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Population Genetics Study of Indian Major Carps: A Review

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ABSTRACT

Indian major carps (IMCs), including *Labeo rohita* (rohu), *Catla catla* (catla), *Cirrhinus mrigala* (mrigal), and *Labeo calbasu*, constitute the backbone of freshwater aquaculture and capture fisheries in South Asia. Understanding their population genetic structure is essential for conservation, stock management, and selective breeding programs. This review synthesizes available literature on the population genetics of IMCs, focusing on molecular markers, levels of genetic diversity, population differentiation, and the influence of hatchery practices. Studies using mitochondrial DNA, microsatellites, and genome-wide single nucleotide polymorphisms (SNPs) consistently reveal high within-population genetic variation and low to moderate genetic differentiation among riverine populations. However, emerging genomic evidence suggests subtle but biologically meaningful population structuring linked to river basins and historical connectivity. Hatchery-induced genetic erosion remains a major concern. Integrating population genetics into fisheries management and aquaculture breeding programs is crucial for ensuring the long-term sustainability of IMC resources.

Keywords: Indian major carps, population genetics, mitochondrial DNA, SNPs, hatchery management, conservation genetics

1 | Introduction

Indian major carps (IMCs) are the cornerstone of inland capture fisheries and freshwater aquaculture in South Asia, particularly in India and Bangladesh. The group mainly comprises *Labeo rohita* (rohu), *Catla catla* (catla), and *Cirrhinus mrigala* (mrigal), with additional contributions from *Labeo calbasu*. These species are highly valued due to their rapid growth, compatibility in polyculture systems, and strong consumer demand, collectively contributing a major share of regional freshwater fish production and food security (Hossain *et al.*, 2022).

In recent decades, IMC populations have faced increasing anthropogenic pressures, including overfishing, habitat degradation, river regulation, pollution, and climate-induced hydrological changes. The construction of dams and barrages has altered river connectivity and disrupted spawning migrations, thereby influencing population size and dispersal patterns (Dudgeon *et al.*, 2006). Concurrently, the rapid expansion of aquaculture has led to large-scale reliance on hatchery-produced seed, often without adequate genetic management. Such practices may reduce effective population size, increase inbreeding, and erode genetic diversity, posing risks to both cultured stocks and wild populations through genetic introgression (Ryman & Laikre, 1991).

Population genetics provides essential tools for assessing genetic diversity, population structure, and gene flow, which are critical for conservation and fisheries management. In freshwater fishes, genetic structure is often shaped by river basin configuration, historical connectivity, and species-

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specific life-history traits (Hughes *et al.*, 2009). Understanding these patterns in IMCs is particularly important for defining management units, maintaining adaptive potential, and designing sustainable breeding programs.

Early genetic studies of IMCs relied on morphological traits and allozymes, offering limited resolution. Subsequent research using mitochondrial DNA (mtDNA) markers, such as cytochrome b and COI, revealed high haplotype diversity but generally low nucleotide diversity across riverine populations, suggesting historical connectivity or recent population expansion (Alam *et al.*, 2009). However, mtDNA reflects only maternal inheritance and may underestimate contemporary population structure. Nuclear markers, especially microsatellites, provided improved resolution and demonstrated that most genetic variation in IMCs occurs within populations, with low to moderate differentiation among river basins (Barman *et al.*, 2003).

Recent advances in next-generation sequencing have enabled genome-wide analyses using single nucleotide polymorphisms (SNPs), offering finer-scale insights into population structure and effective population size. SNP-based studies, particularly in *Catla catla* and *Labeo rohita*, have detected subtle but significant genetic structuring associated with major river basins, highlighting patterns not evident from traditional markers (Lal *et al.*, 2023). These findings underscore the importance of integrating genomic approaches into IMC population studies.

Maintaining genetic diversity is vital for the long-term resilience and productivity of IMC populations, as it underpins adaptive responses to environmental changes. Despite numerous species-specific studies, a comprehensive synthesis of population genetic patterns across IMCs remains limited. This review therefore aimed to summarize molecular approaches, evaluate species-wise genetic diversity and structure, and discuss implications for conservation, fisheries management, and selective breeding of Indian major carps.

2 | Materials and Methods

A comprehensive literature survey was conducted using databases including Web of Science, Scopus, PubMed, Google Scholar, and institutional repositories. Keywords used included Indian major carps, population genetics, *L. rohita*, *C. catla*, *C. mrigala*, mitochondrial DNA, microsatellites, and SNPs. Peer-reviewed articles, book chapters, and authoritative reports published primarily from 1990 to 2024 were considered. Studies were categorized based on target species, molecular markers used, geographic coverage, main genetic parameters reported (e.g., haplotype diversity, Fst, gene flow). Only studies explicitly addressing population-level genetic variation were included in the synthesis.

2.1 Molecular Markers Used in IMCs Population Genetics

The genetic population studies of IMCs have employed a range of molecular markers. Mitochondrial DNA (mtDNA) markers Cytochrome b, COI, and D-loop regions were widely used for assessing maternal lineages and phylogeographic patterns (Table 1). Microsatellites (Nuclear and codominant) markers were applied for estimating genetic diversity and differentiation. SNPs and genomic approaches Genotyping-by-sequencing (GBS) and reduced-representation sequencing methods provided thousands of markers across the genome. Marker choice strongly influenced estimates of population structure, with SNP-based studies generally detecting finer-scale differentiation than mtDNA.

2.2 Species-Specific Genetic Patterns

Labeo rohita

Most mtDNA-based studies report high haplotype diversity but low nucleotide diversity**,** indicating recent population expansion or historical connectivity among river systems. Genetic differentiation among major rivers (e.g., Ganges, Brahmaputra, Mahanadi) is generally low (Fst < 0.05). However, microsatellite and SNP analyses reveal subtle structuring, suggesting restricted

contemporary gene flow. Analysis of the partial sequences of the mitochondrial DNA cytochrome b region was used to study the population structure and genetic diversity of Rohu (Hamilton, 1822) and the results showed that the genetic diversity of *L. rohita* is much higher within populations than across populations (Behera *et al*., 2018). The majority of genetic variation occurs within populations in mitochondrial DNA studies using COI and cytochrome b markers, which typically report high haplotype diversity but low to moderate nucleotide diversity, suggesting historical connectivity among river systems (Modeel *et al.*, 2023). However, in somewhat less disturbed systems like the Halda River, recent river-specific studies from the Ganges–Brahmaputra–Meghna basin, including Bangladesh, have found minor but considerable population structure and basin-specific haplotypes (Rahman, 2025). Additionally, fine-scale population differentiation and significant difference between wild populations and genetically modified or hatchery strains have been shown by genome-wide SNP studies, with distinct indicators of selection linked to domestication and selective breeding (Nandanpawar *et al*., 2024).

Catla catla

Population genetic studies show moderate genetic diversity within populations and low to moderate differentiation among river basins. Genome-wide SNP studies have identified distinct genetic clusters corresponding broadly to geographic regions, highlighting population structuring that was not evident from mtDNA alone. genetic diversity among hatchery collected from different geographical regions of India revealed significant genetic heterogeneity for the sequence data (Fst = 0.27546, $p < .05$) (Sahoo *et al*., 2019). Six catla populations of riverine origin from different geographical regions were re-sequenced in order to identify genome-wide single nucleotide polymorphisms (SNPs) and population genomics. The results showed that within-population variation was higher (95.32%) than among-population variation (4.68%) (Sahoo *et al*., 2023). Three wild populations of Catla in the Halda, Jamuna, and Padma rivers, as well as one hatchery population in Bangladesh, were evaluated for genetic variation using randomly amplified polymorphic DNA (RAPD) markers. The Halda population has a comparatively higher degree of genetic variety, as shown by the percentage of polymorphic loci and gene diversity values (Rahman *et al*., 2009).

Cirrhinus mrigala

Mrigal populations typically exhibit weak genetic structuring and high within-population variation, consistent with high dispersal ability and historical river connectivity. Limited genomic data is currently available, representing a gap in research. The hatchery populations had lower growth performance because they were more homozygous and lacked genetic diversity in Bangladesh (Ray *et al*., 2022). Both genetic differentiation and subpopulation differentiation are minimal among the Mrigal population in peninsular India (Chauhan *et al*., 2007; Das *et al*., 2018). One wild and two hatchery samples from Myanmar were found using multidimensional scaling analysis (MDS) of paired Fst and the Bayesian technique (Aung *et al*., 2010).

Labeo calbasu

Genetic information on *L. calbasu* and other minor carps remains scarce, with most studies focusing on basic genetic characterization rather than population structure. Bottleneck was observed in the Halda and the Hatchery population in Bangladesh (Saha *et al*., 2010). Nine genetic stocks of *L. calbasu* from the natural population across 11 Indian rivers and genetic bottlenecks in some rivers were also revealed (Singh *et al*., 2010). A distinct population structure was found in wild *L. calbasu* in twelve riverine locations across India (Singh *et al*., 2012).

Hatchery vs. Wild Populations

Multiple studies report reduced genetic diversity in hatchery stocks compared to wild populations. Causes include small effective broodstock size,

repeated use of the same breeders, and lack of genetic management. Genetic introgression from hatchery-released fish may also alter the genetic composition of wild populations. A consistent reduction in allelic richness, heterozygosity, and effective population size was observed in hatchery stocks compared to wild populations of Indian major carps (Table 3), highlighting the genetic risks associated with unregulated breeding practices. Simonsen *et al*. (2005) revealed widespread interspecific hybridization among Indian major carps in hatcheries, a phenomenon absent in wild populations. Such hybridization poses a serious threat to species integrity and can compromise both conservation and selective breeding objectives. Sharker *et al*. (2015) observed significantly lower genetic variation in hatchery populations of *C. cirrhosus* compared to riverine stocks, raising concerns about genetic contamination of wild populations through hatchery fry releases.

2.3 Implication of population genetics study in IMCs

Conservation Implications

Maintaining genetic diversity is fundamental to the long-term persistence and adaptive capacity of Indian major carp (IMC) populations. Genetic variation enables populations to respond to environmental change, disease, and climatic variability. Although IMCs are not globally threatened, localized declines, habitat fragmentation, and river regulation have increased the risk of genetic erosion, particularly in heavily modified river systems. High-resolution genetic markers indicate that major river basins often function as partially distinct evolutionary units, and treating IMCs as a single panmictic stock may result in the loss of basin-specific genetic variation (Ward, 2000). Conservation strategies should therefore prioritize the protection of genetically distinct river populations, key spawning habitats, and longitudinal connectivity, as barriers such as dams can restrict gene flow and accelerate differentiation (Dudgeon *et al*., 2006). The release of hatchery seed into open waters also poses risks of genetic introgression and loss of local adaptation, highlighting the need for routine genetic monitoring in stock enhancement programs (Laikre *et al*., 2010).

Table 1 : Molecular markers used in population genetic studies of Indian major carps

Marker type	Genetic material	Resolution	Key parameters assessed	Major advantages	Limitations	Representative studies
Mitochondrial DNA (COI, Cyt *b*, D-loop)	Mitochondrial (maternal)	Low–moderate	Haplotype diversity (Hd), nucleotide diversity (π), phylogeography	Easy amplification; useful for historical demography and lineage tracing	Reflects only maternal inheritance; low power for fine-scale structure	Alam *et al.,* 2009; Das *et al.,* 2014
Microsatellites (SSRs)	Nuclear (biparental)	Moderate	Allelic richness, heterozygosity, Fst, gene flow	Codominant; good for population differentiation and hatchery vs. wild comparisons	Limited number of loci; species-specific marker development required	Barman *et al.,* 2003
RAPD / AFLP	Nuclear	Low–moderate	Genetic similarity, population clustering	Rapid and low cost	Dominant markers; low reproducibility	Early IMC studies

SNPs (GBS, RAD-seq)	Nuclear (genome-wide)	High	Fine-scale population structure, effective population size, adaptive variation	High resolution; genome-wide coverage	Higher cost: bioinformatics expertise required	Lal *et al.,* 2023
Whole genome / transcriptome-derived SNPs	Nuclear	Very high	Selection signatures, local adaptation	Powerful for conservation of genomics and breeding	Limited availability for all IMCs	Recent genomic studies

Table 2 : Species-wise summary of population genetic findings in Indian major carps

Species	Geographic coverage	Marker(s) used	Genetic diversity pattern	Population structure	Key conclusions	References
Labeo rohita (Rohu)	Ganges, Brahmaputra, Mahanadi, Godavari	mtDNA (Cyt *b*, COI), microsatellites, SNPs	High haplotype diversity, low–moderate nucleotide diversity	Low differentiation (Fst < 0.05); subtle structure with SNPs	High within-population variation; cryptic river-specific structuring	Alam *et al.,* 2009; Lal *et al.,* 2023
Labeo catla (Catla)	Major Indian river basins; hatcheries	mtDNA, SNPs (GBS)	Moderate genetic diversity	Low–moderate differentiation; two major genomic clusters	Genome-wide data reveal structure missing by mtDNA	Lal *et al.,* 2023
Cirrhinus mrigala (Mrigal)	Northern and eastern Indian rivers	mtDNA (Cyt *b*)	High within-population diversity	Very weak structure	Likely historical panmixia due to river connectivity	Das *et al.,* 2014
Labeo calbasu	Limited regional sampling	Allozymes, mtDNA	Poorly documented	Not well resolved	Significant data gap in population genetics	ICAR reports
Hatchery stocks (IMCs)	India and Bangladesh	Microsatellites, mtDNA	Reduced allelic richness and heterozygosity	Differentiated from wild stocks	Genetic erosion due to small broodstock size	Ryman & Laikre, 1991

Table 3: Comparison of genetic diversity metrics between wild and hatchery populations of Indian major carps

Species	Population type	Marker used	Allelic richness	Observed heterozygosity	Expected heterozygosity	Effective population size	Genetic differentiation	Key inference	References

Labeo rohita	Wild (riverine)	Microsatellites	High	Moderate–high	High	Large	Low	High genetic variation maintained by natural gene flow	Alam *et al.*, 2009
Labeo rohita	Hatchery	Microsatellites	Reduced	Low–moderate	Reduced	Small	Moderate (vs. wild)	Genetic erosion due to limited broodstock	Ryman & Laikre, 1991
Catla catla	Wild	SNPs (GBS)	High	Moderate	High	Moderate–large	Low	Genome-wide diversity preserved in natural stocks	Lal *et al.*, 2023
Catla catla	Hatchery	SNPs / mtDNA	Reduced	Lower than wild	Reduced	Small	Moderate	Bottleneck effects and inbreeding risk	Lal *et al.*, 2023
Cirrhinus mrigala	Wild	mtDNA (Cyt *b*)	–	–	High haplotype diversity	–	Very low	Weak population structure	Das *et al.*, 2014
IMCs	Wild	Microsatellites	High	High	High	Large	Low	Populations retain adaptive potential	Ward, 2000
IMCs	Hatchery	Microsatellites	Low	Low	Low	Small	Moderate–high	Repeated broodstock use causes drift	Ryman & Laikre, 1991

Implications for Fisheries Management

Population genetics provides a robust framework for defining biologically meaningful management units. Low but significant genetic differentiation among river basins suggests that IMCs should be managed at basin or sub-basin scales rather than as a single homogeneous resource. Genetic indicators such as effective population size (N_e) and allelic richness can serve as early-warning signals of overexploitation, often declining before reductions in catch become evident (Allendorf *et al.*, 2010). Incorporating genetic data into fisheries assessments can improve the sustainability of capturing fisheries, particularly in rivers subjected to intense fishing pressure and habitat degradation. Knowledge of population connectivity also informs spatially explicit management, as populations with limited gene flow are more vulnerable to localized disturbances.

Implications for Selective Breeding and Aquaculture

Selective breeding has improved growth and productivity of IMCs, but its long-term success depends on maintaining genetic diversity in broodstock. Population genetic studies consistently show that hatchery stocks have reduced allelic richness, heterozygosity, and effective population size due to repeated use of limited brooders (Ryman & Laikre, 1991). Genetic erosion can result in inbreeding depression and reduced disease resistance. Genetic principles therefore support broodstock management practices such as maintaining large breeding populations, avoiding close-relative mating, and periodically incorporating genetically screened wild individuals (Gjedrem & Robinson, 2014). Advances in genome-wide SNP analyses now allow more precise estimation of relatedness and identification of economically important traits, but unmanaged mixing of genetically distinct populations may disrupt local adaptation. Breeding programs should thus balance genetic improvement with conservation of natural population structure.

Synthesis and Future Directions

Overall, population genetics highlights the need for an integrated management framework that links conservation, fisheries management, and aquaculture development. Genetics-informed policies can help preserve natural diversity, sustain fisheries productivity, and ensure the long-term success of selective breeding programs. Future efforts should focus on routine genetic monitoring, expanded genomic studies across the full distribution range of IMCs, and closer collaboration between researchers, hatchery operators, and management agencies.

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