

## Section 2

### Executive Summary of the project

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, magnitude of dispersal (gene flow) among *Aedes* mosquito populations is highly important, 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 highly threatened districts in Sri Lanka, namely Colombo, Gampaha and Kandy, with a distance range extending ~100 km. The data were used to determine magnitude of gene flow, genetic diversity, genetic differentiation among *A. albopictus* populations at the macro (among districts) and micro (among cities within district) geographical levels. Allele and genotype frequencies were measured on 62 RAPD loci, 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. 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 from Kandy district ( $N_m = 0.9955$ ). High levels of population differentiation (structuring) was found in both among districts ( $G_{st} = 0.2969$ ;  $N_m = 1.1841$ ;  $\theta = 0.1915$ ) and among cities of each district ( $G_{st} = 0.1558$ – $0.3343$ ). The intra population mean gene diversity,  $H_s$ , in each district is also high and ranged from 0.2009–0.2637. Nei's mean gene diversity,  $H_e$ , in each district ranged from 0.2722 - 0.3173. 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 a significant population differentiation and structuring of *A. albopictus* mosquitoes in Sri Lanka, which may be attribute to dynamic equilibrium between factors that favor differentiation and homogenizing factors in recently established populations.