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Abundance, Diversity, and Distribution of Potential Mosquito Vector Fauna in the Wellamadama Premises of the University of Ruhuna, Southern Sri Lanka

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Abstract

Mosquitoes play a significant role in causing disease outbreaks among humans and animals in many parts of the world. Assessing the risk of disease outbreaks related to vector-borne diseases requires a thorough understanding of the population dynamics of vectors in a specific area. The present study was conducted weekly from August 2023 to October 2023 at the Wellamadama premises of the University of Ruhuna, Sri Lanka. Mosquitoes were collected in two major habitat types, *i.e.*, areas with high anthropogenic activities (HAA) and low anthropogenic activities (LAA), to assess the population structure of potential vector mosquito fauna. Bird-baited traps, mammal-baited traps, CO_2 traps, and light traps were used for mosquito surveillance. All traps were placed at the ground level (1.5-3.0 m), except the bird-bated traps, which were placed 6 m above the ground level. An equal number of traps from each trap type were placed in both HAA and LAA on each sampling date. Collected mosquitoes were identified using standard taxonomic keys. Environmental factors with species abundance and diversity were assessed with canonical correspondence analysis from PAST 4.13. Shannon's diversity index (H') (HAA:1.767, LAA:2.064) and Margalef's index (Mg') (HAA:1.486, LAA:3.194) were used to compare the abundance and diversity of selected habitat types. A total of 423 mosquitoes that belong to 18 species and eight genera (*i.e.*, *Anopheles, Aedeomyia, Aedes*, *Armigeres, Culex, Lutzia, Coquillettidia,* and *Mansonia*) were identified. Even though the diversity was higher in the LAA (18 species) than in the HAA (9 species), the abundance of mosquitoes in the HAA (n=218) is not significantly different from LAA (n=205) (t=0.09, p=0.932). The *Lutzia halifaxii, Ad. catasticta, Ma. unifromis, Cx. sinensis, Cx. pluvialis, Cx. malayi, Cx. gelidus, Ae. vexans,* and *An. jamesii* were only found in LAA, while *An. culicifacies, An. subpictus, An. varuna, Aedes aegypti, Ae. albopictus, Ar. subalbatus, Cx. tritaentorhynchus, Cx. quinquefasciatus*, and *Cq. crassipes* were common to both study sites. With the environmental parameters except for *Coquillettidia* and *Culex,* the rest of the genera were positively correlated with the temperature (r=0.209) and negatively correlated with RH (r=-0.480). The study identified a total of 11 human vector species and 7 non-human vector mosquito species. The high abundance and widespread distribution of vector mosquitoes underscores the potential for mosquito-borne diseases to spread within the university premises.

Keywords: Mosquito taxonomy, Environmental factors, Disease outbreaks, Traps, Risk assessment

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197