

CHAPTER-VI

Summary and Conclusion

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6.1 Genomic DNA extraction based study

- ✦ The molecular and genetic based study required sufficient quantity and quality of genomic DNA which is extracted from the concerned animal for amplification and characterization with specific or arbitrary primers.
- ✦ But if the species concern is threatened in category or its population size is very small then it is necessary to extract the genomic DNA from that species without killing or noninvasively.
- ✦ The present study was basically on two fish species viz., *Badis badis* and *Amblyceps mangois* which are in threatened category as reported by a prestigious fish research institute of India, NBFGR (National Bureau of Fish Genetic Resources, Lucknow, India.
- ✦ The study was carried out with the help of two molecular markers viz., RAPD and ISSR; and it have so many advantages over other molecular markers
- ✦ These markers are cheap, inexpensive, and easy to perform and require very little laboratory expertise in moderately equipped ordinary laboratories and importantly, these markers do not require any prior knowledge of the DNA sequence.
- ✦ Therefore, at first stage of my research I have standardised the gDNA extraction and PCR amplification from two commonly available and phylogenetically related fish species.
- ✦ This allows me to find out minimum quantity of gDNA required to perform sufficient round of PCR amplification for genetic diversity study. Moreover, the protocol which I have modified from previously used protocols is quite efficient and robust and less time consuming. Therefore this procedure can be used not only for the studied species but all other species too.

6.2 Study of the genetic Architecture of *Badis badis* and *Amblyceps mangois*

- ✦ The primary goal of my study was to estimate the available gene pool present within the ornamental and threatened fish *Badis badis* and *Amblyceps mangois* at the rivers of Terai and Dooars region of North Bengal, India.
- ✦ The study region i.e., the Terai and Dooars region is situated at the foothills of Himalaya and different rivers are flowing across this region and the geo-physical conditions make this region a biodiversity hotspot.
- ✦ So the estimation the genetic diversity of this threatened fauna is utmost important for conservation of the genetic resources of this region. Since the population genetic architecture of this ichthyofauna is totally unexplored in that region, therefore, to gain first-hand knowledge of this ichthyofauna of this region is very much essential for their proper management and rehabilitation within the wild.
- ✦ Three major river stream systems and their tributaries are targeted for study viz., Mahananda, Teesta and Jaldhaka. As these rivers are hill streams, so the rivers have a natural altitudinal gradient and monsoon flood sometimes cause admixture of the river waters through overflowing. The irrigation practice and some human made narrow channels are also causative agent for mixing of water of different rivers.
- ✦ The total seventeen populations of *Badis badis* (six population from Mahananda river system, seven population from Teesta river system, four populations from Jaldhaka river system) and fourteen populations of *Amblyceps mangois* (three populations from Mahananda river system, seven populations from Teesta river system, four populations from Jaldhaka river system) were studied for estimation of available genetic diversity.

- ✚ Different diversity indices were used for statistical analyses of the data that were generated after amplification by RAPD and ISSR amplification. Additionally, after achieving the specified objectives of my study, Mitochondrial Cytochrome oxidase (mtCOI) gene of both the species was amplified with specific primer to investigate the genetic diversity and phylogenetic relationship with other geographically/allopatrically isolated populations.
- ✚ After analysing it was found that the both the fish populations *Badis badis* and *Amblyceps mangois* are dwindling across different river streams. But Teesta river system showed highest level of genetic diversity than other two river systems.
- ✚ Although in the Jaldhaka river system the within population diversity is high. But the whole river system population was low compared to the Teesta river system. In Teesta river system the within population diversity was low but the whole river system diversity was high. This situation arises because more number of tributaries are converged to the Teesta river which ultimately lead to the high level of diversity within the Teesta river system.
- ✚ It was observed that there is a break in the diversity pattern as the river flows downward. The richness, evenness and diversity index was altered as the river flows from hilly region to the plain. This is occurred due to different types of anthropogenic and natural pressures which modify or alter the pattern of the diversity.
- ✚ Moreover the river streams hierarchy showed that in the Teesta and Jaldhaka population genetic differentiation was high and significant level of gene flow also occurs between different populations of river systems. Because mixing of waters from different rivers causes significant number of individuals in reproductive proximity which lead to a great amount of gene flow.

- It was also observed that the first order streams of Teesta and second order streams of Jaldhaka have high level of diversity and high degree of differentiation. Therefore these river streams of Teesta and Jaldhaka river system can be considered as an evolutionary significant unit or ESU for proper management and conservation of this ichthyofauna.

- Moreover, conservation of this ichthyofauna is very much significant and essential for the social and economical upliftment of local inhabitants and also biological diversity.