Comparative phylogeography of malaria mosquito vectors In Mageta and Magare Islands of Lake Victoria in Western Kenya

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INTRODUCTION

- Malaria continues to be a major public health concern and a key impediment to socioeconomic development.
- Vector control is the most effective measure to prevent malaria parasite transmission.
- Vector behaviour differs within locations and transmission is geographically specific.
- Knowledge of vector blood-meal sources and genetic variation is important in providing insight into transmission dynamics and strategies for optimal vector control.

METHODS

Study area

Between March 2013 and March 2015, mosquitoes were trapped at 3,093 geo-referenced households (population of 7,221) with Long Lasting Insecticides Nets (LLINs) coverage of 66.78% in malaria-prone islands of Lake Victoria in Western Kenya. We identified both mosquitoes species and their bloodmeals by PCR-high resolution melting analysis (HRM).

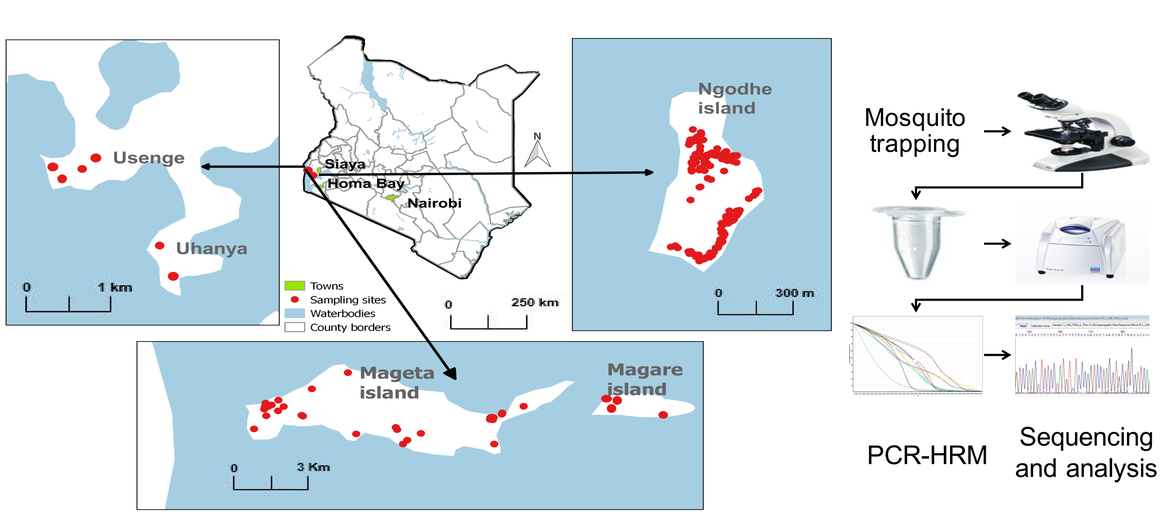

Figure 1: A map of sampling sites in the Lake Victoria region of Kenya.

CONCLUSION

- HRM analyses of *COI* has allowed a reliable and robust differentiation of malaria mosquito bloodmeal from abundant hosts.
- Malaria mosquito vectors feed upon humans when they are active and unprotected with LLINs.
- Additionally, the vectors opportunistically feed upon non-human hosts, presenting an important challenge for control.
- To reduce the levels of malaria transmission, it is necessary to reassess the role of LLINs by integrating other measures into malaria control.

IMPACT

We developed a reliable and robust way to differentiate malaria mosquito species and their bloodmeal hosts to provide insight into malaria transmission dynamics important for optimal vector control.

OBJECTIVES

- Identify mosquito species and sources of their blood-meals.
- Determine the genetic variations of the identified mosquito species.
- Correlate mosquito vector interactions with their host.

RESULTS

We sampled a total of 7883 mosquitoes of which 2693 were malaria mosquitoes (*A. gambiae s. s.*, *A. arabiensis, A. funestus* and *A. coustani*). Out of the total malaria mosquitoes collected, 444 (16.49%) were blood-fed. The blood-fed species were collected indoors by pyrethrum spray collector (PSC; 70.05%) and CDC light trap (15.32%), and outdoors by aspirator (ASP; 10.36%), and CDC light trap (4.28%) (Table 1).

Using (HRM) profiles of cytochrome b (*cyt b*), 16S ribosomal RNA and cytochrome oxidase sub-unit 1 (*COI*) genes, we identified 11 bloodmeal hosts including humans (69.82%), chicken (*Gallus gallus*; 1.80%), cow (*Bos taurus*; 11.26%), and dog (*Canis familiaris*; 1.35%) (Figure 3).

Table 1: Numbers of blood-fed mosquito species captured by different traps.

Species	Type of Traps			
	PSC	Indoor CDC	Outdoor CDC	ASP
A. gambiae s. s.	248 (55.86%)	34 (7.66%)	5 (1.13%)	34 (7.66%)
A. arabiensis	40 (9.01%)	10 (2.25%)	1 (0.23%)	6 (1.35%)
A. funestus s. s	23 (5.18%)	19 (4.28%)	0	16 (1.35%)
A. coustani	0	5 (1.13%)	13 (2.93%)	0
Total	**311 (70.05%)**	**68 (15.32%)**	**19 (4.28%)**	**46 (10.36%)**

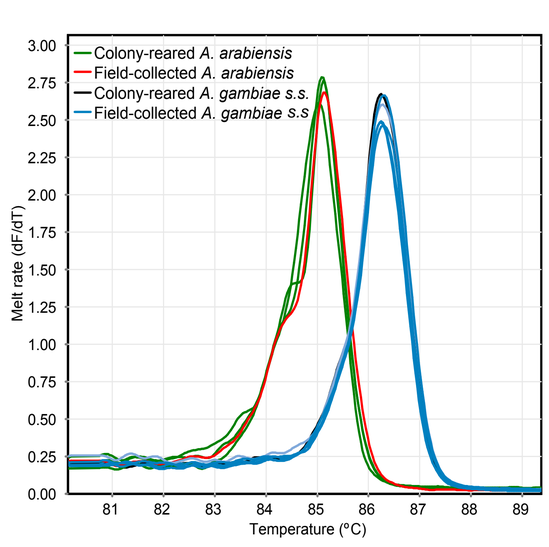

Figure 2: Melt rates of colony-reared and field collected *Anopheles* mosquitoes.

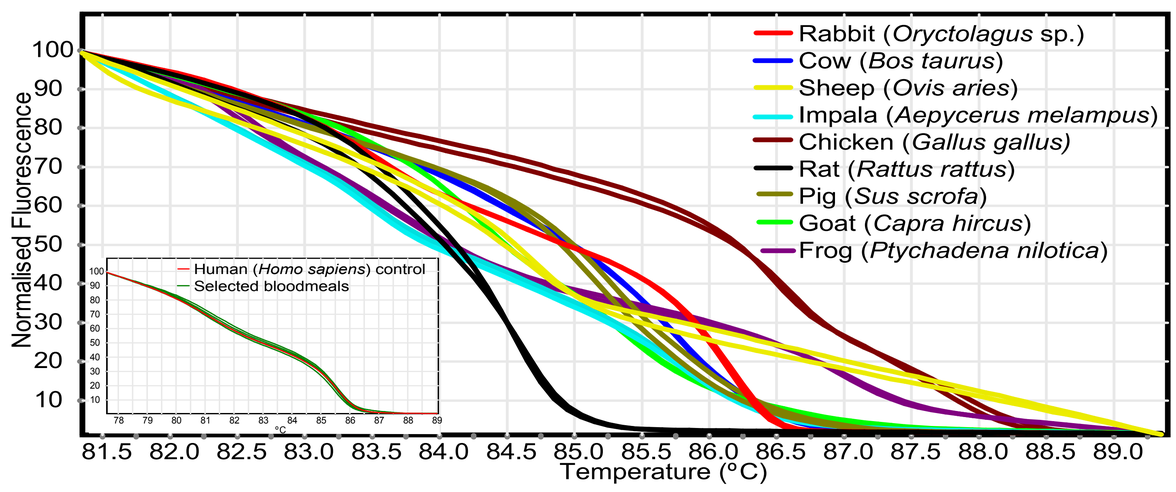

Figure 3: HRM profiles of mosquito bloodmeal sources using *COI*

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