From DNA to Diversity: How Genomics Shapes Conservation Biology

Moorthi Subash[1]* and Anusuya A. S.[2]

[1]ICAR-Central Institute of Fisheries Education, Maharashtra, Mumbai (400 061) India.
[2]College of Fisheries, Karnataka Veterinary, Animal and Fisheries Sciences University, Bidar, Mangalore, Karnataka (575 002), India.

Corresponding Author
Moorthi Subash
Email: subash962002@gmail.com

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ABSTRACT

With the escalating environmental problems and pressures that humankind has been inflicting, genomics is imperative for solving conservation problems for which attention is needed urgently. Conservation genomics increases the precision and success of conservation programs by coming up with cutting-edge ways to monitor endangered species, assess genetic variability, and understand evolutionary processes. Transcriptomics, whole-genome sequencing, and DNA barcoding can all provide comprehensive insights into species adaptation, population structure, and resilience to environmental changes. Such genomic techniques help to identify imperilled populations and restore genetic diversity while framing appropriate policy for ecosystem management. The text shows how genetics can inform conservation programs on the ground and policy decisions by giving real-life examples that worked. Genomic knowledge must be integrated into conservation activities so that species are preserved, ecosystem services are provided, and ecological sustainability is secured in perpetuity.

INTRODUCTION

Well, that's quite an esoteric way of putting it. The planet itself is altered, so that the human population is diverse enough to become extinct and number lesser surviving species. Future generations will, indeed, inherit an impoverished planet with reduced biodiversity, fewer ecosystems service, lesser evolutionary potentials, and a more rapid rate of extinction and collapse of the ecosystem, if species extinctions continue unabated. Protecting endangered species has hence become a very important concern to ecologists and biologists. Population viability analysis, the development of metapopulation theory, species conservation, the role of molecular biology, the creation of global positioning systems, geographical information systems, and remote sensing are just a few of the procedures and initiatives that have been undertaken in this area and are well documented in the literature. Genomics is a rapidly evolving method in conservation biology and an essential component of all biological disciplines in the modern era. Although genomics offers useful tools for characterising biodiversity, there is currently a lack of complete use of genetic approaches in actual conservation. The molecular basis for inbreeding, phylogenetic problems, comprehending genetic illnesses, identifying hybridisation/introgression in species, and current and historical demographic characteristics can all be thoroughly explained by genomic techniques. It can also help understand the mechanisms that link low genetic variation and low fitness, integrate environmental and genetic approaches into conservation biology, and build the newest, fastest monitoring systems.

THE VALUE OF INTEGRATING GENOMICS INTO CONSERVATION

Currently, the whole world is in the shock and trauma of the sixth mass extinction. This particular biodiversity crisis which we are now experiencing is going to devaste ecosystems health and functioning, evolutionary heritage, and species shall adapt creating the ultimate threat to humanity. Genetic variety has always been recognized, understood as essential to biological order at whatever level, but genomics is often absent in conservation and biodiversity assessments. Essential conservation concerns must be addressed if biodiversity is to be preserved-for example, biodiversity monitoring and taxonomic identification. Human activities also put endangered species and their habitats under much demographic strain. Target species/populations must have their genetic diversity restored and increased, tiny populations must be managed, and species adaptation to a changing environment must be supported. To avoid inbreeding depression and preserve adaptive potential, studies stress the significance of preserving genome-wide genetic variation, arguing against a limited focus on functional genetic variation (Kardos *et al*., 2021).

GENOMIC APPROACHES IN BIODIVERSITY RESEARCH

In recent years, high-throughput genomic sequencing methods have progressed from producing primarily short (50–300 bp) DNA sequencing reads to producing significantly longer (>10,000 bp) reads. DNA barcoding/metabarcoding, low representation DNA techniques, transcriptome sequencing (RNA-Seq), and whole genome (re-)sequencing are examples of genetic and genomic methodologies frequently employed in biodiversity research. By connecting genetic data to conservation aims and challenges, conservation genomics can also improve the efficacy of management measures by informing decision-making frameworks (Bernos *et al.,* 2020).

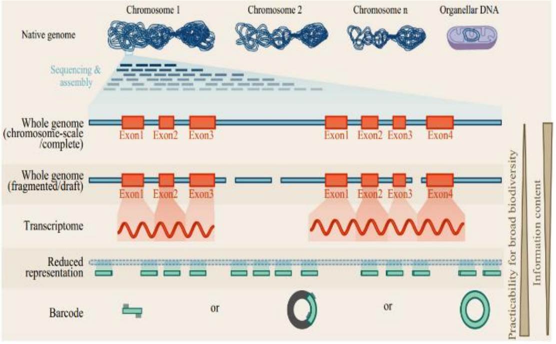

Fig.: Genomic approaches for biodiversity research. Theissinger, K., Fernandes, C., Formenti, G., Bista, I., Berg, P. R., Bleidorn, C., ... & Zammit, G. (2023). How genomics can help biodiversity conservation. Trends in genetics, 39(7), 545-559.

1. DNA barcoding and metabarcoding

DNA barcoding is an effective and commonly used genetic method for species identification and tracking of biodiversity. Using universal or taxon-specific primers that anneal to conserved flanking regions, DNA barcoding sequences reveal relevant DNA locations. At first, the mitochondrial cytochrome c oxidase subunit I (COI) gene served as the basis for DNA barcoding, mostly used in animals, especially invertebrates. Other DNA loci have been used over time to barcode bacteria (16S in rDNA), fungi (ITS in rDNA), protists and nematodes (18S in rDNA), plants (rbcL and matK in cpDNA), and vertebrates (e.g., 12S, 16S, and Cytb in mtDNA). Next-generation sequencing (NGS) and DNA barcoding are combined in DNA metabarcoding, making it possible to analyse complicated samples containing various specimens and/or species. Metabarcoding has been widely employed in ecological network mapping, invasive species detection, and biodiversity evaluation and monitoring. One of the main benefits of metabarcoding is that it allows for high-throughput ecosystem-wide assessments and monitoring in most habitats by avoiding the expensive sorting and processing of materials into individual specimens. Furthermore, ambient DNA is frequently broken down into brief fragments in an environmental medium, making metabarcoding a suitable method for sequencing it. By successfully identifying hybridisation events in endangered species such as the golden perch, genomic techniques have exposed the shortcomings of conventional genetic methods (Attard *et al.,* 2022).

2. Reduced genomic representation

Diminished representation. Most research targeting non-model species uses DNA sequencing (RRS) techniques. Using restriction endonucleases and size selection (e.g., RAD sequence and related techniques), hybridisation with probes (e.g., ultra-conserved elements or custom baits), or a combination of both (e.g., Hy RAD, Rapture), each specimen consistently targets a tiny section of the genome. The genome-wide data provided by RRS techniques is adequate to assess genetic diversity, inbreeding, effective population size, population structure and assignment, gene flow, phylogeographic patterns, and phylogenetic linkages.

3. Gene expression

A novel conservation framework has emerged due to gene expression data, typically RNA-Seqence, which characterises genetic variation in natural populations through functional variation and the quick reactions of individuals or populations to environmental change. Information on gene expression has shed light on how people react to pesticide exposure and how susceptible or resistant they are to certain illnesses. Gene expression data has also identified range changes and adaptive phenotypes or susceptible populations. Furthermore, gene expression data have been utilised to find complete gene networks even when the genes involved are unknown.

4. Whole-genome sequencing

When analysing demographic history, admixture and introgression, recombination and linkage disequilibrium, genetic load, natural selection, and species diversification, whole-genome sequencing (WGS) data provide unmatched power and resolution. To understand evolutionary processes, linkage disequilibrium analyses between several physically distant loci may be required. WGS data make it possible to identify genomic regions subject to selection and look at the' genetic basis and architecture of phenotypic traits.

5. Non-invasive genomic sampling

The primary source of genetic material utilised in wildlife monitoring to shed light on the ecology of endangered species is non-invasive or minimally invasive biological material sampling (e.g., from faeces, feathers, or hair). Low levels of low-quality DNA, frequently tainted with exogenous DNA, are commonly found in non-invasive samples.

CASE STUDIES OF BIODIVERSITY CONSERVATION:

1. Atlantic cod

The Atlantic cod was one of the earliest non-model species with a genomic assembly anchored by chromosomes. Four significant chromosomal inversions that distinguish between migratory and nonmigratory ecotypes in Norwegian and Icelandic seas and are linked to environmental adaptation were discovered using genome assembly in conjunction with population genomic analysis.

2. Crabs with horseshoes

Recent research has produced three of these species' chromosome-level assemblies. Breeding programs and conservation efforts can benefit from these genomic resources.

3. Ash dieback

A novel fungal pathogen known as *Hymenoscyphus fraxineus* was found to be the cause of the ash dieback disease, which quickly spread throughout Europe and killed out ash trees. A global team sequenced the genome of European ash. To help with directed breeding to replenish ash forests throughout the continent, polygenic characteristics linked to decreased sensitivity were utilised to map.

4. European beech

In 2018 and 2019, about two-thirds of European beech trees were died or seriously damaged by extreme drought. A genetic test was created to estimate a beech tree's potential ability to withstand drought. More drought-tolerant trees can now be chosen and propagated using this genetic test.

5. *Iberian lynx*

The genome of an extremely endangered species, the Iberian lynx, was one of the first to be sequenced in its entirety. According to whole-genome resequencing investigations, the species has one of the lowest genetic diversities ever documented due to a history of recurrent population decreases.

6. Freshwater sponge

Accurate SNP calling to evaluate genetic diversity, demographic events, and gene flow has been made possible by the chromosome-level genome of E. muelleri, which has also created new opportunities to study selection and adaptation in sponges. This significant resource will completely transform how we approach conservation in this group of non-model invertebrates. It will help monitor and evaluate their conservation status, which is challenging for invertebrates with little attention.

CONCLUSION

The demand for immediate conservation measures is fueled by the acceleration of the loss of biodiversity worldwide due to anthropogenic influences and rapid environmental change. Genome assemblies provide a basic framework for interpreting and safeguarding biodiversity. To preserve evolutionary potential for adaptive responses to ecological change and diversification in general, and to maximise tactics that minimise the loss of fitness. To do this, we support the advancement of reference genome-based methods in conservation studies and promote information sharing among researchers, conservation professionals, and the general public. We expect that the availability of reference genomes throughout the tree of life will provide a strong, quantitative, and comparable basis for biodiversity assessments, conservation, and restoration, given the significant influence the Human Genome Project has had on the biomedical sciences over the past 20 years.

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