



Assessing risk of Rift Valley fever transmission in a pastoral ecosystem using a One Health approach

Rosemary Sang¹, Mbaabu Murithi², Jacqueline Kasiiti², Nelson Owange², Samwel Arum¹, Ismail Hassan¹, Caroline Tigoi¹, Washington Onyango-Ouma³, Tobias Landman¹, Hippolyte Affognon¹

¹International Centre of Insect Physiology and Ecology, Kenya; ²Central Veterinary Laboratories, Kenya;

³University of Nairobi, Kenya
rsang@icipe.org

INTRODUCTION

Rift Valley fever virus RVF (family *Bunyaviridae*, Genus *Phlebovirus*) is a mosquito-borne viral zoonosis of humans and livestock first isolated from livestock in 1930s in Kenya. It has since been associated with increasing frequency of outbreaks in domestic ruminants and humans every five to ten years with devastating impacts on public health and the fragile economy. However, the fate of the virus between epidemics has remained shrouded in mystery. We used the “one health” approach to investigate virus activity in parts of Garissa County (a major hotspot of RVF) while also determining the associated vector distribution and densities.

DATA COLLECTION

- The activities of this study were conducted between 2012 and 2014 in north-eastern Kenya.



Human sampling (serosurvey)



Livestock tracking and sampling



Vector sampling

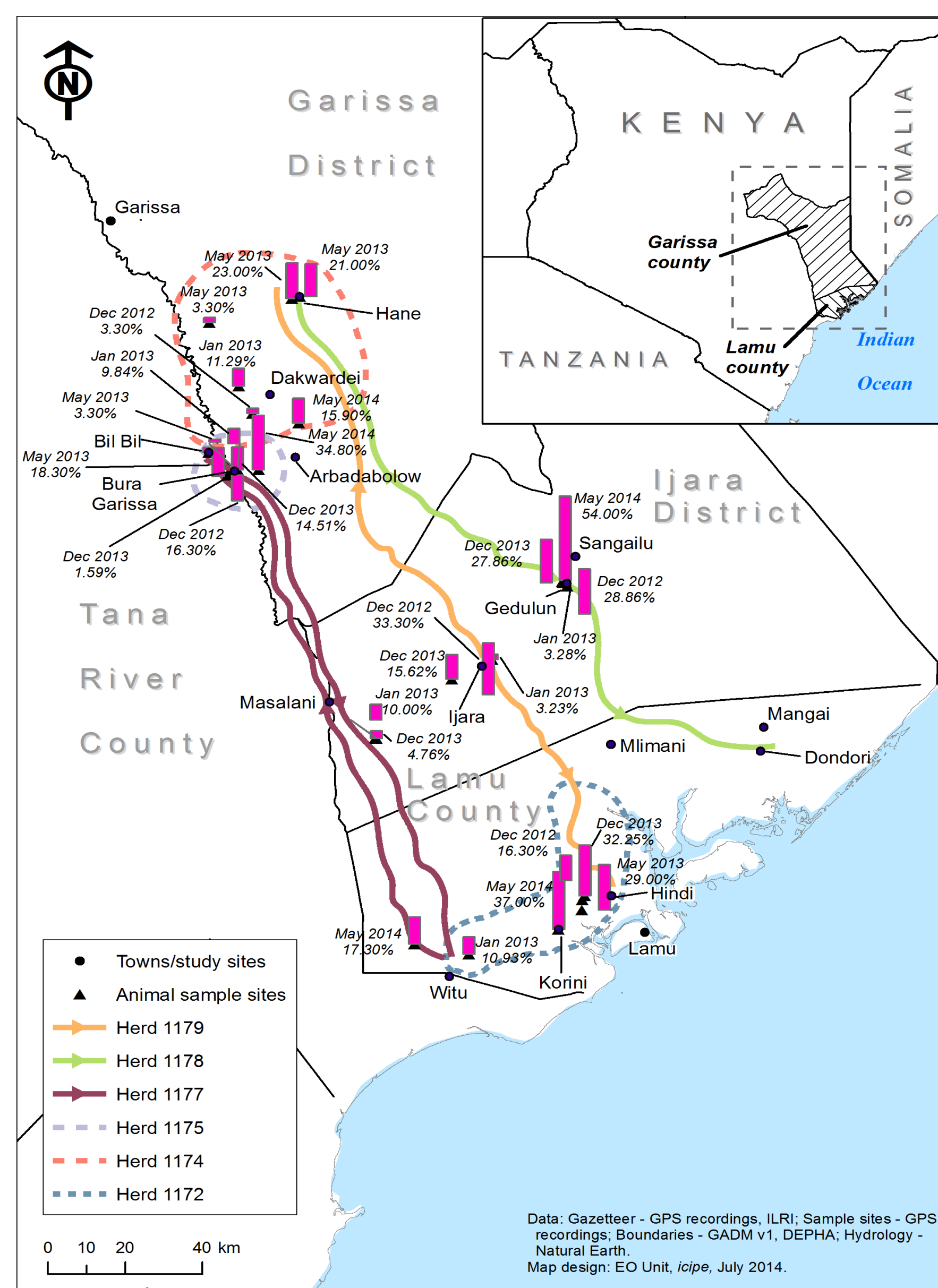


Fig. 1: RVF seroprevalence among livestock

CONCLUSION

- Active circulation of RVF virus persists during inter-epidemic period, spiking during rainy season and more intensely within the forested areas
- Populations living in settlements along nomadic routes and/or adjacent to grazing areas are at risk of virus infection.
- Ae. ochraceus* may have a role in virus transmission from wild ungulates to livestock and also to humans.
- Boni forest could serve as emergence zone for virus persistence and spread through animal movement.

IMPACT

- This study presents integrated data from vectors, livestock, and human studies as a means of understanding Rift Valley fever virus transmission pathways and risks in north-eastern Kenya.
- The data provides vital information that can be used to inform mitigation plans for preventing and controlling RVF outbreaks.

OBJECTIVES

- To understand the dynamics of RVFV transmission in a nomadic pastoral system during inter-epidemic period.
- To determine the distribution, diversity, and feeding preference of RVF vectors within the nomadic movement routes in north-eastern Kenya

RESULTS

Fig. 2: RVFV vector distribution

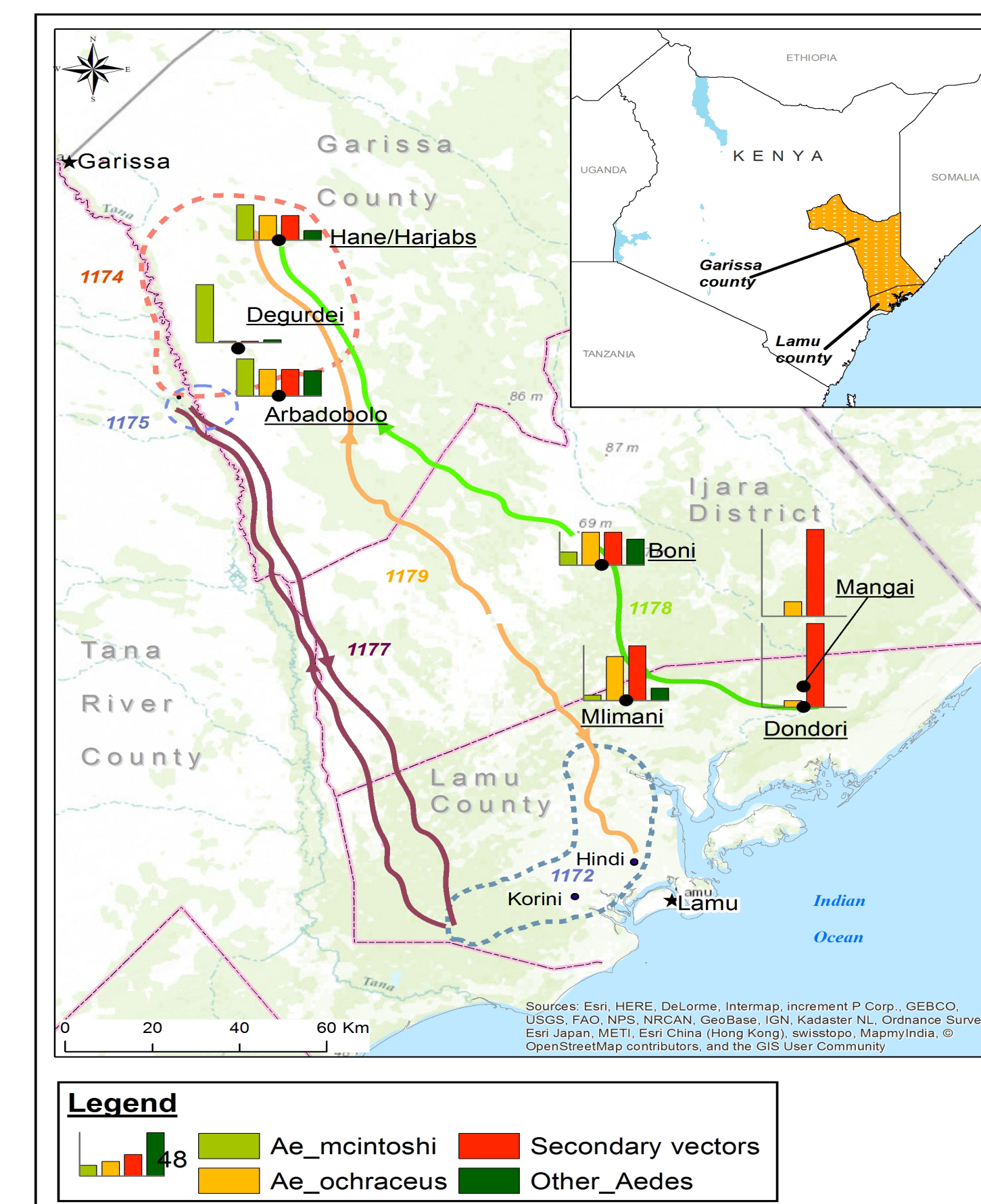
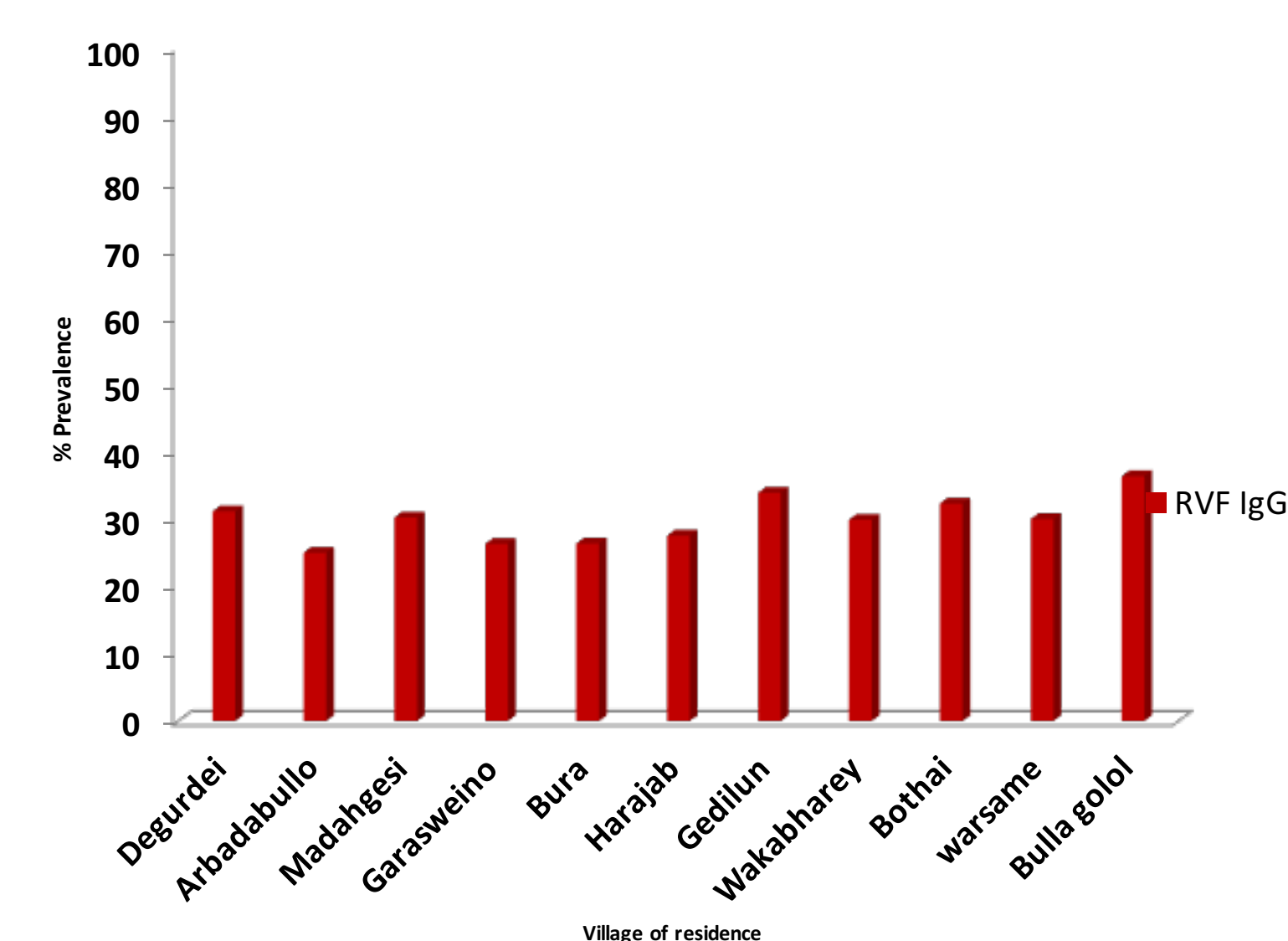


Fig. 3: RVFV IgG Prevalence in humans across settlements



- Ae. mcintoshi* is more prevalent in semi-arid north.
- Ae. ochraceus* is prevalent towards the forest and the coast.
- Mosquito species diversity is highest in Boni forest

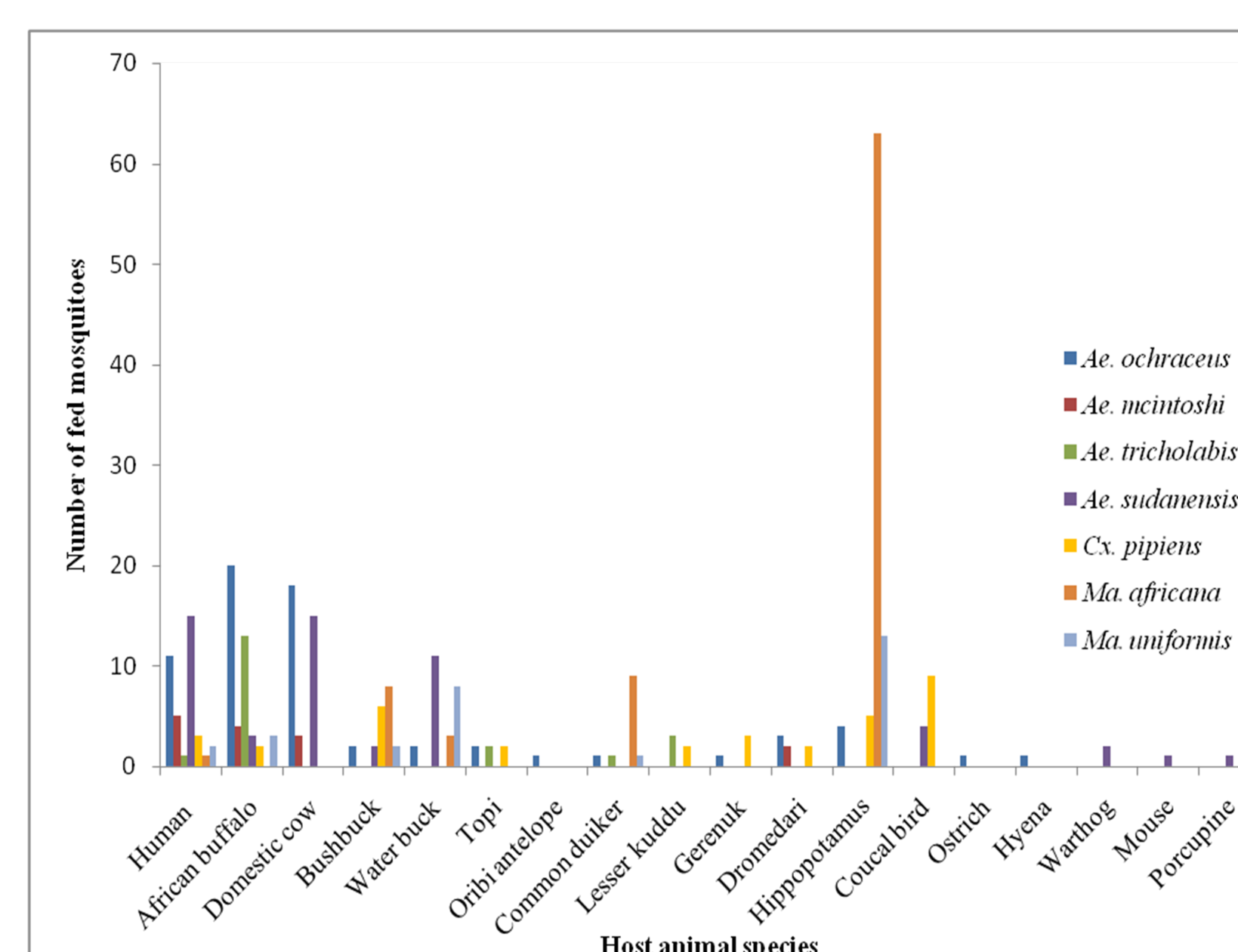
- The was no significant difference in prevalence by village overall prevalence 30%.

EVIDENCE OF RECENT INFECTION:

Five samples from villages in Fafi sub-county tested positive for IgM antibody.

- Arbadobolo-1,
- Bura – 1,
- Harjabs – 2
- Degurdei – 1

MOSQUITO FEEDING PREFERENCE



- Ae. mcintoshi* showed a conserved feeding pattern, feeding mainly on human, and cow.
- Aedes ochraceus* fed on wider range of hosts mainly buffalo, cow, human and camel.
- Ma. africana* had the highest number of fed mosquitoes but was also highly conserved feeder (>90% fed on hippopotamus).

REFERENCES

Arum S.O. et al., *Parasit. Vectors*. 2015 28; 8: 294.

Owange et al., *Preventive Veterinary Medicine* 08/2014; 117(1).

Tigoi et al., *Vector Borne Zoonotic Dis*. 2015 Feb 1; 15(2): 124–132.