

## The Effect of Extensive Mosquito Migration on Dengue Control as Revealed by Phylogeny of Dengue Vector *Aedes aegypti*

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**Abstract :** Dengue has become one of the most important arbo-viral disease in all tropical and subtropical regions of the world. *Aedes aegypti*, is the principal vector of the virus, vary in both epidemiological and behavioral characteristics, which could be finely measured through DNA sequence comparison at their population level. Such knowledge in the population differences can assist in implementation of effective vector control strategies allowing to make estimates of the gene flow and adaptive genomic changes, which are important predictors of the spread of Wolbachia infection or insecticide resistance. As such, this study was undertaken to investigate the phylogenetic relationships of *Ae. aegypti* from Galle and Colombo, Sri Lanka, based on the ribosomal protein region which spans between two exons, in order to understand the geographical distribution of genetically distinct mosquito clades and its impact on mosquito control measures. A 320bp DNA region spanning from 681-930 bp, corresponding to the ribosomal protein, was sequenced in 62 *Ae. aegypti* larvae collected from Galle (N=30) and Colombo (N=32), Sri Lanka. The sequences were aligned using ClustalW and the haplotypes were determined with DnaSP 5.10. Phylogenetic relationships among haplotypes were constructed using the maximum likelihood method under Tamura 3 parameter model in MEGA 7.0.14 including three previously reported sequences of Australian (N=2) and Brazilian (N=1) *Ae. aegypti*. The bootstrap support was calculated using 1000 replicates and the tree was rooted using *Aedes notoscriptus* (GenBank accession No. KJ194101). Among all sequences, nineteen different haplotypes were found among which five haplotypes were shared between 80% of mosquitoes in the two populations. Seven haplotypes were unique to each of the population. Phylogenetic tree revealed two basal clades and a single derived clade. All observed haplotypes of the two *Ae. aegypti* populations were distributed in all the three clades, indicating a lack of genetic differentiation between populations. The Brazilian *Ae. aegypti* haplotype and one of the Australian haplotypes were grouped together with the Sri Lankan basal haplotype in the same basal clade, whereas the other Australian haplotype was found in the derived clade. Phylogram showed that Galle and Colombo *Ae. aegypti* populations are highly related to each other despite the large geographic distance (129 Km) indicating a substantial genetic similarity between them. This may have probably arisen from passive migration assisted by human travelling and trade through both land and water as the two areas are bordered by the sea. In addition, studied Sri Lankan mosquito populations were closely related to Australian and Brazilian samples. Probably this might have caused by shipping industry between the three countries as all of them are fully or partially enclosed by sea. For example, illegal fishing boats migrating to Australia by sea is perhaps a good mean of transportation of all life stages of mosquitoes from Sri Lanka. These findings indicate that extensive mosquito migrations occur between populations not only within the country, but also among other countries in the world which might be a main barrier to the successful vector control measures.

**Keywords :** *Aedes aegypti*, dengue control, extensive mosquito migration, haplotypes, phylogeny, ribosomal protein

**Conference Title :** ICTID 2017 : International Conference on Tropical Infectious Diseases

**Conference Location :** Bangkok, Thailand

**Conference Dates :** December 18-19, 2017