

Molecular Characterization of Malaria Vectors in Gonja-Same District: The Impact of Insecticide-treated Net Interventions

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Introduction: An entomological survey was conducted in the lowland and highland of Gonja Maore and Bombo villages, respectively, in the Same District in northeastern Tanzania. This survey aimed to estimate the malaria vector abundance and determine the malaria vector composition of *Anopheles gambiae* and *Anopheles funestus* sibling species.

Methods: Indoor and outdoor mosquitoes were collected by CDC light traps and MMX traps, respectively, in two villages, each with twelve houses. The collected mosquitoes were sorted morphologically and identified using a dichotomous taxonomic key followed by preservation for molecular genotyping. DNA extraction was done, followed by a polymerase chain reaction to amplify and visualize bands of different species of mosquitoes.

Results: This study indicates that *An. arabiensis* were predominant sibling species 2587 (100%) of the *An. gambiae* complex in the study area followed by *Anopheles rivulorum* 5(71.4%) and *Anopheles lesoni* 2 (28.6%) among malaria vectors. Furthermore, it was found that there has been a marked change in sibling species composition whereby *Anopheles gambiae s.s.* changed from being the most abundant in the past to become a rare species, and *An. arabiensis* had evolved to be the most dominant species in the study area.

Conclusion: The decline in the population of *An. gambiae* complex has excessively affected the most important malaria vector, reducing its role in the transmission of malaria in the study areas. The predominant malaria vector is *An. arabiensis* which feed outdoor when there is an indoor control intervention. We recommend using outdoor control methods such as larviciding and odor bait trapping to control malaria vectors in the study area.

