Abstract No: BO-03

Diversity of microbiota associated with dengue vector mosquito breeding habitats in Udapalatha MOH Division, Sri Lanka

J. Y. Kumari¹, L. D. Amarasinghe^{1*} and H. A. K. Ranasinghe²

¹Department of Zoology and Environmental Management, University of Kelaniya, Sri Lanka ²Department of Biomedical Sciences, CINEC Campus, Sri Lanka. deepika@kln.ac.lk*

Microbiota associated with mosquito breeding habitats are among biotic factors and serve as parasites, pathogens, predators, competitors, non-competitors, and food items for developing larvae. Therefore, there are naturally occurring microbiota species that serve as potential controlling agents against mosquito larvae, causing lethal effects on them. This information can be used in developing novel mosquito vector control strategies. Besides, the degree of parasitic, pathogenic, or predatory effects may also vary with the geographical location, influencing environmental conditions, including abiotic factors and other biotic factors within the habitat. Therefore, the current study was carried out to determine the diversity of microbiota associated with different breeding habitats of dengue vector mosquitoes; Aedes aegypti and Ae. albopictus. Sampling was performed from a variety of breeding habitats at Udapalatha MOH division in Gampola urban area from November 2021 to January 2022. Microbiota in water samples were preserved using Rose Bengal solution and Lugol's iodine and were identified under microscope, using standard identification keys. During the survey, twelve different breeding habitats, namely plastic containers, metal containers, concrete slabs, glassware, tires, leaf axils, tree holes, coconut shells, bamboo trees, ornamental ponds, discarded roof tiles and clay pots, were identified as key breeding sites of Aedes mosquitoes. From the collected samples 54.54% of habitats were positive for Ae. albopictus and 45.46% were positive for Ae. aegypti. Eleven microbiota species; Canthocamptus staphylinus, Canthocamptus sp., Parastenocaris sp., Lepadella ovalis, L. patella, Rotatoria rotatoria, Rotatoria sp., Asplanchna brightwelli, Trichocerca rattus, Euglena sp., and Flagilaria sp. were encountered from breeding habitats associated with Ae. aegypti. Meanwhile, Canthocamptus staphylinus, Parastenocaris sp., L. ovalis, L. patella, R. rotatoria, Rotatoria sp., Euglena sp. and Flagilaria sp. recorded from breeding habitats associated with Ae. albopictus. The highest Shannon Weiner diversity index and gamma diversity relating to the Ae. aegypti were recorded from leaf axils, while for Ae. albopictus, it was from metal containers. For Ae. aegypti, the highest heterogeneity in microbiota diversity was recorded from tire habitats and it was from plastic containers for Ae. albopictus. Out of the microbiota species recorded, no species was identified as parasitic or pathogenic to Aedes mosquito larvae. Updated information from the present investigation would facilitate implementing appropriate vector control interventions.

Keywords: Aedes, Associate, Control, Parasite, Pathogenic