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Phylogenetic analysis of ITS2-rDNA cistron in some *Anopheles* species, subgenus *Cellia* and *Anopheles* (Diptera: Culicidae) in Sri Lanka

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Detailed information on the taxonomic positions, phylogenetic interrelationships and evolutionary affinity among closely related *Anopheles* (*An*) species of medical importance is essential to understand evolutionary patterns among those species. The objective of this study was to conduct studies on genetic characterization of the ITS2 region of rDNA cistron for species identification of some *Anopheles* species in Sri Lanka and to reconstruct the phylogenetic relationship among them. The selection of ITS2 region as a suitable gene marker was proven to be very integral to the success of this study. All Anopheline mosquitoes were identified to its species level by using standard mosquito identification keys, then the rDNA-ITS2 region was PCR amplified and sequenced. The phylogenetic relationships for these mosquitoes were estimated based on ITS2 data and structures facilitated in ProfDistS 0.9.9, and Mega 4.0 software. The phylogenetic relationships inferred from Neighbour Joining (NJ), UPGMA and maximum parsimony analysis revealed unique topology with two distinct monophyletic clades. *An. peditaeniatus*, *An. barbumbrosus*, and *An. nigerrimus* formed one cluster. The remaining Anophelines were grouped to three subclades where *An. culicifacies*, *An. varuna*, and *An. aconitus* were placed in a sister group while *An. jamesii*, *An. maculatus*, *An. pseudojamesii* and *An. karwari* were clustered into a separate single cluster. The other cluster contained *An. subpictus* and *An. vagus*. In this study, the phylogenetic positions of the different malaria vectors that have the potential or are already known to be active in malaria transmission are grouped into two main clusters. The molecular phylogeny obtained in this investigation proximately relates to that of the classical morphological taxonomy and morphological grouping studies. *Anopheles* subgenus and *Cellia* Theobald form distinct unambiguous monophyletic clades. The *Myzomyia* series formed a distinctive cluster while the *Pyrethophorous* and *Neocellia* series formed a separate cluster. Unique secondary structures obtained for each Anopheline has led to species identification and resembled *Anopheles* species diversity in Sri Lanka, while containing compatible helices to symbolize the evolutionary affinity among them.

Acknowledgements: Financial assistance by the NRC research grant (09-21) and the University research grant (ASP/06/RE/2010/18) from the University of Sri Jayewardenepura are acknowledged.

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