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Genetic diversity and population structure of malaria vector mosquitoes *Anopheles peditaeniatus, An. subpictus* and *An. vagus* (Diptera: Culicidae) in five districts of Sri Lanka

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Anopheles subpictus is the secondary vector and *An. peditaeniatus* and *An. vagus* are potential vectors of malaria in Sri Lanka. Understanding population structure of vectors is vital in implementing successful vector control programmes to face the threat of re-emergence of malaria in Sri Lanka. This study reports the genetic diversity and the population structure of *An. peditaeniatus, An. subpictus* and *An. vagus* in five geographical locations in Sri Lanka using their mitochondrial gene, *Cytochrome oxidase subunit* I (*COI*). Adults were collected from Ampara, Badulla, Batticoloa, Jaffna and Kurunegala districts and the *COI* sequences were obtained from morphologically identified species using Polymerase Chain Reaction (PCR) assay. Statistical analyses were conducted using Dnasp 5.10.01 and Arlequin 3.11.

An. peditaeniatus, An. subpictus and *An. vagus* had 8, 15 and 10 haplotypes respectively. All the three species had high genetic diversities. *An. subpictus* had the highest nucleotide diversity (0.025 ± 0.011) while *An. peditaeniatus* had the lowest (0.007 ± 0.002). According to neutrality tests, there is no positive selection driven in any of these species. No significant pairwise differences or genetic structure variations among *An. peditaenatus* or *An. vagus* populations which shows that random mating occurs among different populations of each species.

A significant pairwise difference was observed between Jaffna (northern province) and Kurunegala (northwestern province) *An. subpictus* populations (F_{ST}= 0.965,). *This strongly supports the previous reports on the p*resence of two different sibling species of *An. subpictus* in these two provinces. *Analysis of Molecular Variance (AMOVA) results showed* 82.21% significant genetic structure variation between *An. subpictus* populations (F_{CT}= 0.822) compared to a smaller 17.79% variation within populations (F_{SC}= 1.000), suggesting the existence of different *An. subpictus* sibling species in different geographical areas.

The present study shows that geographic distance between populations has no effect on the population structures of *An. peditaeniatus* and *An. vagus* but affects the population structure of *An. subpictus.* Application of control measures against *An. subpictus* must be done with close monitoring since similar control measures may not be effective for all the populations and the high genetic variation can give rise to the population's resistant to control measures.

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