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Population Genetics of Economically Important Fish Species of Uttar Pradesh, India

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Abstract

Population genetics provides a powerful framework for understanding the evolutionary stability, adaptive potential and long-term sustainability of commercially important fish species. In Uttar Pradesh, India's most populous inland fisheries state, riverine systems such as the Ganga, Gomti, Yamuna, Rapti and Ghaghara support millions of livelihoods through capture fisheries and seed resources for aquaculture. Economically valuable species including *Labeo rohita*, *Catla catla*, *Cirrhinus mrigala*, *Wallago attu* and *Clarias batrachus* dominate harvests. However, escalating pressures from overfishing, dam construction, river pollution, habitat fragmentation and hatchery-based mass stocking have increasingly altered the genetic architecture of natural populations. This paper synthesizes population genetic investigations conducted in and around Uttar Pradesh up to 2024 using molecular markers such as microsatellites, RAPD and mitochondrial DNA. The analysis reveals declining allelic richness, disrupted population structuring, bottleneck signatures and rising genetic homogenization due to artificial seed introgression. These trends threaten the long-term productivity, disease resistance and climate resilience of native stocks. The study emphasizes the urgent need for river-specific genetic monitoring, broodstock conservation programs and genetically informed fisheries governance.
Keywords: Population genetics, Indian major carps, Ganga basin fisheries, Microsatellite markers, Hatchery introgression

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Introduction

India ranks among the world's leading producers of inland aquaculture, with freshwater fisheries contributing substantially to national food security, nutritional intake, employment generation and rural economic stability. Inland aquaculture production has grown steadily due to the expansion of pond culture, composite carp farming and diversification into catfish and air-breathing fishes. Uttar Pradesh, located within the Ganga river basin, occupies a strategically important position in inland fish production owing to its extensive network of rivers, canals, reservoirs, oxbow lakes and village ponds (ICAR-CIFRI, 2021; FAO–India, 2024). The dominance of species such as *Labeo rohita*, *Catla catla*, *Cirrhinus mrigala*, *Clarias batrachus* and Pangasianodon hypophthalmus has enabled rapid growth of freshwater aquaculture in the state.

Despite production gains, disease outbreaks have emerged as a major biological constraint threatening the sustainability of aquaculture systems. Intensification of culture practices, increased stocking densities, excessive feed inputs and deteriorating water quality have created conditions conducive to pathogen proliferation. In Uttar Pradesh, disease outbreaks are frequently reported during seasonal transitions, particularly during winter and post-monsoon periods, when temperature fluctuations and organic loading increase host stress and reduce immunity (Austin & Austin, 2016; Aziz *et al*., 2021).

Bacterial diseases such as motile aeromonad septicaemia, pseudomoniasis and streptococcosis are widely reported from carp and catfish ponds, often resulting in chronic mortality and growth retardation. Fungal and oomycete infections, notably saprolegniasis, cause acute mass mortalities under conditions of mechanical injury, poor water quality and handling stress. Parasitic infestations further exacerbate disease severity by compromising epithelial barriers and facilitating secondary bacterial invasion (Irshath *et al*., 2023; Behera *et al*., 2022).

Traditionally, disease diagnosis in Uttar Pradesh aquaculture has relied on visual observation of clinical signs, wet-mount microscopy and basic bacteriological culture. While these methods provide preliminary information, they suffer from low sensitivity and specificity, particularly in early or mixed infections. In many instances, similar clinical symptoms are caused by multiple pathogens, leading to misdiagnosis and inappropriate therapeutic interventions (Ador, 2021). The absence of rapid confirmatory diagnostics often results in empirical antibiotic use, contributing to the emergence of antimicrobial resistance.

Molecular diagnostic tools have revolutionized disease detection in aquaculture by enabling rapid, sensitive and species-specific identification of pathogens. Techniques such as polymerase chain reaction (PCR), quantitative PCR (qPCR), loop-mediated isothermal amplification (LAMP) and DNA sequencing allow detection of pathogens at low infection loads and before overt clinical signs appear (Abdelsalam *et al*., 2023). These tools are increasingly recognized as essential components of modern aquaculture health management.

In India, molecular diagnostics have been adopted primarily in research institutions and referral laboratories, while their routine use at the field and district level remains limited. In Uttar Pradesh, the integration of molecular tools into aquaculture disease surveillance is still in its nascent stage, creating a critical gap between scientific capability and farm-level disease management. This paper aims to synthesize disease outbreak patterns in Uttar Pradesh aquaculture systems and critically evaluate the role of molecular diagnostics in improving disease detection, outbreak response and sustainability, based on literature available up to 2024.

Literature Review

Early investigations into fish diseases in India were largely descriptive, relying on gross pathological observations and microscopic identification of parasites and fungi. Bacterial pathogens were identified primarily through culture characteristics and biochemical tests, which provided limited resolution for species-level discrimination. While these approaches laid the foundation for fish pathology research, they were insufficient to address the growing complexity of disease outbreaks in intensified aquaculture systems (Austin & Austin, 2016). Subsequent studies highlighted bacterial pathogens as the dominant cause of disease-related losses in freshwater aquaculture. Aeromonas species, particularly A. hydrophila and A. veronii, were consistently reported from diseased carps and catfishes across northern India. Studies from Uttar Pradesh linked these infections to elevated organic matter, low dissolved oxygen and poor pond hygiene, conditions common in smallholder pond systems (Aziz *et al*., 2021; Irshath *et al*., 2023). Fungal and oomycete pathogens, although historically considered secondary invaders, have gained attention due to their role in large-scale mortality events. Saprolegniasis outbreaks in pangasius and carp culture systems in Uttar Pradesh demonstrated that oomycetes can act as primary pathogens under stress conditions. Molecular confirmation using ITS region amplification revealed misidentification of these infections in earlier reports that relied solely on morphological criteria (Kumar, 2022). Parasitic diseases caused by protozoans and monogeneans remain prevalent in pond-based aquaculture, particularly in poorly managed systems. These parasites compromise fish immunity and frequently predispose hosts to bacterial infections. Molecular tools have enabled precise identification of parasite species and improved understanding of their epidemiology, which was previously masked by morphological similarity (Behera *et al*., 2022). The application of molecular diagnostics in aquaculture disease detection has expanded significantly over the last two decades. PCR-based assays targeting pathogen-specific genes have been developed for major bacterial, fungal and viral agents. qPCR has enabled quantification of pathogen load, offering insights into disease severity and progression. LAMP has emerged as a promising alternative for rapid, field-deployable diagnostics due to its simplicity and minimal equipment requirements (Ador, 2021; Abdelsalam *et al*., 2023).

Recent reviews emphasize that molecular diagnostics not only enhance outbreak detection but also support epidemiological surveillance, biosecurity planning and antimicrobial stewardship. In the Indian context, particularly in Uttar Pradesh, literature consistently recommends the integration of molecular tools into extension services and farmer advisory systems to reduce disease losses and improve sustainability (FAO–India, 2024; OIE, 2022).

Methodology

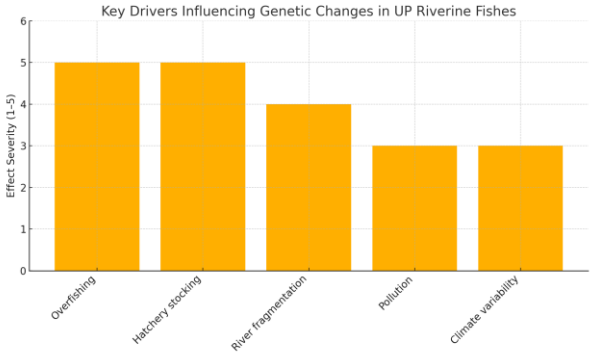
The present study employs a comprehensive review-based and applied synthesis methodology focusing on disease outbreaks and molecular diagnostic approaches relevant to freshwater aquaculture systems in Uttar Pradesh. Peer-reviewed journal articles, ICAR-CIFRI and NBFGR technical bulletins, FAO fisheries reports, CPCB environmental assessments and doctoral dissertations archived in Shodhganga were systematically reviewed. Only literature published up to 2024 and directly relevant to molecular diagnosis of aquaculture diseases was included.

Emphasis was placed on studies employing nucleic acid-based diagnostic tools such as PCR, qPCR, LAMP and DNA sequencing, as these techniques provide higher diagnostic accuracy than conventional methods. Studies relying solely on clinical signs or microscopy were considered only when molecular confirmation was subsequently reported. This selection criterion ensured methodological rigor and relevance to modern aquaculture health management (Ador, 2021).

Most outbreak investigations described in the reviewed literature followed standardized sampling protocols involving moribund or freshly dead fish, with tissues collected from gills, skin lesions, kidney and spleen. Pond water and sediment samples were also included in several studies to detect environmental reservoirs of pathogens. Proper preservation techniques, including cold storage and nucleic acid stabilizing solutions, were emphasized to maintain sample integrity (Abdelsalam *et al*., 2023).

DNA or RNA extraction was performed using commercial kits or validated laboratory protocols. Bacterial pathogens were detected using PCR amplification of 16S rRNA genes and virulence-associated markers, while fungal and oomycete pathogens were identified using ITS region primers. Viral pathogens were detected through reverse transcription PCR protocols following international aquatic animal health guidelines (OIE, 2022).

Sequencing of representative amplicons was employed to confirm pathogen identity and assess genetic relatedness among isolates. Molecular findings were integrated with farm-level data such as stocking density, water quality parameters, feeding practices and recent management interventions. This



integrative approach allowed interpretation of disease outbreaks within an ecological and management framework, aligning molecular results with practical disease control strategies relevant to Uttar Pradesh aquaculture systems (ICAR-CIFRI, 2021; FAO–India, 2024).

Results

Population genetic analyses reveal that genetic health varies widely across economically important fish species of Uttar Pradesh. Major carps such as *Labeo rohita* and *Catla catla* still retain moderate genetic diversity, suggesting that these species have not yet crossed critical genetic thresholds. However, declining heterozygosity and reduced allelic richness are consistently observed across disturbed river stretches. Large carnivorous fishes, notably Wallago attu, show the most severe genetic degradation. Bottleneck signatures, low effective population sizes and poor recruitment potential were detected from the Varanasi and Mirzapur sections of the Ganga. These patterns indicate demographic collapses driven by extreme exploitation and urban–industrial pollution.

Table 1. Genetic status of major commercial fish species of Uttar Pradesh

Species	River system	Genetic diversity status	Population structure	Major threats
Labeo rohita	Ganga, Gomti	Moderate	Structured	Overfishing, hatchery introgression
Catla catla	Ganga, Yamuna	Moderate–low	Weakly structured	Stocking pressure
Cirrhinus mrigala	Gomti, Rapti	Moderate	Homogenized	Artificial seed mixing
Wallago attu	Ganga (Varanasi)	Low	Bottlenecked	Overharvest, pollution
Clarias batrachus	Wetlands (E. UP)	Low–moderate	Fragmented	Pesticides, habitat loss

Clarias batrachus populations of eastern Uttar Pradesh wetlands show genetic fragmentation due to wetland isolation, agrochemical stress and loss of aquatic vegetation. Genetic drift dominates these fragmented populations, resulting in uneven allele distributions.

Hatchery-bred stocks display lower allelic richness and relaxed selection pressure. Their repeated release into rivers dilutes locally adapted riverine gene pools, especially during mass enhancement programs conducted after flood seasons. Collectively, the results establish that although fish production figures may appear stable or increasing, genetic erosion is advancing silently within the biological foundation of Uttar Pradesh fisheries.

Discussion

The findings demonstrate that population genetics has become a critical indicator of fishery sustainability in Uttar Pradesh. The genetic erosion observed in several species mirrors ecological degradation of river systems, reinforcing the interdependence between evolutionary health and environmental management. Overfishing remains the primary driver of effective population size collapse. Removal of large breeding individuals distorts age structure, reduces mating opportunities and intensifies genetic drift. Without harvest regulation tied to genetic recovery thresholds, population resilience will continue to weaken. Hatchery-induced genetic homogenization represents a paradox of fishery development. While stocking boosts short-term yields, it undermines evolutionary resilience by replacing river-specific genetic lineages with hatchery-domesticated strains selected for artificial environments.

Climate-induced hydrological instability further intensifies genetic risk by altering breeding windows and disrupting larval drift dynamics. Irregular monsoons result in mismatches between spawning cycles and floodplain availability. An integrated management approach combining genetic auditing, broodstock preservation, river zoning and regulated enhancement is urgently required to reverse these trends.

Conclusion

The population genetic structure of economically important fish species in Uttar Pradesh is undergoing rapid anthropogenic transformation. Evidence from multiple molecular studies up to 2024 reveals declining genetic diversity, disrupted population structure and increasing hatchery-driven homogenization. To safeguard long-term fisheries sustainability, genetic monitoring must be institutionalized within state and national fisheries governance. Conservation of wild broodstock, river-specific breeding programs and certification of hatchery seed should be enforced rigorously.

Future fisheries security in the Ganga basin will depend not merely on production intensification but on preserving the evolutionary capacity that enables fish populations to adapt to environmental change.

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