Two-Gene High Resolution Melting Mosquito Bloodmeal Analysis: Unravelling Host-Vector-Arbovirus Interactions in a Kenyan Wildlife–Livestock Interface

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INTRODUCTION

Blood-feeding patterns of mosquitoes are linked to the spread of the pathogens that they transmit. Efficient identification of arthropod vector bloodmeal hosts can reveal the diversity of vertebrate species involved in disease transmission cycles, including disease reservoirs (Omondi et al., 2015).

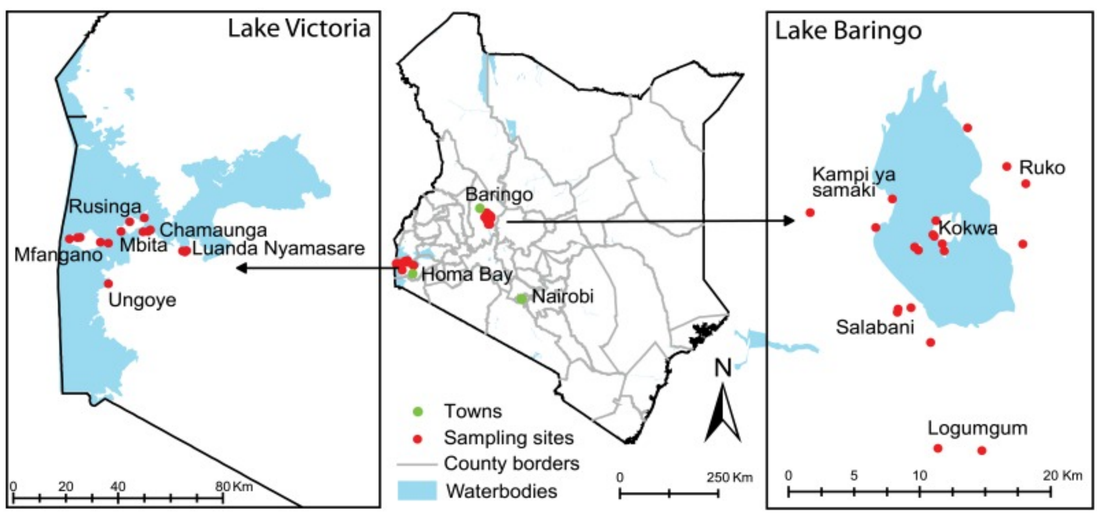
Using High Resolution Melting (HRM) analysis of cytochrome *b* (*cytb*) and 16S rRNA PCR products, we improved mosquito bloodmeal identification to identify diverse vertebrate host species found at the geographical interface of wildlife with livestock farming, and of aquatic/wetland with terrestrial ecosystems, along the shores and adjacent islands of lakes Victoria and Baringo in Kenya (Figure 1).

OBJECTIVES

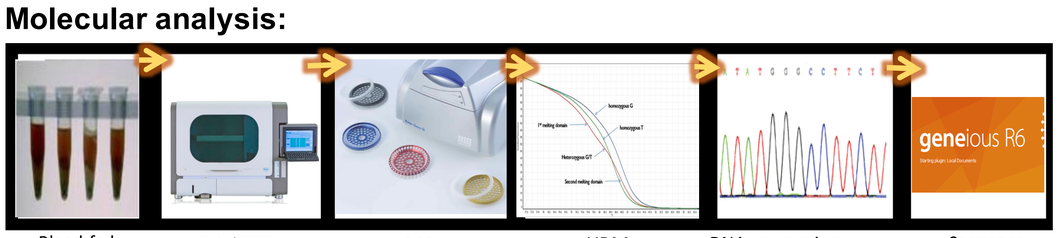
- To determine bloodmeal sources of blood-fed mosquitoes sampled along the shores and selected islands of lakes Baringo and Victoria in Kenya.
- To determine the presence of arboviruses in blood-fed mosquitoes.

METHODS

Figure 1. Mosquito sampling areas in Kenya



Molecular analysis:



RESULTS

Figure 2. Bloodmeal HRM based on two markers. We identified 33 bloodmeal hosts (including humans, 8 domestic animal species, 6 peridomestic animal species and 18 wildlife species) by HRM analysis.

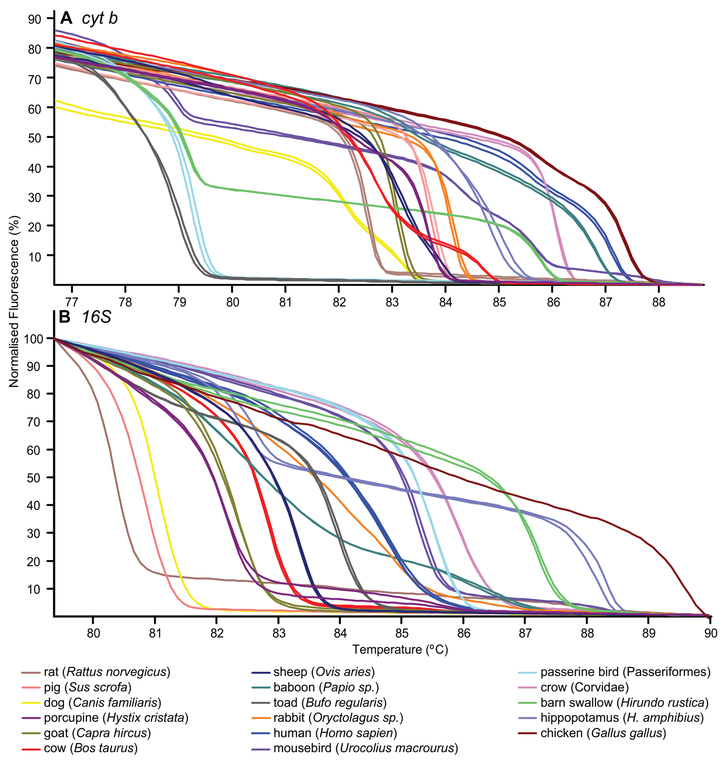
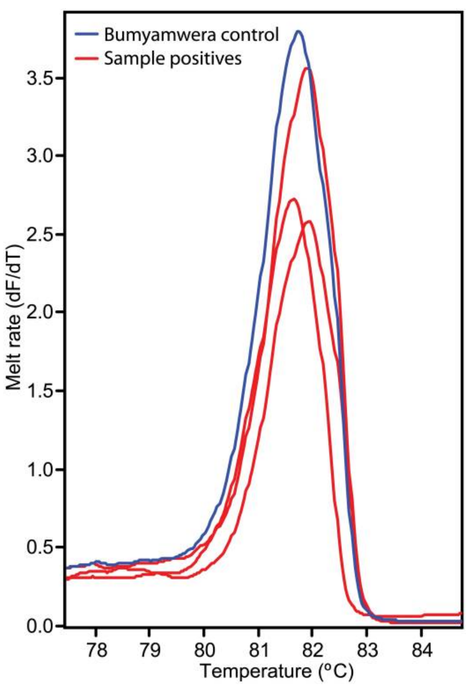


Figure 4. Arboviruses detected in blood-fed mosquitoes. We detected Sindbis and Bunyamwera viruses in blood-fed mosquito homogenates by Vero cell culture and RT-PCR in *Culex*, *Aedeomyia*, *Anopheles* and *Mansonia* mosquitoes from Baringo that had fed on humans and livestock.



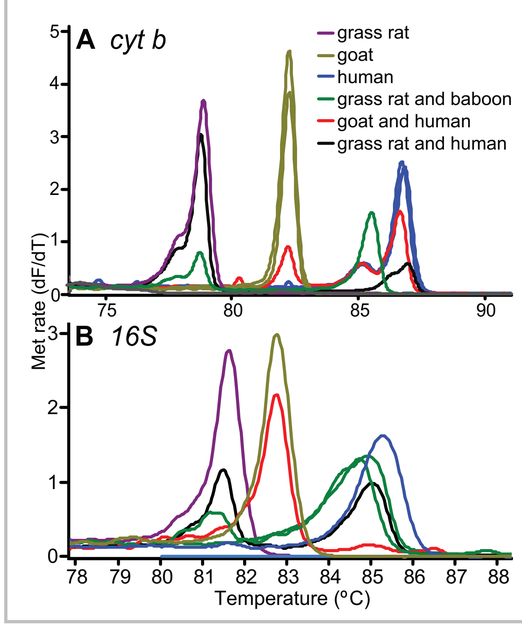


Figure 3. Mixed mosquito bloodmeals. Identified by HRM in a *Culex pipiens* from Mbita that had fed on a goat and a human, and in two *Mansonia africana* mosquitoes from Baringo that each had fed on a rodent (*Arvicanthis niloticus*) in addition to a human or baboon.

IMPACT

This study provides an efficient bloodmeal identification of field-collected vectors that is pivotal to disentangling disease transmission dynamics, identifying ecological reservoirs during inter-epidemic periods, and developing appropriate disease control and response strategies based on mosquito bloodmeal patterns.

CONCLUSION

This study demonstrates the improved resolution of HRM-based bloodmeal analysis by using two distinct molecular markers, revealing broad opportunistic host feeding patterns among mosquito vectors, including migratory birds and wildlife, which are important in the epidemiology of arboviruses endemic in these regions of Kenya.

REFERENCES

Omondi D., Masiga D.K., Ajamma Y.U., Fielding B.C., Njoroge L. and Villinger J. (2015) Unraveling host–vector–arbovirus interactions by two-gene high resolution melting mosquito bloodmeal analysis in a Kenyan wildlife–livestock interface. *PLoS ONE* 10(7), e0134375.

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