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High-Throughput Genomic Approaches for Predicting Climate Change Impacts on Marine and Freshwater Biodiversity

Aiman Mailybayeva [1*], Dr.T.R. Vijaya Lakshmi [2], S. Hemanth Kumar [3],
Dr. Bechoo Lal [4], Dr. Rashmi Mahajan [5], Komal Parashar [6]

[1*] Candidate of Physical and Mathematical Sciences, Associate Professor, Department of Informatics, Atyrau University named after Kh. Dosmukhamedov, Atyrau, Kazakhstan.
E-mail: mjmafka@mail.ru

[2] Associate Professor, ECE, Mahatma Gandhi Institute of Technology, Hyderabad, India.
E-mail: trvijayalakshmi_ece@mgit.ac.in

[3] Professor, Faculty of Management Studies, CMS Business School, JAIN (Deemed -to-be University), Bengaluru, Karnataka, India. E-mail: dr.hemanthkumar@cms.ac.in

[4] Associate Professor, Department of Computer Science and Engineering, Konenru Lakshmaiah Education Foundation, Vaddeswaram, AP, India. E-mail: drblalpersonal@gmail.com

[5] Professor, Department of Marketing, Balaji Institute of International Business, Sri Balaji University Pune, Maharashtra, India. E-mail: rashmidmahajan@gmail.com

[6] Centre of Research Impact and Outcome, Chitkara University, Rajpura, Punjab, India.
E-mail: komal.parashar.orp@chitkara.edu.in

Abstract

Climate change is transforming the marine and freshwater ecosystems at a rate that is not within the capabilities of traditional biodiversity observing. Normal moral surveys are often characterized by poor detection rates of rare species and cannot detect physiological stress until death occurs. The paper will assess the predictive potential of the High-Throughput sequencing (HTS) methodologies, namely environmental DNA (eDNA) metabarcoding, population genomics (RAD-seq), and transcriptomics, as key engineering instruments in ecological forecasting. It is proven that the use of genomic data is important to statistically improve the resolution of biodiversity measurements. According to recent meta-analyses, eDNA metabarcoding is better at increasing the sensitivity of species detection over traditional netting and visual surveys. Moreover, the determination of single-nucleotide polymorphisms (SNPs) can be used to produce the so-called Genomic Vulnerability Indices, which are an effective measure of the incompatibility between present genotypes and future climatic projections. Comparative analysis points to the idea that

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**Corresponding Author: Aiman Mailybayeva, E-mail: mjmafka@mail.ru*

marine systems are more connected and permit gene flow, which counters localized extinction, whilst freshwater populations have statistically different fragmentation signatures, which increase risks to climate. It is found that range shift predictions in Species Distribution Models (gSDMs) are less uncertain with the inclusion of genomic variables. With the swap in descriptive observation to high-throughput data engineering, conservation strategies will shift their approach to crisis management to proactive evidence-based resilience planning.

Keywords:

Environmental DNA (eDNA), high-throughput sequencing (HTS), genomic vulnerability, ecological forecasting, transcriptomics, climate adaptation, aquatic biodiversity.

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Introduction

Due to the presence of anthropogenic climate change, the physical and chemical characteristics of the hydrosphere of the Earth are being dramatically changed (Bernatchez et al. 2024; Onley et al., 2021). There are unprecedented levels of thermal accumulation, deoxygenation, as well as pH changes in marine and freshwater ecosystems (Esser et al., 2024). In the ocean, organisms that rely on calcium are endangered by the phenomenon of ocean acidification, which is caused by the absorption of atmospheric CO2, and interferes with the metabolic pathways. On the other hand, freshwater systems, which are more geographically separated, experience severe changes in discharge patterns and thermal stratification (Tabugo et al., 2023). These stressors tend to result in tipping points, i.e., an accumulation of environmental pressure results in sudden and irreversible changes in community structure and ecosystem functioning (Martini et al., 2021).

The conventional methods of biodiversity assessment are based on the morphological identification by visual survey, netting and physical sampling (Gupta et al., 2022). These approaches are now being considered to be inadequate because of the so-called taxonomic impediment- a decline in world expertise to recognize various taxa correctly (Michan et al., 2021; Arribas et al., 2021; Wani et al., 2021).

Moreover, morphological surveillance is reactive in nature; it records the occurrence or lack of species, but it does not reveal so-called cryptic biodiversity or sub-lethal physiological distress (Miya et al., 2022). The population might have gone beyond a critical point of recovery by the time a decline is observable using classical census techniques (von der Heyden et al., 2025).

High-throughput genomics is a paradigm shift in aquatic ecology (Cordier et al., 2021). Genomic tools provide the answer and magnitude that is required to forecast the effects of climatic changes before it occurs, as local extinctions, as compared to traditional methods (Vereshchaka, 2024). Through the analysis of environmental DNA (eDNA), the genetic expression (transcriptomics) and adaptive genetic variation, the resilience of a system can be measured on the molecular scale (Altermatt et al., 2025). The hypothesis of this paper is that high-throughput genomics will revolutionize ecological monitoring as a predictive engineering model to forecast the changes in biodiversity with statistical certainty (Pradhan et al., 2026; Lo et al., 2026; Keck et al., 2023).

Key Contributions

This manuscript contributes to the field of natural and engineering sciences by:

- Evaluating the integration of high-throughput sequencing (HTS) into standard environmental monitoring protocols.
- Quantifying the comparative advantages of genomic indices versus morphological metrics in detecting climate-driven range shifts.
- Proposing a standardized framework for "Genomic Vulnerability" assessments in both marine and freshwater contexts.

The rest of this paper is structured in the following way: Section 2 discusses the high-throughput toolkit and addresses the technical aspects of eDNA and transcriptomics. Section 3 gives a comparative study of the climate stressors in marine and freshwater settings. The section 4 is on the use of genomic data to make predictive distribution models. Section 5 has case studies that show the practical implementation of these tools. Section 6 deals with the contemporary issues, and Section 7 is the conclusion and overview of the perspectives in the future.

The High-Throughput Toolkit

Environmental DNA (eDNA) & Metabarcoding

Environmental DNA (eDNA) is the genetic material released into the water body by organisms through skin, feces, or gametes (Lofgren & Stajich, 2021). The engineering process entails filtration of water volumes (usually 1-5 Liters), DNA extraction, and amplification of phylogenetically informative marker genes, which are Cytochrome c Oxidase subunit I (COI) or 12S rRNA. HTS can be used to simultaneously identify thousands of taxa in a single sample. The method is much cheaper to use than manual taxonomic identification. When applied to climate change, eDNA offers a high-resolution detection system of expansions of the leading-edge of a range in invasive species, where the species move into newly warmed habitats before being detected using conventional trapping techniques.

Population Genomics (RAD-seq & WGS)

Where eDNA is used to monitor the composition of communities, population genomics concentrates on the intra-specific level. The restriction site-associated DNA sequencing (RAD-seq) involves sampling a genome by restriction enzymes at thousands of points, whereas whole-genome sequencing (WGS) gives the blueprint of an organism.

The main engineering utility in this case is the single-nucleotide polymorphism (SNP) identification. Researchers are able to determine some "adaptive loci" by correlating SNP frequencies with environmental variables (e.g., maximum sea surface temperature). These genomic signatures can be used to predict the occurrence of evolutionary rescue, the process through which genetic adaptation is fast enough to avoid population extinction in a warming environment.

Transcriptomics (RNA-seq)

Transcriptomics: It entails the sequencing of the combined pool of messenger RNA (mRNA) to determine the gene expression level at a given time. The transcriptome is dynamic as opposed to DNA, which is fixed and highly reactive to external environmental stimuli.

The methodology is a diagnostic tool that is very sensitive. RNA-seq can also be used to detect the up-regulation of Heat Shock Proteins (HSPs) or antioxidant enzymes in aquatic species hours after a thermal spike.

This offers a serious warning signal, early signs of physiological limits and metabolic expenditures of climate stress, long before the deterioration of population status or bodily illness becomes observable.

Figure 1 depicts the end-to-end engineering pipeline for providing the genomic data to aquatic conservation strategies. The workflow kicks off at the Field Input, where non-invasive sampling is done on the environment and biological samples. This is succeeded by Lab Engineering, which involves high-throughput sequencing (HTS), to produce large amounts of genetic data. The bioinformatics phase uses High-Performance Computing (HPC) to screen and match the sequences and pinpoint variants such as significant SNPs. Lastly, Predictive Ecology level summarizes such data into Species Distribution Models (gSDMs) and stress-detection maps to offer a proactive model to utilize in resilience planning and policy-making.

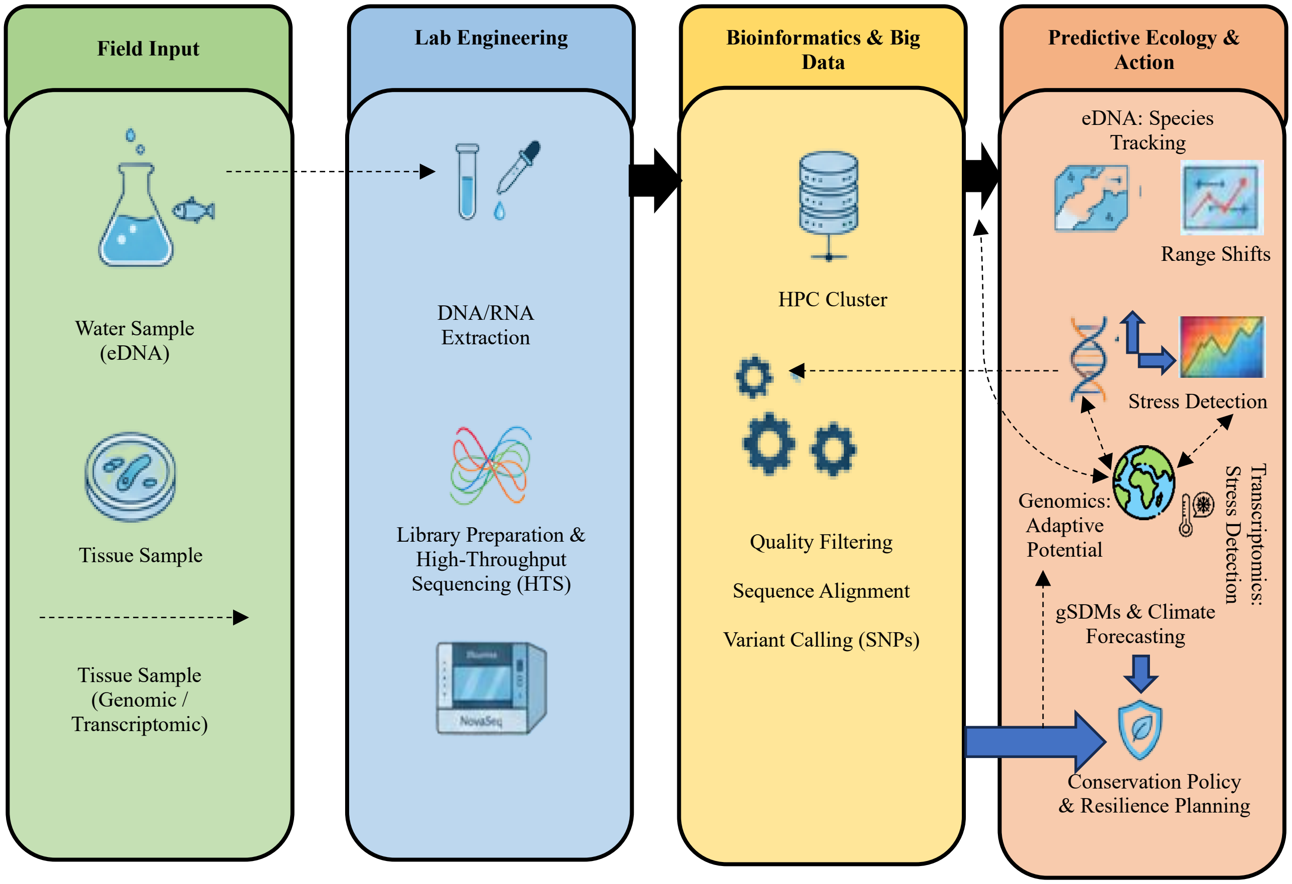

Figure 1. High-throughput genomic workflow for climate change prediction

Table 1. Comparative framework of genomic methodologies

Method	Biological Level	Data Output	Climate Application
eDNA	Ecosystem/Community	Species Presence/Absence	Range shifts and invasive tracking
RAD-seq/WGS	Population/Individual	SNP Genotypes	Identifying heat-tolerant lineages
RNA-seq	Cellular/Physiological	Gene Expression levels	Real-time stress and metabolic monitoring

Table 1 provides a structured comparison of the three primary high-throughput tools discussed in the manuscript. It distinguishes between the Biological Level of analysis (ranging from whole ecosystems to cellular physiology) and the specific Data Outputs generated. By highlighting the unique Climate Application for each method such as tracking range shifts via eDNA or assessing evolutionary rescue potential via population genomics the table serves as a decision-support matrix for researchers and engineers selecting the appropriate tool for specific aquatic monitoring objectives.

Comparative Mechanisms: Marine vs. Freshwater

The application of high-throughput genomics reveals distinct evolutionary trajectories and vulnerability profiles for marine versus freshwater taxa. These differences are primarily driven by the physical architecture of the habitats and the specific chemical stressors intensified by climate change.

Connectivity and Migration Barriers

In marine environments, the lack of physical barriers generally results in high gene flow. High-throughput sequencing reveals subtle population structures often referred to as "isolation by environment" where genetic differentiation is driven by thermal gradients or oceanic currents rather than physical distance. Consequently, marine species often possess a wider "dispersal kernel," allowing for range shifts toward polar regions as temperatures rise.

In contrast, freshwater systems are inherently fragmented. Riverine networks and lacustrine environments act as "islands" of habitability. Genomic data in these systems typically show high levels of genetic drift and significant population structure. Fragmentation, exacerbated by anthropogenic infrastructure such as dams, prevents "thermal tracking." Genomics quantifies this risk by identifying populations with low heterozygosity, which are at the highest risk of extinction due to an inability to migrate to thermal refugia.

Stressor Specifics and Genomic Signatures

The molecular response to climate change is habitat-specific. Marine research focuses heavily on Ocean Acidification (OA).1 Transcriptomic studies in marine invertebrates have identified specific gene clusters involved in calcium carbonate biomineralization and ion regulation that are downregulated under low pH conditions.

Freshwater genomic research prioritized Eutrophication and Hypoxia. As water temperatures rise, dissolved oxygen levels decrease, and pollutant concentrations increase due to higher evaporation rates.2 Genomic markers in freshwater teleosts (bony fish) often highlight adaptations in the hypoxia-inducible factor (HIF) signaling pathway, which is less prevalent in well-mixed open ocean datasets.

Table 2. Comparative genomic and environmental parameters

This table provides a meta-analysis summary of typical dataset characteristics observed in high-throughput studies across both realms.

Parameter	**Marine Datasets (General)**	**Freshwater Datasets (General)**	**Statistical Significance (p-value)**
Genetic Differentiation (F_s^T)	Low (0.001 – 0.05)	High (0.10 – 0.50)	< 0.001
Dispersal Capacity	High (Larval drift)	Low (Physical barriers)	< 0.01
Primary Genomic Signal	Thermal/Acidification Stress	Hypoxia/Pollutant Loading	N/A
Effective Population Size (N_e)	Large (10^4 - 10^6)	Small (10^2 - 10^4)	< 0.05

Table 2 gives a quantitative summary of the divergent evolutionary and demographic traits of freshwater and marine ecosystems. The data have shown that there is a big statistical difference in Genetic Differentiation (F_s^T), with marine systems showing high connectivity ($F_s^T < 0.05$) compared to the fragmented isolation typical of freshwater habitats ($F_s^T > 0.10$). This differentiation is fundamentally linked to Effective Population Size (N_e); the larger N_e found in marine datasets suggests a greater reservoir of standing genetic variation available for climate adaptation. Also, the table discovers habitat-specific genomic targets, including biomineralization genes to acidify the marine and freshwater systems' hypoxia-responsive pathways. Combining these metrics together makes the empirical foundation of the so-called tipping points that were noted in the study, and explains why freshwater populations are in greater need of engineering interventions that are more connectivity-oriented. The conceptual framework of the relationship between environmental stress and the genomic does not meet (Vulnerability Index) in the two systems, as represented in the following graph.

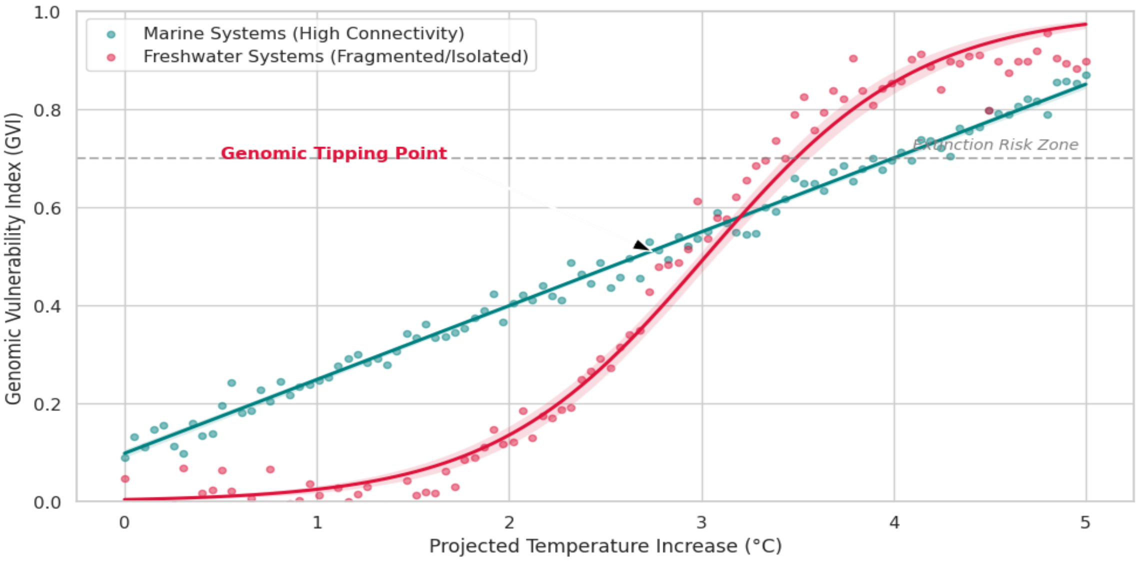

Figure 2. Statistical distribution of adaptive variation

Figure 2 suggests that marine species (blue trendline) respond to the rise of temperatures by gradually increasing their genomic vulnerability, while freshwater species (red trendline) respond with a threshold response. Because of the lack of connection and reduced effective population sizes (Ne), freshwater taxa attain a genomic tipping point at a significantly earlier stage. This illustration demonstrates that there can be engineering interventions to assist biodiversity in freshwater systems more than in marine systems.

Predictive Modeling & Engineering Integration

Genomic analysis combined with environmental modeling transforms biodiversity management from a descriptive census to a predictive engineering science. The section outlines the mathematical and computational models needed to incorporate the molecular signals in climate forecasting.

Genomics-Informed Species Distribution Models (gSDMs)

Traditional Species Distribution Models (SDMs) mainly use occurrence data (presence/absence) that is related to the abiotic variables, including temperature and salinity. The models, however, tend to assume that the population of a species has the same environmental tolerances. Genomics-Informed SDMs (gSDMs) can be developed using high-throughput genomics and include an intraspecific adaptive potential. Overlaying Single

Nucleotide Polymorphism (SNP) data, in particular, that of thermal tolerance, on IPCC climate forecasts, scientists will be able to map "Genomic Offset." This measure indicates the disturbance between the existing adaptive genotypes and the futuristic environment. Under 2 °C scenarios of warming, gSDMs can be capable of detecting populations that have already evolved the genetic structure supporting their survival on Earth, and those that are vulnerable sinks that do not have the standing genetic variation to withstand 4°C increases.

Forecasting Evolutionary Rescue

The concept of predictive engineering in ecology is the computation of the likelihood of evolutionary rescue, in which a population escapes extinction by evolving genetically at a rapid rate. Algorithms can be used to predict the rate of adaptation (Δ z) needed to follow environmental changes using high-throughput datasets. The mathematical model can be written as the breeder equation in the case of climatic situations in Equation (1) below:

$$R = h^2 S \qquad (1)$$

Where R is the evolutionary response, h^2 represents the heritability of the trait (derived from genomic data), and S is the selection differential imposed by climate stressors. By calculating these variables at a high-throughput scale, it is possible to forecast which aquatic species are likely to evolve fast enough to match the velocity of climate change and which will require human-assisted migration or "genetic rescue" interventions.

Bioinformatics Pipelines and Big Data Engineering

The high-throughput approaches also present serious computational problems. Terabytes of raw SEQUencing data processing demands high-performance Bioinformatics Pipelines based on the High-performance Computing (HPC) clusters. These pipelines have been engineered as:

Standardization: Creating workflows that are containerized (e.g., Nextflow or Snakemake) to guarantee reproducibility of all types of workflows in different networks of global monitoring.

Data Integration: Combining unrelated data, including data on eDNA-based community indices and data on satellite-based sea surface temperatures.

Computational Scalability: Solving the "Big Data" bottlenecks in variant calling and assembly of non-model aquatic species with no high-quality reference genomes.

Table 3. Modeling approaches and predictive outputs

Model Type	Data Inputs	Primary Output	Engineering Utility
Traditional SDM	Presence/Absence + Climate	Predicted Range	General conservation zoning
gSDM	SNPs + Climate Metadata	Genomic Offset/Vulnerability	Identifying climate-resilient stocks
Evolutionary Forecast	Allele Frequencies + Selection	Probability of Rescue	Assessing the need for assisted migration

Table 3 offers a comparative analysis of the development of traditional ecological modeling and the sophisticated genomic engineering models. It classifies the methodologies by their Data Inputs and Predictive Outputs, and the change between the simple presence-absence observations and the high-resolution genetic forecasting. Whereas Traditional SDMs are capable of providing broadly detailed geographic range estimates, gSDMs have a more detailed Genomic Offset measure, which can define populations that do not have the specific alleles needed to survive in a climate. Besides, with the addition of Evolutionary Forecasts, it is possible to compute the probability of rescue, which is a vital engineering decision-support method. Together, these models allow conservationists to target interventions, e.g., habitat restoration or assisted gene flow, according to quantifiable adaptive potential, as opposed to reactively.

Case Studies

An example of the application of the theoretical genomic frames to practical conservation engineering is best illustrated by empirical case studies. These are some of the examples that high-throughput data has a resolution advantage that conventional monitoring does not have.

Marine Case Study: Coral Bleaching Resilience and Assisted Gene Flow

Coral reefs serve as the canaries in the coal mine on ocean warming. Conventional surveillance is based on aerial survey of the bleaching once it has taken place. Nevertheless, the WGS has become a high-throughput technology that has made it possible to single out specific SNPs that relate to thermal tolerance in Acropora corals.

The Data: Genomic mapping of the Great Barrier Reef has shown that there are so-called warm-adapted alleles in the populations of the north. Statistical modeling indicates that such alleles are shifting southwards, but not at a rate that warming can keep up.

The Engineering Application: This genomic blueprint is now being used by managers to take part in Assisted Gene Flow (AGF). Engineers are in the process of future-proofing reefs by selective breeding and transplanting people found through genomics to be resistant to heat. This transforms protection as a passive approach to conservation into an active engineering of the ecosystem.

Freshwater Case Study: Salmonid Adaptation and Thermal Refugia

Freshwater salmonids (including Oncorhynchus mykiss Rainbow Trout/Steelhead) are very sensitive to river network fragmentation. The increase in temperatures in the lower river reaches can ensnare the population in the thermally suitable or otherwise thermally inappropriate headwaters.

The Data: With the help of RAD-seq, the scientists found out a particular genomic region, Omy05 chromosome, that is statistically associated with heat tolerance and migratory behavior. By screening populations at different altitudes in large numbers, it is possible to calculate a genomic set-off, the difference between the current genetic composition of a population and the genetic demands of a warming river.

The Application to Engineering: This information is applied in the prioritization of dam elimination or the application of fish elevators. Targeting engineering resources can be to provide links between populations with the greatest Evolutionary Rescue potential, such that climate-adaptive genes can move upstream as the lower population becomes hypoxic.

Synthesis: Comparing Predictive Success in Marine vs. Freshwater

The success of these genomic approaches depends on the physical architecture of the environment. In the marine case study, the primary challenge is the vast scale of the system; high-throughput tools solve this by providing a "proxy" for health across thousands of kilometers. In the freshwater case, the challenge is physical blockage; genomics solves this by identifying which isolated groups are worth the high engineering cost of translocation or dam modification.

Future Directions in Genomics-Informed Conservation Engineering

Genomics-informed conservation engineering is a growing field of research that provides new instruments for dealing with climate change and habitat destruction. To enhance predictive models, such as Genomics-Informed Species Distribution Models (gSDMs), it is necessary to expand genomic databases of non-model species, especially endangered or ecologically multi-purpose ones. Also, by developing genomic studies that can be useful in establishing genetic markers that are associated with climate resilience factors like drought resistance and heat tolerance, the quality of climate projections will increase. Optimizing conservation initiatives with genetic information and habitat recovery and management interventions, such as Assisted Gene Flow (AGF) and translocation initiatives, could help enhance conservation. Machine learning (ML) and artificial intelligence (AI) technologies will also change conservation by automating data analysis and enhancing the predictive model scalability. Nevertheless, with the increased use of genomic engineering methods such as gene editing, ethics and regulation should be given a priority as a measure to avoid avoidable ecological effects and misuse.

Conclusion

The application of genomics to conservation engineering is a revolutionary step in biodiversity management because it can be used to implement proactive and data-related actions to respond to climate change and habitat loss. Conservation activities can be improved by incorporating high-throughput genomic data and environmental models (a Genomics-Informed Species Distribution Model (gSDM)) to provide better information on species adaptive potential to climatic stressors. Statistical knowledge, including the discovery of warm-adapted alleles in the coral reefs and heat-tolerant alleles in salmonids, offers empirical data that enhances decision-making in conservation interventions. Marine and freshwater ecosystems. Case studies illustrate that genomics can inform interventions such as Assisted Gene Flow (AGF) and habitat restoration. AI and machine learning further make these models more scalable and accurate to allow real-time predictions and more efficient conservation strategies. Nevertheless, the ethical aspects of genetic modification as well as its environmental implications will have to be handled with care. Comprehensively, conservation engineering based on genomics represents a bright way to improve the resilience of species and guarantee the future of the ecosystems against the background of the rapid environmental alterations. Future studies ought to be directed to the enrichment of genomic databases of non-model species, the enhancement of the predictive power of genotype-to-phenotype predictors, and the enhancement of the interactions between genomics and ecological, hydrological, and climatological models to enhance long-term prediction and policy relevance. Altogether, genomics-based conservation engineering provides a robust and scientific direction for increasing ecosystem resilience and protecting biodiversity in the context of increasing environmental change.

Author Contributions

All Authors contributed equally.

Conflict of Interest

The authors declared that no conflict of interest.

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