

Where n = sample size, t = value of the normal distribution (Student t) for a 95% confidence level ($t = 1.96$), L = accepted error or precision (5%), and SD = weighted disease prevalence (%). With This technique, the number of animals determined for random sampling was 242; collected into identified plastic bags; and observed at microscope.

Results: 194 (80.16%) positive to ticks; and 211 (79.92%) positive to fleas *Ctenocephalides* spp.

Conclusion: Is considerable number of positives animals and to continue in the present conditions, this problem can take importance in the society, because frequently these dogs are on different points from the town and can pass the infection of other healthy animals, visitors and even the same family.

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34.018

Phenotypical and genotypical traits of *Listeria monocytogenes* strains isolated from tonsils of wild boars hunted in Switzerland

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Background: During the last decades, wild boar populations have increased in Europe and spread over the entire continent. The population densities of wild boars in Switzerland are among the highest reported in Western Europe. High wild boar densities and increasing popularity of outdoor ranging of fattening pigs may intensify the risk of contacts between wild boars and domestic pigs and, therefore, the transmission of microorganisms and parasites. With this background and with the background of increasing per capita consumption of wild boar meat and the high per capita consumption of pork, knowledge of the situation of the food-borne pathogens circulating in the wildlife population is an important public health issue.

Methods: In this study, tonsils of 153 wild boars hunted in the Western part of Switzerland were enriched overnight in TSB and screened on the presence of *L. monocytogenes* using VIDAS®. Positive samples were cultured on two selective agar media. Presumptive positive colonies were biochemically identified. *L. monocytogenes* strains were further characterized by serotyping and genotyping methods.

Results: *L. monocytogenes* are food-borne pathogens that are distributed in a wide variety of environments. Human infection may lead to a serious and potentially life threatening illness known as listeriosis. Reports from the USA show that *L. monocytogenes* infections are responsible for the highest hospitalization rates (91%) amongst known food-borne pathogens. *L. monocytogenes* were isolated from tonsils of twenty-six (17%) animals. Of the 26 isolates, 45% were of serotype 4b, 38% were of serotype 1/2a and 17% were of serotype 1/2b. Epidemiological data from different countries shows that the majority of human infection outbreaks are primarily associated with three *L. monocytogenes*

serotypes (1/2a, 1/2b and 4b), despite the fact that there are 13 serotypes potentially capable of infecting humans. Further genotyping results of the isolated strains will be presented.

Conclusion: This study shows, that tonsils of wild boars are not only a reservoir for *Yersinia enterocolitica* and *Yersinia pseudotuberculosis*, but also for *Listeria monocytogenes*. This has mainly to be considered by the hunters, who may be handling carcasses under minimal hygiene conditions. Moreover, outside rearing of domestic pigs and close contact to wild boars may increase the risk of transmission.

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The "One Health" Initiative: Using open source data for disease surveillance

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Background: We have created a self-organizing ontology that allows us to organize and filter external data by relating email exchanges through their references into "reference-connected sets". These sets of messages can be generated dynamically and constructed in real-time to identify subject categories (e.g. disease outbreaks) as they evolve. This allows the filtering of less important information into sets of messages that uniquely identify events so the user is not overwhelmed with irrelevant information.

Methods: This paper describes the approach as it is applied to ProMEDmail, an Internet-based system dedicated to rapid global dissemination of information on infectious diseases. This official program of the International Society of Infectious Diseases has the largest reporting base of any health organization and can be used as a model for a bio-threat surveillance system that takes advantage of decentralized, Internet-based social networks.

Results: The presenter will demonstrate how the technique was used in an analysis of the evolution of pandemic influenza messages. The presenter will also discuss the benefits of expanding the approach through new science and technology solutions to increase global health security.

Conclusion: A medical informatics solution to surveillance of outbreaks of zoonotic diseases can be achieved through user-friendly graphic interfaces; automated extraction and formatting of data; expert systems for epidemiologic analysis; powerful algorithms for data and information fusion; interconnection with other networks (public health agencies, hospitals, animal/zoonotic disease surveillance); standard forms through an internet.

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