



Diversity of zoonotic arbovirus and malaria parasites in urban-restricted non-human primates

Maamun Jeneby^{1,2*}, Villinger Jandouwe¹, Daniel Masiga¹, Rosemary Sang^{1,3}

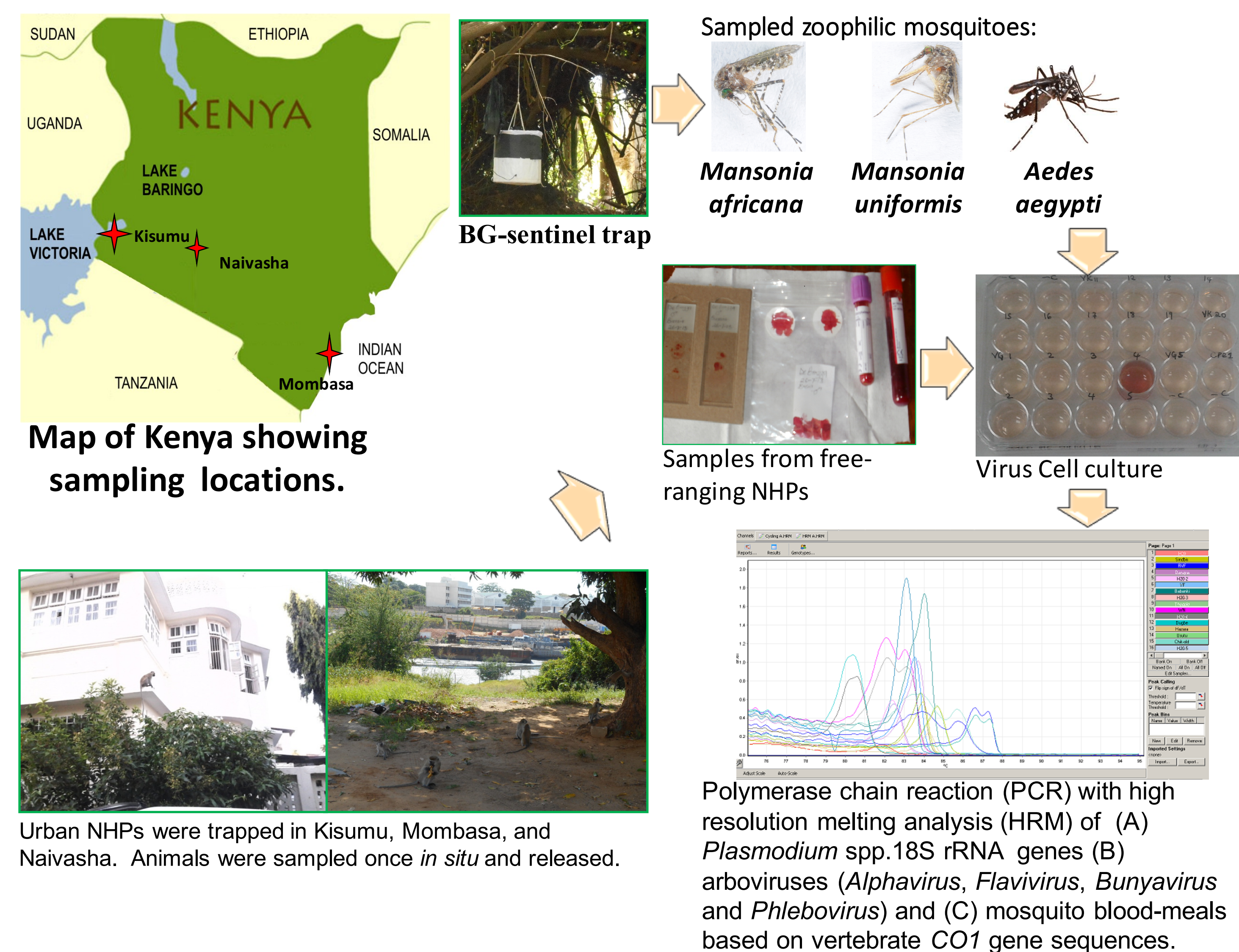
¹International Centre of Insect Physiology and Ecology (*icipe*), Kenya; ²National Museums of Kenya, Kenya; ³Kenya Medical Research Institute, Kenya

jmaamun@icipe.org

INTRODUCTION

Urban centres in East Africa have witnessed increasing zoonotic disease outbreaks in recent decades (1). Among these are a series of endemic zoonotic infections, some of which originate from monkeys (1) and are mosquito-borne (2,3). Endemic foci of zoonotic pathogens, including dengue virus, yellow fever virus and simian malaria parasites, usually refer to rural villages. However, the focal distribution of pathogens may also occur in urban areas with suitable conditions and habitats for animal hosts, vectors, pathogen transmission and susceptible human populations. It is thus important to understand the role of potential vectors and animal reservoirs constituting the so-called 'zoonotic disease ecology' in densely populated urban centres such as Kisumu and Mombasa, in Kenya, East Africa.

METHODS



CONCLUSIONS

The study findings indicate that African green monkeys and baboons in Mombasa and Kisumu urban centres are infected with a diversity of malaria parasites and arboviruses of medical importance. With the presence of zoophilic mosquitoes, NHP hosts and exposed human population, there is potential risk of zoonotic pathogen transmission to humans.

IMPACT

- Although *P. falciparum* and *P. berghei* are thought to be human and rodent-specific malaria parasites, respectively, NHPs may also be important parasite reservoirs.
- Arboviruses of medical importance are circulating in urban primates.
- Mosquitoes that bite humans in urban centres are also zoophilic, feeding on other vertebrate animals.

OBJECTIVES

To investigate, for the first time, the distribution of dengue virus, yellow fever virus and simian malaria parasite in free-ranging non-human primates (NHPs) and zoophilic mosquitoes within densely populated urban centres in Mombasa and Kisumu, Kenya, East Africa.

RESULTS

Sampled NHPs

- Chlorocebus aethiops* (African green monkeys) (120) and 10 *Papio anubis* (baboons) were sampled in Mombasa (N=51), Kisumu (N=53) and Naivasha (N=26).
- Mosquitoes (5617) were collected from within the monkey home ranges, identified and processed into 1517 pools of up to 25 mosquitoes/pool.

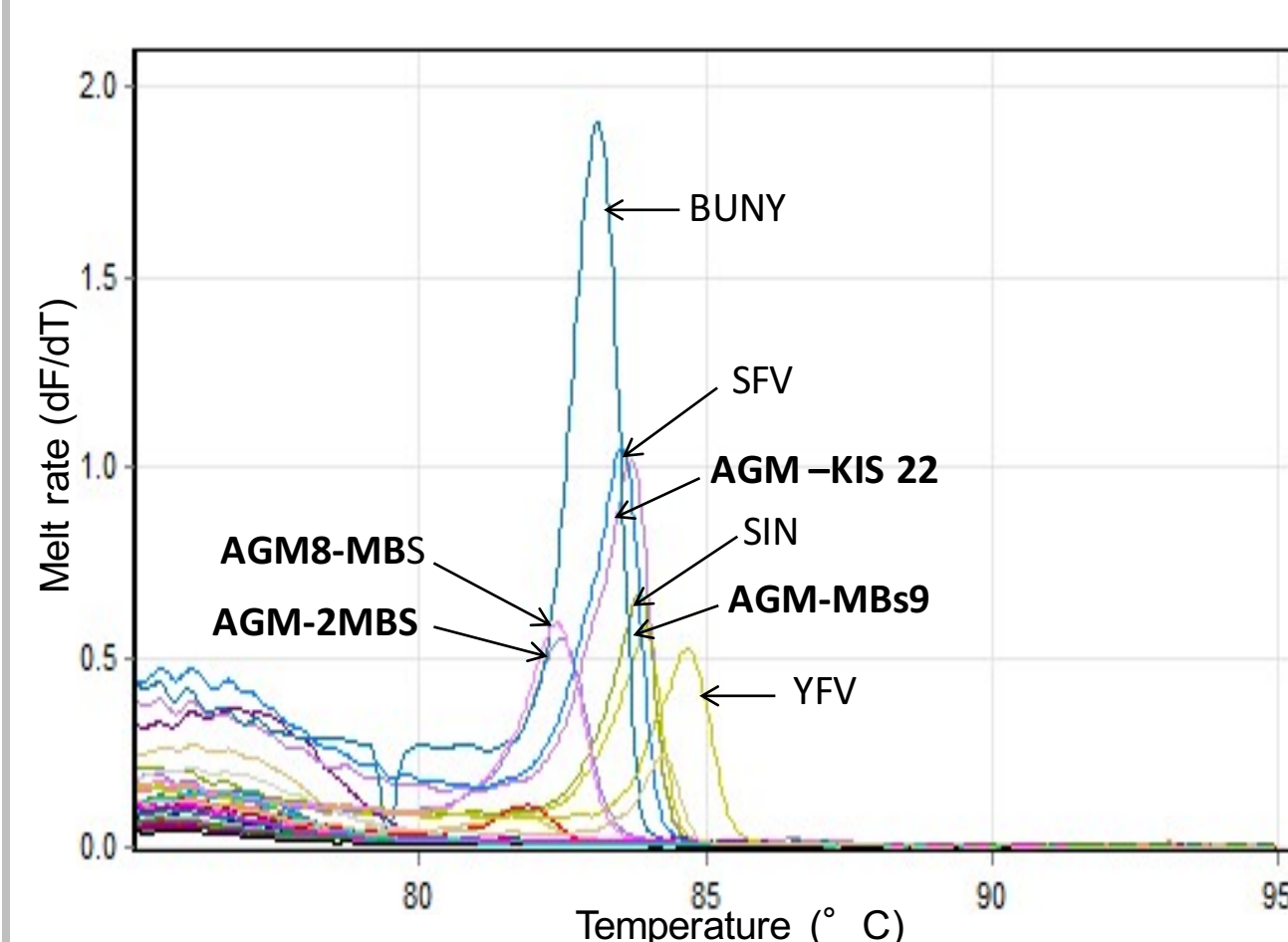


Fig. 1. PCR-HRM high throughput pan arbovirus detection of Bunyavirus (BUNV), Semliki Forest virus (SFV), Chikungunya virus (CHIK) and Sindbis virus (SINV) in 15% of the primate samples. **Bolded annotations** are representatives of samples from African green monkey (AGM) from Mombasa (MSA), and Kisumu (KIS).

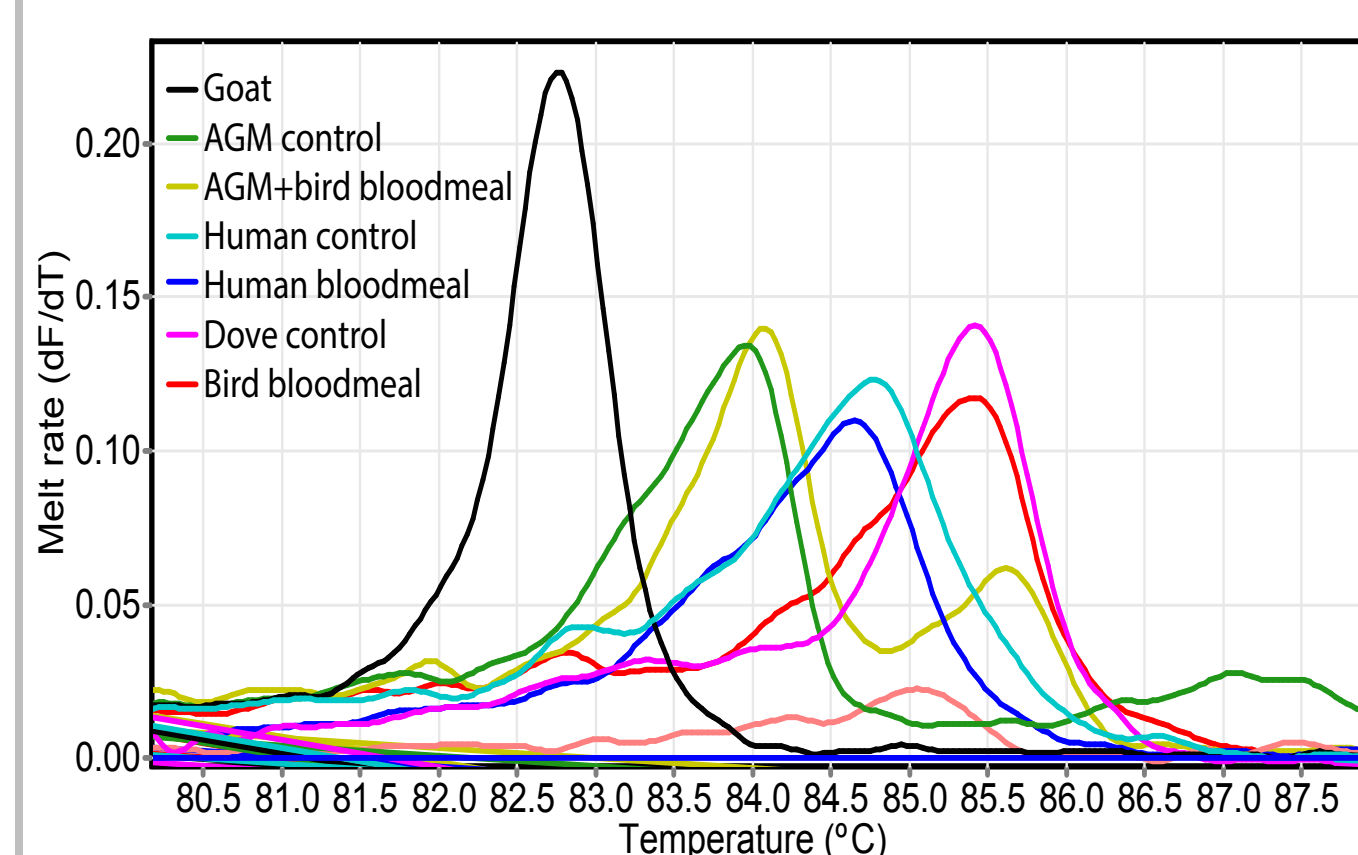


Fig. 3. Mosquito blood meal analysis using PCR-HRM (2). Blood meal indicated that zoophilic mosquitoes, *Aedes aegypti*, *Culex pipiens* and *Culex zombaensis* feed on humans, birds, goats as well as urban monkeys.

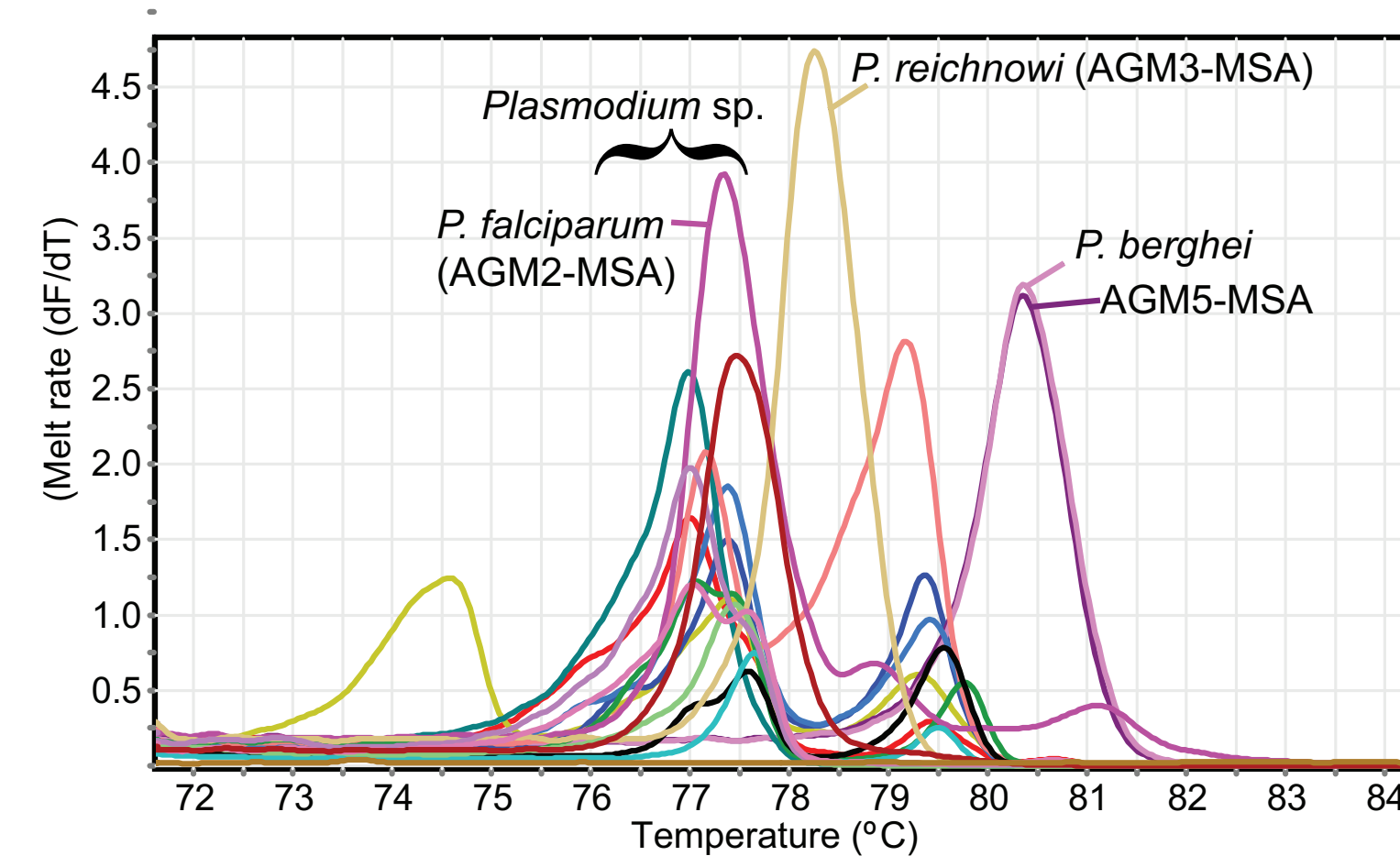


Fig. 2. Nested PCR-HRM for detection of *Plasmodium* spp. (4). This test detected a diversity of *Plasmodium* species including *P. falciparum*, *P. reichnowi* and *P. berghei* in blood samples from African green monkeys in Mombasa urban centre.

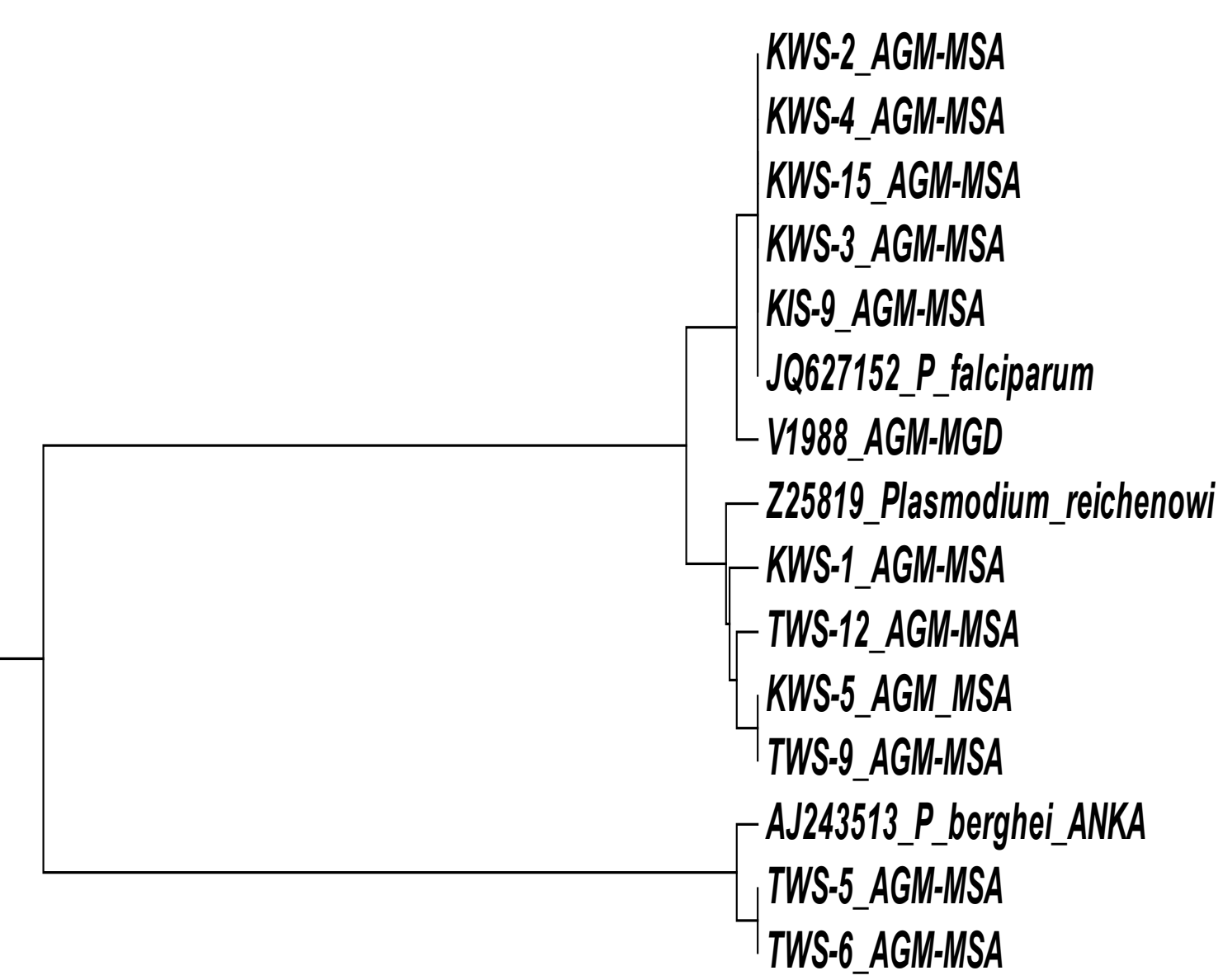


Fig. 4. Phylogenetic relationships between the 18S rRNA sequences obtained in the study and those of known *Plasmodium* species (represented by their accession number)

REFERENCES

- Weaver S.C. (2013) Urbanization and geographic expansion of zoonotic arboviral diseases: mechanisms and potential strategies for prevention. *Trends Microbiol.* 21, 360–363.
- Omondi D. et al. (2015) Unravelling Host-Vector-Arbovirus Interactions by Two-Gene High Resolution Melting Mosquito Bloodmeal Analysis in a Kenyan Wildlife-Livestock Interface. *PLoS One.* 10(7).
- Odhiambo C. et al. (2015) Phylogenetic analysis of Bunyamwera and Ngari viruses (family Bunyaviridae, genus *Orthobunyavirus*) isolated in Kenya. *Epidemiology & Infect.* 1: 7.
- Kipanga P.N. (2014) High-resolution melting analysis reveals low *Plasmodium* parasitaemia infections among microscopically negative febrile patients in western Kenya. *Malaria J.* 13: 429.
- Omondi D., Masiga D. K., Ajamma Y. U., Fielding B. C., Njoroge L., and Villinger J. (2015) Unravelling host-vector-arbovirus interactions by two-gene high resolution melting (HRM) mosquito bloodmeal analysis in a Kenyan wildlife-livestock interface. *PLoS ONE*, 10(7): e0134375. doi:10.1371/journal.pone.0134375.