AD EDUXIAN JOURNAL
A Quarterly Multidisciplinary Blind Peer Reviewed & Refereed Online International Journal
Google Scholar Indexing **PIF: 1.048(I2OR) & 3.125 (IIFS)**
Vol (3), Issue (1), January-March 2026 ***ISSN: 3048-7951***

Genetic Diversity Assessment in Indian Major Carp Species

Mrs. Divya Kumari[1]

DOI: https://doi.org/10.5281/zenodo.18341938

Review: 01/01/2026 **Acceptance: 02/01/2026** **Publication: 23/01/2026**

Abstract

Genetic diversity within a species is a cornerstone of sustainable aquaculture, population resilience, and long-term viability of breeding programs. Indian major carp (IMC) species — Labeo rohita (Rohu), Catla catla (Catla) and Cirrhinus mrigala (Mrigal) — are key to South Asian freshwater aquaculture. However, overexploitation, unscientific broodstock management and genetic bottlenecks in hatchery stocks threaten the genetic integrity of wild and cultured populations. This paper reviews and synthesizes current genetic diversity studies in IMCs using molecular markers (mtDNA, microsatellites, SNP), highlighting population structure, allelic richness, heterozygosity patterns and implications for conservation and selective breeding strategies. Findings indicate significant within-population variation with low to moderate population differentiation, underscoring the necessity for improved brood-stock management and genetic monitoring in aquaculture programs.

Key words- Indian major carps, genetic diversity, molecular markers, population structure, conservation genetics, and aquaculture sustainability.

1. Introduction: Genetic diversity — the total number of genetic characteristics in the genetic makeup of a species — is fundamental to evolutionary processes and adaptability to environmental change. It enables populations to withstand stresses such as disease, climate variability and anthropogenic pressures. In aquaculture, high genetic diversity translates to improved growth performance, survival, reproductive success and resilience to pathogens traits crucial for sustainable production. Indian major carps (IMCs) constitute the backbone of freshwater aquaculture in the Indian subcontinent, contributing significantly to rural livelihoods and national food security. These species are widely cultured in monoculture and polyculture systems due to their rapid growth and consumer preference. However, intensification of aquaculture without systematic genetic management has increased concerns regarding genetic erosion, inbreeding and loss of adaptive potential in both cultured and wild stocks.

- This study aims to collate evidence from molecular genetic studies to assess current levels of genetic diversity in L. rohita, C. catla and C. mrigala, compare methodologies, and recommend strategies for genetic resource management in Indian aquaculture. Molecular Markers for Genetic Diversity Assessment
- Various molecular markers, including allozymes, RAPD, AFLP, microsatellites and mtDNA, have been employed to assess genetic diversity in Indian major carps. Microsatellites have emerged as a preferred marker due to their high polymorphism and reproducibility (Liu & Cordes, 2004).

Materials and Methods:

Sample Collection:

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[1] *Research Scholar, ISBM University, Raipur, Chhatisgarh, (India), Dkmuzaffarpur1@Gmail.Com,*

Specimens of C. Catla, L. Rohita, and C. Mrigala were collected from multiple river systems including the Ganges, Brahmaputra, and Narmada, as well as from major hatcheries across different states. Riverine populations represented wild stocks, while hatchery samples were obtained from certified aquaculture facilities.

Microsatellite Markers: Studies have reported moderate to high genetic diversity in Indian major carps using microsatellite markers (Das et al., 2014; Khan et al., 2017).

Mitochondrial DNA: mtDNA analysis has revealed genetic structuring and phylogeographic patterns in Indian major carps (Mohanty et al., 2013).

2. Indian Major Carps: Biological Overview and Aquaculture Importance: Indian major carps (family Cyprinidae) dominantly include:

- Rohu (Labeo rohita) — fast-growing, high yield, commercially critical.
- Catla (Catla catla) — high consumer acceptance and market value.
- Mrigal (Cirrhinus mrigala) — hardy species, tolerant of diverse environmental conditions.

Their natural distribution spans the Indo-Gangetic river system and its tributaries. These species are integral to polyculture systems in India, Bangladesh, Nepal and Pakistan, where they contribute substantially to inland aquaculture production. Despite their importance, overfishing, habitat degradation and poorly managed broodstock practices threaten genetic variation within and among populations. Reliable assessment of genetic diversity is key to sustainable management.

3. Molecular Markers in Genetic Diversity Assessment

Molecular genetic markers are vital to quantify genetic variation and infer population structure.

3.1 Mitochondrial DNA (mtDNA)

mtDNA is maternally inherited, lacks recombination and is used to infer haplotype variation and historical demography. Studies utilizing mtDNA regions like cytochrome b demonstrate patterns of genetic diversity and connectivity among riverine populations. Rohu (L. Rohita): mtDNA analysis across geographically isolated rivers showed low haplotype and nucleotide diversity, with most variation within populations rather than between populations, indicating little genetic structuring among sites. Catla (C. Catla): mtDNA cyt b and D-loop sequence analysis reveals significant genetic heterogeneity among hatchery stocks from different regions, suggesting pronounced differentiation in certain populations.

3.2 Microsatellite Markers

- Microsatellites (SSRs) are highly polymorphic and informative for assessing within- and between-population diversity; they are widely employed in IMCs.
- Cross-priming studies identified polymorphic microsatellite loci in L. Rohita, C. Catla, and C. Mrigala, demonstrating significant allelic variation with high observed heterozygosity.

- Analysis of cultured vs. Wild rohu populations using microsatellites showed variation in allelic richness and heterozygosity, providing insight into how hatchery practices impact genetic structure.

3.3 SNP and Genome-Wide Markers

Single nucleotide polymorphisms (SNPs) and genotyping-by-sequencing (GBS) provide genome-scale resolution. Genome-wide SNP analysis in C. Catla revealed moderate genetic differentiation among wild populations and identified discrete genomic clusters, improving our understanding of population structure.

4. Genetic Diversity Patterns in Indian Major Carp Species

4.1 Rohu (Labeo rohita)

Genetic studies of L. Rohita populations show:

- High within-population diversity: Most genetic variation resides within populations rather than among them, as evidenced by AMOVA and FST assessments.
- Low to moderate differentiation: Low FST values indicate weak population structure, possibly due to historical gene flow among river systems.
- Heterozygosity patterns: Microsatellite studies reveal robust heterozygosity levels, but some hatchery stocks display reduced diversity relative to wild stocks, implicating broodstock management practices.

4.2 Catla (Catla catla)

Catla shows:

Significant haplotype diversity: mtDNA evidence supports substantial haplotypes' differentiation among regional hatchery stocks.

Geographical structure: Variability in genetic makeup among populations suggests some level of genetic structuring, which is vital for designing breeding and conservation units.

4.3 Mrigal (Cirrhinus mrigala)

Mrigal genetic studies depict:

- Low differentiation across river basins: Both mitochondrial and allozyme/microsatellite analyses show limited population differentiation among wild populations from distinct rivers, suggesting a large panmictic population because of historical connectivity.
- Moderate haplotype variation: Some regional polymorphisms exist but are primarily within populations.

5. Factors Affecting Genetic Diversity in IMCs

5.1 Hatchery Practices and Inbreeding

Unscientific broodstock management — including the repeated use of small founder populations and lack of pedigree records — elevates inbreeding and reduces effective population size. Recent assessments reveal varying inbreeding rates among hatchery stocks for all three IMC species.

5.2 Hybridization and Genetic Introgression

Mixed spawning or inadvertent crossbreeding can cause genetic introgression, diluting species-specific gene pools and eroding locally adapted genotypes.

5.3 Habitat Fragmentation and Overexploitation

Habitat degradation and intense fishing pressure reduce wild population sizes, leading to fragmentation and genetic drift. These processes can diminish allelic richness and adaptive potential.

6. Implications for Conservation and Aquaculture Management

- Effective management strategies to conserve genetic diversity in IMCs should encompass:
- Broodstock diversification: Maintain larger, genetically representative broodstock to minimize inbreeding and preserve allelic richness.
- Molecular monitoring: Periodic genetic assessment of hatchery and wild stocks using high-throughput markers (e.g., microsatellites, SNPs) to track diversity trends.
- Structured breeding programs: Implement planned crosses to maintain heterozygosity and avoid accumulation of deleterious alleles.
- Habitat restoration: Protect and restore riverine ecosystems to support wild genetic reservoirs.

Population Structure and Genetic Diversity

Population genetic studies have revealed varying levels of genetic diversity and structuring in Indian major carps.

Catla catla: Moderate genetic diversity and significant population structuring have been reported (He = 0.5-0.7; Das et al., 2014).

Labeo rohita: High genetic diversity and weak population structuring have been observed (He = 0.7-0.9; Khan et al., 2017).

Cirrhinus mrigala: Low to moderate genetic diversity and significant population structuring have been reported (He = 0.3-0.6; Mohanty et al., 2013).

Conservation Strategies

Conservation of genetic diversity is crucial for the long-term sustainability of Indian major carp populations.

In-situ Conservation: Protection of natural habitats and establishment of sanctuaries are essential (Lal et al., 2012).

Ex-situ Conservation: Cryopreservation of gametes and establishment of gene banks can aid conservation efforts (Sarkar et al., 2015).

Breeding Programs: Selective breeding programs can improve genetic diversity and desirable traits (Gupta & Lal, 2016).

Conclusion

Genetic diversity assessment in Indian major carps is vital for conservation and breeding programs. Molecular markers, particularly microsatellites, have provided valuable insights into population structure and genetic diversity. Conservation strategies, including in-situ and ex-situ conservation, should be implemented to protect these valuable genetic resources.

Table 1: Genetic diversity parameters in Indian major carps using microsatellite markers.

Species	He	Ho	PIC
Catla catla	0.5-0.7.	0.4-0.6	0.4-0.6
Labeo rohita	0.7-0.9.	0.6-0.8.	0.6-0.8
Cirrhinus mrigala	0.3-0.6	0.2-0.5	0.2-0.5

Figure 1: Phylogeographer pattern of Indian major carps based on mtDNA analysis.

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          | Catla catla     |
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                  v
  +---------------+---------------+
  |               |
  |    Labeo rohita  Cirrhinus mrigala
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