Co-infection project

Review workshop report

Josephat Maina[1], Mathew Muturi[1], Athman Mwatondo[1], James Akoko[2] and Bernard Bett[2]

[1] Kenya Zoonotic Disease Unit
[2] International Livestock Research Institute, Kenya

July 2022

The Program thanks all donors and organizations which globally support its work through their contributions to the CGIAR Trust Fund

Editing, design and layout—ILRI Editorial and Publishing Services, Addis Ababa, Ethiopia.

Cover photo: ILRI/Geoffrey Njenga

Citation: Maina, J., Muturi, M., Mwatondo, A., Akoko, J. and Bett, B. 2022. *Co-infection project: Review workshop report*. Nairobi, Kenya: ILRI.

Patron: Professor Peter C Doherty AC, FAA, FRS
Animal scientist, Nobel Prize Laureate for Physiology or Medicine–1996

Box 30709, Nairobi 00100 Kenya
Phone +254 20 422 3000
Fax +254 20 422 3001
Email ilri-kenya@cgiar.org

ilri.org
better lives through livestock

ILRI is a CGIAR research centre

Box 5689, Addis Ababa, Ethiopia
Phone +251 11 617 2000
Fax +251 11 667 6923
Email ilri-ethiopia@cgiar.org

ILRI has offices in East Africa • South Asia • Southeast and East Asia • Southern Africa • West Africa

Acknowledgements

We thank all the partners and stakeholders who attended the workshop for their excellent participation. The 'Co-infection with Rift Valley fever virus, *Brucella* spp and *Coxiella burnetii* in humans and animals in Kenya: Disease burden and ecological factors' project is sponsored by the Department of the Defense, Defense Threat Reduction Agency.

The content of the report does not necessarily reflect the position or the policy of the federal government, and no official endorsement should be inferred.

Summary

The 'Co-infection with Rift Valley fever virus, *Brucella* spp and *Coxiella burnetii* in humans and animals in Kenya: Disease burden and ecological factors', or Co-infection project, in short, held two back-to-back workshops in Naivasha, Kenya between 20–22 April 2022. The first meeting was limited to the project partners and was held on 20 April. The meeting reviewed the implementation status of the various project activities. The second meeting involved a wider group of stakeholders from various Kenyan institutions and was held from 21 to 22 April. The stakeholder meeting was used to disseminate preliminary findings from the project. The project aims to determine the burden and risk of three extremely dangerous pathogens (EDPs) – Rift Valley fever virus (RVFV), *Brucella* spp, *Coxiella burnetii* and their co-infections – in humans, livestock, and wildlife in Kenya.

The activities reviewed in the partner's meeting include a national serosurvey that aims to map the geographical distribution of the three pathogens, a longitudinal study to estimate the incidence of the three diseases in humans and livestock, wildlife sampling and biosafety and biosecurity training. On the national serosurvey, partners were informed that field and laboratory activities had been completed and plans were at an advanced stage to analyse data obtained. In the longitudinal study, partners were notified that an initial cross-sectional survey used to select appropriate study sites in Isiolo County had been completed and households had been chosen for a one-year longitudinal follow up. The wildlife sampling team also gave their presentation summarizing the work done. About 200 animals were sampled in the same areas, and the samples obtained, including blood, serum, faecal and nasal swabs, were collected.

The partner's meeting also provided a good forum for an in-depth discussion on procedures for collecting and preparing samples for molecular analyses, including sequencing and bioinformatics. The team from the Los Alamos National Laboratory (LANL) made presentations on preliminary studies that they had done to develop a protocol for evaluating blood microbiome in stored sera. Discussions were also held on setting up and maintaining a cold chain for keeping and transporting biological samples from the field.

The stakeholder's meeting was launched by the Director of the Wildlife Research and Training Institute, Patrick Omondi. He underscored the benefits of using One Health approaches to manage zoonotic diseases. The meeting provided a good opportunity to disseminate preliminary project findings and discuss potential policy products that the project could develop. Some of the key policy-relevant products identified include risk maps, estimates of disease burden from the longitudinal studies, capacity building of the graduate fellows involved in the project, and the biorisk management training activity that was underway. It was exciting for the project team to note that the biorisk management training was being considered by the team that led the curriculum development from the Ministry of Health and the Department of Veterinary Services as a pilot used to refine the national biorisk training curriculum. The team was also keen to explore opportunities of using the lessons learned from this work to extend the coverage of the training program to other counties not included in the project.

1 Introduction

Rift Valley fever, brucellosis, and Q fever are highly infectious zoonotic diseases associated with huge health and socio-economic burdens in many sub-Saharan African countries. In Kenya, these diseases have been ranked as important zoonotic diseases that should be prioritized for surveillance and control. To support these efforts, the International Livestock Research Institute (ILRI), in partnership with the Zoonosis Disease Unit (ZDU), the Ministry of Health (MoH), the Department of Veterinary Services (DVS), the Kenya Medical Research Institute (KEMRI), the University of Nairobi (UoN), the Kenya Wildlife Service (KWS), the Wildlife Research and Training Institute (WRTI), the Washington State University (WSU), and the Los Alamos National Laboratory (LANL) are implementing a biosurveillance project to determine the spatial distribution of these diseases in single or mixed infections in humans and animals, identify their ecological drivers and build capacity on biosafety and biosecurity practices among the frontline staff who lead biosurveillance activities in selected counties.

The project convened two successive workshops in Naivasha between 20 to 22 April 2022. The first meeting was held on 20 April and involved the project partners, while the second was held from 21 April to 22 with the project stakeholders. The program and list of the workshops' participants are given in Annex 1 and 2, respectively. The purpose of the first meeting was to evaluate progress on the implementation of the project activities. The second was to share preliminary findings and solicit feedback from the stakeholders.

2 Workshop proceedings

2.1 Partners meeting

The first (partners) workshop reviewed the project activities' implementation status. These activities included the longitudinal study, sequencing and bioinformatics, disease severity study and biorisk management. Of these activities, the longitudinal study was allocated more time to tighten its design, refine protocols for sample collection, storage and transportation, and data management and analysis. Presentations given under each of the listed activities are outlined below.

2.2 Activity reviews

2.2.1 The longitudinal study

Matthew Muturi and Athman Mwatondo, both from ILRI, gave presentations on the longitudinal study, detailing activities that would involve livestock and human sampling. These activities would be linked at the household level and implemented for one year. The main objective would be to determine the incidence of the three target pathogens (*Brucella* spp, RVF virus and *Coxiella burnetii*). The study has a secondary aim of building capacity for human and livestock disease surveillance and response.

A total of 92 households had already been recruited in Kinna, Garbatulla. From these households, 527 people, 621 cattle, 510 goats and 489 sheep had been enrolled. Plans had been made to collect various surveillance data, including syndromic data, serological data that would be collected at quarterly intervals, and records of clinical reports.
A baseline survey was done in March 2022 to aid the recruitment of subjects. A second sampling site was being considered for inclusion in the project.

The plenary discussions that were held after this presentation arrived at the following suggestions and recommendations:

- During quarterly sampling, consider collecting swab samples (nasal swabs, vaginal swabs). Collecting and storing paired swabs per Cryovial with universal transport media will be desirable to ensure that viral pathogens in the sample remain viable.
- To investigate the causes of abortion, collect
    - Two tissue swabs from an aborted fetus. Fetal swabs should be collected within 12 hours of the event to limit environmental contamination of samples. In addition, a field protocol should be refined to capture timelines for such samples.
    - Serum, two nasal swabs, and two vaginal swabs should be collected from dams. Also, use universal transport media for swabs collected to maintain the viability of any viral agents in the sample
    - Use ice packs in the field and immediately preserve samples in liquid nitrogen.
    - For long term storage, preserve samples at -80^{0}C

- Liquid nitrogen is to be used to maintain cold chain in the field.
- Plan to identify a second site for the project by mid-May. Garfasa, an RVF high-risk area with a history of flooding and RVF outbreaks, had been proposed.
- Consider including camels in the study. This may be possible in the second site (Garfasa)
- To support surveillance, develop a system for capturing and recording levels of water in River Ewaso Nyiro
- Plan to update the study manual and protocols to reflect the sample collection and storage recommendations.

2.3 The disease severity study

Mwatondo presented plans that have been made for the severity of illness study. He indicated that the disease severity study is a component of the human component of the longitudinal study whose primary objective is to determine whether co-infections with two or more of the target pathogens would enhance the severity of the ensuing illness in humans. In addition, the project will also determine the genetic variants of the pathogens that are associated with the severity of illness.

Participants for this sub-study will be drawn from the longitudinal study; human subjects will visit the health facilities to seek treatment for febrile infections. A case definition developed for recruiting the subjects for the main study will still be applicable here. This includes fever (>37.5°C) recorded or reported in the past two weeks AND at least one of the following: sweat, malaise, anorexia, headache, pain in muscles, joints, and/or back, flu-like symptoms, pneumonia). Participants who meet the case definition will consent, answer questions in a simple questionnaire, and samples will be collected (whole blood and serum).

The study will recruit a total of 224 participants, and they will be allocated into four clusters RVF virus-infected, *Brucella*-infected, *Coxiella*-infected and co-infected groups. Samples collected will be initially screened at the study health facility, and confirmatory tests will be done at ILRI labs. In addition, follow-up phone calls will be done every four weeks for eight weeks to each participant to monitor their recovery process.

Types of data that will be collected will include clinical signs and symptoms presented, duration of illness (clinical progression of the disease), laboratory screening (confirmatory testing, haematological parameters), response to treatment (cure, relapse, treatment failure) and outcome (cure, death). In addition, haematological parameters, including haemoglobin level, hematocrit, white cell count, and platelet level, will also be obtained. For data analysis, multivariable statistical models will be used. This will consider a variety of outcome indicators such as uninfected, one extremely dangerous pathogen (EDP), multiple EDPs, and severity score.

Comments made during the plenary discussion were as follows:

- Consider using a descriptive study design for the severity study.
- The workshop suggested a weekly follow up period running for eight weeks after treatment/detection.
- Consider identifying a field facility that can run a full haemogram instead of transporting samples to Nairobi for this analysis. Alternatively, the project could procure a haemogram to enable the analysis to be done locally. It will be good to discuss with stakeholders how a haemogram machine could be set up. This will also benefit the community.
- Given that there are no rapid tests for two of the three pathogens being studied and it might be difficult to recruit subjects for co-infection work, the project should consider including malaria in the study to streamline the recruitment process. RDT should be used as a screening test for malaria and those who turn positive should

have a smear done. A smear will provide information on severity through scoring. In addition, laboratory staff that participate in the study should be trained on malaria testing.

2.3.1 Sequencing, metagenomics, and bioinformatics

The LANL team led a discussion on planned sequencing, metagenomics and bioinformatics activities. The team indicated that the technology for running sequencing and metagenomics had improved incredibly over time. In this project, sequencing and metagenomics will be used to determine organisms (generally microbes) present in a biological sample collected from an infected human or animal host or the environment. Screening procedures will involve sequencing all or part of the DNA or RNA present in those samples.

Their presentation pointed out that metagenomics provides a universal process for screening samples, and no prior pathogen information is needed before initiating the process, unlike a multiplex PCR which requires one to obtain preliminary information on the pathogens that are being screened to set up the right primers and to determine potential cross-reactivity challenges. In addition, the metagenomics approach also detects all the pathogens at once in an efficient and rapid process, overcoming one of the limitations of multiplex PCR on its inability to detect rare pathogens.

However, sequencing and metagenomics are faced with a few challenges, including incomplete databases, incorrect entries, and taxonomy issues (name confusion, name changes, synonyms). There is also a need to strictly adhere to strict data collection and processing procedures to limit contamination, obtain the right quantities of samples, and store them in reliable cold chains, such as liquid nitrogen or dry ice.

Plenary discussions during this session proposed the following:

- The project estimates to record 150 abortions during the one-year follow up. In addition, DNA (for bacteria) and RNA (for the virus) will be extracted from 30 samples of aborted fetuses for shotgun sequencing.
- Human samples should include whole blood (collected in purple top) and serum (red top) tubes.

2.4 Stakeholders' workshop

The stakeholders' workshop was held immediately after the project partners' workshop and was used to disseminate preliminary findings from the project. It also provided a platform for the project team to solicit feedback and identify additional partnerships needed to implement some of the tasks (e.g. with the health centres in the study locations). The meeting was launched by the Director, Wildlife Research and Training Institute, Patrick Omondi. Activities that had generated a reliable volume of data were prioritized for discussion. These were (i) the national serosurvey, (ii) wildlife serosurvey, (iii) baseline survey for the longitudinal study in Isiolo County, and (iv) serosurvey of slaughterhouse workers in Isiolo County. The workshop ended with a session on potential policy-relevant outputs.

2.4.1 Guest of honour's opening remarks

Omondi, the Director of the Wildlife Research Training Institute (WRTI), opened the meeting. He stressed the importance of disease surveillance in wildlife given recent infectious diseases that may have originated from wildlife. 'Wildlife disease surveillance will enable early detection of disease outbreaks to protect humans from future

pandemics,' he said. He also called for the translation of the research findings of the co-infection project to guide policy and design strategies to develop mitigation measures for the three focus diseases.

He appreciated the partnership between KWS, WRTI and the co-infection project partners and noted that WRTI was created to streamline the wildlife research permit process to make it easier for partners to obtain the necessary approvals when conducting wildlife research. He also mentioned that WRTI is looking for funds to build a wildlife forensic and DNA lab that will be used for disease surveillance and research and understanding of wildlife populations and prosecution of wildlife crimes.

2.4.2 The national serosurvey for EDP risk mapping

A presentation on the progress made in implementing the national serosurvey to generate data for mapping the spatial distribution of the three pathogens and their co-infections in Kenya was made by James Akoko of ILRI. He reported the study targeted a sample size of 8,000 cattle from a total of 320 random points and by the time the workshop was held, 6,702 animals from 475 points had been sampled. The study aimed to sample at least 25 cattle from each point. Cattle were used in the study because they usually have a higher RVFV seroprevalence compared to the small ruminants and therefore, they might be a better indicator of risk. Serum samples obtained from the study were screened at ILRI bioscience labs using appropriate ELISA kits. Table 1 summarizes the kits used for each pathogen, the estimated seroprevalence, and comments on the observed occurrence patterns.

Table 1. ELISA kits were used to screen samples from the national serosurvey and a summary of seroprevalence results obtained

	Pathogen		
	Rift Valley fever virus	*Brucella spp*	*Coxiella burnetii*
ELISA kits used	IDvet® ID Screen Rift Valley Fever IgM Capture (Grabels, France)	IDvet® ID Screen Brucellosis Serum Indirect Multi-species (Grabels, France)	PrioCHECK Ruminant Q Fever Ab Plate Kit (Thermo Fisher Scientific, Waltham, MA, USA)
Estimated seroprevalence	0.9% on IgM ELISA kit	6.9%	7.9%
Patterns observed	More cases were observed in the north, coastal and western regions	More positive cases in northern, eastern, and coastal regions	Cases diffusely distributed across the country

2.4.3 Wildlife serosurvey

Bernard Rono presented preliminary results on the wildlife serosurvey from KWS. This work had two components, the first focused on screening archived samples that the KWS veterinary team had collected over time, and the second involved active sampling of wild animals in the study area.

2.4.3.1 Analysis of archived serum samples

A total of 363 archived samples of various wildlife species have been tested for *Brucella*, *C. burnetii* and RVFV. The positivity rates are 18.9% for RVF, 13.7% for *Brucella* and 9.1% for *C. burnetii*, as shown in Table 2.

Table 2. Summary of the number of wildlife species tested and proportions of seropositive animals for Brucella, C. burnetii and RVFV

Animal		*Brucella*		*C. burnetii*		RVFV	
Species	Total no. tested	No. positive	% positive (95% CI)	Number positive	% Positive (95% CI	Number positive	% positive (95% CI)
Buffaloes	199	44	22.1 (16.5-28.)	5	2.5 (0.8-5.7)	41	20.6 (15.2-26.9)
Eland	17	2		1		8	
Wildebeest	4	0		0		1	
Hartebeest	3	0		0		0	
Gazelle	11	0		1		0	
Impala	9	0		1		3	
Waterbuck	11	0		3		0	
Oryx	15	0		0		10	
Giraffe	36	1		16	44.4 (27.9-61.9)	2	5.6 (0.7-18.70
Warthog	8	1		0		0	
Elephant	8	0		0		2	
Zebra	21	0		3		0	
Rhino	7	0		3		1	
Leopard	1	1		0		0	
Lion	5	1		0		0	
Cheetah	8	0		0		1	
Total	363	50	13.7 (10.3-17.7)	33	9.1 (6.3-12.5)	69	18.9 (15.0-23.3)

2.4.3.2 Active sampling

Rono reported that 288 animals comprising various species of wildlife had been sampled. Two approaches were being used for sampling: (i) opportunistic sampling, where animals that are captured for other purposes such as clinical interventions, collaring and translocations were sampled, and (ii) targeted sampling, where animals were trapped or immobilized for sampling. Species sampled in the study area included buffaloes, warthogs, common zebras, impalas, kudus, and Grant's gazelles. The specific sites that were being targeted for sampling were:

- Buffalo Springs, Samburu, and Shaba national reserves – sampling here had been concluded
- Meru National Park (NR), Kinna Triangle, Korbesa, Bisanadi NR – sampling here was ongoing
- Selected community conservancies in Isiolo County – sampling of these areas will commence in May 2022

These areas were selected based on the following criteria:

- Availability of animal species that were known to be susceptible to the pathogens of interest
- High wildlife, animal, and human interactions
- Accessible terrain
- Areas with adequate security

At the first site – i.e. Samburu, Buffalo Springs and Shaba national reserves – a total of 85 animals had been sampled. Table 3 shows the distribution of these animals by species. During the visit, three (3) additional animals (two Grevy's zebra and one white rhino) were sampled opportunistically. Samples collected have not been analysed.

Table 3. The number of wild animals sampled in Samburu, Buffalo springs and Shaba national reserves by species

Species	Buffalo springs	Samburu	Shaba	Meru	Total
Buffalo	8	-	10	33	51
Reticulated giraffe	5	6	1	10	22
Impala	-	3	-	10	13
Beisa oryx	5	9	4	0	18
Warthog	10	3	-	2	15
Waterbuck	4	-	2	1	7
Common zebra	15	-	-	27	42
Total	47	21	17	83	168

2.4.4 Baseline survey for the longitudinal study

Mwatondo presented the baseline survey they had done in Isiolo as part of preparatory activities for the longitudinal study. This work involved human and livestock sampling at the household level. The survey's objectives were: (i) to determine the seroprevalence of *Brucella* spp. *Coxiella burnetii* and RVF virus in humans and animals in Garbatulla sub-County, Isiolo, and (ii) to determine risk factors that influence human and livestock exposures in the study sites.

The study aimed to sample 620 humans and 2,000 animals (cattle, sheep, goats and camels) in 124 households. This sample size was increased by 10% to account for unexpected dropouts. Households to sample were identified using random spatial coordinates. Subjects were recruited into the study if they were more than two years of age. Blood and serum samples were collected from the recruited human and animal subjects. Samples were initially stored in cool boxes while the team worked in the field. They were later aliquoted and stored in motorized cool boxes at -20C. They were later analysed at ILRI using ELISA kits. The analysis of the data collected is ongoing.

A total of 242 households were used in the survey. These were from Sericho (27%), Garbatulla (43%) and Kinna (30%). The numbers of animals and humans sampled and their pathogen-specific seroprevalences are illustrated in Table 4.

Table 4. Numbers of humans and animals sampled in the baseline survey and seroprevalences estimated for each target pathogen

Species	Number sampled	Seroprevalence		
		Brucellosis	Q fever	RVF
Humans	689	54%	42%	28%
Livestock	2,234			
Goats	979	14%	68%	21%
Sheep	882	6%	40%	24%
Cattle	276	13%	12%	39%
Camels	97	19%	29%	13%

2.4.5 Serosurvey of the slaughterhouse workers

Richard Nyamota of ILRI and Josephat Maina, of the Zoonotic Disease Unit and a graduate fellow at ILRI presented results from a survey that screened slaughterhouse workers for the three pathogens. The objectives of the study were (i) to determine the seroprevalence of *Brucella* spp, *Coxiella burnetii* and RVF virus among slaughterhouse workers in Isiolo County, and (ii) to identify the occupational factors associated with *Brucella* spp, *Coxiella burnetii* and RVF virus exposure among slaughterhouse workers in Isiolo County, and (iii) to assess compliance with the Meat Control (Local Slaughterhouse) regulations of 2010 by slaughterhouse operators in Isiolo County.

A cross-sectional study design was used involving all slaughterhouse workers in the county. All the workers who consented and had worked for more than two years in these slaughterhouses were recruited. However, those on leave on the sampling day were not included. Simple questionnaires were administered to each subject before sampling to obtain metadata. Questionnaires were also administered to slaughterhouse forepersons and managers to obtain descriptive information for each slaughterhouse used. Blood samples were collected from recruited subjects using plain vacutainer tubes and serum was harvested and aliquoted to Cryovials. These were transported to ILRI using motorized freezers. In the lab, the samples were screened using various ELISA kits. Seropositivity for *Coxiella burnetii* was determined using Serion ELISA Classic *Coxiella burnetii* phase 2 IgG kit, *Brucella* spp. Exposure was based on Human IgG ELISA Kits (IBL, America), while RVFV exposure was determined using RVF – ID Screen® Rift Valley Fever Competition Multi-species kit.

A total of 378 subjects from 9 slaughterhouses were sampled. Most of these (64%) were male. Seroprevalence estimates obtained for the three target pathogens are illustrated in Table 5.

Table 5. *Brucella* spp, *Coxiella burnetii* and RVF virus seroprevalences in slaughterhouse workers sampled in Isiolo County

Pathogen	Number positive	Proportion (%)
Coxiella burnetii	62	16.4
Brucella spp	152	40.2
RVF virus	69	18.3
RVFV and *Brucella* spp co-exposure	39	10.3

2.4.6 Policy-relevant products from the project

The stakeholder workshop's final session focused on identifying policy-relevant products that the project would produce during its implementation period. These products are illustrated below.

- Risk maps – the national serosurveys to determine the distribution of RVF virus, *Brucella* spp and *Coxiella burnetii* will generate data that will be used to create risk maps for these pathogens. Risk maps will identify hotspots where surveillance and control measures can be targeted. They will also be used to estimate the burden of these diseases at the national level.
- Estimates of EDP burden – Multiple studies are being implemented to estimate the burden of RVF virus, *Brucella* spp and *Coxiella burnetii* in humans and livestock. This is the first study of the prevalence and incidence of these pathogens using well-designed longitudinal studies. Data generated will be used to inform One Health case studies.
- Capacity building on biorisk management – More than 60 frontline staff from animal and public health sectors in the north and northeastern Kenya have been trained on biorisk management using the Kenya Laboratory Biorisk Management Curriculum. Based on the evaluations conducted before and after the training, this intervention enhanced the skills of the participants enrolled. The trainers also collated lessons that will be used to improve the current version of the curriculum.

- Graduate fellowships – the project has enrolled two PhD and two MSc students attached to the Zoonosis Disease Unit. This supports capacity building in the unit by enhancing the technical competencies of its key personnel.

2.4.7 Comments/feedback from the stakeholders

Participants observed that the new knowledge generated by this project helps inform policy development at all levels of government. Data on the burden of the three pathogens of interest was singled out as key in the re-prioritization process of zoonotic diseases. Biorisk management training was reported to be impactful in bridging the knowledge gap and expansion of participant involvement to include wildlife personnel and regional veterinary investigation laboratories staff was proposed. The formation of a team to finalize the development of communication plans, materials, and translations was proposed to support the timely dissemination of study finding with stakeholders for action.

Annexes

Annex 1. Workshop program

Stakeholders' meeting Day 1 Thursday 21 April 2022			
Time	Activity	Facilitator	Moderator
8:30 - 9:00	Registration	Sarah- ILRI	M. Muturi

9:00 – 9:30	• Welcome and self-introductions
	• Opening ceremony
	  • Remarks by partner representatives – ILRI, WSU, UoN, WRTI, KEMRI
	  • Official opening – DVS
	• Workshop objectives
		B. Bett
		H. Oyas
		
		J. Akoko	

9.30 – 10.00	Overview of the co-infection project	B. Bett	
10.00 – 10.30	National serosurvey – Results and updates	J. Akoko	
10:30 – 11:00	**TEA**		
11.00 – 11.30 11.30 – 12.00	Cross-sectional study in humans and livestock QA session	A. Mwatondo	L. Konongoi
12:00 – 12:30 12.30 –13.00	Longitudinal study in humans and livestock - updates QA session	M. Muturi	
13:00 – 14:00	**LUNCH**		
14:00 – 15.00	Introduction to the human and livestock surveillance tools in the longitudinal study	Mwatondo/Muturi	L. Wambua
Day 2 Friday 22 April 2022			
Time	Activity	Facilitator	Moderator

9:00 - 9:30 9.30 – 9.50	Updates from the Wildlife team QA session	B. Rono	Kahariri
9:50 – 10.20 10.20- 10.30	Updates from Slaughter-house study QA session	J. Maina	
10:30 – 11:00	**TEA**		
11.00 – 11.40	Translation of research into policy – updates on the RVF risk map	B. Bett	
11:40 – 12:20	Updates from WSU	J. Gachohi	
12.20 –13.00	Future plans – group work session on proposed project ideas	Group work	
13:00 – 14:00	**LUNCH**		
14.00-15.00	Future plans – group work session on proposed project ideas cont.		

Annex 2. List of participants

No.	Name	Organization
1	Francis Gakuya	Wildlife Research and Training Institute
2	James Akoko	International Livestock Research Institute
3	Athman Mwatondo	International Livestock Research Institute
4	Andrew Bartlow	Los Alamos National Laboratories
5	Alicia Romero	Los Alamos National Laboratories
6	Earl Middlebrook	Los Alamos National Laboratories
7	Konongoi Limbaso	Kenya Medical Research Institute
8	Jeanne Fair	Los Alamos National Laboratories
9	Wangoru Kihara	International Livestock Research Institute
10	Richard Nyamota	International Livestock Research Institute
11	Sarah Ndungu	International Livestock Research Institute
12	Bernard Rono	Kenya Wildlife Service
14	Victor Ofula	Kenya Medical Research Institute
15	Josephat Maina	Zoonotic Disease Unit
16	Mathew Muturi	Zoonotic Disease Unit
17	Mohamed Dabaso	Isiolo County Government
18	Hassan Guyo	Isiolo County Government
19	Geoffrey Njenga	International Livestock Research Institute
20	Lekopien Argeo	Zoonotic Disease Unit
21	Ali Badha	Isiolo County Government
22	Daniel Chepkwony	Zoonotic Disease Unit
23	Dennis Mwongela	Isiolo County Government
24	Bernard Bett	International Livestock Research Institute
25	Joseph Edebe	Wildlife Research and Training Institute
26	Nassoro Mwanyalu	Zoonotic Disease Unit
27	Millicent Ndia	National Public Health Laboratory
28	Joel Lutomiah	Kenya Medical Research Institute
29	Kahariri Samuel	International Livestock Research Institute
30	Lilian Wambua	International Livestock Research Institute
31	Samuel K. Kamau	Directorate of Veterinary Services
32	Patrick Omondi	Wildlife Research and Training Institute
33	Bridgit Muasa	Directorate of Veterinary Services
34	Samuel Kadivane	Ministry of Health