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A preliminary study on the identification of genetic polymorphisms of Aedes aegypti using Randomly Amplified Polymorphic DNA (RAPD).

Dengue fever, dengue haemorrhagic fever and dengue shock syndrome caused by an arbo-viral complex, is an alarming health problem in Sri Lanka. A thorough knowledge on the population structure of *Aedes aegypti,* the vector of the virus in the urban areas is of central importance in management of Dengue. Fourty-seven species of *Ae. aegypti* have been reported in Sri Lanka. This paper describes an attempt made to assess the genetic diversity of the mosquito in ten populations in western and north-western provinces of Sri Lanka by detection of Random Amplified Polymorphic DNAs (RAPDs).

DNA was isolated from five individuals per population and screened for RAPDs using the standard RAPD-PCR protocol with eight pre-tested 10-mer Operon primers, A02, A04, A14, B10, B15, C05, D15 and E07. PCR products were scored in 1.2% agarose after electrophoreses for

presence and absence of bands. Pair-wise distances were calculated and dendrogram was constructed to depict the genetic relationships.

An average of 6.4 bands per primer was observed and among 51 bands amplified, 48 exhibited polymorphism. The dendrogram depicted a clear separation of populations into two groups. The first group comprised *Ae. aegypti* collected from three towns, Maharagama, Gangodawila and Nugegoda, which are within a very close proximity. Other cluster comprised mosquitoes collected from seven locations, which are located relatively apart from one another. The overall results clearly indicated the enormous potential of the RAPDs for ready detection of DNA polymorphisms in *Ae. aegypti* collected from different locations. Such characterizations are useful in epidemiological studies of vector populations.