

SC

**BREEDING STRUCTURE OF DENGUE
VECTOR, *Aedes albopictus* IN AREAS AT RISK
OF EPIDEMICS USING DNA MARKERS**

By

M. M. S. T. Mapa

A dissertation submitted to the Faculty of Graduate studies, University of Kelaniya, Kelaniya, Sri Lanka in partial fulfillment of the requirements for the Degree of Master of Philosophy in Molecular Biology.

December 2009



ABSTRACT

Dengue fever is currently considered to be the most serious vector-borne disease in Sri Lanka. *Aedes aegypti*, and *Aedes albopictus* have been implicated to be the most important vectors of dengue transmission. To understand the transmission of the disease, knowledge of the population (breeding) structure and magnitude of dispersal (gene flow) among *Aedes* mosquito populations is essential, as it directly influences dengue virus transmission. Random amplified polymorphic DNA (RAPD) analysis was undertaken to examine breeding structure in 19 *A. albopictus* populations from three worst affected districts in Sri Lanka, namely Colombo, Gampaha and Kandy, with a distance range extending ~100 km. The data were used to determine the genetic diversity, differentiation, magnitude of gene flow among *A. albopictus* populations at the macro (different districts) and micro (different sites in a district) geographical levels. Allele and genotype frequencies were measured on 62 RAPD loci. Allele frequencies were estimated assuming that RAPD alleles segregate as dominant markers and the genotype frequencies at those loci are in Hardy–Weinberg equilibrium. The investigation showed that *A. albopictus* appears to be the dominant mosquito species of the sampled areas of each district. Nei's mean gene diversity, H_e , in each district ranged from 0.2722 - 0.3173. High levels of population differentiation (structuring) was found in both among three districts ($G_{st} = 0.2969$; $N_m = 1.1841$; $\theta = 0.1915$) and among different cities of each district ($G_{st} = 0.1558-3343$). The intra population polymorphism, H_s , in each district is also high and ranged from 0.2009-0.2637. The level of gene flow among *A. albopictus* populations within Colombo district is moderate ($N_m = 1.6711$ mosquitoes per generation). Highest values of gene flow were observed in Gampaha district ($N_m = 2.7096$) with lowest values observed from Kandy district ($N_m = 0.9955$). Cluster analysis based on Nei's genetic distance, indicate that populations from neighboring areas in each district are clustered according to their geographical origin. The result indicate significant population differentiation and structuring of *A. albopictus* mosquitoes in Sri Lanka, which may be attributed to dynamic equilibrium between factors that favor differentiation and homogenizing factors in recently established populations.