Spatial distribution of non-clinical Rift Valley fever viral activity in domestic and wild ruminants in northern Tanzania

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SUMMARY

Rift Valley fever (RVF) is an acute zoonotic viral disease of domestic ruminants in mainland Africa and Madagascar. The disease may exist in non-clinical form in apparently health animals. This study was designed to investigate the existence and spatial distribution of non-clinical form of RVF virus (RVFV) activity in wild and domestic animals in six districts in northern Tanzania. A retrospective cross-sectional study involved testing a total of 285 and 100 serum samples from domestic ruminants and wildlife species, respectively. The samples were subjected to IgG and IgM enzyme-linked immunosorbent assay (ELISA) as well as to the Real-time Polymerase Chain Reaction (RT-PCR). Based on ELISA test, the seroprevalence of RVF-specific IgG antibodies was: African buffalo (40.9%, n=22), African elephant (33.3%, n=3), cattle (11.8%, n=93), sheep (11.3%, n=97) and goats (8.4%, n=95). Two serum samples from goats tested positive for IgM. All samples tested were RVFV-negative based on RT-PCR test. The highest intra-village sero-prevalence of IgG was observed in two villages (Kimotorok and Lormorije) of Simanjiro district. Domestic ruminants from herds that were located

at an elevation below 1000m were at higher risk (OR=2.32, 95% CI 1.05 – 5.16, p=0.04) of RVFV infection. Findings of the current study indicate existence of a wide range of domestic and wildlife hosts which could serve as potential reservoirs of RVFV during inter-epidemic period. This calls for adoption of one health approach in responding to RVF epidemics as well as during implementation of RVF controlling measures with the ultimate goal of eradicating RVF in Tanzania.

Key words: Rift Valley fever, inter–epidemic period, seropositivity, spatial distribution, ruminants, Tanzania.

INTRODUCTION

Rift Valley fever (RVF), is an acute, mosquito-borne zoonotic viral disease that has a significant global threat to humans and livestock (Woods *et al.,* 2002). The causative agent, RVF virus (RVFV), belongs to the genus *Phlebovirus* of family *Bunyaviridae,* a group of enveloped RNA-viruses (Bouloy and Flick, 2009). The disease affects many species of animals including sheep, cattle, goats, buffalo, camels, monkeys and humans as well as rodents (Swanepoel 1994; Swanepoel and Coetzer, 2004; Mandell and Flick, 2011). The primary amplifying hosts are domestic ruminants (Swanepoel, 1994). Humans can be exposed through contact with infected animal tissues, blood or body fluids or through the bite of an infected mosquito most commonly the *Aedes* species (endemic vectors) and *Culex, Mansonia, Anopheles, and Eretmapodites* (epidemic vectors) (Meegan and Bailey, 1988; Swanepoel and Coetzer, 2004; Me´tras *et al.,* 2011).

The disease is characterised by high mortality and abortion rates and has severe socio-economic consequences, including restrictions in international movement of animals and their products (Pepin *et al.,* 2010). Infection in humans may be asymptomatic but is usually associated with moderate influenza-like illness, may cause hepatitis, hemorrhagic fever, encephalitis, retinitis and permanent vision impairments (Swanepoel and Coetzer, 2004). Fatality rate in human ranges from 0.5 to 2% (Swanepoel and Coetzer, 2004).

Tanzania is among the countries in the sub-Saharan Africa where RVF is endemic. At present, it is not known how RVFV was introduced in Tanzania. According to the Tanzanian Animal Disease Act, RVF is a notifiable disease (URT, 2004). Previous studies postulated a possibility for the existence of RVF viral activity during the inter-epidemic period (IEP) (Swai and Schoonman, 2009; Heinrich *et*

al., 2012). Furthermore, a study by Masambu (2009) reported presence of antibodies specific to RVFV in apparently health unvaccinated cattle population in Iringa (Southern highland zone) and Morogoro (Central zone) regions in Tanzania.

Although northern zone of Tanzania remains the RVF hot spot (Corso *et al.,* 2008; Woods *et al.,* 2002), the spatial distribution and clinical aspects of RVF viral activity in domestic and wild animals during IEP in this area have not been investigated. Besides its survival in *Aedes* mosquitoes, RVFV is believed to circulate at very low level without noticeable clinical manifestation in animals (Pepin *et al.,* 2010; Rostal *et al.,* 2010). The animal-mosquito cycling may involve low-level of infections in domestic and wild animals during IEP and these animals might remain the reservoirs (Linthicum *et al.,* 1985; Crabtree *et al.,* 2012). Immunogeno-protective response is associated with production of antibodies specific to RVFV in infected animals within 3–5 days post-infection; therefore detection of antibody against RVF in animals is one of the indicators of exposure (FAO, 2003).

Here we report the results of a study that involved examination for RVFV activity in serum samples that had been randomly collected from domestic ruminants during an IEP between July and September 2007. We also tested limited serum samples from wild animals collected between January 2002 and June 2006. The objectives were (i) to assess any RVFV circulation that had possibly remained undetected in unvaccinated domestic and wild animal population without RVF clinical disease and (ii) to describe spatial distribution of RVFV activity in northern Tanzania.

MATERIALS AND METHODS

Study area

The source of domestic ruminant (cattle, sheep and goats) serum samples for this study were the districts (respective names of villages in parentheses) of Handeni (Magamba, Mazingira, Msaaje, Taula and Zavuza); Mbulu (Endahargadet, Haraa, Khaday and Masqaroda); Monduli (Emareite, Lolkisale, Mbashi, Mfereji, Orkatan); Same (Makokane, Ndungu, Njoro and Vumari); Simanjiro (Kimotorok, Loondrekes, Lormorije, Losinyai, Naberera and Sukuro). Wildlife samples were from Ngorongoro Conservation Area (NCA) in Ngorongoro district where domestic animals and humans interact freely with wildlife. All these districts are located in Northern Tanzania (Latitude 2^{o} to 6° S and Longitude 32° to 40°E) that is comprised of four administrative regions and 26 districts. Large part of northern Tanzania is mountainous and includes Mount Meru, an active volcano, Mount Kilimanjaro, a dormant volcano, and the Usambara and Pare mountain ranges. West of those mountains is the Gregory Rift

Valley, which is the eastern arm of the Great Rift Valley (Mhita and Venalinen, 1992). On the floor of the Rift Valley are a number of large salt lakes, including Natron in the north, Manyara in the south and Eyasi in the southwest. The rift also encompasses the Crater highlands, which include the NCA and the Ngorongoro Crater. Towards the north-eastern there are a number of national parks (Figure 2).

In the study area the hottest period extends between November and February (25–35 °C) while the coldest period occurs between May and August (15–20 °C). The northern zone has a savannah climate which is modified by altitude and experiences two distinct wet periods – the short rains (or "*Vuli*") in October to December and the long rains (or "*Masika*") from March to May (Mhita and Venalinen, 1992; Kabanda and Jury, 1999). The amount of rainfall falling in these seasons is usually 50□200mm per month but varies greatly between regions, and can be as much as 300 mm per month in the wettest regions and seasons. One of the most well documented ocean influences on rainfall in this region is the *El Niño* Southern Oscillation (ENSO). *El Niño* episodes usually cause greater than average rainfalls in the short rainfall season (OND), whilst cold phases (*La Niña*) bring a drier than average season (Kabanda and Jury, 1999). For descriptive purposes of this study area elevation was arbitrarily categorized into low (below 1000m above the sea level), medium (≥ 1000 and ≤ 1500m) and high (> 1500m above the sea level).

Between September and November 2006 short-rain season, the amount of rainfall exceeded 600 mm in the northern zone. The excess rainfall resulted in anomalous vegetation growth, with departures ranging between 20 and 100% above normal as illustrated by satellite derived Normalized Difference Vegetation Index (NDVI) anomalies (Anyamba *et al.,* 2010). Persistence of elevated and widespread rainfall resulted in abundant vegetation growth from September through December 2006 and created ideal conditions of dambo formations (Anyamba *et al.,* 2010). It is believed that the flooding of dambos induces the hatching of transovarially infected *Aedes mcintoshi* mosquito eggs and supports multiplication of Culex and other potential vectors of RVFV (Linthicum *et al.,* 1984; 1985; 1987).

Study design and study population

This was a retrospective cross-sectional study that involved laboratory examination of RVFV activity in the stored serum samples that had been previously collected during IEP from domestic ruminants and mixed species of wildlife. Serum samples that were included in this study were those from animals without RVF clinical disease, history of vaccination against RVF and whose epidemiological information was available.

Between July and September 2007 (after the latest RVF outbreaks had ended in the country in May 2007) a cross-sectional blood sampling was carried out in the herds of domestic ruminants without history of vaccination against RVF in 130 villages in 26 districts of northern Tanzania. Selection of the villages and animals had been made through multi-stage random sampling procedures whereby an average of 5 villages (range 4-10) were selected in each district and 15 domestic ruminants (average 5 of each species) were randomly selected from each village.

Wildlife serum samples were collected in the NCA between January 2002 and June 2006 by Tanzania Wildlife Research Institute (TAWIRI) and Ngorongoro Conservation Area Authority (NCAA) during the course of routine investigation of wildlife diseases or animal rescues. The domestic ruminant and wildlife serum samples were stored at -20^{o}C and had never been examined for RVFV activity.

Selection of serum samples from animal population without clinical disease for laboratory examination of RVFV activity

A serum bank comprising 2093 serum samples collected from domestic ruminants was used to obtain a total number of 285 samples that were included in this study. Inclusion criteria for the samples analysed were: i) Availability of identification/label of the sample, ii) Being samples from farms/herds/flocks with history of absence of clinical RVF disease, iii) Availability of epidemiological information collected using a questionnaire. The information included locality, date sampled, biodata (species, age, sex), history of vaccination against RVF, clinical signs of RVF or any other ill health condition during sample collection and if the history of RVF clinical disease within the herd/flock during 2006-2007 RVF outbreak.

A total of 100 serum samples collected from mixed wildlife species (African buffalo=22, African elephant=3, lion=18, Thomson Gazelle=11, warthog=9, wildebeest=13 and zebra=24) in NCA that had necessary epidemiological information were also included in the study.

Serum samples selected for this study (285 domestic ruminants and 100 wild animals) were shipped on ice packs in April 2012 to the Center for Emerging and Zoonotic Diseases, National Institute for Communicable Diseases, of the National Health Laboratory Service, Sandringham, South Africa (CEZD NICD/NHLS) for laboratory examination.

Laboratory examination for RVFV activity: IgM, IgG, virus antigen and viral nucleic acid

All serum samples included in this study were inactivated at 56 °C for 60 minutes in a water bath before performing specific laboratory procedures. Animal serum samples were tested for the presence of anti-RVF antibodies using three enzyme-linked immunosorbent assay (ELISA) formats according to the manufacturer's (Biological Diagnostic Supplies Limited, UK) instructions. These included RVF inhibition ELISA (Paweska *et al.,* 2003), IgM-capture ELISA (Paweska *et al.,* 2005) and antigen detection ELISA (Jansen Van Vuren and Paweska, 2009).

Initially all samples were tested using RVF inhibition ELISA. Serum samples that were positive on inhibition ELISA and 20 randomly selected serum samples that were negative on inhibition ELISA were subjected to IgM-capture ELISA. All ruminant serum samples that were positive on inhibition ELISA were tested for nucleocapsid protein of RVFV by antigen detection ELISA.

Real-Time Polymerase Chain Reaction (RT-PCR) was used as described by Drosten *et al.,* (2002) using the LightCycler® RNA Amplification kit HybProbe® (Roche Diagnostics, Germany) and the LightCycler® instrument (Roche) for the detection of the RVFV RNA in samples that were positive on IgM and antigen detection ELISA formats.

Cut-off values for ELISA tests

For RVF inhibition ELISA, a specific activity of each serum (net optic density {OD}) was calculated by subtracting the non-specific background OD in the wells with mock antigen from the specific OD in wells with virus antigen. The mean net OD readings for replicate tests were converted to a percentage inhibition (PI) value using the equation: [(100− (mean net OD of test sample/ mean net OD of negative control) ×100]. Internal quality control was observed according to the manufacturer of the kits. Interpretation of the results was made using the cut-off threshold specified by the manufacturer of the kit. Sera samples with PI equal to or greater than 41.9, 41.4, 38.4 and 34.2 were considered seropositive for RVF inhibition in cattle, goat, sheep and buffalo, respectively. The cut-off values for other wild animals were based on that of buffalo.

For RVF IgM ELISA conversion of net OD readings into percentage positivity (PP) was carried out using the equation below:

$$PP=\frac{\text{Net OD serum (Control- or Test serum) X 100}}{\text{Net mean OD C++}}$$

Threshold PP values; sheep and goat sera producing PP values ≥7.9 and 9.5, and bovine sera producing PP values ≥ 14.3, respectively were considered to be positive, and less than these values were considered to be negative.

For RVF recNP Antigen detection ELISA the results of optic density readings were expressed as a percentage of the mean high-positive control antigen (PP) using the formula: (mean net OD of duplicate test specimen/ mean net OD of high-positive control) ×100. Threshold values producing PP values ≥ 5.0 were considered to be positive and less than these values were considered to be negative.

Data analysis

Stata statistics software (version 12, Statacorp, College Station, TX, USA) was used for all statistical analyses. Descriptive statistics was carried out and Chi-square was employed to compare the proportion of seropositivity amongst animal species and other predictable variables including age, sex and location. Logistic regression was used to compare seropositivity and elevation. Significance of parameter estimate (p) was considered at the level below 0.05.

All GPS points were projected to Universal Transverse Mercator (UTM) coordinate system and later overlaid on the respective district map using ArcGIS 10 (ESRI, Eastern Africa). The respective district map was extracted from the country shape file. We mapped the spatial point pattern for the prevalence based on the RVF inhibition ELISA and RVF IgM ELISA laboratory results.

Ethical considerations

The purpose of the study had been made clear to animal owners and authorities of the Ministry of Livestock and Fisheries Development (MoLFD) and the Tanzania Wildlife Research Institute (TAWIRI) before obtaining oral consent for animal sampling. Blood sampling was carried out by Veterinarians according to standard protocol. Observation as well as the maintenance of the physical and physiological condition of the animals during the time of sampling was given the priority. Before exporting the serum samples to the Republic of South Africa, the import and export permits of samples were obtained from the respective Directorate of Animal Health Import-Export Policy Unit, Department of Agriculture, Forestry and Fisheries, Republic of South Africa, and the Directorate of Veterinary Services, MoLFD, United Republic of Tanzania.

RESULTS

Epidemiological data

Domestic ruminants (n=285) that were recruited into this study were all of indigenous breeds, local indigenous Tanzanian short horn zebu breed, Small East African goat and mix of the Red

Maasai and Black head Persian (BHP) sheep reared under pastoral and agro-pastoral production systems.

All 74 interviewed livestock owners (with herds without RVF clinical disease) did not report signs suggestive of RVF such as increase of abortion rates/history of massive abortion and death of new born/neonatal animals in their herds. All (n=285) domestic ruminants included in this study had not been vaccinated against RVF. Physical examination of domestic ruminants revealed no signs compatible with RVF and all animals were apparently health at the time of sampling. It was not possible to obtain information on clinical examination of wild animals. However, there have been no reports of RVF clinical disease in wildlife in Tanzania.

Serostatus of antibodies specific to RVFV, specific antigen and nucleic acid in animal population without clinical disease

The range of RVF Inhibition and IgM detection ELISA values for domestic animal serum samples tested for RVFV activity is indicated in Table 1.

Relatively larger proportion of domestic ruminant serum samples examined (n=285) in this study were from Same district (26.32%) followed by Handeni (25.61%), Simanjiro (21.75%), Monduli (17.54%) and Mbulu (8.77%) (Table 2). A total of 30 (10.53%, n=285) and 10 (10%, n=100) serum samples from domestic and wild ruminants respectively tested positive for IgG specific to RVFV (Table 2, 3). The specific species seroprevalence of IgG was: African buffalo (40.91%, n=22), African elephant (33.33%, n=3), cattle (11.83%, n=93), sheep (11.34%, n=97) and goats (8.42%, n=95). Two (including the one that was positive on RVF inhibition ELISA) of the three elephant serum samples were collected in September 2005 and the third one was collected in October 2003. Of the nine positive serum samples from buffalo three were collected in June 2006, one in February 2005, three in April 2004 and two in June 2002.

Of the 60 sera that were subjected to IgM ELISA only two sera (collected in August and September 2007) tested positive for IgM antibodies and both were from adult goats giving the intra-species prevalence of 3.33%. Both the IgM-positive sera also had tested positive for IgG antibodies and all 20 sera that were negative on RVF inhibition ELISA were also negative on IgM ELISA.

In overall a relatively higher proportion of seropositivity was observed in the domestic ruminant samples that were collected in July (13.79%, n=87) and August (12%, n=75) followed by September (8.22%, n=73) and June (6%, n=50). However, there was no sufficient evidence of seropositivity to significantly vary with the month of sampling (p=0.45). RVFV nucleocapsid protein and RNA nucleic acid were not

detected in any of the serum samples tested.

Table 1. Range of RVF Inhibition and IgM detection ELISA values for domestic animal serum samples tested for RVFV activity

Animal	Inhibition ELISA		IgM detection ELISA	
	Negative	Positive	Negative	Positive
Goat	-5.38519-26.90663	56.6193-100.2992	-1.39505-3.428997	14.8383-16.487
Sheep	-1.57589-29.44421	65.63233-100.6856	-2.53646-13.88713	-
Cattle	-11.6463-36.44513	49.11901-100.127	-3.65263-6.187104	-

Spatial distribution of RVFV IgG and IgM in domestic ruminants in the study areas

A total of 24 (18.5%, n=130) villages were not clinically involved in the latest (2007) disease outbreak and its domestic ruminants had not been vaccinated against RVFV. Of the 24 villages without RVF clinical disease 14 (58.33%) had herds of domestic ruminants in which at least one animal tested positive for IgG. Significant variation existed in seropositivity across all 24 villages and 74 herds/ farms ($p<0.001$). A total of 21 (28.38%, n=74) herds (ranging from one to three herds per village) had IgG seropositivity. The highest intra-village sero-prevalence of IgG in the herds/ farms with non-clinical disease was observed in Kimotorok village (80%, n=5) followed by Lormorije village (42.86%, n=7) in Simanjiro district. Both the IgM-positive sera were from two villages namely Makonane and Zavuza (Figure 1) in Same and Handeni districts respectively. These villages were located at 121 km apart. Domestic ruminants that were located at ≤1000m above the sea level had higher odds of being IgG seropositive than those located at an elevation above 1000m (OR=2.32, 95%CI 1.05 – 5.16, p=0.04). This association held even after allowing for the confounding effects of age (adjusted odds ratio=2.32, 95% CI: 1.05 – 5.16, p=0.93) and species (adjusted odds ratio=2.16, 95% CI: 1.00 – 4.82, p=0.06).

Table 2. The anti-RVF IgG serostatus in villages without RVF clinical disease in domestic ruminants

District	Village	Sheep No. examined	Sheep No. positive (%)	Goat No. exami-ned	Goat No. positive (%)	Cattle No. exami-ned	Cattle No. positive (%)
Handeni	Magamba	0	-	11	0 (0.0)	1	1 (100.0)
	Mazingira	0	-	2	0 (0.0)	0	-
	Msaje	18	1 (5.6)	0	-	5	1 (20.0)
	Taula	0	-	9	0 (0.0)	1	1 (100.0)
	Zavuza	7	1 (14.3)	3	1 (33.3)	16	0 (0.0)
Mbulu	Endahargadet	0	-	0	-	9	1(11.1)
	Haraa	0	-	0	-	4	0 (0.0)
	Khaday	0	-	0	-	4	0 (0.0)
	Masqaroda	0	-	0	-	8	0 (0.0)
Monduli	Emareite	3	0 (0.0)	4	0 (0.0)	0	-
	Lolkisale	6	0 (0.0)	5	0 (0.0)	0	-
	Mbashi	7	1 (14.3)	4	0 (0.0)	0	-
	Mfereji	5	0 (0.0)	5	0 (0.0)	0	-
	Orkatan	4	2 (50.0)	7	0 (0.0)	0	-
Same	Makokane	5	1 (20.0)	3	1 (33.3)	4	2 (50.0)
	Ndungu	2	0 (0.0)	2	0 (0.0)	6	2 (33.3)
	Njoro	10	0 (0.0)	16	0 (0.0)	0	-
	Vumari	10	1 (10.0)	2	0 (0.0)	15	2 (13.3)
Simanjiro	Kimotorok	0	-	5	4 (80.0)	0	-
	Loondrekes	7	2 (28.6)	0	-	10	0 (0.0)
	Lormorije	6	2 (33.3)	1	1 (100.0)	0	-
	Losinyai	7	0 (0.0)	2	1 (50.0)	1	1 (100.0)
	Naberera	0	-	8	0 (0.0)	9	0 (0.0)
	Sukuro	0	-	6	0 (0.0)	0	-
	Total	97	11(11.3)	95	8 (8.4)	93	11 (11.8)
Sex	Male	25	4 (16.0)	18	1 (5.6)	35	3 (8.6)
	Female	72	7 (9.7)	77	7 (9.0)	58	8 (13.8)
	Total	97		95		93	
Age group	Young	10	0 (0.0)	17	0 (0.0)	51	4 (7.8)
	Adult	87	11(12.6)	78	8 (10.0)	42	7 (16.7)
	Total	97		95		93	

Table 3. Prevalence of immunoglobulin G (IgG) specific to RVFV in wild animals in Ngorongoro Conservation Area

Species	Total tested	No positive (%)
African Buffalo	22	9 (40.9)
African Elephant	3	1 (33.3)
Lion	18	0 (0.0)
Thomson Gazelle	11	0 (0.0)
Warthog	9	0 (0.0)
Wildebeest	13	0 (0.0)
Zebra	24	0 (0.0)
Total	100	10 (10.0)

DISCUSSION

RVF remains endemic in Tanzania (FAO, 1999; Woods *et al.,* 2002; WHO, 2007; Corso *et al.,* 2008; Swai and Schoonman, 2009; Masambu, 2009; Sindato *et al.,* 2011; Fyumagwa *et al.,* 2011) and the northern zone had been severely affected by the past outbreaks (Corso *et al.,* 2008; Woods *et al.,* 2002; Sindato *et al.,* 2011; Fyumagwa *et al.,* 2011). Besides its survival in mosquitoes, RVFV is believed to circulate at very low level without noticeable clinical manifestation in animals (Pepin *et al.,* 2010; Rostal *et al.,* 2010).This study attempts to describe the clinical aspects of RVF viral activity in domestic and wild animals as well as its spatial distribution during IEP in order to contribute to the development/ implementation of strategic control initiatives to combat severe outbreaks in livestock and humans.

Our results indicate that RVFV life cycle exist without clinical disease in multi-host animal species during IEP in the northern Tanzania. Detection of anti-RVF IgG in African buffalo and elephant born before the 2006/2007 outbreak, suggests that virus transmission continued in the wild life during an IEP. This observation is consistent with previous studies that had reported evidence of RVF infection in African buffalo and other wildlife species during the Inter-epidemic periods (IEPs) (Gonzalez- Scarano *et al.,* 1991; Anderson and Rowe, 1998).

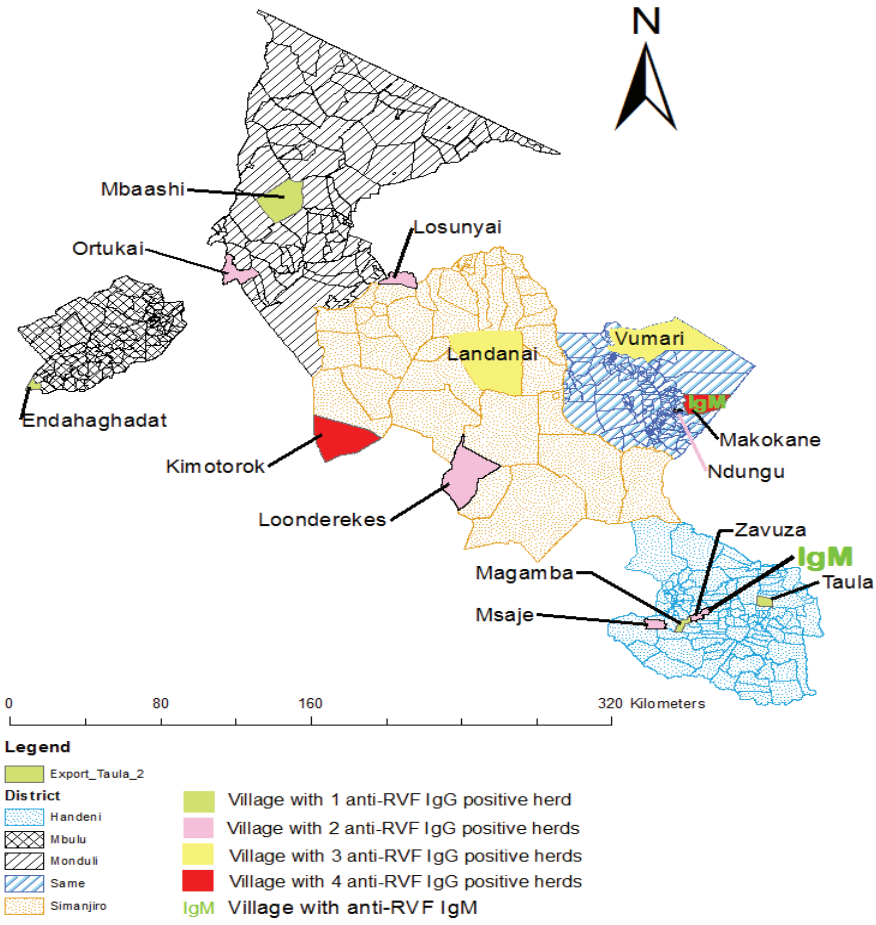

Figure 1. Distribution of villages with non-clinical RVF positive herds in northern Tanzania. The insert is map of Tanzania showing the study districts.

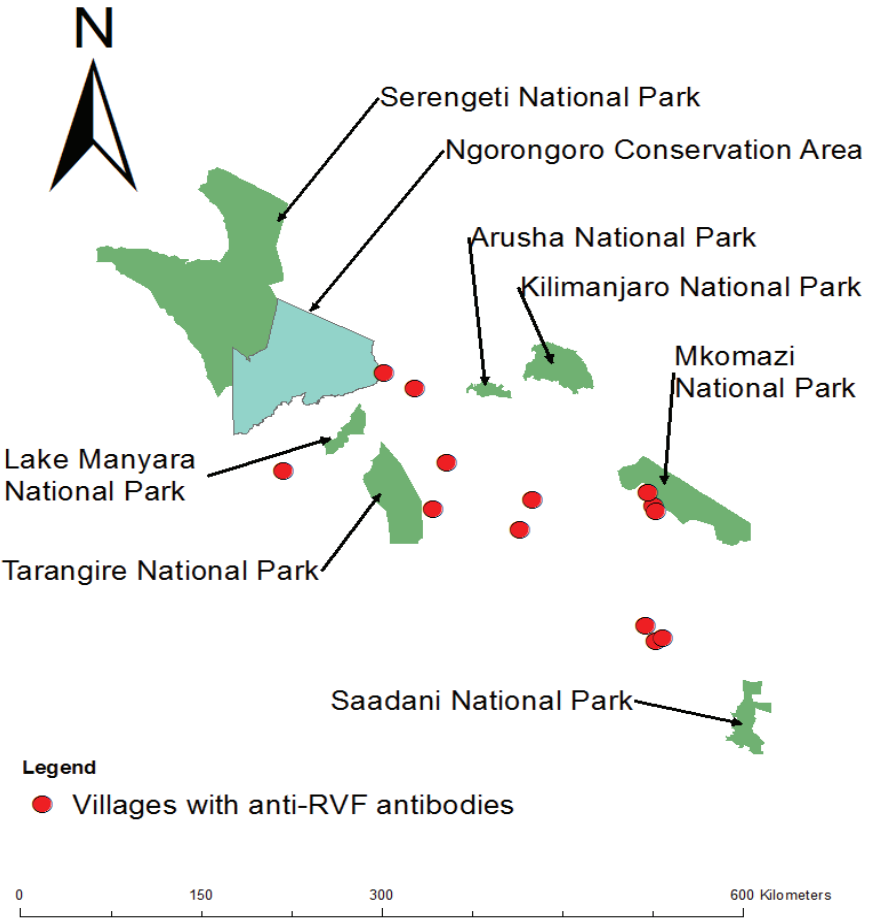

Figure 2. Distribution of villages with anti-RVF antibody in relation to the location of National Parks and Conservation Area

Detection of antibodies against RVFV in apparently health population of buffalo, elephant, cattle, sheep and goats in the study area suggests that these animals may be susceptible to RVFV infection but tolerant to clinical disease or had mild infection. A study by Rostal *et al.* (2010) reported serological evidence of infection with no clinical disease in sheep and goats born after the 1997/1998 but before the 2006 RVF outbreaks in Kenya. In Africa indigenous ruminant breeds infection is usually subclinical. A

high level of genetically determined resistance to RVF in indigenous breeds of sheep, goats and cattle has been reported in Africa (FAO, 2003).

The Northern zone of Tanzania where the study districts are located had reported sporadic RVF cases in animals in 1997/1998 outbreak (Woods *et al.,* 2002) and was heavily affected by the RVFV outbreak of 2006/2007 that involved both livestock and humans (Corso *et al.,* 2008). In this study relatively larger proportion of seropositive herds were located <1000m above the sea level implying that elevation is an important spatial predictor for RVF seropositivity. This observation is consistent with previous studies in Tanzania, Kenya and Madagascar (Nguku *et al.,* 2010; Chevalier *et al.*, 2011; Heinrich *et al.*, 2012). This observation suggests that the risk of RVFV infection increases with decrease in elevation and this scenario may be partly explained by the fact that the lower-lying areas support mosquito breeding and survival over longer periods contrary to higher elevations.

A very low proportion of domestic ruminants were found to be IgM positive. This suggests that there was no high level of active infection at the time of sampling. This explanation is supported by the fact that IgM persists for only 6 to 8 weeks after initial infection (Paweska *et al.,* 2005; 2007). Even though the PCR and antigen detection results were negative, detection of IgM-positive sera in goats from two villages that were located 121 km apart suggests presence of active infection in this species during the time of sampling. This detection of IgM in goats at least two months post-epidemic contrasts with the findings of a study in South Africa that reported IgM in cattle screened 20 days post-epidemic (Mapaco *et al.,* 2012). However, in our study it remains inconclusive as to why IgM was detected only in goats. While the scattered distribution of the two IgM samples might indicate introduction of these seropositive animals from active foci elsewhere into these villages; we are unable to unveil such a possibility since the information about animal introduction and/or herd replacement practices in specific herds was not obtained.

The presence of antibodies against RVFV in wildlife and domestic ruminants without clinical disease does not exempt these animal species from being reservoirs of RVFV in a sylvatic cycle. The fact that the surveyed districts are in close proximity with a number of national parks and conservation area and that the sampled conservation area had IgG in some wild ruminants, implies that the possibility of spread of infection from wildlife to domestic ruminants and vice-versa should not be underestimated. A study by Linthicum *et al.* (1985) suggested that infected wild animals, particularly buffalo, can develop viraemia and play a role as reservoirs.

CONCLUSION

Our results indicated that circulation of RVFV without clinical disease occurred in multi-animal species of wild and domestic ruminants during inter-epidemic period including the wildlife-domestic animals-human interaction areas in northern Tanzania. Furthermore the findings suggest that elevation is an important predictor of RVF seropositivity. These findings suggest wide-ranging host preference of mosquito vectors for domestic and wild ruminants and the proportion of animals infected with RVFV might remain the reservoirs. This emphasises on the need to strengthen one health approach of inter-sectoral collaboration towards strategic control initiatives to combat severe RVF outbreaks in livestock and humans in Tanzania.

ACKNOWLEDGEMENTS

We acknowledge the livestock keepers, Tanzania National Parks Authority (TANAPA), Tanzania Wildlife Research Institute (TAWIRI) and Ministry of Livestock and Fisheries Development. Special thanks to Arusha Veterinary Investigation Centre for providing the serum samples. The technical and material support kindly provided by the Special Pathogens Unit of the National Institute of Communicable Diseases, South Africa is acknowledged. This study was funded by the Ministry of Livestock and Fisheries Development and Southern African Centre for Infectious Diseases Surveillance through Wellcome Trust Grant.

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