

VII ABSTRACT

Microbiota associated with mosquito breeding habitats serve as parasites, pathogens, predators, competitors, non-competitors, and food items for developing larvae. Identification of microbiota species that cause lethal effects against mosquito larvae would be beneficial for potential larval controlling approaches in an environmentally- friendly manner. Mosquito gut symbiotic bacteria could be genetically modified to express effector molecules and then reintroduced into the mosquito, where they produce desired effects by influencing disease transmission potential. These approaches may prove to be a highly valuable tool for mosquito control strategies. The present study was carried out to determine selected biotic and abiotic factors associated with the mosquito larvae in a range of mosquito breeding habitats encountered in selected areas of four districts in Sri Lanka (Gampaha, Kegalle, Kandy and Kurunegala). Midgut bacteria in different life stages of selected vector mosquitoes were screened.

The study revealed that the relative distribution of mosquito species ($X^2=143.248$; $P < 0.001$) and naturally occurring microbiota species/taxa associated with mosquito breeding habitats ($X^2=257.029$; $P < 0.01$) were significantly different among four districts studied. A total number of 83 microbiota species/taxa were identified from a range of natural and temporary mosquito breeding habitats within four districts in Sri Lanka and *Vorticella microstoma*, *Zoothamnium* spp. and *Chilodinella* sp. were found as possible parasitic, epibiont, and pathogenic agents against mosquito larvae respectively. Laboratory bioassays revealed that there is a potential of *V. microstoma* as a bio-controlling agent against *Culex tritaeniorhynchus*, *Culex gelidus* and *Anopheles subpictus* mosquito larvae.

The relative distribution of midgut bacteria in adult *Cx tritaeniorhynchus*, *Cx gelidus* and *Mansonia annulifera* mosquitoes were significantly different ($X^2=486.091$; $P < 0.000$) from each other. Midgut bacterial composition of *Aedes aegypti* and *Aedes albopictus* adults ($X^2=556.167$; $P < 0.001$) and larvae ($X^2=633.11$; $P < 0.001$) respectively, are significantly different from each other. The relative distribution of midgut bacteria among field captured *Ae. aegypti* and *Ae. albopictus* larvae

($X^2=84.981$; $P < 0.000$) and adults ($X^2=48.974$; $P < 0.000$) from the different localities; Brandiyamulla, Gampaha, and Miriswaththa, in Gampaha Medical Office of Health (MOH) area were significantly different from each other. Besides, field captured mosquitoes (both larvae and adults) and the lab-reared colony of *Ae. aegypti* (both larvae and adults) harbor a significantly different gut bacterial composition. The study revealed that mosquito midgut bacterial composition is influenced by the life stage, species, and the locality they inhabit.

The majority of microbiota species co-exist with mosquito larvae and there are species, serve as parasites, pathogens, and food items for developing larvae. Microbiota composition in breeding habitats varies with locality. Identified gut microbiota from field captured mosquito species could incorporate with the modified strains of mosquitoes through open release programmes in novel vector approaches, to generate compatible organisms with the wild population, thereby achieving higher competitiveness, fitness, and survival.

Keywords: Biotic, *Culex*, epibiont, interactions, parasite, pathogen, polymorphism.