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Sympatric gene clusters in microsatellite marker depicted population genetic structure of *Anopheles culicifacies s.l.* (Diptera: Culicidae) sibling species E in Sri Lanka

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The understanding of the vector population genetic structure is important in malaria vector control and prevention of re-occurrence programs. However, the genetic structure of the major malaria vector mosquito, *Anopheles culicifacies* in Sri Lanka has not been investigated yet. Therefore, this study was carried out to understand the population genetic structure of the malaria vector *An. culicifacies* sibling species E in Sri Lanka. Cytogenetically identified mosquitoes collected from six different localities during 2010-2012 were genotyped using eight microsatellite markers developed for sibling species A in the complex and tested for the Hardy-Weinberg equilibrium, linkage disequilibrium, isolation by distance and Bayesian clustering algorithm. Six microsatellite loci were highly polymorphic across localities with high allelic richness (1.000-10.432). Five localities deviated from Hardy Weinberg equilibrium ($P<0.006$) with heterozygosity deficits after the Bonferroni correction. Genetic differentiation in population pairs (Fst : 0.03331 - 0.23184) was not supported by the isolation by distance model ($r^2 = 0.3057$, $p= 0.0180$). Bayesian clustering analysis identified the presence of three gene clusters in the population studied. Percentage of individuals of each cluster was varied in six localities. Isolation by distance was not detected in any pair of cluster. Possible barriers to the gene flow in the topography of Sri Lanka were not recognized, suggesting that the force to gene clustering in the population could be due to ecological and microhabitat conditions of the localities. The sympatric occurrence of all three gene clusters was observed and it supports the fact that differentiation of clusters has taken place over a long time and the variation in percentages of individuals in each cluster could be due to the ecological variations in sampling localities.

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