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Population variations of the whitefly *Bemisia tabaci* using RAPD-PCR

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Bemisia tabaci is considered as the vector of Begomoviruses. Little is known about the genetic variations of these populations in Sri Lanka. Knowledge of the genetic variation within *B.tabaci* populations is necessary for their efficient control and management. The objectives of the present study were (1) To develop a low cost protocol for isolation of insect genomic DNA, (2) To determine the use of RAPD-PCR markers to analyze population variations of *B.tabaci* and to ascertain the population variations due to geographical differences, (3) To prepare a dendrogram to indicate the relationships between five populations obtained through RAPD-PCR analysis. In this study five random primers (OPA-2, OPA-12, OPB-11, OPB-12, OPE-17) were used to identify genetic diversity of *B. tabaci* populations obtained from the Institutes of Department of Agriculture from four host species namely guava (Angunakolapelessa), manioc (Angunakolapelessa), pumpkin (Mahailupallma) and brinjal (Peradeniya and Mahailupallma). The operon primer B-11 amplified three populations (guava, manioc and pumpkin) while the E-17 amplified four populations (guava, manioc, brinjal (Peradeniya and Mahailupallma). A2, A12, B12 primers differentiated all the five populations. These primers were identified as important molecular markers since they gave good indications of polymorphism existing among the five populations. Brinjal populations collected from the same host, but from two different locations, Mahailupallma and Peradeniya also exhibit genetic diversity. The dendrogram that was created using UPGMA algorithm reveals that in the case of five populations under consideration namely guava, manioc, pumpkin and brinjal populations are distinctly different populations of *B.tabaci*.