak evidence of seasonality with the highest relative risk of sample submission being observed in March and September, the final months of the dry seasons.

Conclusion: The results of these studies can be used to inform the development of a risk-based FMD control strategy and as a baseline for evaluating future interventions used in FMD management programmes.

Key words: Semi-structured interview, smallholder farming system, spatial survey, passive surveillance, regression

Modelled foot-and-mouth disease (FMD) outbreak frequency and characteristics following disease incursions

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ABSTRACT

Worldwide, foot-and-mouth disease (FMD) has the greatest economic impact of any livestock disease. The epidemiology of this highly infectious viral disease remains poorly understood, particularly in endemic regions, hindering effective control.

Within-herd outbreak frequency in endemic settings is controlled by rate of disease incursion and intrinsic factors including population turn-over (herd management) and impact on herd susceptibility of past incursions. We explore the incursion-outbreak relationship using a Susceptible-Exposed-Infectious-Recovered-Carrier disease dynamic to model within-herd transmission, and a threshold proportion of susceptible individuals as an indicator of outbreak risk.

When a herd suffers an outbreak, disease incursion is less likely to lead to a subsequent outbreak due to a reduced proportion of susceptibles. Results show that following an outbreak, higher rates of population turn-over reduces the time until the population is once again at significant risk of an outbreak. Further reductions in the duration of this low risk period are observed when repopulating the herd with a greater proportion of susceptible individuals. Overall, higher rates of incursion lead to smaller, but more frequent outbreaks and a higher overall burden of disease. Counter intuitively, this suggests that as incursion risk reduces farmers may perceive an increase in the frequency of outbreaks, assuming that small more frequent outbreaks are more likely to go unnoticed.

Modelled outbreaks occur less frequently than observed in endemic regions of Cameroon, particularly if only large outbreaks are observable. This discrepancy is robust to uncertainty in model parameterisation suggesting real world outbreaks result from circulation of multiple strains without significant cross immunity. Future models should account for multiple FMD strains and the heterogeneous landscape of farms within which they circulate.

Key words: Foot-and-mouth disease, endemic, outbreak risk

Research within international non-governmental organisations: building research capacity through development of a global research group

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ABSTRACT

Robust evidence-generation in an organisation necessitates (a) locally-available and strong research skills and (b) a systematic approach to identifying research priorities. Brooke is an international non-governmental organisation (iNGO), with staff in seven low and middle-income countries, aiming to implement sustainable, evidence-based animal health and welfare programmes. Brooke research had seen success with locally-relevant projects, however there were limited fora for answering large, strategic questions. Individual country programmes had limited opportunity to collaborate, access peer-support and share ownership of the organisation's research portfolio. Relevant research disciplines for the organisation are diverse, including epidemiology, socioeconomics and ethology, introducing a challenge in ensuring appropriate internal capacity in all subjects. Initiation of an internal Animal Welfare and Ethical Review Body was a pivotal point in raising the profile and improving quality of organisational research work and highlighted the need for its global coordination.

Formation of an International Research Group (IRG) was proposed. Workshops in each country were held August–September 2017, facilitated by the relevant research lead, and including representatives from each organisational function and level. Workshops outputs were consolidated during a meeting of research leads in London, September-2017. Draft terms of reference for the IRG were created alongside a six-month vision. IRG members were recruited through an application process, and the group's first meeting was in December-2017, with participants from 5 countries, using video conferencing facilities. It meets every six weeks.

The IRG is a community hub for research activities at Brooke providing expertise, coordination and communication, and curating a common organisational vision of research. Initial priorities include development of clear, universal understanding of all the organisation's research; application and review process for future research; a framework for external collaboration so external expertise can be sourced; and clear research priorities following an evidence gap-mapping process aligned to assumptions within the organisation's theoretical framework for programmatic impact.

Key words: Research capacity, LMICs, research

History and Epidemiology of Foot and Mouth Disease in Afghanistan: A retrospective study

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ABSTRACT

Foot and Mouth Disease (FMD) is endemic in Afghanistan. A retrospective study of data collected through passive surveillance of outbreaks of FMD from 1995 to 2016 was undertaken. A total of 1471 outbreaks were reported between 1995 and 2008 and 4845 samples were test positive between 2009 and 2016 in 34 provinces. The number of outbreaks did not differ significantly (P = 0.24) between 1995 and 2008. However, during this period there was a strong correlation between the number of outbreaks reported and the number of districts containing infected animals (r = 0.74, P = 0.002). From 2009 onwards, the distribution of the disease based on test positive samples was significantly different (P < 0.001) between years (2009 to 2016). Serotype O was the predominant serotype detected, however serotypes A and Asia1 were also detected. Cattle were involved in all outbreaks reported. The study also highlights the spatio-temporal distribution of test positive samples in Afghanistan. Herat province in the North-West (bordering Iran), Nangarhar province in East (bordering Pakistan) and Kabul province in the centre of the country were found to have infections in all years. The findings from this study provide valuable direction for further research to understand the epidemiology of FMD in Afghanistan.

Key words: Foot and mouth disease, Retrospective, Epidemiology, Afghanistan.

Spatial epidemiology of Highly Pathogenic Avian Influenza A H5N6 poultry outbreaks in Korea, 2016-2017: Case-case study to identify hotspot-related factors

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ABSTRACT

Objective: In 2003, the first outbreak of Highly Pathogenic Avian Influenza (HPAI) had occurred in Korea. Since then, only H5N1 and H5N8 has been developed in poultry. In November 2016, H5N6 was first reported in poultry in Korea, which lead to culling about 40 million poultry to curb the epidemic. Especially in Gyeonggi Province, 32.2% (123 of 382 cases) of total H5N6 outbreaks in Korea had occurred. Understanding local risk factors is key to help design interventions to reduce the risk of poultry outbreaks in hotspot regions. This study aims to identify specific H5N6 hotspots and quantify factors that differentiate hotspots from other areas in Gyeonggi Province, Korea.

Materials and methods: Data were selected from 123 HPAI-affected farms during 2016-2017 in Gyeonggi Province. To identify HPAI-hotspots, purely spatial scan statistic using farm coordinates was performed. A case-case study was conducted to compare within-hotspot cases and outside-hotspot cases to identify the hotspot-related risk factors, Six poultry industry factors, such as poultry density and farm density, and three wild migratory bird factors including Normalized Difference Vegetation Index (NDVI) and elevation are considered in a multivariable logistic regression model.

Results: Primary and secondary hotspots in Gyeonggi Province were demonstrated. There were 40 and 21 cases (61 cases; 49.6% of total outbreak in the Province) each and risk ratios were 3.9 ($P<0.01$) and 4.32 ($P<0.01$), respectively. Results of the multivariable regression model showed that within-hotspot cases were significantly associated with increased poultry density [Odds Ratio (OR) = 1.03, Confidence Interval (CI): 1.03-1.04], reduced farm density (OR= 0.74, CI: 0.58-0.92), higher elevation (OR = 1.07, CI : 1.04-1.11), and lower NDVI (OR for IQR change = 0.02, CIs : 0.01-0.18) compared to outside-hotspots cases.

Conclusion: Our study indicates that the HPAI-affected farms within identified hotspots were primarily located in areas characterized by large-sized intensive poultry-industry and inversely associated with environmental indicators of wild migratory bird presence. Further, investigation is required to understand the role of poultry movement and airborne dissemination in farm-to-farm transmission within-identified hotspots.

Key words: Avian influenza, spatial analysis, spatial scan statistic, risk factor, Korea

Development of a conceptual framework and assessment tools to assess the Foot and Mouth Disease (FMD) control program in the proposed FMD-free zone in Thailand

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ABSTRACT

Objective: This study aims to propose a conceptual framework and assessment tools for using in the assessment of the current FMD control policy and its implementation in the proposed FMD-free zone in Thailand.

Materials and methods: To develop the framework and assessment tools, data and information were collected to identify: (i) a list of essential elements of successful FMD control programs; (ii) a list of stakeholders; and (iii) a list of relevant regulations and other documents for the development. The framework and assessment tool were developed under the assumptions that: (i) testing and diagnostic systems were adequate, rapid, and satisfied international standards, and (ii) the reporting system had an appropriate design.

Results: The proposed framework included essential characteristics of policy design and implementation that should be found in the FMD control program in Thailand. The assessment tools included an assessment matrix and three sets of questionnaires. The assessment matrix identified shortcomings of policy design, policy implementation, veterinary capacity, and stakeholder engagement. The questionnaires were designed to collect supporting information to verify if elements of the FMD control program had been met with criteria in the assessment matrix.

Conclusion: The proposed framework and assessment tools are currently being applied to assess the proposed FMD-free zone in Thailand. The expected outputs from the assessment will indicate whether the FMD control system in Thailand meets the international requirements for FMD-free status. This assessment process will help the researchers to make recommendations for improvements of the FMD control program in Thailand.

Key words: Foot and Mouth Disease, disease control, FMD-free zone, assessment, Thailand

Temporal and geographic distribution of weather conditions favorable to airborne spread of foot-and-mouth disease in the coterminous United States

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ABSTRACT

Objectives: Under favorable weather conditions, airborne transmission of foot-and-mouth disease (FMD) can hinder the ability to rapidly contain an outbreak and minimize economic consequences. Although not the predominant route of infection, airborne transmission has been implicated in previous outbreaks. Our objective was to identify seasonal and geographic differences in patterns of conditions favorable to airborne FMD spread in the United States to inform effective Federal and State control strategy planning and preparedness.

Materials and methods: Data from a national network of surface weather stations were examined for three study years (December 2011–November 2012, December 2012–November 2013, December 2014–November 2015). Weather conditions favorable to airborne transmission were taken from the literature where possible and sensitivity analysis was performed around key weather parameters.

Results: Weather conditions were found to be most frequently favorable to airborne spread during the winter. Geographically, conditions were most frequently favorable to airborne FMD spread in the upper Midwestern United States, a region where swine and cattle populations are common. Generally, mild weather conditions with few extremes were more favorable for FMD spread. National patterns in risk areas for airborne FMD spread were similar across study years even though the degree of risk differed based on variations in weather patterns among study years.

Conclusion: Our findings suggest that airborne transmission could contribute to FMD spread in the coterminous United States, and that some geographic areas are at an increased seasonal risk. To our knowledge, this is the first study to characterize the seasonal and geographic variation in weather conditions favorable to airborne FMD spread on a national scale in the United States. The findings presented here can be used to enhance preparedness and surveillance activities by identifying geographic areas in the United States where airborne spread is most likely to be a risk factor for transmission during an outbreak.

Key words: Foot-and-mouth disease, environment, weather, geographic information systems

Infection dynamics of Foot-and-Mouth Disease in contact-exposed pigs are determined by the estimated exposure dose

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ABSTRACT

Objective: Understanding of the variability of foot-and-mouth disease (FMD) infection dynamics which may occur in naturally exposed pigs is essential to better plan for epidemic preparedness. The current study utilized data from novel experimental studies of FMD transmission in pigs to 1) estimate the minimum shedding quantity of FMD virus (FMDV) in oropharyngeal fluid (OPF) that delineates the transition from latent to infectious phases in inoculated donor pigs and 2) estimate the exposure dose that contact-exposed pigs receive and how that influence FMDV infection dynamics.

Materials and methods: Generalized Additive Mixed Models were used to investigate FMDV infection dynamics in groups of pigs that had been infected through simulated-natural intra-oropharyngeal inoculation, or via direct contact exposure to inoculated donor pigs that were shedding varying quantities of virus.

Results: The estimated threshold for onset of infectiousness based upon FMDV quantitated in OPF was on average $10^{3.18}$ $TCID_{50}$/ml. In parallel to the estimated FMDV shedding quantities from the infected donor pigs, the estimated exposure dose effectively received by the contact-exposed pigs predicted the variation of the subsequent infection dynamics. Specifically, the exposure dose determined the time of the first detection of FMDV RNA in OPF and serum, and the appearance of clinical signs.

Conclusion: The outcomes of these modeling approaches for dose-quantitation and dose-dependency of FMD infection dynamics in pigs provide a practical insight of the interpretation of experimental studies results which may be applied to field scenarios. Robust understanding of the variability of infection dynamics is necessary for improved preparedness planning, including surveillance and control strategies.

Key words: Foot-and-Mouth disease, infection dynamics, swine, shedding, exposure-dose

OIE veterinary education twinning programme: Postgraduate education by research

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ABSTRACT

Objective: The OIE Veterinary Education Twinning Programme between the Royal Veterinary College (RVC) and the Jordan University of Science and Technology (JUST) started in 2015 and is one of the first education twinning programmes endorsed by the World Organisation for Animal Health (OIE). The aim of the program is to establish a knowledge exchange platform to share best educational and research practices in the broad field of veterinary public health, and to use this platform to facilitate long term collaboration between RVC and JUST in Veterinary Public Health training and research in the Middle East and Arab region.

Materials and methods: An ambitious component of this program was the postgraduate education by research, which aimed to promote intense educational exchange between a large team of students and supervisors, from the UK and Jordan. It consisted in a series of paired Master of Research (MRes) and Master of Science (MSc) projects, in which students were trained by means of conducting parallel and coordinated research on complementary topics related to veterinary public health. Students and their supervisors had the opportunity visit both countries, attend face-to-face meetings and coordinate work on a number of specific research topics (chosen to fit well within the OIE remit and be aligned with the priorities and strengths of JUST and RVC), which were used as vehicle for postgraduate education by research.

Results/ Conclusions: The parallel research conducted by RVC-JUST has been a very successful branch of the OIE Veterinary Education Twinning Programme. Students have obtained their MRes and MSc degrees, and several scientific publications, manuscripts (in preparation for publication), and oral communications in conferences have been co-authored by the students and supervisors from JUST and RVC. The academic qualifications and technical skills gained during the post graduate component contributed for students successfully securing jobs in academic research, scientific publishing, and PhD programs.

Key words: JUST, OIE, RVC, twinning programme, veterinary education

Identification of areas at risk for foot-and-mouth disease virus circulation in Ecuador using maximum entropy models

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ABSTRACT

Most of South American veterinary services in collaboration with livestock sectors and the Pan American Centre for Foot-and-Mouth Disease of the Pan American Health Organization (PANAFTOSA-PAHO) have significantly advanced in the control and eradication of Foot-and-Mouth disease (FMD) in their territories. Thus, out of a population of just over 350 million cattle, 97% of all the herds and 95% of the total cattle have been recognized by the OIE as FMD-free, the majority still being part of zones where vaccination is practiced. Since bovine population is considered the reservoir for FMD virus infection in the Region, this scenario of vaccination might hamper the detection of potential residual viral transmission still present; which would challenge the regional elimination efforts. For that reason, the identification of areas with potential persistence of viral transmission, such as subpopulation with insufficient herd immunity, is key to implement risk-based surveillance and control strategies and more rapidly achieve eradication. This multi-institutional collaboration between the National Veterinary services of Ecuador "Agencia de Regulación y Control Fitozoosanitario" (Agrocalidad), PANAFTOSA and the University of California, Davis aimed to identify areas that due to their geographic, demographic, epidemiological, and socio-economic characteristics are at higher risk to still have virus circulation or low levels of herd immunity within the country. We used species distribution modeling (Maxent) for such purpose. Data regarding the demographic characteristics of the farms, immunity status of a sample of the cattle population and movements within Ecuador were provided by Agrocalidad. We also collected publicly available data regarding the bioclimatic, socio-economic and geographical characteristics of the farms such as: temperature, precipitation, altitude, land use, density of roads, human development index, population density. The risk maps obtained provide valuable information to inform further strategies for surveillance and control and, hopefully, will accelerate the advancement towards the eradication of the disease.

Key words: FMD, herd immunity, Species distribution modeling, Maxent, risk-based strategies

The reproductive number: an elegant method for determining vaccination impact on Highly Pathogenic Avian Influenza outbreak transmission in backyard poultry populations on Java

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ABSTRACT

Objective: Research was implemented on Java, Indonesia, to determine appropriate vaccination program design against H5N1 highly pathogenic avian influenza, and potential impact on disease incidence. It was hypothesized that quarterly vaccination in backyard and semi-commercial poultry would reduce disease incidence. It can be difficult to determine the incidence of H5N1 outbreaks in mixed poultry populations, because of the preponderance of per-acute death prior to serological conversion. Thus a multi-methods approach was used to assess the impact of H5N1 vaccination on outbreak incidence.

Materials and methods: Methods included longitudinal operational research comparing disease incidence in three treatment groups (vaccination with Legok 2003 H5N1, co-vaccination with Legok 2003 H5N1 and HB1 Newcastle disease, and an unvaccinated control), analysis of national surveillance outbreak data in the research area, and study of H5N1 transmissibility in the aforementioned vaccinated and unvaccinated groups.

Results: All three methods showed that relatively modest levels of population immunity significantly interrupted H5N1 outbreak occurrence. 63.8% of birds in a household flock need to be immune to H5N1 to interrupt transmission within the flock, 51.7% of household flocks in a neighborhood. Two of the methods were found to be relatively time and resource demanding. The transmissibility study was the most modest in terms of resources, involving a single field epidemiologist relying on available national data to intensively study laboratory confirmed outbreaks of H5N1.

Conclusion: The advantages of using the reproductive number calculated from modified event tree data collected using participatory epidemiological methods are discussed, including providing additional data to support a disease control program such as morbidity, mortality, and case fatality, outbreak lengths, proportion of susceptible units affected, time and distance between households during outbreaks, and risk factors such as the presence of Muscovy ducks, commercial poultry, and bird contact between households.

Key words: Highly Pathogenic Avian Influenza, vaccination, backyard poultry, transmissibility, Indonesia

Life Cycle Assessment of Swine and Poultry Production in the Philippines: A Comparison of Housing with Natural and Tunnel Ventilation

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ABSTRACT

Objective: A life cycle assessment (LCA) of swine and poultry production was carried out to compare the environmental performance of raising the farm animals in houses with natural and tunnel ventilation system. This study used the attributional LCA approach wherein the impacts were measured based on the material and energy flows.

Materials and methods: The system boundary was the operation involving grower-finisher pigs reared in 16 to 17 weeks and broilers harvested after 30 days. Inventory analysis was conducted in the facility of selected farm cooperators both for swine and poultry. The following were specifically quantified: number of swine and poultry animals, feeds, volume of water required for each of the life cycle stage, volume of diesel used for transportation, electricity consumption, amount of LPG used for warming the air inside the animal house, amount of solid wastes, excess nitrogen (N) and phosphorus (P), CO_2 and SO_2 emissions. The functional unit used is per harvested animal. The impact categories include global warming potential (GWP), atmospheric acidification potential (AP) and eutrophication potential (EP). Results revealed that broiler production could be more preferable than swine production due to its lower potential impacts to the environment.

Results: The outcomes also showed that farms utilizing natural ventilation had lower impacts compared to the tunnel ventilated production but only on a relatively minimal amount. It was found out that in the process of raising one grower-finisher pig, the impacts in terms of GWP, AP, and EP for natural and tunnel ventilation setting were 0.98, 0.0016, and 3.36, and 9.71, 0.0154, and 6.88, respectively. Meanwhile, the environmental impacts for the production of one broiler chicken were 0.1833, 3.24E-05, and 0.0090, and 0.2083, 3.14E-05, and 0.0175, respectively.

Conclusion: These findings serving as benchmark could guide swine and poultry farm operators and policy makers in crafting solutions to reduce environmental emissions of this industry.

Key words: life cycle assessment, tunnel ventilation, swine, poultry, environmental impact

Seroprevalence of Bovine Coronavirus antibodies in dairy cows in Prachuap Khiri Khan Province, Thailand

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ABSTRACT

Objective: Bovine coronavirus (BCoV), a positive sense single-stranded RNA virus, is an important causative agent of Winter dysentery in dairy cattle worldwide. The purpose of this present study was to assess the seroprevalence of BCoV's antibodies in 1 dairy farm in Prachuap Khiri Khan Province, Thailand.

Materials and methods: A total of 119 dairy cows sera from 1 dairy herd were collected every week for 5 weeks and examined for BCoV's antibodies by commercial BCoV ELISA test kit.

Results: Of these 119 samples, 61.54%, 92.31%, 100% 100% and 100% were positive for antibodies to BCoV in week 1,2,3,4 and 5 respectively. Twelve samples (10.08%) were negative for antibodies to BCoV in week 1 and 2. All the week in dairy farm in Prachuap Khiri Khan Province were positive.

Conclusion: The seroprevalence of BCoV among week can be regarded as very high. Further consideration should be given to investigating and intiating control programmes for dairy herds in Thailand.

Key words: Bovine coronavirus, serum samples, dairy cattle, ELISA, Winter dysentery disease

Network for Evaluation of One Health: A Systems approach for better integration

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ABSTRACT

Objective: One Health (OH) is promoted as an approach for health challenges arising from the intertwined spheres of humans, animals and the ecosystems constituting their environment. The EU COST funded "Network for Evaluation of One Health (NEOH)" identified characteristic features of OH initiatives and developed an evaluation framework with tools to assess these characteristics systematically.

Materials and Methods: The NEOH hypothesises that OH initiatives tackle complex problems at the animal-human-environmental interface. Therefore, they require adaptive leadership to apply systems thinking, transdisciplinary working, and inclusive and flexible planning. In addition, infrastructures providing opportunities for individual, team and organizational learning are essential, thereby requiring sharing of data, information and experiences. With the NEOH tools, these characteristics are assessed systematically in a semi-quantitative way and summarized in a OH-index and OH-ratio. These can then be compared to selected outcomes in line with the initiative's theory of change. Application of the framework to 10 international case studies allowed identifying gaps and opportunities for further development.

Results: The framework proved useful to systematically assess the characteristics of OH initiatives within the relevant context. However, system mapping and analysis wered traceabi found challenging for OH practitioners and evaluators. The OH-index currently only provides an approximate indication of the degree of integration achieved by an initiative due to professional judgment, whereas the OH-ratio illustrates quite clearly the match between OH behaviour and enabling infrastructure. The measurement of interdisciplinary and OH outcomes was a limiting factor for full evaluations in the case studies.

Conclusion: The NEOH framework provides the foundation for comparisons of OH initiatives. Systems thinking and associated techniques require good training to be effective for project planning, implementation and evaluation. The framework and its application – documented in a new handbook - is not only useful for evaluation, but also for planning of OH initiatives.

Factors influencing animal rabies in southern Thailand, January 2014 – June 2017

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ABSTRACT

Objective: Rabies is an important zoonotic viral disease in Thailand. Human and animal rabies, predominantly, dogs still occur throughout the country. This study described the characteristics and distribution of rabid animals by animals, times and places, and to evaluate the influencing factors of dog rabies.

Materials and methods: We included all rabies diagnostic cases in southern Thailand from January 2014 to June 2017, which were available on the Thairabies.net database. We evaluated the association between dog rabies and influencing factors: vaccination status, owner status, habitat status, age of dogs, clinical signs and seasons, by logistic regression models.

Results: The overall animal rabies was 66.58% (263/395). Majority of rabies positivity was 77.57% in dogs (204/263) and 20.53% (54/263) in cattle. Rabid animals were found in eight provinces, the top three rabies positive provinces were 68.82% (181/263) in Songkhla, 9.13% (24/263) in Nakon-Si-Thammarat and 7.60% (20/263) in Trang. In addition, rabies dynamically occurred all year round in the same areas. The univariate odds ratio was higher in dogs with aggressive signs (OR=5.50;95%CI=2.80-10.78), free-roaming dogs (OR=3.45;95%CI=1.21-9.81) and stray dogs (OR=1.98;95%CI=1.01-2.76). Moreover, the multivariate analysis showed that dog rabies was associated with dogs aged> 1 year old (OR=1.61;95% CI=1.05-20.03) as well as aggressive signs (OR=5.17; 95%CI=2.05-14.55). We found that animal rabies repeated in some areas. Dog with aggressive sign, free-roaming dogs, stray dogs and dogs aged > 1 year old had a high opportunity of being rabies.

Key words: Animal rabies, dog, logistic regression, southern Thailand

Teaching One Health and epidemiology as tools for applied critical thinking

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ABSTRACT

Objective: Over the past decade, there has been a significant increase in the number of undergraduate programs in public health. Many have embraced One Health as an integral part of their curriculum. The University of Illinois at Chicago, School of Public Health, has incorporated One Health as one of the six "Curricular Themes" that bring core content into confluence, "promoting coherence within and across courses along the entire educational sequence."

Materials and methods: The principles of epidemiology serve as the basis for a two-course sequence in critical thinking. Within those two courses are extensive, student-centered instruction on: study design, survey development, the hierarchy of evidence, analysis of selected public health journal articles, Bloom's taxonomy of educational objectives, and the logical fallacies commonly employed in argumentation, especially in discussion of public policy.

Results: The Applied Critical Thinking course is a 2 credit-hour 300 level course for undergraduate students in the University of Illinois Chicago School of Public Health baccalaureate program. The goal of the course is to use applied epidemiology, to prepare students to make reasoned, intelligent decisions about public health matters. At the conclusion of the course students are be equipped to: 1) argue issues more clearly, precisely, accurately, and fairly; 2) create cogent analyses in support of conclusions; 3) use tables and graphs to communicate quantitative information effectively in written and oral forms; 4) valuate the quality of the evidence, and 5) translate numbers into information .

Conclusion: The curriculum is designed to help students recognize the strengths and limitations of study design and methodology, assess data quality, evaluate the significance of results and their applicability to real world populations, and communicate findings in an effective manner to a community audience. A recommendation has been made to extend training in epidemiology and public health beyond those students who elect to major in public health.

Key words: One Health, critical thinking, applied epidemiology, public health

Determinants of foot-and-mouth disease in Iran: A farm level case control study

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ABSTRACT

Objectives: Foot-and-mouth disease (FMD) is one of major contagious animal. The purpose of this study was to evaluate the determinants associated with FMD occurrence in farms.

Materials and methods: A case- control study was carried out in cattle farms. The cases were farms with new reports of FMD and controls were units without any report of F
MD in last 6 month. For assessing the risk factors, a researcher- made questionnaire was used. Statistical analyses were done with SPSS version 16 using the logistic regression test.

Results: Purchase of new livestock [OR: 14.69 (CI95%: 4.29, 5 0.36)] and passing migratory livestock [OR: 13.32 (CI 95%: 1.74, 101.87) were identified as the risk factors of the disease. Visiting the farm by the vaccinator in last 2 weeks [OR: 0.17 (CI 95%: 0.05, 0.63)] and buying new livestock from the same village/ city where the farm is located [OR: 0.16 (CI 95%: 0.04, 0.58)] were considered as protective factors.

Conclusion: Considering the role of infected livestock in the country, the most important steps for effective preventation are: areadherence to biosecurity as well as quarantining new purchased animals, and informing and training farmers to not purchase new animals from farms that are located in the infected areas and around the times of outbreak.

Key words: Case control study, risk factors, foot and mouth disease

Willingness-to-pay/Willingness-to-accept to air and water quality improvement/ degradation among households in swine and poultry farm communities in the Philippines

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ABSTRACT

Objective: In the Philippines, there is an increasing trend in swine and poultry raising both backyard and commercial to meet the increasing demand in meat consumption. This contribute to alarming problems such as foul odor emission and occurrence of numerous flies in communities where the farms are located. While there are regulations setting the distance of farms to built-up areas, still there are cases in the country wherein households co-exist with swine and/or poultry farms in a barangay thereby creating conflict because of the previously mentioned environmental problem.

Materials and methods: This study determined the WTP and WTA of households residing near a swine farm and households residing near two different poultry farms, naturally and tunnel ventilated. The contingent scenario was to invest in a water quality monitoring and treatment facility and air quality monitoring equipment. The knowledge, attitude, and perception of households were also determined. Data were obtained through household survey using pre-tested structured questionnaires.

Results: There were a total of 336 respondents for the survey near swine farm while 52 and 124 respondents for the survey near conventional and tunnel ventilated poultry farms, respectively. Results showed that the mean WTP and WTA per household near the swine farm are PhP 403.82/month and PhP 1,430.65/month, respectively. On the other hand, the mean WTP per household near the naturally ventilated and tunnel ventilated poultry farms are PhP 1,131.30/month and PhP 363.56/month, respectively while the mean WTA per household are PhP 2,468.30/month and PhP 366.16/month.

Conclusion: These results could guide policy makers or the whole community in resolving their environmental issues and could be a benchmark in other places experiencing the same situation.

Key words: Willingness-to-pay, willingness-to-accept, tunnel ventilated, swine, poultry

Molecular epidemiology of Iranian Foot-and-mouth disease (FMD) viruses based on full genome sequencing data, 2017

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ABSTRACT

Objective: Foot-and-mouth disease (FMD) is a severe infection caused by a picornavirus that affects livestock and wildlife and causes significant economic losses in Iranian livestock. FMD virus has a high mutation rate, leading to extensive genetic variation. Here are seven different serotypes, each with a diversity of topotypes, genetic lineages and strains. Some lineages have different properties that may contribute to sporadic spread beyond their recognized endemic areas.

Materials and methods: RNA extracted from clinical bovine samples, demonstrating the feasibility of full-genome sequencing from strong positive samples taken from symptomatic animals.

Result: Phylogenetic analysis based on Full genome and VP1 gene revealed that the Iranian FMD isolates are classified in Asia1 clade and viruses were most closely related to isolates collected in Pakistan and Turkey.

Conclusion: It is the first full genome sequencing result in Iran. Data obtained from this study provide valuable information on the FMDV serotypes circulating in Iran and their genetic relationship with strains causing FMD in neighbouring countries.

Key words: Foot-and-mouth disease, Iran, molecular epidemiology, phylogenetic study

Economic and social analyses of avian influenza A (H7N9) control strategies in southern China

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ABSTRACT

This study investigates the economic value and social factors of China's H7N9 control strategies. An empirical study was conducted in five provinces of south China to: document the broiler chicken trade and its production systems; assess the economic impact of H7N9 to the industry; and review the current policy and interventions applied.

H7N9 avian influenza has become a serious public health issue in China, including concern over the potential for pandemic development, since it was first detected in humans in March 2013. It caused more than 1,600 human cases with a high case fatality rate and has spread widely in the poultry population in China.

In addtion, H7N9 created significant economic impacts to the poultry industry, especially yellow broilers (yellow feather chickens). Yellow broilers are the major source of chicken meat in south China producing approximately half of China's annual broilers due to consumer preference. Previous studies have identified LBMs as critical control points; however they are only part of a complex production and trade system.

Chinese veterinary authorities have conducted various interventions to tackle H7N9. However, China's diversified broiler production system and the complexity of its trade network constrain the success of these interventions. The limited understanding of the broiler production industry, the economic motivation behind adoption practices and factors associated with stakeholders' behaviour have also reduced the effectiveness of control measures. The study aims to fill in these gaps and the outcomes may assist Chinese policy-makers to more effectively control and prevent outbreaks of H7N9.

Key words: H7N9, economic impacts, policy

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