Keywords: Acephate, organophosphate, reproductive toxicant, sperm function

dinithipeiris@gmail.com Tel: 0714018537

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A preliminary study on genetic estimates of population structure of *Aedes aegypti* populations in three districts, Sri Lanka

H S D Fernando[1], M D Hapugoda[2] and B G D N K De Silva[1*]

[1]*Department of Zoology, Faculty of Applied Sciences, University of Sri Jayewardenepura, Nugegoda*

[2]*Molecular Medicine Unit, Faculty of Medicine, University of Kelaniya, Kelaniya*

Dengue disease has become a high risk epidemic in Sri Lanka. *Aedes aegypti* is the main vector of the disease. Vector control is the primary way to prevent dengue as no efficient therapies are available for the disease. Understanding the dispersal and population structure, of *Ae. aegypti* in Sri Lanka would enable effective control strategies to suppress mosquito populations. A preliminary study was done to determine the level of variations in microsatellite loci in Sri Lankan *Ae. aegypti* populations. Primarily, three *Ae. aegypti* populations from Colombo (n = 15), Jaffna (n = 25) and Batticaloa (n = 10) were studied. DNA was extracted from sampled adults and larvae - (reared to adults). PCR amplification was carried out for 9 microsatellite loci, AT1, AG7, AC1, AG5, AG2, AC2, AC5, AG4 and AC4 with forward primer of each pair fluorescently labeled with HEX or FAM dye. Post PCR products were sent to Macrogen Inc. Korea for genotyping and results were analyzed using ARLEQUINE, version 3.1.

All loci except AC5 were polymorphic showing a distinct number of alleles ranging from 2 (AC2) to 7 (AG4). As locus AC5 failed to amplify consistently it was excluded from the study. Over all loci, genetic diversity appeared higher in Jaffna populations. Significant departures from Hardy–Weinberg proportions were observed with several loci ($P > 0.05$). However, the test for Hardy–Weinberg equilibrium revealed that some loci did not meet the expectations of this model. The observed heterozygosity was less than expected heterozygosity in most cases, indicating an excess of homozygote genotypes at most loci. However, deviation from Hardy-Weinberg equilibrium might correspond to heterozygote deficits. Null alleles also generate apparent heterozygote deficits and mutations in the region may prevent PCR amplification resulting in a heterozygote being scored as a homozygote. This is the first attempt to use microsatellite analysis for assessing the population structure of *Ae. aegypti* in Sri Lanka. However, as this was a preliminary study, requirement exists for further studies on

different spatial scales to confirm the population structuring of this mosquito species in Sri Lanka.

Keywords: *Aedes aegypti*, microsatellites, population structure

nissankakolitha@gmail.com Tel: 0724258715