Preliminary study on genetic variation between the populations of *Aedes aegypti* and *Aedes albopictus*

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In the past 12 years the incidence of dengue fever and dengue haemorrhagic fever has showed a dramatic increase in Sri Lanka. Now it has become a major public health problem in the country and still, little is known about the population structure of the vectors (*Aedes aegypti* and *Aedes albopictus*) in Sri Lanka. This study assessed the genetic diversity between the populations of *Aedes aegypti* and *Aedes albopictus* by using 10- base primers in random amplified polymorphic DNA polymerase chain reaction (RAPD-PCR) Genomic DNA extracted from 21 individual mosquitoes from 7 populations of *Aedes aegypt*i and 15 individual mosquitoes from 5 populations of *Aedes albopictus* collected from different areas of Sri Lanka were used for RAPD-PCR assay. Nei and Lei's genetic distance analysis were applied for identifying the genetic relatedness of the mosquitoes from different geographic populations. The results indicate that five RAPD primers, OPA-01,OPA-02, OPB 01, OPB-18, OPC-01 clearly

elucidated the genetic diversity of *Aedes aegypti* populations but fails for *Aedes albopictus* populations. More primers are required to assess *Aedes albopictus* population.

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