Novel tick-borne *Rickettsia* sp. from wild ticks of Kenya: Implications for emerging vector-borne disease outbreaks

M. M. Mwamu1, 2, E. Kariuki3, D. Omondi1, J. Kabii1, D. Odongo2, D. K. Masiga4 and J. Villinger1

1International Centre of Insect Physiology and Ecology, Nairobi, Kenya; 2School of Biological Sciences, University of Nairobi, Nairobi, Kenya; 3Kenya Wildlife Service, Nairobi, Kenya

mwananje@gmail.com

**INTRODUCTION**

Ticks are important vectors of emerging infectious zoonotic pathogens that contribute to public and animal health burdens (De la Fuente et al., 2008). Limited understanding of pathogen diversity and their tick vectors, especially in areas of intensified human–livestock–wildlife interactions, often limits development of disease prevention and control strategies (Walker, 2011). We studied the diversity of questing ticks and tick-borne pathogens during the dry and wet seasons of 2013 and 2014 from the Shimba Hills National Reserve (SHNR), one of Kenya’s high biodiversity areas facing human encroachment.

**OBJECTIVES**

- To systematically collect and identify tick diversity in Shimba Hills National Reserve.
- To identify and characterise tick-borne pathogens circulating within the Shimba Hills human–livestock–wildlife interface.
- To identify tick–pathogen interactions.

**METHODS**

Tick collection

- PCR HRM
- Sequence analysis
- DNA/RNA Auto extraction
- HoTShot DNA extraction

**RESULTS**

Three species from two genera of the ixodidae family were identified: *Amblyomma eburneum* (n=118), *Rhipicephalus maculatus* (n=88) and *Amblyomma tholloni* (n=3). We report the first molecular detection of *Rickettsia africae* in *A. eburneum*, and two novel *Rickettsia*-like species, in *R. maculatus* ticks.

**CONCLUSIONS**

- Increasing incidences of emerging tick-borne infectious diseases require adequate control strategies.
- Surveillance in areas of intensified human–wildlife interactions is critical to improve understanding of pathogen diversity and their tick vectors.

**IMPACT**

- Our results may explain the occurrence of some unidentified febrile illnesses contributing to human morbidity in the region.
- The detection of *R. africae* will be useful in describing cases of African tick-bite fever.
- Novel pathogens are possible future disease threats.
- Results will contribute to better tick and tick-borne disease control.

**REFERENCES**
