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eDNA Metabarcoding and Population Genomics of Commercially Important Marine Fish for Biodiversity Assessment and Sustainable Fisheries Management Along the Pakistan Coast

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ABSTRACT

The northern Arabian Sea along Pakistan's 1,001 km coastline represents a biologically productive yet increasingly threatened marine ecosystem, supporting over 500 cataloged fish species of substantial commercial and ecological importance. Escalating anthropogenic pressures, including overfishing, illegal, unreported, and unregulated (IUU) fishing, habitat degradation, and the intensifying Arabian Sea Oxygen Minimum Zone (OMZ), have severely altered fish community structures and precipitated declines in key commercial stocks. Traditional monitoring approaches, reliant on catch landings, net trawling, and morphological taxonomy, are constrained by phenotypic plasticity, cryptic speciation, specimen damage, and an inability to identify early life stages or processed products. This review synthesizes the transformative potential of two complementary molecular technologies environmental DNA (eDNA) metabarcoding and population genomics for biodiversity assessment and sustainable fisheries management along the Pakistan coast. eDNA metabarcoding enables non-invasive, high-throughput, multi-taxa community profiling through mitochondrial markers (COI, Cyt b, 12S/16S rRNA), facilitating detection of elusive, endangered, and cryptic species, including remnant sawfish populations and coral-associated assemblages in Astola Island MPA. Population genomics, leveraging SNPs and mitochondrial sequencing, resolves stock boundaries, genetic diversity, and demographic histories, revealing distinct Evolutionary Significant Units in silver pomfret (*Pampus argenteus*) and genetic connectivity patterns in Spanish mackerel (*Scomberomorus commerson*). Integrated applications extend to seafood traceability via DNA-based QR codes, IUU fishing detection, and Blue Economy policy alignment with SDG 14. Key challenges include eDNA degradation under high temperatures, PCR bias, incomplete regional reference databases, and infrastructural capacity gaps. Strategic multi-institutional partnerships and sustained investment are essential for operational implementation, offering a paradigm shift toward resilient, evidence-based fisheries governance in Pakistan.

Introduction

The northern Arabian Sea represents one of the most oceanographically dynamic and biologically productive marine ecosystems on the planet (Qasim,1982). Spanning an Exclusive Economic Zone (EEZ) along a coastline of approximately 1,001 kilometers, Pakistan's marine environment comprises two distinct coastal provinces: the Sindh coast, dominated by the expansive Indus

River Delta and complex mangrove creek systems, and the Balochistan (Makran) coast, characterized by deep-water bays, rocky headlands, narrow continental shelves, and proximity to high-energy upwelling zones (Pakistan, 2016). This hydrographic heterogeneity supports over 500 cataloged fish species, including roughly 298 marine teleost and elasmobranch taxa, with at least 250 demersal and 50 small pelagic species holding direct commercial significance. These resources form the backbone of local coastal economies, contributing significantly to domestic food security and international trade revenues (Steven et al., 2023).

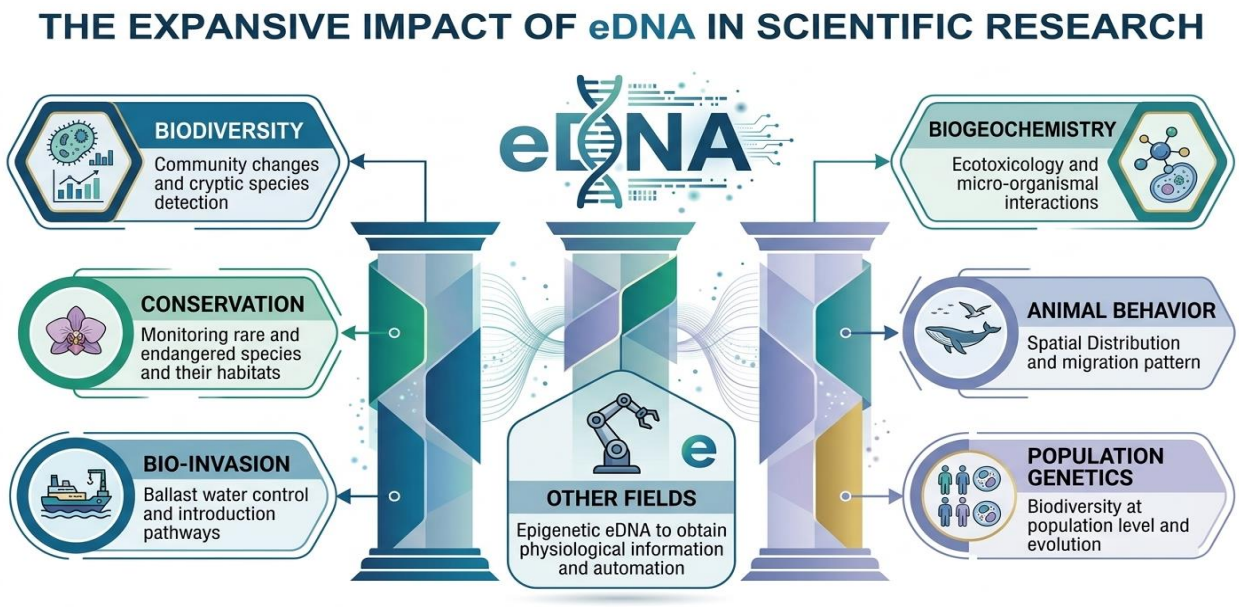
Despite its ecological and socio-economic importance, the marine fish biodiversity along the Pakistan coast faces escalating anthropogenic and climatic pressures (Mehak et al., 2023). Unregulated overfishing, destructive harvesting practices, habitat degradation, coastal industrial pollution, and intense illegal, unreported, and unregulated (IUU) fishing have severely altered fish community structures and precipitated stock declines across major commercial fisheries (Widjaja et al., 2023). Historical monitoring reveals that key apex and demersal taxa such as sawfishes (family Pristidae) have experienced localized extirpations, while major commercial stocks including silver pomfret (*Pampus argenteus*), narrow-barred Spanish mackerel (*Scomberomorus commerson*), croakers (family Sciaenidae), and ponyfishes (family Leiognathidae) demonstrate signs of recruitment impairment and reduced catch-per-unit-effort (Dulvy et al., 2016). Compounding these stress factors is the intensification of the Arabian Sea Oxygen Minimum Zone (OMZ), a profound subsurface hypoxic body that extends across mid-water depths and compresses pelagic and demersal habitats toward the surface and immediate coastal fringes (Singh et al., 2023).

Traditional methods of assessing ichthyofaunal diversity and monitoring stock health rely heavily on catch landings, net trawling, visual censuses, and classical morphological taxonomy. While foundational, these approaches suffer from substantial limitations (Fisher, 2014). Morphological identification of marine fishes is frequently impeded by high phenotypic plasticity, cryptic speciation, damage to specimens during capture, and an inability to accurately identify early life stages (eggs and larvae) or processed commercial products. Furthermore, net trawling is inherently invasive, spatially restricted, labor-intensive, and inadequate for sampling fragile, low-abundance, or highly mobile species (Santana-Garcon et al., 2018).

To address these critical monitoring gaps, molecular ecology has introduced two complementary paradigm-shifting technologies: Environmental DNA (eDNA) metabarcoding and population genomics (Wan et al., 2026). eDNA metabarcoding extracts cellular and extracellular genetic material directly from water samples, enabling non-invasive, high-throughput identification of whole biological communities without capturing or disturbing organisms. Concurrently, population genomics leverages high-density single nucleotide polymorphisms (SNPs) and targeted mitochondrial sequencing to resolve fine-scale genetic differentiation, define stock boundaries, quantify genetic diversity, and evaluate demographic histories (Mandal & Das, 2025).

Synthesizing molecular progress within Pakistan's marine waters reveals how integrating eDNA metabarcoding and population genomics can transform regional biodiversity assessment, establish resilient fisheries management frameworks, enforce supply chain traceability, and advance sustainable Blue Economy objectives along the Pakistan coast (Ali & Hussain, 2026).

Figure 1. Multi-Disciplinary Conceptual Framework Illustrating the Expansive Impact of Environmental DNA (eDNA) Across Scientific Research and Ecological Monitoring.



Oceanographic Dynamics and Marine Biodiversity Along the Pakistan Coast

The structure and distribution of ichthyofaunal communities along the Pakistan coast are directly governed by the physical oceanography of the northern Arabian Sea. The coastal marine domain is geographically divided into two major ecoregions: the Sindh coast to the east and the Balochistan (Makran) coast to the west, each exhibiting contrasting geomorphological and oceanographic regime (Manilo & Bogorodsky, 2003).

The Sindh coast is heavily influenced by the discharge of the Indus River, which forms the Indus Fan a massive sub-marine sediment accumulation extending over 1,500 kilometers into the Indian Ocean, originating at the shelf break of the Indus Canyon (Raza et al., 2023). The nutrient-rich alluvial runoff, coupled with vast mangrove ecosystems (primarily *Avicennia marina*), creates vital estuarine and nursery habitats for juvenile sciaenids, clupeids, penaeid shrimps, and flatfishes (*Pseudorhombus arsius*, *Psettodes erumei*, and *Cynoglossus cynoglossus*). However, high coastal runoff from urban centers like Karachi introduces urban and industrial pollutants that stress local fish populations and degrade estuarine water quality (Beilfuss et al., 2000).

In contrast, the Balochistan coast features a narrow continental shelf dropping precipitously into deep oceanic waters, interspersed with high-biodiversity bays such as Sonmiani Bay and Ormara, and offshore oceanic islands like Astola Island (Pakistan, 2016). Sonmiani Bay comprises a 60-kilometer-long lagoon system connected to the Arabian Sea via a narrow 4-kilometer mouth, functioning as a critical transition zone between estuarine and open-ocean ecosystems. Seasonal monsoon dynamics dictate primary biological productivity across these areas (McClanahan, 1988). During the Southwest (SW) summer monsoon (June to September), strong wind-driven upwelling brings cold, nutrient-dense waters from the deep slope to the surface, sparking phytoplankton blooms that fuel dense assemblages of small pelagics and predatory teleosts. Conversely, during the Northeast (NE) winter monsoon (November to February), water stratification and elevated salinity levels induce seasonal shifts in species richness, equitability, and abundance (Koochaknejad et al., 2025).

Overlaying these physical parameters is the Arabian Sea Oxygen Minimum Zone (OMZ), one of the thickest and most severe subsurface oxygen-depleted layers globally (Lackher et al., 2023). Driven by high surface biological productivity and restricted ocean ventilation, the OMZ encroaches upon the continental shelf, compressing the vertical habitat of oxygen-sensitive species such as scombrids, carangids, and stromateids into thin surface layers. This spatial compression amplifies species vulnerability to commercial surface gear, accelerating local overexploitation (Waller et al., 2024).

Table 1: Regional Oceanographic Profiles and Ichthyofaunal Diversity Dynamics Along the Coast of Pakistan

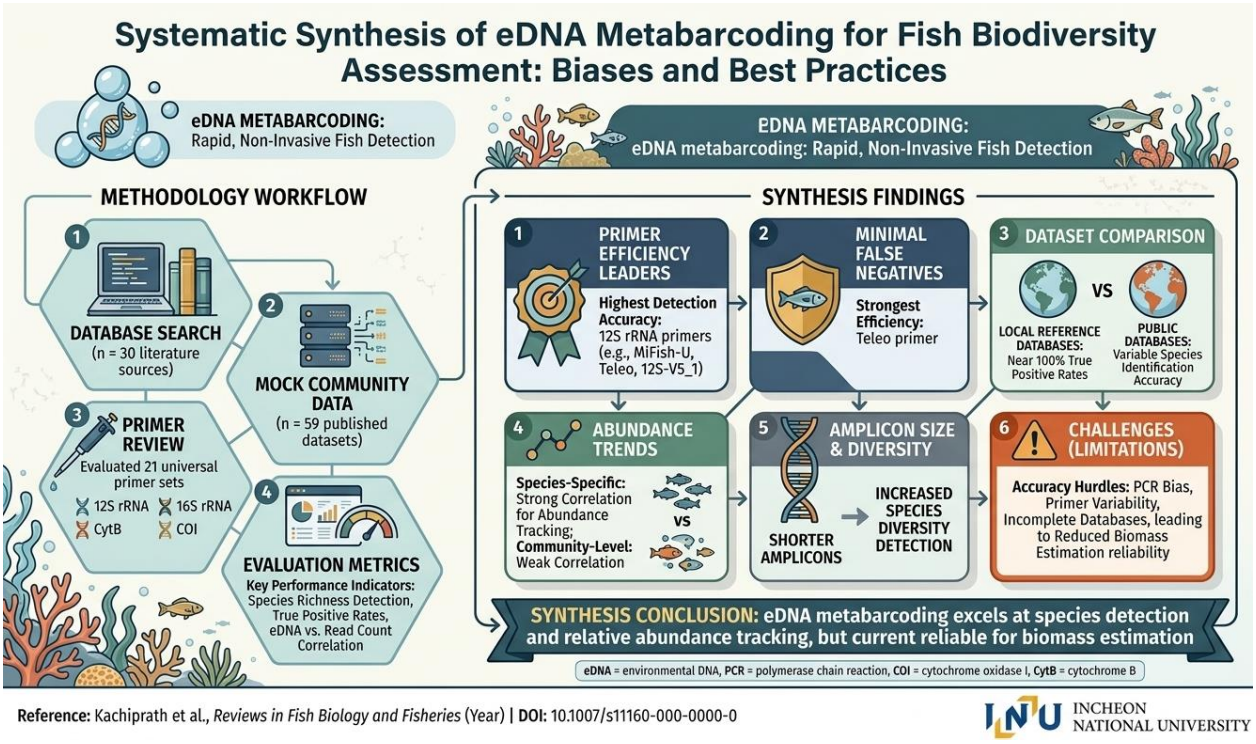
Coastal Region	Physical & Oceanographic Features	Dominant Marine Habitats	Key Commercial & Vulnerable Fish Taxa	Environmental Stressors & Drivers
Sindh Coast (Indus Delta to Karachi)	Broad continental shelf; Indus Canyon sediment fan extending >1,500 km; heavy riverine runoff	Estuarine mangrove creeks, shallow muddy bottoms, intertidal flats	Sciaenidae (croakers), Clupeidae, Flatfishes (*Psettodes*, *Cynoglossus*), Ariidae	Industrial pollution, estuarine degradation, juvenile overharvesting, siltation
Eastern Balochistan (Sonmiani Bay to Ormara)	Intermediate shelf; 60 km enclosed lagoon system at Sonmiani; seasonal monsoonal influx	Sandy-muddy bays, sheltered lagoons, open coastal waters	Leiognathidae (*Leiognathus*, *Secutor*, *Karalla*), Stromateidae (*Pampus argenteus*)	Salinity spikes during NE monsoon, habitat alterations, localized trawl pressure
Western Balochistan (Pasni, Gwadar to Jiwani)	Extremely narrow shelf; proximity to deep ocean trenches; intense seasonal upwelling	Rocky headlands, sandy beaches, coral patch reefs (Astola Island MPA)	Scombridae (*S. commerson*), Sphyraenidae, Epinephelidae, Carangidae	Hypoxic expansion via OMZ, climate-induced sea surface warming, IUU fishing

Environmental DNA (eDNA) Metabarcoding: Principles, Markers, and Applications

Environmental DNA (eDNA) metabarcoding represents a transformative biological monitoring tool for marine ecosystems. The technique operates on the premise that macro-organisms shed genetic material into their surrounding aqueous environment via skin cells, mucus, epidermal shedding, gametes, metabolic waste, and decaying tissue (Stat et al., 2017). By collecting water samples, filtering cellular debris, extracting total environmental DNA, and executing target PCR amplification coupled with Next-Generation Sequencing (NGS), researchers can simultaneously identify complex multi-taxa assemblages without capturing a single organism (Lee at al., 2019).

The standard operational workflow for marine eDNA metabarcoding begins with field water collection across targeted coastal or offshore stations, followed by immediate on-site or laboratory filtration through specialized micro-porous membranes such as Sterivex units (Jerney et al., 2023). Extracted genomic material undergoes high-fidelity PCR amplification using locus-specific barcode primers. High-throughput sequencing platforms, including Illumina and Oxford Nanopore MinION systems, generate millions of sequences reads that are bioinformatically filtered, clustered into Amplicon Sequence Variants (ASVs) or Operational Taxonomic Units (OTUs), and queried against global reference databases to yield taxonomic identity assignments (Iyer et al., 2019).

Figure 2. Systematic Framework of the eDNA Metabarcoding Workflow, Performance Findings, and Methodological Challenges for Marine Fish Biodiversity Assessment.



Marker Selection and Taxonomic Resolution

The success of eDNA metabarcoding in marine fish assessment depends on selecting mitochondrial markers that balance hyper-variable regions for species-level differentiation with conserved primer binding sites for broad taxonomic amplification (Maracle, 2025). The mitochondrial Cytochrome c Oxidase Subunit I (COI) gene serves as the classical standard for DNA barcoding and metabarcoding in metazoans, yielding standard target fragments between 652 and 655 base pairs. COI demonstrates robust discriminatory power across marine teleosts, showing substantial barcode gaps with mean pairwise Kimura 2-parameter (K2P) distances of 6.34% within species, 17.12% within genera, and 26.8% to 36.9% within families along the Pakistani coast (Abidin et al., 2024).

Table 2: Molecular Marker Performance and Nucleotide Dynamics in Marine Fish Genomics Along the Pakistan Coast

Marker Locus	Target Fragment Size (bp)	Average Nucleotide Composition (% AT / % GC)	Primary Taxonomic & Evolutionary Utility	Pairwise K2P Divergence Range / Resolution
Mitochondrial COI	~652 – 655 bp	52.8% AT / 47.2% GC (57.6% GC at 1st codon position)	Standard metabarcoding & species identification; resolves cryptic taxa	High species-level gap; 6.34% intra-species, 17.12% intra-genus
Mitochondrial Cyt b	~1,141 bp	53.73% AT / 46.26% GC (marine teleosts)	Phylogenetic reconstruction, species authentication, SNP QR code generation	Inter-family distance 0.369; inter-order distance 0.337
12S rRNA / 16S rRNA	~100 – 300 bp (eDNA mini-barcodes)	Variable across structural stem-loop domains	High-throughput eDNA metabarcoding from degraded environmental samples	Broad multi-species detection; lower resolution for closely related congeners

In addition to COI, the mitochondrial Cytochrome b (Cyt b) gene (~1,141 bp) provides deep phylogenetic clarity and high species-level diagnostic capability. In marine fishes from the region, Cyt b displays an overall nucleotide composition skewed toward AT richness (~53.73% AT vs. 46.26% GC) (Bakar, 2018). At the codon level, the first position exhibits elevated GC content (up to 57.60%), whereas the third position displays extreme evolutionary degeneracy and sequence variability, making it an ideal candidate locus for identifying fine-scale Single Nucleotide Polymorphisms (SNPs). Short sub-regions of 12S rRNA and 16S rRNA are increasingly utilized for environmental mini-barcodes because shorter loci withstand environmental degradation in warm coastal waters (Kyriacou et al., 2024).

Non-Invasive Biodiversity Detection and Cryptic Taxa Resolution

eDNA metabarcoding significantly enhances traditional biodiversity survey protocols along the Pakistan coast by detecting elusive, rare, endangered, and ecologically sensitive species that evade standard sampling nets (Çevik & Çevik, 2025). Surveys employing eDNA monitoring in the Arabian Sea have uncovered previously overlooked genetic diversity across complex groups including sciaenids, clupeiforms, flatfishes, and grunts (Sawh et al., 2025).

Furthermore, eDNA offers a crucial monitoring mechanism for detecting the remnant presence or extirpation of critically endangered taxa. For instance, despite the historic presence of four sawfish species (*Pristis* spp.) along the Makran and Sindh coasts, directed capture surveys have recorded zero specimens in recent decades, leading to assumptions of local extinction (Beng & Corlett, 2020). eDNA sampling across historical habitats such as the Indus Delta and Miani Hor lagoon provides a high-sensitivity, non-invasive method to search for micro-refugia of these imperiled elasmobranchs (Suhail et al., 2025). Similarly, eDNA metabarcoding facilitates real-time spatial monitoring of fragile marine ecosystems like the Astola Island Marine Protected Area (MPA), mapping spatial variations in coral-associated fish assemblages without physical habitat disruption (Yang et al., 2024).

Population Genomics and Phylogeography of Commercial Marine Fishes

While eDNA metabarcoding provides qualitative and semi-quantitative multi-species community profiles, population genomics evaluates intra-specific genetic health, stock structure, gene flow, and evolutionary adaptability (Yuan et al., 2026). For commercially exploited marine teleosts along the Pakistan coast, defining whether landing sites exploit a single panmictic population or multiple genetically isolated stocks is essential for sustainable harvest limits (Osmany & Moazzam, 2022).

The standard population genomic methodology relies on acquiring tissue specimens from representative landing centers (such as Karachi, Pasni, and Gwadar), extracting genomic DNA, and subjecting samples to restriction site-associated DNA sequencing (RAD-seq) or target mitochondrial amplicon sequencing (Sarwar & Sarwar, 2026). Bioinformatic pipelines calculate population differentiation indices (F_{ST}), nucleotide diversity (π), and haplotype diversity (h), followed by spatial clustering using Principal Component Analysis (PCA) and Bayesian structure models. These parameters establish the boundaries of Evolutionary Significant Units (ESUs) and inform adaptive management strategies (Morin et al., 2021).

Stock Differentiation and Population Dynamics of Key Commercial Species

Population genomic analyses utilizing mitochondrial markers and nuclear SNP panels have revealed pronounced phylogeographical patterns and genetic structuring among key commercial fishes across the Arabian Sea, Persian Gulf, and wider Indo-Pacific regions (Yin et al., 2026).

Silver Pomfret (Pampus argenteus)

Silver pomfret (*Pampus argenteus*) represents one of the most economically valuable marine teleosts in the northern Arabian Sea, yet it experiences severe overexploitation. Population differentiation (F_{ST}) analyses demonstrate significant genetic structure separating *P. argenteus* populations along the Pakistani coastline from those in the Persian Gulf, East China Sea, and Australasia (Mohitha, 2016). Principal Component Analysis (PCA) and pairwise F_{ST} heatmaps place Pakistani *P. argenteus* stocks into a unique genetic cluster exhibiting marked divergence (F_{ST} values up to 0.33 when compared against Australian/USA cohorts), while showing closer genetic affinity to contiguous Indian stocks ($F_{ST} \approx 0.05 - 0.08$) (Sial et al., 2024). This pronounced regional differentiation indicates that Pakistani pomfret populations constitute a distinct Evolutionary Significant Unit (ESU) requiring localized conservation and dedicated stock management rather than regional broad-scale management (Sun et al., 2013).

Narrow-Barred Spanish Mackerel (*Scomberomorus commerson*)

As a highly migratory pelagic predator, *S. commerson* is widely targeted along the Makran coast. Molecular barcoding and Cyt b SNP profiling show high haplotype diversity coupled with low nucleotide diversity, a pattern characteristic of historical population expansion following marine glacial bottlenecks (Dimech et al., 2026). Despite its migratory capacity, physical

barriers imposed by seasonal upwelling cells and the subsurface OMZ create variable spatial-temporal genetic connectivity between populations in the Gulf of Oman and the central Arabian Sea (Figueroa, 2024).

Ponyfishes (Family Leiognathidae)

Ponyfishes comprise a major component of demersal trawl catches in Sonmiani Bay and along the Sindh coast. Systematic surveys resolved ten species across three genera (*Leiognathus*, *Nuchequula*, *Secutor*, and *Karalla*), with *Secutor interruptus* dominating monsoon catches and *Karalla daura* occurring in lower densities (Kashani et al., 2026). Genetic diversity and equitability metrics within leiognathid populations follow monsoonal shifts, peaking during the post-monsoon season (0.74 ± 0.69) and plunging during the high-salinity NE monsoon. High environmental fluctuation drives strong seasonal demographic expansions, underscoring the necessity of dynamic seasonal fishing bans aligned with genomic recruitment pulses (Verba et al., 2026).

Barcode Gap Analysis and Cryptic Diversity

Barcode Gap Analysis (BGA) across Pakistani marine ichthyofauna confirms that mitochondrial COI and Cyt b loci provide a robust "barcode gap" where interspecific genetic divergence significantly exceeds intraspecific variation (Amir et al., 2022). In extensive evaluations of coastal specimens, intraspecific distances remain consistently low (typically $< 1.0\%$), whereas mean interspecific distances within genera average 17.12%, and inter-family distances reach 26.8% to 36.9%. This diagnostic gap allows unambiguous species assignment for over 95% of sampled marine teleosts (Rock et al., 2008). Crucially, BGA has unveiled several cryptic species complexes within commercially targeted groups such as grouper (*Epinephelus stoliczkae*), flathead (*Cociella punctata*), and grunt (*Pomadasys aheneus*) that were historically managed as single panmictic species. Failing to recognize cryptic diversity risks the silent extirpation of genetically distinct, low-abundance subpopulations masked under broader taxonomic groupings (Papaiakovou, 2025).

Applications in Fisheries Management, Traceability, and Blue Economy Policy

The synthesis of eDNA metabarcoding and population genomics offers direct, actionable solutions to long-standing challenges in Pakistan's marine fisheries sectors (Ali & Hussain, 2026). Broad implementation follows an integrated policy pipeline connecting laboratory discovery to real-time enforcement:

First, molecular diagnostic signatures derived from target loci are deployed for supply chain authentication. Second, non-invasive eDNA assays are integrated into routine coastal vessel patrols to verify habitat protection compliance. Third, population genomic metrics are incorporated into state policy frameworks to fulfill national obligations under international maritime and environmental agreements (Öz & Üstüner, 2026).

Seafood Traceability and Market Fraud Mitigation

Seafood mislabeling, species substitution, and fraudulent trade are widespread in commercial fisheries (Jacquet & Pauly, 2008). In local landing sites and retail export markets, lower-value demersal fillets are frequently mislabeled as high-value species like silver pomfret (*P. argenteus*) or Spanish mackerel (*S. commerson*). Because morphological diagnostic characters are lost during filleting, freezing, or cooking, conventional inspection methods are ineffective (González-Soñora et al., 2026).

To resolve this issue, molecular workflows leveraging targeted SNP diagnostic loci within the Cyt b and COI genes have been translated into scannable Quick Response (QR) codes (Dennis et al., 2026). By converting unique single-nucleotide diagnostic signatures into standardized 2D QR codes, seafood inspection authorities can verify species identity in real time across the supply chain using handheld smartphone scanners. This low-cost, molecular-to-digital framework prevents fraudulent substitutions, safeguards export revenues, and ensures compliance with international market standards (Sophian, 2026).

Combating IUU Fishing and Enhancing MPA Governance

Illegal, Unreported, and Unregulated (IUU) fishing undermines stock sustainability along the Pakistan coast, particularly along porous maritime borders and within Marine Protected Areas (MPAs). eDNA metabarcoding serves as an efficient forensic tool to detect illegal fishing activities (Lina & Murad Zaib Butt, 2025). By analyzing water samples collected along protected boundary zones such as Astola Island MPA authorities can detect the recent spatial footprint of commercially targeted teleosts or shark species, identifying illegal extraction zones without relying exclusively on physical maritime patrols (Letessier et al., 2017). Furthermore, integrating eDNA bio-monitoring into MPA management provides objective baseline biodiversity metrics to measure ecological recovery following enforcement actions (O'Brien et al., 2021).

Policy Frameworks and Blue Economy Integration

Pakistan's marine policy is increasingly orienting toward Blue Economy expansion, aiming to maximize sustainable ocean wealth while meeting international commitments under United Nations Sustainable Development Goal 14 (Life Below Water) and International Maritime Organization (IMO) conventions (Jattak at el., 2023). Incorporating eDNA and genomic monitoring directly into national policy addresses several key requirements:

- Modernizing stock assessment protocols by replacing static catch-effort models with genomic estimates of effective population size (N_e), gene flow, and stock boundaries
- Mitigating environmental compression by utilizing eDNA spatial mapping to track climate-driven OMZ shifts and adjusting Total Allowable Catches (TACs) for pelagic teleosts accordingly.
- Fostering transboundary cooperation by harmonizing regional genetic reference databases across Arabian Sea littoral states to manage shared migratory fish stocks (Maggini, 2025).

Challenges, Knowledge Gaps, and Future Horizons

While the integration of eDNA metabarcoding and population genomics presents immense promise, several technical, environmental, and institutional challenges must be resolved to achieve operational implementation along the Pakistan coast (Patin & Goodwin, 2023).

Technical and Environmental Dynamics of eDNA

- **eDNA Decay and Transport**: High sea surface temperatures ($> 30°C$ during summer) and intense solar UV radiation in the Arabian Sea accelerate enzymatic eDNA degradation, rapidly reducing molecule half-lives in surface waters (Harrison et al., 2019). Concurrently, strong monsoon-driven coastal currents induce significant spatial transport, complicating the precise physical localization of detected biological signals (Phattananuruch & Pokavanich 2024).
- **PCR Bias and Quantification Limitations**: Universal metabarcoding primers (e.g., standard COI or 12S loci) can exhibit differential amplification efficiency across diverse teleost families, leading to PCR bias where specific taxa are over-represented while others remain undetected. Quantitative interpretation of read counts as absolute biomass metrics remains challenging due to variable shedding rates across life stages and specie (Rujiter et al., 2021)

Reference Database Gaps

A primary bottleneck facing eDNA metabarcoding in Pakistani coastal waters is the incompleteness of regional DNA sequence reference libraries (GenBank and BOLD). Although global databases contain thousands of fish sequences, many endemic, demersal, and deep-sea species native to the northern Arabian Sea lack curated, full-length reference barcodes (Sawh et al., 2025). Unrepresented taxa lead to unassigned operational taxonomic units (OTUs) or misclassifications during bioinformatic pipelines. Sustained efforts to physically collect, morphologically identify, and sequence voucher specimens across all 500+ coastal fish species remain imperative (De Santiago et al., 2025).

Infrastructure, Capacity Building, and Resource Allocation

Implementing molecular fisheries management requires robust laboratory infrastructure, high-throughput sequencing access, bioinformatic computing capacity, and specialized personnel (Berry et al., 2026). At present, molecular ecology facilities within marine institutions along the Pakistan coast require modernization and sustained research funding. Bridging these resource gaps necessitates structured multi-institutional partnerships between regional universities, government fisheries departments (e.g., Sindh and Balochistan Wildlife and Fisheries Departments), and international marine scientific organizations (Yogel et al., 2025).

Conclusion

The integration of eDNA metabarcoding and population genomics represents a paradigm shift in biodiversity assessment and sustainable fisheries management along the Pakistan coast. This review demonstrates that traditional morpho-taxonomic and catch-based monitoring approaches are insufficient to address the escalating pressures of overfishing, IUU fishing, habitat degradation, and climate-driven oceanographic changes, including the expanding Arabian Sea Oxygen Minimum Zone. eDNA metabarcoding offers a non-invasive, high-throughput, and cost-effective means to profile entire fish communities, detect rare and endangered taxa such as sawfishes, and monitor protected areas like Astola Island MPA without habitat disruption. Population genomics, through mitochondrial markers and SNP panels, provides critical insights into stock structure, genetic diversity, and demographic history, revealing distinct Evolutionary Significant Units in commercially vital species such as silver

pomfret and Spanish mackerel, thereby informing localized management strategies. The translational applications of these technologies spanning seafood traceability via DNA-based QR codes, forensic detection of illegal fishing, and alignment with Blue Economy objectives and SDG 14 underscore their policy relevance. However, operational implementation faces significant barriers, including rapid eDNA degradation in warm tropical waters, PCR bias, incomplete regional reference databases, and inadequate laboratory infrastructure and human capacity. Addressing these challenges requires coordinated multi-institutional partnerships, sustained research funding, and harmonized regional genetic databases across Arabian Sea littoral states. By bridging molecular discovery with enforcement and policy frameworks, Pakistan can transition toward resilient, evidence-based fisheries governance that safeguards marine biodiversity, secures coastal livelihoods, and advances sustainable ocean wealth for future generations.

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