Summary


- A systematic survey on Anophele: species abundance, bionomics and habitat preference in relation to malaria was conducted for three years in Thenzawl. A total of 10 species Anopheles campestris (25.8%), An.nivipes (24.0%), An.vagus (20.6%), An.jamesii (15.1%), An.jeyporiensis (11.4%), An.maculatus (1.7%), An.philippinensis (0.7%), An.annularis (0.26%), An.sinensis (0.23%) and An.peditaeniatus (0.22%) were collected.
Because of its consistency, abundance and bionomics, \textit{An. campestris}, \textit{An. jeyporiensis}, and \textit{An. nivipes} may have played a role in malarial transmission. However, further cytological or molecular identification should be carried out to find the specific vectors of malaria in Mizoram.

The present study was also designed to characterize \textit{Anopheles} species of Mizoram. Their characterization was carried out in the following manner –

- \textit{Insecticide susceptible/resistance characterization}: A commonly used pesticide used for vector control in the state (Deltamethrin) was tested against four species and the order of tolerance was found to be \textit{An. vagus}<\textit{An. campestris}<\textit{An. jamesii}<\textit{An. nivipes}. The similar pattern was observed in the enzyme biochemical assay studies. Heterogeneity in enzyme production was observed - \textit{An. nivipes} produced the maximum with a value of 0.0177 α–naphthol/min/mg protein and \textit{An. dirus} with a value of general esterase with a value of 0.0611 β–naphthol/min/mg protein, it produced the minimum for Glutathione S-transferase; \textit{An. nivipes} (1.26183 ± 0.068) produced the maximum Mixed function Oxidase; and while for GST, it was \textit{An. maculatus} (1.9580 ± 0.0422).
Molecular characterization through resistant allele studies: Expression of the gene was carried out in nine *Anopheles* species. What was however, unique in this study was different expression pattern of CYP 6 gene. It is possible that due to the wider use of melathion than deltamethrin [Anonymous, 2012], the mechanism of insecticide detoxification is dominated by mutant *AChE* than CYP. However, the expression profiling of *CYP6* needed further investigation, isolation of the CYP protein, synergic studies and real time (RT) – PCR may facilitate in determining the expression status of the gene and its role in resistance mechanism in *Anopheles* species of Mizoram.

Molecular characterization through phylogenetic relationship: The study was performed in accordance with the traditional trend of similar morphological characteristic relatedness. RAPD profile gave a range of 19 – 26% polymorphic bands that revealed 65.4 ± 4.04 % polymorphism; however, RAPD-PCR profiling did not significantly aid in identification of Anopheline population. CO1 and ITS gene solved the purpose of molecular phylogeny of the anophelines, since the phylogeny inferred both sequences were unequivocally supported by analysis of morphological characters as described by Christophers (1924), Sallum *et al.* (2002) and Harbach *et al.* (2004).
Molecular characterization through secondary structure prediction studies of ITS2 sequences. Among the 10 ITS2 secondary structures constructed, 2 species belonged to type I, 3 species were of type II, 2 species were of type III, and 3 species were of type IV. Type I, III, IV and Type III, IV structures were observed in Neocellia and Pyrethroporus series. In contrast, type II was only seen in the series Myzomyia.