

Joint analysis of human and bovine serological data: new insight on the risk and mechanisms of transmission of Rift Valley fever in Madagascar

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Purpose:

In 2008-09, an outbreak of Rift Valley fever (RVF) virus occurred in Madagascar. Spatial heterogeneity in seroprevalence (SP) and case occurrence frequencies suggested that some areas are more favorable to RVF circulation. The objectives of our study were to identify environmental factors in favor to human and cattle infections; test the relevance of using local cattle infection as human infection predictor and give a new insight on the respective role of direct and vectorial transmission both in human and cattle.

Methods:

We used 2 independent cattle and human serological datasets originating from two national surveys (2009 and 2011-13). Multiple Factor Analysis (MFA) was used to characterize environments of the whole island in terms of climate and landscape. The datasets were analyzed independently using a generalized linear mixed model (GLMM) with the individual serological status- human or cattle- as the binomial response. Explicative variables were age and MFA factors for cattle model (M1) and age, gender, MFA factors and contact with ruminants and their product for human model (M2). Then human and cattle data were analyzed jointly by GLMM with the human individual status as binomial response. In addition to the previous explicative variables cattle SP predicted by M1 was used. Models accuracies were tested using ROC curve method.

Results:

Four MFA factors were selected. Age and factor4 - humid (irrigation, lake, marshland) environment - had a positive effect on SP of cattle and human living in rural areas ($p < 0.001$ and $p < 0.01$) while factor1 - warm, dry and herbaceous environment - had a negative effect ($p < 0.05$). Humans consuming raw milk were at risk. Predicted cattle SP were associated with human SP ($p < 0.05$).

Conclusions:

Our results support an endemic transmission of RVF in rural area with humid landscape settings in both human and cattle populations suggesting the predominance of vectorial transmission for both populations. Local cattle infection seems to be a good predictor of human infection.

Relevance:

This joint analysis allowed deciphering transmission mechanisms and should help health and veterinary authorities to assess risk of RVF and optimize surveillance network.