

CHARACTERIZATION OF BACTERIAL ISOLATES FROM BREEDING WATER OF DENGUE VECTOR MOSQUITO, *Aedes albopictus*

**W.M.S.H. Wijesundara^{1,2}, K.P.W.C. Kavindi¹, T.C. Weeraratne¹
and W.A.P.P. de Silva^{1*}**

¹Department of Zoology, Faculty of Science, University of Peradeniya, Sri Lanka

²Postgraduate Institute of Science, University of Peradeniya, Sri Lanka

*depriyanka@sci.pdn.ac.lk

The microbial composition of mosquito breeding grounds, which varies according to microhabitat conditions, climatic factors, and geographical regions, plays a crucial role in larval development, fecundity, and host-pathogen interactions of mosquitoes. Considering the relatively high fitness and wider distribution of *Aedes albopictus* mosquitoes, we characterised the bacteria associated with their breeding grounds. Samplings were carried out from Kurunegala and Kandy districts in Sri Lanka (May to November 2023). Twenty-five water samples were collected and cultured on Luria Broth media (LB) and Nutrient agar plates (NA). Identified morphologies were sub-cultured, and 80% glycerol stocks were prepared for pure colonies. Molecular identification of the pure colonies was conducted by sequencing the 16s rRNA gene. Morphological identification, based on shape, size, colour, margin, opacity, and elevation, confirmed 20 different bacterial morphologies and molecular identification confirmed 17 different bacterial isolates. *Aeromonas hydrophila* was the most abundant bacteria observed in all breeding grounds (100%). The second most abundant was *Acinetobacter proteolyticus* (32%). The remaining bacterial composition was represented by three *Staphylococcus* spp. viz., *S. cohnii* (20%), *S. pseudoxylois* (12%), *Staphylococcus* sp. strain 20 (16%); *Bacillus subtilis* (20%); two *Fictibacillus* spp. viz., *F. phosphorivorans* (20%) and *F. halophilus* (12%); *Pseudomonas mosselii* (12%); *Citrobacter braakii* (28%); *Chromobacterium haemolyticum* (8%); *Exiguobacterium indicum* (28%); *Arhrobacter* sp. (8%); *Luteimonas terrae* (28%); *Micrococcus luteus* (24%) and *Deinococcus* sp. (12%). Two to eight different species were reported from each mosquito breeding site. A maximum of four to five distinct species were reported from the majority of *Aedes* mosquito breeding sites (64%). The findings identified the microbes that are commonly associated with *Aedes albopictus* mosquitoes, and further studies will be carried out using different culture media to assess the bacterial diversity in the breeding habitat water of *Aedes albopictus*.

Financial assistance from the Multi-Disciplinary Research Grant (Grant No. 136) is acknowledged

Keywords: Dengue vectors, Larval habitats, Microbiota