

## ABSTRACT

Malaria, a vector borne disease is still a public health problem in sub-Saharan Africa. In western Kenya, malaria is endemic with the predominant vectors being *An. gambiae s.s.*, *An. arabiensis* and *An. funestus*. Pyrethroid-based long lasting insecticidal nets and indoor residual spraying are currently major effective tools employed to control malaria vectors in endemic areas in western Kenya. However, they are currently threatened by insecticide resistance. Malaria vectors exhibit varied geographical distributions and *An. gambiae s.s.*, *An. arabiensis* and *An. funestus* are the primary vectors in Busia, Ahero and Bondo respectively. Knockdown resistance has been documented as a mechanism of resistance against pyrethroids. Recently, both L1014S and L1014F mutations associated with knockdown resistance have been reported in western Kenya. Whether these mechanisms correlate with sporozoite rates in *Anopheles gambiae s.l.* mosquitoes in western Kenya is unknown. The overall aim of this study was to investigate whether knockdown resistance had impact on malaria transmission. Specifically, this study investigated rate of deltamethrin phenotypic resistance; *P. falciparum* sporozoite rate and *Anopheles* densities between wild-caught female *An. gambiae s. l.* and *An. funestus* mosquitoes; determined whether *kdr* genotypes (L1014S and L1014F) frequency has association with *P. falciparum* sporozoite rate in *An. gambiae s.s.* and *An. arabiensis*; compared the knockdown resistance allele frequency in larval raised and wild-caught female *An. gambiae s. l.* Samples were collected from Ahero, Bondo and Busia in western Kenya. In the laboratory-based experimental design, larval raised adults and wild caught *Anopheles* were exposed to 0.05% deltamethrin using the WHO tube assays to test for susceptibility. Conventional PCR and real-time PCR were used for species identification and *kdr* genotyping respectively. Sporozoite rates were determined using ELISA in all wild-caught female mosquitoes. Of 4,360 wild-caught *Anopheles* sampled, 32.8% were *An. funestus* and the rest were *An. gambiae s.l.* A total of 2,186 larvae raised adults *An. gambiae s.l.* were also used for the study. Independent t-test showed that *An. funestus* were more phenotypically resistant compare to *An. gambiae s.l.* ( $P < 0.001$ ). Independent t-test also showed that wild-caught adult mosquitoes were more phenotypically resistant than larval raised ones ( $P < 0.001$ ). Independent t-test showed that *An. funestus* had higher sporozoite infectivity rate than *An. gambiae s.l.* ( $P < 0.001$ ). Two-way classification chi-square test of association revealed that there was a significant association between *kdr* east (L1014S) and sporozoite rate in *An. gambiae s.s.* ( $X^2_1 = 5.49$ ,  $P = 0.032$ ). It also showed that the L1014S and L1014F allele frequencies in larvae raised and wild *An. gambiae s.l.* were not statistically significant. The finding of a higher level of resistance in wild versus larval raised adults could be alluded to other mutations and mechanisms of resistance. It also suggests that wild mosquitoes should be considered in assessment of phenotypic resistance. The observation of high sporozoite rates in *An. funestus* in Bondo and Busia compared to *An. gambiae s.l.* indicates that this re-emerged species could be driving malaria transmission in the sub-Counties. The significant association between *kdr* east (L1014S) and sporozoite rate in *An. gambiae s.s.*, suggest the epidemiological importance of that marker; it could drive malaria transmission. The insignificant difference observed in *kdr* (L1014S and L1014F) frequencies in wild and larval raised adults which did not reflect in phenotypic resistance suggest that other mechanisms of insecticide resistance might contribute to resistance in wild mosquitoes. The findings of this study will help in insecticide resistance monitoring and assessment programmes.

