

CHAPTER-6:

SUMMARY

This study has shown the power and efficacy of COI barcodes for diagnosing ornamental fishes of Manipur. For a barcoding approach to species identification to succeed within-species DNA sequences need to be more similar to one another than to sequences in different species. In our study, out of the 27 sequences, 2 sequences belong to same species, i.e., *Wallago attu*, 2 belong to *Channa punctata* and another 2 belong to *Puntius sophore*. The respective groups form tight clusters in NJ tree and their DNA sequences are highly similar to one another. 4 sequences belong to *lepidocephalus sp.* and they represent a clade in the NJ tree. The 21 species of ornamental fishes examined in this study possess COI sequences that permit their separation from any other taxon included in this study. In all of these cases, COI sequences were tightly clustered. The present study is the first of its kind being conducted to explore ornamental fishes of north eastern India in molecular level. It has been widely appreciated that the fragmentation of the rivers and lakes from continental freshwater networks leads to more pronounced genetic structure among populations and deeper divergence among haplotypes than in the marine realm. Most of the ornamental fishes found in Manipur analyzed in this study exhibit a similar pattern of genetic diversity at COI, each being a single cluster of tightly related mtDNA sequences distinct from all other species. Our current study will result in a significant improvement of our knowledge concerning the systematics of the ornamental fish species found in North eastern India, to facilitate monitoring changes in the geographic distribution of species that will probably occur in the future and ultimately to generate a DNA barcode library for all the ornamental fishes found in this region and hence making easy access to specimen identification.