Fishes make up the most abundant class of vertebrates, both in terms of number of species and of individuals. They exhibit enormous diversity not only in size, shape and biology but also in the habitats they occupy. There are about 450 families of freshwater fishes globally. Roughly 40 are represented in India. About 25 of these families contain commercially important species. Snakehead fishes or Murrels are members of family Channidae and are native to Asia, Malaysia, Indonesia and Africa. Snakeheads are air-breathing fishes, several capable of overland migrations and are distinguished by their somewhat elongated and cylindrical bodies, the presence of large scales on the head, flattened heads, and dorso-lateral eyes on the anterior part of the head. They have supra branchial chambers for aerial respiration with the ventral aorta divided into two parts to permit bimodal respiration.

Most Channid species are important food fishes in southern Asia and China and the flesh is considered a delicacy. Murrels are also considered potential candidate species for diversification of aquaculture. Some medium to large species are cultured in ponds or in cages set in slow running rivers. The systematics of family Channidae is a matter of continuing debate, especially because of the similarities in their external morphology and internal anatomy. Morphological and physiological data have produced inconclusive
taxonomies. Among murrels, large sized *Channa marulius* is the most important due to consumer preference and high market price. It is considered as an important food fish and a significant component of freshwater fishery. It is somewhat cosmopolitan in distribution with native range extending from tropical to temperate climates. *C. marulius* has a wide distribution occurring in almost all states of India, Sri Lanka, Bangladesh, Pakistan, Burma and Thailand. In India, it is found in freshwaters of West Bengal, Uttar Pradesh, Madhya Pradesh, Bihar, Punjab, Orrissa, Maharashtra, Gujrat, Andhra Pradesh, Tamil Nadu, Karnatka and Kerala.

*Channa marulius* is reported to be the largest in family Channidae, reaching a length of 120-122 cm. Dark spots are seen on the lateral sides of the body and 4-6 round black blotches followed by white spots, little below the lateral line are also present. A large black prominent ocellus with white or orange boundary at upper part of the base of caudal fin characterizes the species. The accessory respiratory organs of the pharyngeal region are well developed in *C. marulius* and these serve as air sacs to breath atmospheric oxygen.

*C. marulius* constitutes the mainstay of wild freshwater fisheries in India, especially in peninsular region. The culture of this giant murrel has not been traditionally popular for its highly voracious feeding habits in tertiary level. Pronounced cannibalism and heavy mortality, right from earlier stages of life, are primary factors for unsuccessful
culture. Being a local migrant, it travels for a short distance for the purpose of feeding or for locating suitable breeding grounds or in search of new water bodies to avoid stress conditions of existing ecosystem.

The fish is considered as a potential aquaculture species in addition to an important capture fishery resource. Due to declining abundance of *C. marulius* in wild, the fish has been assessed at lower risk- near threatened (LRnt) status. Understanding of population genetic structure of a species provides critical information for developing conservation and management strategies for natural fish populations as well as fishes having threatened status. In addition to protein and nuclear DNA markers, different mtDNA gene sequences have been used to determine variation at interspecific and intraspecific levels in fishes. The fast rate of mtDNA evolution coupled with maternal inheritance have made mtDNA an extremely useful genetic system for studying gene flow, hybrid zones, population structure and other population related questions.

Murrels are considered potential candidate species for diversification of aquaculture and *Channa marulius* which is most important due to consumer preference and high market price. The identification of molecular markers and documentation of genetic diversity of *Channa marulius* is, therefore, important considering that such information is valuable in breeding programmes, genetic stock
identification and fishery management, besides to provide insight into evolutionary genetics of species. Stock identification will improve our understanding about the genetic structure of natural populations. This information is helpful in decision making during introduction or rehabilitation of a declining or threatened stock. To fill the knowledge gap on population genetic structure of wild *C. marulius*, the present study has been undertaken with the objectives given below:

a) Identification of Polymorphic Mitochondrial DNA (mtDNA) markers in *Channa marulius*.

b) Analysis of genetic diversity in natural population of *Channa marulius* using mtDNA markers.

c) Identification and Characterization of Microsatellite DNA markers in *Channa marulius*.

The treatise consists of 7 chapters, 24 figures and 8 tables in support of the text. The study is summarised as follows:

- Samples of mature *C.marulius* were collected from major river systems of northern India during the period of study. Blood was extracted through caudal puncture and fixed in 95% ethanol.

- Total Genomic DNA was isolated and amplified using Universal Primers for mtDNA Cytochrome b and ATPase 8 and ATPase 6 regions respectively. The purified PCR Product was sequenced
on an automated DNA sequencer. DNA sequences were aligned and then analysed for genetic variation using relevant softwares.

- Analysis of partial Cytochrome b region revealed the suitability of this region in determining the genetic diversity in *C. marulius* population. Results obtained also demonstrated that partial mtDNA Cytochrome b fragment (307 bp) is a potential marker for studying variation both within as well as among populations in *C. marulius*.

- Analysis of Molecular Variance (AMOVA) for Cytochrome b region within 15 populations revealed that out of total variation, 84.69% of variation was seen among the populations and within the population, variation was approximately 15%. Population structuring was revealed by Fst value of 0.84.

- Samples from river Brahmaputra, Yamuna, Mahanadi and Teesta exhibited population specific haplotypes. Most common haplotype was found across 5 populations namely Ganga, Sone, Sindh, Chambal and Tons. Total 34 variable sites were identified and 18 of them were parsimony informative.

- The present study also evaluated the potential of complete ATPase region of mitochondrial DNA as a marker region to determine the phylogeography of *C. marulius* from Indian rivers.
The results revealed that 842 bp of ATPase 6/8 region could be a promising marker for determining variations at interpopulation as well as intrapopulation levels in wild *C. marlius*.

- AMOVA analysis for ATPase region within 15 populations revealed that out of total variation, 63.78% was seen among populations and 14.49% variation was present within populations. Fst value of 0.584 revealed population structuring.

- Samples from river Ganga, Gomti 1, Tons, Sone, Sharda, Sindh, Chambal, Brahmaputra, Teesta1&2 and Mahanadi showed the presence of unique haplotypes. Most common haplotype was found across 12 populations except Son, Chambal and Teesta 2. Total 47 variable sites were identified out of which 23 were parsimony informative.

- In our study, ATPase 8 and 6 genes not only expressed intraspecific diversity but were also able to resolve haplotypes in each population as well as variation in the progeny. Also it detected the native haplotypes present in each population. However on a finer level it was less effective in resolving populations having recent evolutionary history. Our findings demonstrated the utility of this otherwise less studied region of
mtDNA for population genetics, conservation and management of wild *C. marulius* fishery.

- Overall, results from Cytochrome b as well as ATPase region analysis, when put together, revealed the presence of 10 distinct genetic stocks of *Channa marulius* present in Indian rivers. These stocks were the populations from following rivers: Ganga, Gomti, Teesta1, Teesta2, Brahmaputra, Yamuna, Sone, Tons, Chambal and Mahanadi.

- In order to obtain basal information on microsatellite repeats in *C. marulius*, an enriched genomic library was constructed. Out of 200 plasmids screened, 44 clones confirmed the presence of an insert. Sequencing of 44 clones yielded 6 microsatellite repeats.

- 5 out of 6 repeats were found to have optimum flanking sequences for primer designing and the primers were tested in *Channa marulius* and related species like *Channa punctatus*, *Channa striatus*, *Channa gachua* and *Channa orientalis*. The primers amplified successfully in *C. marulius* and also cross amplified homologous loci in other *Channa* species. One locus CML-93 was also found to be polymorphic, when tested across 2 different populations.
- The results indicated that these specific microsatellite loci identified in *C.marulius* have potential in use for genetic diversity studies of wild populations.

- In conclusion, present work is the first comprehensive study on identification of molecular markers and genetic diversity of commercially important murrel *C.marulius* in wild. The mitochondrial DNA analysis using Cytochrome b and ATPase 8 and 6 genes determined the presence of at least 10 genetic stocks. The high level of differentiation observed appear to be a likely phenomenon in view of biology of this fish.