

## 5. CONCLUSION

Five districts of Kerala encompassing the high land, midland and low land regions were selected for the observation of odonates. Seventy three different habitats of Thrissur, Ernakulam, Palakkad, Wayanad and Idukki districts of Kerala were observed that including streams, rivers, ponds, lakes, paddy fields, ditches and estuaries. The reserved forests and protected areas were excluded from the study.

During the study period, a total of 71 species belonging to 43 genera and 10 families were recorded. Of these 33 species were damselflies and 38 species were dragonflies. Four Western Ghats endemic species viz. *Aciagrion approximans krishna*, *Agriocnemis keralensis*, *Pseudagrion indicum* and *Protosticta graveleyi* were recorded. *Paracercion malayanum* was recorded as the first report from central and northern Kerala. The observed species richness was more in dragonflies than in damselflies. Coenagrionidae and Libellulidae were the most dominant families of damselflies and dragonflies respectively. The observed species richness was high in vegetated ponds, lakes and streams and minimum in unvegetated habitats. Taxonomic keys for the observed 71 species of odonates were prepared.

Representing 28 genera, molecular characterisation of 34 species was done. Partial COI gene, 18S rRNA gene sequences and translated protein sequences were generated. The sequences were deposited in the GenBank database and received accession numbers. Of these twelve COI gene sequences and twenty three 18S rRNA gene sequences are the first records in worldwide databases. The obtained COI gene sequences are useful for precise and faster species level identification and phylogenetic analyses while the 18S gene sequences are beneficial in higher level phylogenies.

Phylogenetic analyses of two suborders and selected families were carried out based on both marker genes. The effectiveness of both genes in discriminating relationships was compared. A detailed comparison of trees revealed the efficiency of COI over the 18S rRNA gene in resolving family and suborder trees. In the majority of analyses, COI yielded better resolution than 18S rRNA gene.

COI based phylogenetic trees were constructed for selected 27 genera and estimated intraspecific and interspecific divergence values. Low genetic variability

was exhibited by the majority of odonates analysed except eight species. According to the literature, the occurrence of intraspecific divergence can be because of their highly sensitive gene sequences. Interspecific divergence values were also estimated and found maximum and minimum values in genus *Tholymis* and *Dysphaea* respectively.

Close genetic similarities without any divergence were observed between different species of geographically distant regions was another significant finding of this work.