ABSTRACT

Mosquitoes have been the focus of investigations since the time the first human disease was linked to them. Compared to other insects, they cause more human suffering, serving as cyclic or mechanical but exclusive vectors of important diseases of man such as malaria, dengue, yellow fever, filariasis, encephalitis etc. Mosquito populations even within a species vary in their behaviour and morphology that attributes to their complex interaction with the environment and also in their vectorial capacity. Thus, the study of mosquito ecology and genetics at different foci is important to understand their evolution and diversification. The existing endemicity of several mosquito borne diseases and in particular dengue and chikungunya in Karnataka state, India, prompted the author to study diversity of mosquitoes in forest and rural habitats with respect to differential ecology and in addition to the systematics, bioassay, biochemical and molecular aspects in *Aedes aegypti* and *Aedes albopictus*. The outcome of the study yielded twenty nine species of mosquitoes from the rural areas and sixty species could be collected from the forest habitats. Insecticide susceptibility tests shown that the rural populations of both *Ae. aegypti* and *Ae. albopictus* are more tolerant to the insecticides tested. Of the synthetic pyrethroids tested deltamethrin was found to be the most effective. Isozyme analysis indicates that the populations of *Ae. aegypti* and *Ae. albopictus* from rural and forest habitats are different in their electrophoretic pattern. The higher frequency of common alleles in rural population could be correlated with the higher tolerance level to insecticides. Quantitative estimation of enzymes has shown the significant difference in their activity in both *Ae. aegypti* and *Ae. albopictus*. Here also a higher level of enzyme activity in rural population could be correlated with the tolerance level to insecticides. RAPD analysis done by the author showed that sub-populations of mosquitoes of *Ae. aegypti* i.e., rural and forest areas, cluster together. As *Ae. aegypti* are peripherally located in forest habitats and/or associated with human settlements. The gene flow would have led to homogeneity of gene pool of both the populations. On the other hand *Ae. albopictus*, habitually are found more towards the interior of the forest areas and hence there could be restricted gene flow between rural and forest populations. Thus greater genetic diversity was noticed between *Ae. albopictus* populations. The study also agrees with the congeneric relationship between the species *Aedes aegypti* and *Aedes albopictus* based on their genetic identity.