

Microbiota Diversity associated with Mosquito Breeding Habitats in Kegalle District, Sri Lanka

H.A.K. Ranasinghe* and L.D. Amarasinghe

Department of Zoology and Environmental Management, University of Kelaniya

**Corresponding Author E-mail: achinikoshilaa@gmail.com, TP: +94774794083*

The distribution, abundance, and individual fitness of mosquitoes are known to be dependent on associated microbiota composition with developing larvae. Identification of such naturally occurring microbiota and their interactions on mosquito larvae, in terms of parasitic, pathogenic, competitive or predatory organisms against larvae is beneficial. Such agents can be used for potential larval controlling approaches, in an environmental- friendly manner. Thus, the present study aimed to investigate the diversity of microbiota associated with mosquito larval habitats. Sampling was performed from a variety of breeding habitats in Kegalle district, Sri Lanka. Microbiota in water samples were preserved using Rose Bengal solution and Lugol's iodine, and were identified observing under the microscope, using standard identification keys. A variety of mosquito breeding habitats indicated the presence of 37 microbiota species under 9 phyla, belong to; Amoebozoa, Arthropoda, Ciliophora, Charophyta, Chlorophyta, Cyanobacteria/ Cyanophyta, Euglenozoa, Ochrophyta/ Heterocanthophyta and Rotifera. Except in coconut shells, every breeding habitat type investigated had the prevalence of rotifers, at least with one species. Thus the phylum Rotifera displayed the highest percentage of abundance (30.83%) of total microbiota. Species under phylum Charophyta had the lowest abundance among recorded (2.19% of total microbiota). *Philodina citrina* and *Euglena pisciformis* were found as species showing all three categories of abundance types; constant, common and accidental/or rare. Although the highest number of microbiota species were recorded from paddy field breeding habitats, all the species were existed as accidental or rare species in the habitat type according to their abundance. Only ponds and tree holes were recorded with beta diversities over 50% (high heterogeneity) in microbiota composition among the systems. Paddy fields, marshy lands, blocked drainages, metal containers, and leaf axils had beta diversities between 20 and 50%, indicating intermediate heterogeneity. The rest of the other habitats had beta diversities below 20%, indicating low heterogeneity. Paddy fields exhibited the highest gamma diversity (16) and Shannon-Weiner diversity (52.17) values. From the microbiota species recorded, *Zoothamnium* sp. was identified as an epibiont in *Culex gelidus* and *Culex tritaeniorhynchus* mosquito larvae. Updated information from the present investigation would be facilitated for implementing appropriate vector control interventions.

Keywords: Abundance; Constant; Heterogeneity; Rotifers