

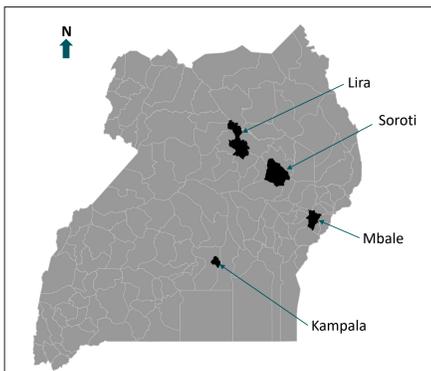
Surveillance of climate-sensitive zoonotic diseases: Leptospirosis at livestock slaughterhouses in three regions of Uganda

Lordrick Alinaitwe^{1,2,3}, Martin Wainaina⁴, Kristina Roesel¹, Clovice Kankya³, Salome Dürr², Martin Richter⁴, Elizabeth Cook¹, Anne Mayer-Scholl⁴

- 1 International Livestock Research Institute (ILRI), Animal and Human Health Program, Kenya
- 2 University of Bern, Veterinary Public Health Institute, Switzerland
- 3 Makerere University, College of Veterinary Medicine, Animal Resources and Biosecurity, Uganda
- 4 German Federal Institute for Risk Assessment, Department of Biological Safety, Germany

Leptospirosis is an important bacterial zoonosis worldwide and is disproportionately associated with low-income settings and with extreme weather events due to climate change. Transmission to humans often occurs when infected rodents and domestic animals contaminate the environment via urine as the bacteria preferentially colonise kidneys. Leptospirosis causes significant morbidity and loss of productivity in humans and animals, and inadequate control measures are in place in Uganda. Surveillance of leptospirosis at slaughterhouses can therefore be useful in providing information on vast areas of a country and screening for diseases that are not considered during animal inspections.

Methods



Study sites in Uganda

Slaughterhouse sampling

Slaughterhouses from northern, eastern and central regions.

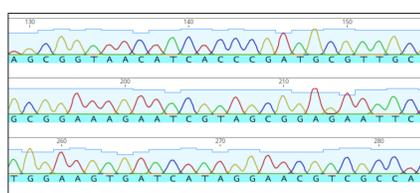
2,030 livestock (820 cattle, 761 pigs, 335 goats, 114 sheep), and 117 small mammals.

Kidney samples obtained.



Laboratory testing

PCR testing – pathogenic leptospires, single- and multi-locus sequence typing.



Sanger sequencing

Species identification.

Determining sequence types.

```

mlst_sequences <- readAStringSet(mlst_lepto)
slst_sequences <- readAStringSet(slst_lepto)

#multiple sequence alignments
aligned_mlst <- msa(mlst_sequences, "ClustalOmega")
aligned_slst <- msa(slst_sequences, "ClustalOmega")

#view alignment
print(aligned_mlst, show="complete")
print(aligned_slst, show="complete")

#convert alignment to a seqinr alignment object
aligned_mlst_seqinr <- msaconvert(aligned_mlst, type="seqinr::alignment")
aligned_slst_seqinr <- msaconvert(aligned_slst, type="seqinr::alignment")

#compute distance matrices
library(seqinr)
distance_matrix_mlst <- dist.alignment(aligned_mlst_seqinr, "identity")
as.matrix(distance_matrix_mlst)[2:15, "CK0810", drop=FALSE]
distance_matrix_slst <- dist.alignment(aligned_slst_seqinr, "identity")
as.matrix(distance_matrix_slst)[2:15, "CK0810", drop=FALSE]

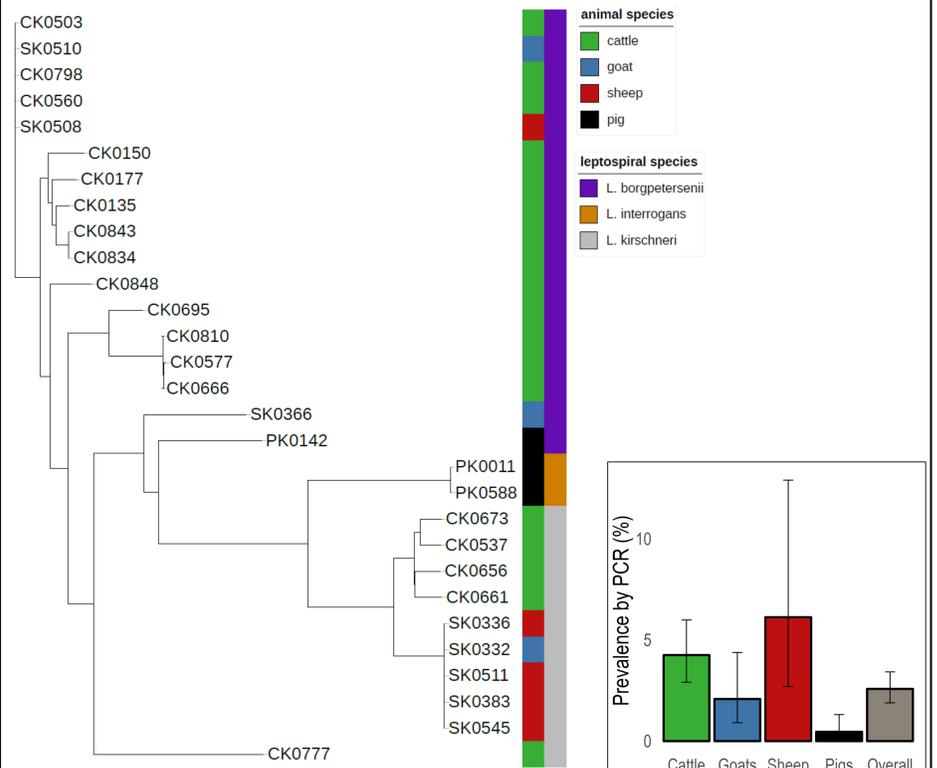
```

Data analyses:

Prevalence by PCR.

Phylogenetic relatedness.

Preliminary Results



Phylogeny from multi-locus sequence typing (MLST)

Diverse sequence types observed.

Pathogenic leptospires from PCR testing

Detected in various hosts. High prevalence observed.

Conclusion

Slaughterhouse data are important and cost effective in surveillance of zoonotic diseases in Uganda. This approach can be scaled-up to include other animal diseases of public health or veterinary importance.



Contact:

Martin Wainaina • Tel. +49-30-18412-24332.
Email: Martin-Wainaina.Kimari@bfr.bund.de