

RESEARCH PAPER

Mitochondrial DNA variation in economically important fish species

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Abstract

Mitochondrial DNA (mtDNA) markers (COI, cytochrome b, D-loop, ATPase 6/8) have become essential tools for assessing genetic variation, population structure, and phylogeography of economically important freshwater fishes. This review synthesizes mtDNA-based studies on Indian freshwater fishes, highlights results relevant to rivers that flow through Uttar Pradesh (particularly the Ganga basin), and evaluates marker performance for stock identification and conservation. Available studies indicate moderate-to-high mtDNA diversity in many carp and catfish taxa, frequent shallow spatial structuring for widespread species, and evidence that habitat fragmentation and anthropogenic pressures can reduce genetic connectivity. For Uttar Pradesh, published molecular sampling is relatively sparse; targeted mtDNA surveys across major Ganga tributaries are urgently needed to inform stock management and hatchery supplementation programs. Key recommendations include coordinated mtDNA barcoding and control-region surveys across UP rivers and integration with nuclear markers for robust management decisions.

KEYWORDS:

Mitochondrial DNA, COI, cytochrome b, genetic diversity, Uttar Pradesh

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Introduction

Mitochondrial DNA (mtDNA) has been one of the most extensively used molecular tools in fisheries genetics due to its maternal inheritance, absence of recombination, relatively rapid mutation rate, and high copy number in cells. These characteristics allow reliable amplification from small or degraded tissue samples and facilitate comparative studies across laboratories and regions. In fishes, mtDNA has been widely applied for species identification, population genetic structure analysis, phylogeographic reconstruction, and inference of historical demographic events, making it particularly valuable in regions where genomic resources are limited or unevenly distributed (Das et al., 2013; Cermakova et al., 2023).

Among mitochondrial markers, cytochrome c oxidase subunit I (COI) has become the global standard for DNA barcoding and species authentication, while cytochrome b (cyt b) is commonly used for resolving inter- and intra-specific relationships and population-level differentiation. Additional regions such as ATPase 6/8 and the non-coding control region (D-loop) are especially informative for assessing recent demographic history and fine-scale population structuring because of their higher mutation rates. Comparative studies demonstrate that marker choice strongly influences the temporal and spatial resolution of inferred genetic patterns (Gao et al., 2020; Clark et al., 2024).

In India, mtDNA-based studies have played a central role in documenting freshwater fish diversity across river basins, particularly for carps, catfishes, and clupeids. Extensive barcoding initiatives and population genetic studies using COI, cyt b, ATPase 6/8, and control-region sequences have revealed cryptic diversity, clarified taxonomic ambiguities, and provided baseline data for stock identification. These studies have also highlighted substantial regional variation in genetic diversity driven by riverine history, hydrological connectivity, and anthropogenic pressures (Kumar et al., 2017; Roy et al., 2024).

Economically important freshwater fishes in Uttar Pradesh, including major carps such as *Labeo rohita*, *Cirrhinus mrigala*, and *Catla catla*, as well as selected catfishes and mastacembelids, form the backbone of inland fisheries and aquaculture in the state. Genetic information is essential for sustainable management of these resources, particularly for broodstock selection, hatchery seed quality control, and conservation of wild genetic diversity. MtDNA markers provide an accessible means to assess maternal line diversity and detect potential genetic erosion associated with overexploitation and hatchery-mediated translocations (Modeel et al., 2023; Kumar et al., 2017).

Studies on *Labeo rohita* across South and Southeast Asia using cyt b and other mtDNA markers have consistently reported shallow population genetic structure, often interpreted as the result of historical connectivity, high dispersal potential, and extensive anthropogenic movement of seed. However, subtle but significant local differentiation has been detected in some river systems, underscoring the importance of regional genetic assessments when sourcing broodstock for aquaculture and ranching programmes (Modeel et al., 2023).

For minor carps and medium-value species such as *Labeo gonius*, mtDNA ATPase 6/8 and control-region analyses have revealed high haplotype diversity and evidence of phylogeographic structuring across Indian rivers. These findings suggest that historical river capture events, basin isolation, and localized adaptation have shaped contemporary genetic patterns, reinforcing the need for basin-specific management rather than uniform stocking strategies (Roy et al., 2024; Das et al., 2013).

Catfishes and other non-cyprinid taxa have also benefited from mtDNA-based investigations in India. Studies using cyt b and 16S rRNA markers have resolved taxonomic uncertainties, identified cryptic species, and clarified population boundaries in genera such as *Ompok* and *Tenuulosa*. Such genetic clarification is particularly relevant for Uttar Pradesh fisheries, where accurate species identification is critical for regulation, trade, and hatchery practices (Malakar et al., 2013; Choudhury, 2021).

Despite the demonstrated utility of mtDNA, much of the existing Indian literature is concentrated in select river systems, and comprehensive mtDNA sampling within Uttar Pradesh—especially across its Ganga tributaries—remains limited in the peer-reviewed record up to 2024. Given the state's ecological importance and fisheries dependence, this represents a significant knowledge gap. Addressing this gap requires synthesis of existing mtDNA evidence alongside identification of priorities for future genetic monitoring.

Finally, it is widely acknowledged that mtDNA provides only a maternal perspective on population history and can be influenced by introgression, incomplete lineage sorting, and mito-nuclear discordance. Consequently, fisheries genetics literature increasingly recommends integrating mtDNA with nuclear markers such as microsatellites or SNPs for robust management decisions. Nonetheless, mtDNA remains a cost-effective and informative first step for stock assessment and conservation planning, particularly in data-limited contexts such as many inland fisheries of Uttar Pradesh (Clark et al., 2024; Kumar et al., 2017).

Methodology

This paper adopts a structured literature-synthesis approach to evaluate the application of mitochondrial DNA markers in economically important freshwater fishes of India, with particular relevance to Uttar Pradesh river systems. Peer-reviewed articles, institutional reports, and credible grey literature published up to 2024 were compiled to create a comprehensive overview of mtDNA-based genetic studies relevant to fisheries management. The synthesis focuses on commonly used mitochondrial loci including COI, cytochrome b, ATPase 6/8, the control region, and near-complete mitochondrial genomes where available (Modeel et al., 2023; Roy et al., 2024).

Literature searches were conducted using academic databases such as PubMed, Web of Science, Google Scholar, and institutional repositories. Search terms combined keywords related to mitochondrial genetics and Indian freshwater fishes, including “mitochondrial DNA,” “COI,” “cytochrome b,” “ATPase,” “control region,” “India,” and major river systems such as the Ganga, Yamuna, Ghaghara, and Rapti. This strategy ensured inclusion of both basin-wide studies and species-specific investigations relevant to Uttar Pradesh fisheries (Kumar et al., 2017).

Each selected study was systematically reviewed and tabulated according to species examined, mitochondrial marker(s) used, geographic coverage, sample size, and primary genetic metrics reported. These metrics included haplotype diversity, nucleotide diversity, population differentiation indices, and evidence of demographic expansion or bottlenecks. Where authors explicitly discussed management or conservation implications, these interpretations were recorded for comparative assessment (Modeel et al., 2023; Roy et al., 2024).

To ensure reliability, quality-control criteria were applied during synthesis. Priority was given to studies that deposited DNA sequences in public databases such as GenBank and provided clear locality information. Studies reporting standard

analytical approaches, including haplotype network construction, AMOVA, and pairwise population differentiation statistics, were considered higher confidence. Research lacking accession numbers or precise sampling locations was retained but interpreted cautiously (Malakar et al., 2013; Choudhury, 2021).

Special attention was paid to studies addressing anthropogenic drivers such as dams, pollution, and hatchery-mediated translocations, as these factors strongly influence genetic patterns in Indian rivers. Papers explicitly linking mtDNA variation to river fragmentation or stocking practices were highlighted, given their direct relevance to fisheries management in Uttar Pradesh (Thapliyal, 2020; Kumar et al., 2017).

Because Uttar Pradesh-specific mtDNA datasets are relatively sparse, the synthesis incorporated findings from geographically proximate or hydrologically comparable river systems. Such comparative inference was applied cautiously, with emphasis on ecological similarity and shared evolutionary history. This approach allowed broader interpretation while avoiding overgeneralisation beyond available data (Das et al., 2013; Roy et al., 2024).

The synthesis also evaluated marker-specific strengths and limitations by comparing outcomes across loci. COI and cyt b studies were examined primarily for species identification and broad-scale structure, while ATPase 6/8 and control-region studies were emphasised for insights into recent demographic events and fine-scale population differentiation (Gao et al., 2020).

Finally, gaps in the existing literature were systematically identified, including limited sampling within Uttar Pradesh, over-reliance on single mitochondrial loci, and a lack of integrated mito–nuclear studies. These methodological gaps inform the interpretative framework of this paper and provide the basis for recommendations aimed at strengthening genetic monitoring and fisheries management in Uttar Pradesh and comparable Indian river systems (Clark et al., 2024; Kumar et al., 2017).

Results

Synthesis of the literature shows that mtDNA markers routinely recover moderate-to-high haplotype diversity in many Indian freshwater fishes, but geographic structuring is species-dependent: widespread carp species often show shallow structure (suggesting recent gene flow or human-mediated translocations), while species with limited dispersal show clearer differentiation by basin. Studies of *Labeo rohita* and related carps frequently reported shallow but detectable population partitions, whereas control-region studies in other taxa revealed fine-scale structure.

A major pattern is that anthropogenic factors (dams, pollution, habitat alteration, hatchery releases) tend to reduce realized connectivity; several mtDNA studies from Indian rivers document reduced effective population size or signatures of demographic change in impacted populations. This has direct implications for UP, where river regulation and urban impacts are significant.

Table 1 (below) summarizes representative mtDNA studies relevant to species of economic importance and to UP-comparable basins (authors, year, species, marker, location). Each entry cites the original study so managers can consult primary data.

Table 1 — Representative mtDNA studies (surveyed literature; selection).

Study (author, year)	Species (common)	Marker(s) used	River / region sampled
Modeel et al., 2023	<i>Labeo rohita</i> (rohu)	mtDNA (COI/cyt b)	South & Southeast Asia (comparative) — implications for Indian rivers. PubMed
Roy et al., 2024	<i>Labeo gonius</i> (minor carp)	ATPase 6/8, D-loop	Indian rivers across five basins (comparison relevant to Ganga). Frontiers
Malakar et al., 2013	<i>Ompok bimaculatus</i> (butter catfish)	cyt b	Riverine populations across India (taxonomic & population analysis). PubMed
Thapliyal, 2020	<i>Mastacembelus armatus</i>	cyt b	Studies of dam impacts on genetic diversity (Indian river case studies). EnvironCJ Journal
Choudhury , 2021	<i>Tenualosa</i> spp.	cyt b	Population study (coastal-riverine comparisons) — methodological reference. CABI Digital Library

Marker-specific performance and practical considerations (sensitivity, resolution, pros/cons) are summarized in Table 2, drawn from method and review literature.

Table 2 — mtDNA markers: suitability summary (synthesis from literature).

Marker	Typical use / strength	Limitations
COI	Species identification (DNA barcoding); broad reference libraries available. Nature	Lower within-species resolution for very recent divergence.
Cytochrome <i>b</i>	Good for phylogeography and moderate-resolution population studies. CABI Digital Library	Single-locus, maternal-only perspective.
Control region (D-loop)	High variability — sensitive to recent demographic events. MDPI	Alignment/indel issues; homoplasmy possible.
ATPase 6/8	Useful in some carps and minor species; informative haplotypes. Frontiers	Less widely used — fewer reference sequences.

Overall, the literature synthesis indicates that a two-marker approach (COI or *cyt b* + control region or ATPase) is cost-effective to balance species ID and within-population resolution, while combined mito–nuclear designs are preferable for management-level decisions.

Discussion

The surveyed studies illustrate that mtDNA variation captures important signals for fisheries management: it can identify cryptic species, detect population partitions important for defining management units, and reveal historical demographics that inform restoration priorities. For UP rivers, these capabilities could help differentiate locally adapted stocks from translocated hatchery-derived fish and detect populations suffering diversity loss.

However, relying solely on mtDNA is insufficient for some decisions: mito-nuclear discordance, male-mediated gene flow, and hatchery introgression require nuclear data to confirm patterns. Thus, while mtDNA barcoding and control-region surveys are recommended as first-line actions for UP, follow-up analyses using microsatellites or SNP panels should be planned for any management action affecting broodstock movement or stock enhancement.

Practical constraints in Uttar Pradesh include limited published genetic sampling focused on UP tributaries, variable sample reporting, and a need for capacity-building (molecular labs, voucher specimen curation). A coordinated program linking local fisheries departments, academic institutions in UP, and national sequence repositories would maximize the utility of mtDNA data for sustainable fisheries.

Mitochondrial DNA markers provide an efficient and informative toolkit for assessing genetic variation in economically important freshwater fishes. Available Indian studies up to 2024 show meaningful mtDNA diversity in many taxa, and marker choice (COI, *cyt b*, D-loop, ATPase) should be matched to the study aim (species ID vs. fine-scale structure).

For Uttar Pradesh specifically, the published record through 2024 shows limited, scattered mtDNA sampling; targeted, basin-wide mtDNA surveys (COI + control region / ATPase) across key species are a high priority to inform hatchery broodstock selection, stock enhancement, and conservation of wild genetic resources. Integration with nuclear markers will strengthen management recommendations.

Implementing a UP-focused genetic monitoring program (standardized sampling, public sequence deposition, and combined mito-nuclear analyses) will help secure long-term sustainability of UP’s freshwater fisheries and the livelihoods that depend on them.

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