Mapping the risk of Rift Valley fever in Uganda

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Introduction

- Rift Valley fever (RVF) is a mosquito-borne viral zoonosis that mainly affects cattle, sheep, goats and camels. Its epidemics are associated with above-normal persistent rainfall and flooding.
- Uganda has had multiple RVF epidemics mainly in the southwestern and central parts of the country since 2016. No analyses have been done to map the risk of the disease.
- We compare spatial distribution of epidemic and endemic infections (based on serological data) to gain deeper understanding of the epidemiology of the disease. Uganda provides a unique setting for these analyses since (i) no RVF vaccination has ever been done in the country and (ii) multiple epidemics have been reported at more frequent intervals since 2016.

Materials and methods

Data: Data were obtained from three sources: (i) surveillance records on epidemics kept by the Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), (ii) de novo serological surveys involving cattle, sheep and goats and (iii) online spatial data on climate and other ecological variables.

Analyses: Observed epidemics were mapped to obtained occurrence maps. Serological data were also analysed using random effects logistic regression model to identify animal-level factors associated with RVF virus exposure. Furthermore, a geostatistical model, implemented using RINLA was fitted to serological data to predict spatial patterns of endemic infections. A mesh generated for this purpose is shown in Figure 2.

Predictions: The final model developed from the analysis of serological data was used to predict the spatial range of exposure. Predictors used comprised ecological variables only.

Results and recommendation

- Initial epidemic was observed in Kabale, southwestern Uganda in March 2016 after periods of heavy rains.
- For the serological survey, a total of 3,962 animals were sampled from 198 households and 150 villages. Random effects model fitted to the data suggested that adjusted intra-herd correlation coefficient (ICC) was 0.35, while the ICC estimate between animals from different herds was 0.15.
- Prediction from serological data suggested that endemic transmissions occur in many parts of the country (including northeastern parts), but no outbreaks have been observed in many of these areas.
- More active surveillance for the disease is needed in areas predicted to have high transmission risk based on serological data, especially during the wet seasons.

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