

A PRELIMINARY STUDY TO ANALYZE *Aedes aegypti* DIVERSITY IN SRI LANKA USING MITOCHONDRIAL DNA VARIATIONS.

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Aedes aegypti is the primary vector of dengue- which has become a major public health problem in Sri Lanka during the recent past. In the absence of an effective drug and vaccine, mosquito control appears to be the only way to protect human from this deadly virus. This in turn reveals the need for more detailed understanding of the diversity and distribution of this mosquito species in Sri Lanka.

A preliminary study was done to analyze genetic variability of *COI* region in *Aedes aegypti* mosquitoes in Sri Lanka. Mitochondrial *Cytochrome C Oxidase subunit 1 (COI)* gene was sequenced and analyzed from 50 mosquito samples collected from five districts, Colombo, Jaffna, Galle, Ratnapura and Batticaloa. DNA was extracted from sampled adults and larvae- which were reared to adults. PCR amplification was carried out for *COI* region. Post PCR products were sent to Macrogen Inc. Korea for sequencing and the results were analyzed using DnaSP, v. 5.0.

A total of 9 haplotypes were identified from the fifty individuals sequenced. Mainly two haplotypes were shared among populations. Haplotype 1 was present in all districts except Ratnapura, whereas haplotype 6 was present in all districts. Majority of haplotypes (4) were only found within a single district. Haplotype 7 was only present in Colombo and Ratnapura district whereas haplotype 5 was present in Galle, Ratnapura and Batticaloa populations. The nucleotide diversities were characterized in 13 polymorphic sites, of which 12 sites were parsimony informative. The overall nucleotide diversity per site was 0.01099 ± 0.00056 , whereas haplotype diversity was 0.726 ± 0.051 indicating low levels of genetic diversity.

This is the first study to analyze the genetic diversity of *Ae. aegypti* populations in Sri Lanka using mitochondrial DNA variations. Although low levels of genetic diversity among the populations is revealed, the need for further studies exists in order to have an insight into the role of control programmes in shaping the genetic composition of the mosquito populations. Further, the study would pave the way in predicting the dispersal patterns and the behavior of the mosquito species enabling more effective mosquito control.

Keywords: *Aedes aegypti*, mitochondrial DNA, *COI*, haplotype diversity