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# Genomic Innovations: A Tool for Conserving Fisheries Resources

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**SUMMARY**

Conservation genomics is an emerging field that integrates genetic and genomic tools to support the conservation and management of fisheries resources. Genomics provides valuable insights for biodiversity monitoring, species identification, and habitat restoration by analysing genetic diversity, population structure, and adaptive traits. Techniques such as DNA barcoding, environmental DNA (eDNA), whole-genome sequencing, and gene expression analysis help detect endangered species, assess genetic health, and guide sustainable fisheries management. These approaches also play a crucial role in combating overfishing, mitigating climate change impacts, and enhancing aquaculture sustainability. Additionally, genomics aids in understanding evolutionary processes, tracking invasive species, and restoring depleted fish stocks. Integrating genomic data into conservation policies enables more precise decision-making, ultimately ensuring aquatic ecosystems' long-term resilience and sustainability in the face of environmental and anthropogenic pressures.

## INTRODUCTION

Biodiversity is the variety of all life forms, and it is essential to the existence and proper functioning of all ecosystems. Biodiversity supports habitats for all species by providing many unique environments in which species can exist; these include ecosystems of all types and sizes, rare ecosystems, and corridors between habitats. Although genetic diversity has long been recognized as fundamental to all levels of biological organization (individuals, populations, species, communities, and ecosystems), more attention should be paid to biodiversity assessments and conservation efforts. Biodiversity preservation critically depends on addressing key conservation issues. These include taxonomic identification and biodiversity monitoring associated with aquatic ecosystem protection and restoration (e.g., for invasive species management). At the same time, human activities exert significant demographic pressures on habitats and endangered species. This requires managing small populations, restoring and increasing the genetic diversity of target species/populations, and supporting species adaptation to a changing environment. Genomic data can help tackle these issues by allowing us to characterize and monitor genetic diversity through various emerging tools. The novel insights that can be obtained from genomic data have led to several national and international initiatives aiming to expand the genomic resources available for non-model species. At the same time, scientists and practitioners are collaborating to (i) standardize protocols for detecting and monitoring the genetic diversity of the species and their adaptive potential and (ii) integrate genetic and evolutionary knowledge into conservation planning. These actions are critical to promoting transboundary management to ensure the persistence of populations and species and, ultimately, the continued provision of nature-based ecosystem services. Here, we provide an overview of how genomics can help conserve fisheries resources.

### Conservation Genomics

Conservation genomics is an interdisciplinary field that combines genetics, genomics, and conservation biology to study the genetic diversity, population structure, and evolutionary processes of endangered or threatened species. It plays a crucial role in informing conservation strategies and ensuring the long-term survival of vulnerable species. It is the application of genomic analysis to preserve the viability of populations and the biodiversity of living organisms. Genomic methods can be used to argue about species identity, degree of hybridization, genetic diversity, demographic history, and effective population size. As a branch of conservation biology, conservation genomics focuses on studying endangered mechanisms and conservation strategies for endangered species that aim to protect the species' survival ability and reduce the risk of extinction. This field integrates theoretical ideas of genetics and analytical methods of genomics.

### Genomics for fisheries resource conservation

Conservation genomics protects endangered and vulnerable fish species by providing insights into their genetic diversity, population structure, and adaptive potential. By analyzing the genetic makeup of threatened populations, scientists can identify inbreeding risks, genetic bottlenecks, and loss of diversity, critical factors affecting species survival. Genomic tools help track endangered fish's movement and breeding patterns, informing habitat protection and restoration efforts. DNA barcoding and environmental DNA (eDNA) enable the non-invasive detection of rare species, reducing the need for disruptive sampling methods. Additionally, genomics supports captive breeding and restocking programs by ensuring the genetic health of reintroduced populations and preventing the spread of maladaptive traits. Understanding genetic adaptations to environmental changes also aids in developing strategies to enhance species resilience against climate change, habitat destruction, and other anthropogenic threats. By integrating genomic data into conservation policies, fisheries managers can design targeted recovery plans that maximize the chances of survival for endangered and vulnerable fish species.

**Tools used in conservation genomics**

**1. DNA barcoding and metabarcoding**

DNA barcoding has become an efficient genetic approach for species identification and biodiversity monitoring. DNA barcoding sequences the informative DNA loci with universal or taxon-specific primers. Initially, DNA barcoding was based on the mitochondrial cytochrome c oxidase subunit I (COI) gene and mainly focused on animals, particularly invertebrates. Over the years, additional DNA loci have been utilized to barcode vertebrates (e.g., 12S, 16S, and Cytb in mtDNA), plants (rbcL and matK in cpDNA), fungi (ITS in rDNA), protists and nematodes (18S in rDNA), and bacteria (16S in rDNA). DNA metabarcoding combines the principles of DNA barcoding with next-generation sequencing (NGS), enabling the analysis of complex samples containing a mixture of specimens and/or species. Metabarcoding has been widely used in biodiversity assessment and monitoring (e.g., species turnover during ecosystem restoration, mapping of ecological networks, or detection of invasive species). A key advantage of metabarcoding is bulk sampling and sequencing, circumventing costly sorting and processing of samples into individual specimens, thereby enabling high-throughput ecosystem-wide assessments and monitoring in most environments. Moreover, metabarcoding is an appropriate approach to sequence eDNA, often degraded into short fragments in an environmental medium. However, the short length of the DNA regions targeted in barcoding and metabarcoding can often limit accurate characterization of a community's genetic and taxonomic diversity, failing to discern closely related taxa or taxa with introgressed nuclear genes or organellar genomes. Genome skimming circumvents some of the experimental biases in metabarcoding, potentially allowing more accurate metagenomic estimates of biodiversity and wildlife forensic investigations.

**2. Reduced genomic representation**

Reduced representation DNA sequencing (RRS) approaches are predominant in studies aimed at non-model species. RRS approaches provide genome-wide data in large sample sizes at a comparably reduced cost. A small fraction of the genome is reproducibly targeted in each specimen, either using restriction endonucleases and size selection (e.g., RAD seq and related methods) or captured by hybridization using probes (e.g., ultra-conserved elements or custom baits) or a combination of both (e.g., HyRAD, Rapture). Although RRS approaches only capture a small portion of the genome, they provide sufficient genome-wide data to estimate genetic diversity, inbreeding, effective population size, population structure and assignment, gene flow, phylogeographic patterns, and phylogenetic relationships. However, combining RRS-derived data from different studies necessitates identical experimental protocols, which limits replicability. Moreover, RRS approaches utilizing restriction endonucleases (and PCR) may be subject to allelic dropout. Although RRS approaches can be conducted without a reference genome, alignment to a reference genome improves inferences from RRS data. Furthermore, a reference genome provides genome coordinates for most SNPs, thereby facilitating the identification of linked loci, which is key to many population-genetic inferences.

**3. Gene expression**

Gene expression data (usually RNA-Seq) have given rise to a new conservation framework by characterizing genetic variation in natural populations through functional variation and rapid responses of individuals or populations to environmental change. Differences in gene expression have been linked to life history traits and population dynamics, aiding in identifying candidate genes potentially affecting eco-evolutionary processes. Gene expression data have provided insights into pesticide exposure responses and susceptibility or disease resistance. Gene expression data have also been used to predict range shifts and identify vulnerable populations or adaptive phenotypes.

### 4. Whole-genome sequencing

Whole-genome sequencing (WGS) data offer unparalleled power and resolution in analyses of demographic history, admixture and introgression, recombination and linkage disequilibrium, genetic load, natural selection, and species diversification. Elucidating evolutionary processes may require linkage disequilibrium analyses between many physically distant loci. WGS data enable the detection of genomic regions under selection, mutations in regulatory elements, rare variants and structural variation, and investigation of the genetic basis and architecture of phenotypic traits (e.g., disease susceptibility/resistance in endangered species). WGS data can also provide unique insights into phylogenetic relationships, evolutionary history, extinct and cryptic taxa, and ancestral intraspecific genetic diversity and structure, which are valuable in assessing temporal genomic erosion and guiding conservation and restoration efforts. Since samples of extinct or endangered species usually are rare, WGS data maximize the genomic information obtained from each sample. The highly fragmented DNA in museum and subfossil specimens (often <100 bp) requires the availability of reference genomes for WGS read mapping and downstream evolutionary analyses.

### 5. Noninvasive genomic sampling

Noninvasive or minimally invasive selection of biological material (e.g., from faeces, feathers, or hair) is commonly used in wildlife monitoring as the primary source of genetic material to provide insights into the ecology of endangered species. Noninvasive samples typically contain low amounts of poor-quality DNA, often contaminated with exogenous DNA.

### 6. Genome editing: engineering adaptation, gene drives, and de-extinction

Genome-editing tools, such as CRISPR-Cas9, allow precise modification of genes and genomes of living organisms. Genome editing can be applied to mediate locus-specific genetic rescue in endangered species threatened with high frequencies of deleterious mutations or to increase resistance to infectious diseases and resilience to anthropogenic environmental change. Modifications could even involve gene drives to assist the spread of harmful mutations through invasive populations. However, this is still controversial due to possible unintended outcomes and the need for an international regulatory framework for safe and responsible use.

## CONCLUSION

Conservation genomics transforms how fisheries resources are managed and protected by providing powerful insights into genetic diversity, population dynamics, and adaptive potential. By leveraging tools such as DNA barcoding, reduced representation sequencing, gene expression analysis, whole-genome sequencing, and noninvasive sampling, scientists can monitor biodiversity, detect endangered species, and implement effective conservation strategies. These genomic approaches not only aid in mitigating the impacts of climate change, habitat destruction, and overfishing but also support the development of sustainable fisheries management practices. As genomic technologies evolve, their integration into conservation policies will be essential for preserving aquatic biodiversity and ensuring the long-term resilience of fish populations and ecosystems.

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