

A preliminary assessment of Rift Valley fever epidemiology in two wildlife/livestock/human interfaces areas in Zimbabwe

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**Purpose:**

Rift Valley Fever (RVF) is an emerging disease threatening human and livestock health in Africa and the Middle-East. The role of wildlife in the maintenance and transmission of the virus at human/livestock/wildlife interfaces in Southern Africa remains unclear. In order to elucidate RVF epidemiology in the Great Limpopo (GLTFCA) and the Kavango-Zambezi (KAZATFCA), we combined preliminary data from serology, entomology, telemetry and field experiments in Zimbabwe.

**Methods:**

At each site, blood samples were taken between 2008 and 2011 from livestock and buffalo. The samples were tested with I-ELISA for RVF antibodies and the data analysed with Generalized Linear Model. Four mosquito trapping sessions were conducted at water holes used by livestock and/or wildlife. Potential contacts between wildlife and cattle were assessed using data of GPS collared cattle and buffalo published elsewhere. Bags of viscera were used as a proxy to estimate residence time of aborted fetus and potential infectious contacts between livestock and wild ruminants.

**Results:**

KAZATFCA serological results were all negative. In GLTFCA, the seroprevalence was 4.6% in cattle (27/587), 3% in small ruminants (2/66) and 6.8% in buffalo (14/205). The disease was endemic in livestock, with 2009 prevalence lower than 2008 ( $p=0.04$ ). Buffalo prevalence was significantly higher in 2010 ( $p=0.05$ ). Six species of mosquitoes were captured, including 3 potential RVF vectors: *Culex quinquefasciatus*, *C. theileri* trapped at both sites; *Anopheles coustani* identified in KAZATFCA only. Home ranges of sympatric cattle and buffalo overlapped, with significant differences in seasonality and frequency of indirect contacts across sites. Estimated residence time of aborted fetus ranged between a few hours and several days.

**Conclusions:**

These results indicate that RVF circulates in cattle and buffalo populations within the GLTFCA, with inter-annual and spatial variations, and that transmission between wild and domestic compartments may be due to both vectors and direct contacts

**Relevance:**

This innovative study combining different field data will contribute to improving zoonotic RVF at wild/domestic interfaces in Africa