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Molecular Evolution of Invasive Species and their Ecological Impacts on Global Fisheries and Aquaculture Systems

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Abstract

The increasing rate of international trading and global warming has supported the fatality of introducing non-native species in large numbers, which is a major threat to aquatic biodiversity and world food security. In this paper, consider the molecular evolution of the invasive species and the implications that it has had

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on the global fisheries and aquaculture systems. Recent discoveries in genomics, such as epigenetic plasticity, hybridization, and adaptive evolution at high rates, are combined to describe how the invasive population of a species can break the founder effect and initial genetic bottleneck to conquer new environments. Nature is found to be unstable through molecular shifts in invasive taxa that cause much ecological disturbance, including genetic pollution of wild stocks by introgression and introduction of new pathogens that annihilate commercial aquaculture. It also elaborates on the effect of the Trojan horse, where the genomic strength of invaders enables them to act as unrelenting vectors of diseases in warming oceans. The shortcomings of conventional ecological modeling are shown through analysis of case studies, including the Lessepsian migration and the invasion of Atlantic lionfish, which are in favor of merging the environmental surveillance systems of environmental DNA (eDNA) and genomic biosecurity. As a possible way to reduce the invasive effects, the potential and ethical aspects of biotechnological interventions, including CRISPR-based gene drives, are considered. Conclusion: It is determined that to have a sustainable management of the global blue economy, knowledge of the molecular basis of invasiveness is a prerequisite. To protect the sustainability of fisheries and the socio-economic well-being of coastal societies all over the globe, the integration of genomic insights into international policy is needed.

Keywords:

Molecular evolution, invasive species, genomic biosecurity, environmental DNA (EDNA), fisheries management, aquaculture sustainability, rapid adaptation.

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Introduction

The Invasive Species-Fisheries-Aquaculture nexus is a major collision point whereby biological changes are directly in conflict with food security on a global scale. With the growing dependence of the world on the blue economy, the health of the wild-capture fisheries and the development of intensive aquaculture are threatened by the introduction (Zehra et al., 2025; Oficialdegui et al., 2025; Singh, 2021). This is not just space occupation; these species change the architecture of functional ecosystems and cause a cascading effect that will undermine not only the natural biodiversity but also the economic feasibility of aquatic protein production (Tan et al., 2023; Kovalenko et al., 2021; Bernery et al., 2022).

Human activities have broken down the ancient biogeographic boundaries and created a rate of species introduction that has never been witnessed in evolutionary history (Morisette et al., 2021; Yao et al., 2022; Britton et al., 2023). The main agents of these invasions are the release of ballast water by international shipping, the release of organisms by the ornamental trade, and escapes of poorly contained aquaculture installations (Singh, 2021; Robin et al., 2023; Seshagiri et al., 2021). Moreover, climate change is the driving force, which is shifting thermal regimes and allowing the invasion of the higher latitudes, which used to be hostile (Atique & An, 2022; Siddiqui et al., 2023). These stressors establish disturbed environments in which opportunistic non-native species tend to do well in competition with native specialists (Jawdhari et al., 2022; Chan et al., 2021).

Although traditional ecology would give a paradigm through which one can observe the population decline, it tends to be ineffective in explaining the mechanisms through which a small population of a founder species can flourish in an exotic ecosystem (Kovalenko et al., 2021; Atique & An, 2022). It is required to shift the focus towards a molecular approach to find the "genomic toolkit" of successful invaders (Fricke & Olden, 2023; Siddiqui et al., 2023). This incorporates rapid sequence evolution, epigenetic changes, and hybridization mechanisms, which offer the physiological versatility needed to make use of the new niches. It is these molecular foundations that urgently need to understand to stop reacting to management, but to proactively predict and contain based on genomes (Pukk et al., 2021; Jerde, 2021; Dubreuil et al., 2022).

This paper aims to synthesize the impact of molecular evolution on the success of invasive species and then destabilize the global sectors of the blue economy. This review demonstrates that the combination of genomic adaptation and ecological influence on the area is the reason why molecular surveillance has to be considered as a part of fisheries and aquaculture management to provide socio-economic and biological stability in the long term.

The remainder of the paper is as follows: Section 2: Molecular Mechanisms of Invasiveness determines the mechanism of overcoming low genetic diversity by epigenetic plasticity and hybridization to build highly adaptable, so-called genomic toolkits to new environments. Section 3: Pathways of Impact on Global Fisheries looks at the decline of wild stocks due to genetic pollution (introgression) and the introduction of cryptic pathogens to destabilize the natural ecological conditions. Section 4: Disruptions in Aquaculture Systems examines the economic cost of invasive biofuels and parasites with resistance to treatments, resulting in siphoning of nutrients and destruction of infrastructure. Section 5: Case Studies gives empirical evidence of Atlantic lionfish and Lessepsian migrations to illustrate how molecular adaptations are then converted into success in colonization. Section 6: Management and Mitigation using Biotechnology Environmental DNA (eDNA) monitoring and CRISPR-based gene drives should be considered as new technology to provide the opportunity to detect and control the proliferation of invasive species at the earliest possible stage. Section 7: Conclusion and Future Directions conclude by outlining the need to have a "Genomic Biosecurity" system in place to safeguard the global blue economy against continued evolutionary changes of the invasive taxa.

Molecular Mechanisms of Invasiveness

This part discusses the so-called genomic toolkit, with the help of which non-native species can change a small number of struggling representatives into the dominant eco-power. Whereas traditional ecology is concerned with environmental fit, molecular evolution describes biological strategies of internal biology to avoid extinction.

Genetic Bottlenecks vs. Rapid Adaptation

The inception of invasions is usually an instance of a founder effect in which a limited number of individuals have a decreased portion of the genetic diversity in the original population. This was previously believed to curtail invasive possibilities (the genetic paradox of invasion). Nevertheless, rapid evolution happens when the mutation rates are high or the numerous events of the introduction (admixture) supply sufficient raw material on which the natural selection can work within only a few generations.

Epigenetic Plasticity

Epigenetic plasticity, in particular, DNA methylation, is one of the most important processes of survival in the short term. This enables a species to make changes to the gene expression, either by switching off or switching on some characteristics, but does not alter the DNA sequence itself. This phenotypic plasticity is crucial in the adaptation of aquatic organisms to varying salinities of the ballast water or varying temperatures of new latitudes.

Horizontal Gene Transfer (HGT)

Although it is a common occurrence in bacteria, Horizontal Gene Transfer (HGT) is a developing field of research in invasive algae and microbes in aquaculture. Invaders may acquire local functional genes, thereby gaining instant advantages over local competitors, such as antibiotic resistance or metabolism of local nutrients, or invaders may acquire a Darwinian fitness advantage by acquiring new genes that provide a short-term competitive advantage to their host.

Hybridization: The "Evolutionary Rescue"

It is by hybridization that an invader species will breed with a closely related native species or even another introduced strain. It gives rise to evolutionary rescue in which the new hybrid offspring have heterosis (hybrid vigor). Most of these hybrids tend to be more aggressive and grow quicker than the parent species over diverse environmental conditions with extreme conditions.

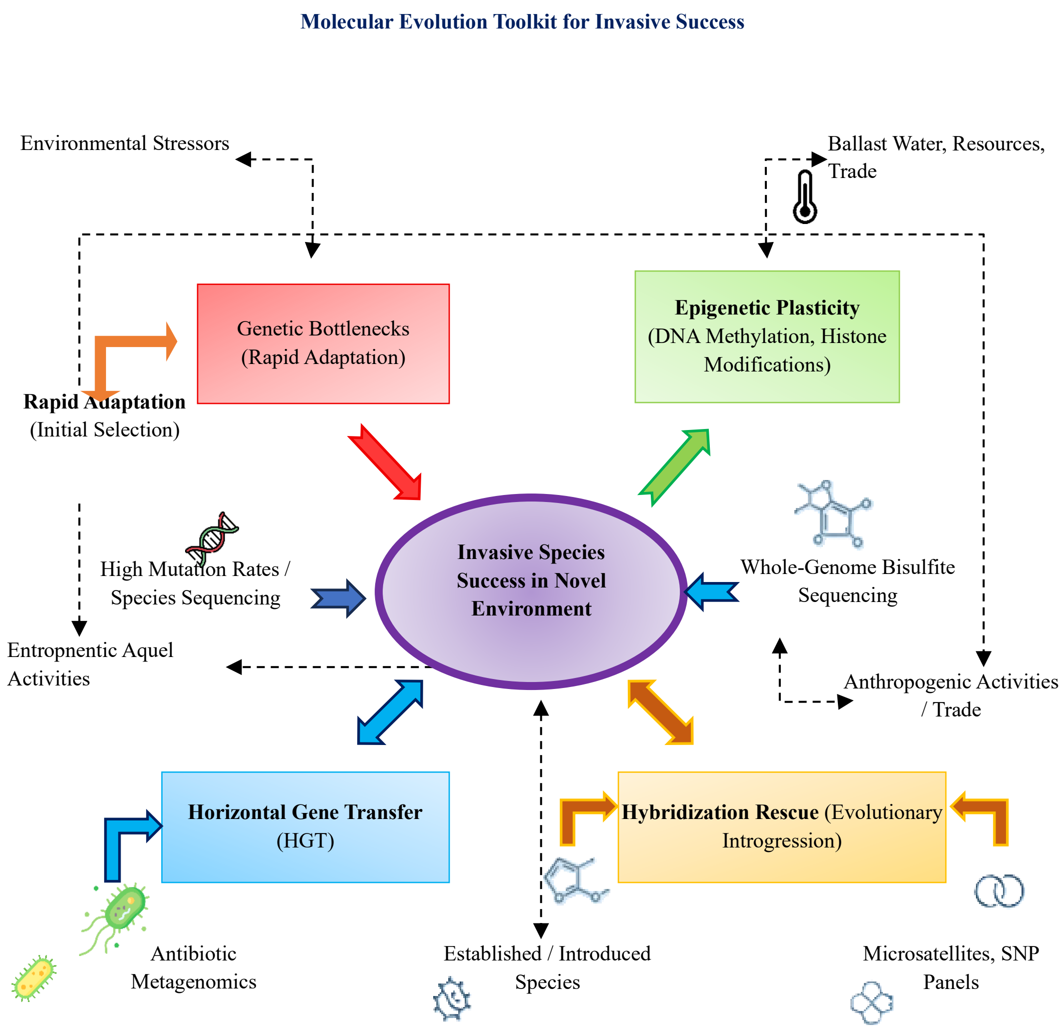

Figure 1: Molecular evolution toolkit for invasive success

Figure 1 shows an example of an overall Molecular Evolution Toolkit where there is synergy between anthropogenic stressors and genomic adaptation, which promotes invasive success. Identically, the architecture demonstrates that invasive species overcome the constraints of a so-called founder effect by exploiting Genetic Bottlenecks as a catalyst for fast selection and Epigenetic Plasticity (i.e., DNA methylation) to promptly tune their physiology to novel environments. The model extends Hybridization Rescue and Horizontal Gene

Transfer (HGT) as processes of obtaining new aggressive capabilities by interspecific breeding or by obtaining microbial genes. Connecting these internal (molecular) processes with external (both the ballast water and the overall trade) drivers, the figure proves that the invasive dominance is not accidental but the consequence of the multidimensional process involving the usage of the external data, which has a biological basis.

Pathways of Impact on Global Fisheries

This Section discusses the alteration of molecular response into environmental destabilization, in particular, the connection between the genomic accomplishments of invasive species and the destruction of wild-catch fisheries.

Genetic Introgression and "Genetic Pollution"

Genetic introgression takes place when the invasive species or escaped domestic strains (e.g., Atlantic Salmon) breed with native populations. This causes genetic pollution in which a locally adapted complex of genes is disrupted. Introduction of the model can be used to forecast the loss of native fitness. A simplified version of the Wahlund Effect, or the change in frequency of a native allele (q) over time (t) due to gene flow (m) from an invasive population with allele frequency (q_m), can be expressed as:

$$q_t = (1 - m)^t (q_0 - q_m) + q_m \qquad (1)$$

This equation (1) illustrates that the genetic identity of wild stocks can be rapidly altered even when there are small but consistent escape events of aquaculture or invasive pulses, and this causes loss of specialization as a result of migration time or predator avoidance.

Trophic Displacement and Competition

Molecular markers like DNA metabarcoding of gut contents and stable isotope (δ15N and δ13C) can also be used to measure the precise amount of competition that invaders have on native species. An invasion results in a niche shift among native populations due to the replacement of an invasive species with one that occupies a similar functional niche. The extent of competitive overlap and the following displacement can be estimated with the help of the Niche Overlap Index of Pianka (O_{jk}):

$$O_{jk} = \frac{\sum p_{ij} p_{ik}}{\sqrt{\sum p_{ij}^2 \sum p_{ik}^2}} \qquad (2)$$

From Equation (2), p_{ij} and p_{ik} represent the proportions of resource i used by the invasive species j and native species k. High overlap values ($O_{jk} \rightarrow 1$) indicate intense competition that typically results in the exclusion or stunted growth of native fishery targets.

Co-introduction of Pathogens (The "Trojan Horse" Effect)

The invasive species frequently serve as vectors of so-called cryptic pathogens, viruses, bacteria, or parasites that the native stocks have not met before. The identification of these pathogens can be done ahead of a clinical outbreak using Molecular tracing, through High-Throughput Sequencing (HTS). The effects on the fishery are frequently quantified in terms of the Basic Reproduction Number (R0) of the introduced pathogen in the native population:

$$R_0 = \beta \cdot c \cdot d \qquad (3)$$

Equation (3), β represents the likelihood of a contact being transmitted, c represents the rate of contact between invasive and native fish, and d represents the infectious period. In the case of $R_0<1$, the pathogen that is invaded will propagate, which may result in the collapse of the commercial fishery.

Disruptions in Aquaculture Systems

This segment discusses the discrete molecular and biological processes of how invasive species compromise the performance and economic sustainability of the global aquaculture processes.

Biofouling Genomics and Treatment Resistance

The Mediterranean mussel (Mytilus galloprovincialis) or any of the tunicates cause enormous expenses in aquaculture by passing through nets, pipes, and cages. The genomics of biofouling studies the evolution of these species to adapt to the conventional anti-fouling agents, including copper-based coatings or heat treatments. The molecular race frequently results in the upregulation of Heat Shock Proteins (HSPs) or metal-binding Metallothioneins so that such organisms can survive eradication attempts that would otherwise result in the disappearance of the native species. It is possible to quantify the higher metabolic cost of the farmed species as the decrease in Specific Growth Rate (SGR):

$$SGR = \frac{\ln(W_f) - \ln(W_i)}{t} \times 100 \qquad (4)$$

According to Equation (4), W_f and W_i, the weights of the farmed stock at time t are the last and initial. Invasive biofouling results in a significant decrease in SGR because it forms a hypoxic micro-environment.

Pathogen Evolution in High-Density Environments

Aquaculture systems are referred to as evolutionary pressure cookers in which high host density enables an easy, rapid evolution of the invasive parasites and microbes. Upon the introduction of a new pathogen by a species, the pathogen tends to evolve virulence to take advantage of the large farmed host population. Molecular surveillance demonstrates how these pathogens can soil farmed stocks after having leaped out of invasive "reservoirs" and, in most cases, change to avoid the immune system of the host. This may be represented as the change in virulence (alpha) in relation to the transmission (beta) in the dense environment of a farm, repositioning the optimal virulence upwards, resulting in increased mortality rates (m) in the aquaculture system, expressed in Equation (5):

$$m = \alpha + \text{background mortality} \qquad (5)$$

Resource Competition and Nutrient Siphoning

Coastal and open-water aquaculture. Invasive filter feeders (like invasive oysters or macroalgae) directly compete with farmed species in the competition for particulate organic matter and dissolved nutrients. DNA metabarcoding the surrounding water column gives molecular support for the process of nutrient siphoning, in which invasive biomass blocks primary production to the farmed crop. This decreases the efficiency of the Feed Conversion Ratio (FCR) in the semi-natural systems since the natural part of the diet is exhausted. Even the economic effect may be quantified as Competition Coefficient (α_{12}) in a modified Lotka-Volterra model, the effect of the invasive species on the carrying capacity of the farmed species.

Case Studies

This segment is based on the theoretical molecular processes of practical applications and proves the success of high-profile aquatic invasions through the use of genomic data.

The Lionfish (Pterois volitans/miles): Genomic Expansion

One of the fastest spreading species of the sea is the Indo-Pacific lionfish in the Western Atlantic and the Caribbean. The population has flourished despite a harsh case of genetic bottleneck at the time of its inception. The association of specific loci with faster adaptation to changing depths and temperatures has been determined by genomic studies that used RAD-seq.

Table 1. Genomic and ecological profile of the lionfish (pterois) invasion

Metric	**Detail**
Origin	Indo-Pacific (Bali/Philippines)
Genetic Marker	Mitochondrial DNA (mtDNA) & SNPs
Molecular Success	High levels of "Admixture" from multiple introduction events
Impact	65%–95% reduction in native reef fish recruitment

Table 1 gives a diagnostic breakdown of the Atlantic Lionfish invasion, which provides an explanation of the molecular data in one of the most aggressive marine expansions in history. Through RAD-seq and SNP panels, the scientists were able to discover that the success of the population was not due to one introduction but instead Admixture, where the individuals of one source population mixed with another to produce a genetically strong super-invader. This genomic mixing allowed the species to adapt fast to different levels of depth and temperatures, and this has caused the catastrophic 65-95 percent decrease in the native fish recruitment, as shown in the table.

The Mediterranean Lessepsian Migration

The Suez Canal is a saltwater passageway, which has enabled Lesssepsian migrants of the tropical Red Sea to penetrate the cooler Mediterranean. Epigenetic tuning is indicated through molecular signatures in the Rabbitfish (Siganus luridus). The characteristic of differential DNA methylation enables the tropical fish to endure winter in the Mediterranean without the need to wait till some advantageous mutation can occur.

Zebra Mussels (Dreissena polymorpha) in North America

The classic biofouling genomics is the zebra mussels. It was brought in through the ballast water, and their distribution across the Great Lakes and inland waters has been monitored through High-Throughput Sequencing (HTS). Genomic mapping shows that genes that deal with the production of byssal threads are highly expressed, which enables them to stick to virtually any substance, and hence easily transported through commercial shipping.

Population Growth Comparison

The concept of the following graph consists of the illustration of the normal Lag phase against the normal Expansion phase facilitated by the molecular adaptation.

Population Density

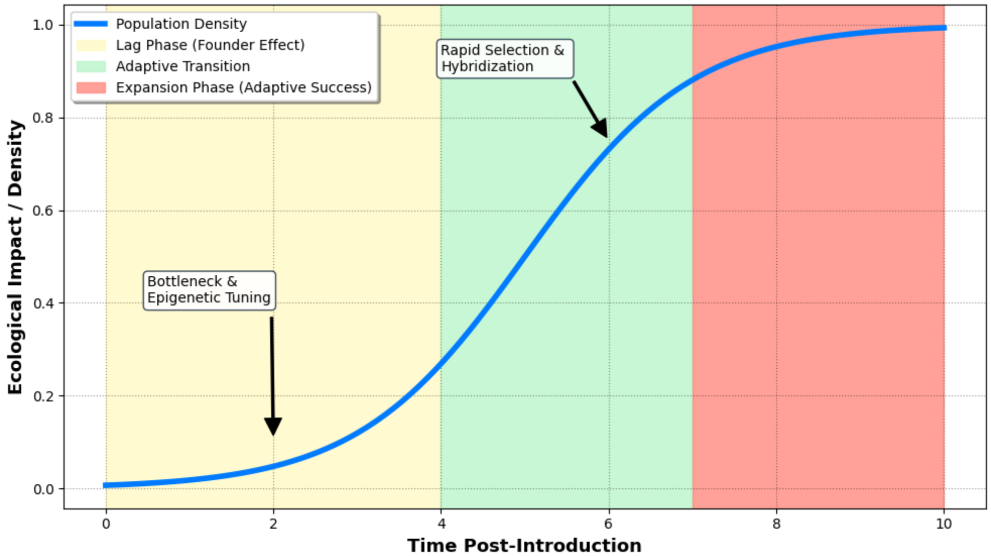

Figure 2. Invasive species population dynamics

Figure 2 is divided into three separate areas that provide a correlation between population density and time. The first stage of survival is the Lag Phase (Yellow), which is usually the period when the species is mostly unnoticed and requires epigenetic plasticity to facilitate the adaptation between its native biology and the new environment. The Adaptive Transition (Green) is the point at which there is a molecular breakout, i.e., a breakthrough in the form of hybridization rescue, or the buildup of favorable mutations occurs to conflict with the original genetic bottleneck. This will culminate in the Expansion Phase (Coral), in which the explosive growth of the species has captured the maximum competitive benefits, and the native fisheries are rapidly forced out, resulting in a permanent alteration in the aquatic ecosystem.

Table 2. Comparative summary of case studies

Species	Primary Molecular Driver	Ecological Impact	Economic Sector Affected
Lionfish	Admixture/Rapid Selection	Trophic Collapse	Coral Reef Fisheries
Rabbitfish	Epigenetic Plasticity	Habitat Alteration	Mediterranean Coastal Fisheries
Zebra Mussel	Gene Over-expression	Biofouling/Nutrient Siphoning	Freshwater Aquaculture & Power Plants

Table 2 is the summary of the direct causal relationship between internal molecular strategies and their subsequent socio-economic outcomes, which shows that the success of aquatic invasions is dependent on particular biological toolkits. The table identifies the different ecological impacts of the category of species, such as the Lionfish, Rabbitfish, and Zebra Mussel, including trophic collapse, habitat change, and industrial biofouling (as different examples of admixture and epigenetic plasticity). After all, this comparative structure demonstrates that the decline of the wild fisheries and aquaculture systems is a foreseeable consequence of the power of an invader to adapt to its new environment, on a molecular level.

Management and Mitigation through Biotechnology

This section examines the way to be able to reverse the "molecular script" of invasiveness in order to develop high-tech defense systems. Through these genomic principles that have made these species successful, to detect, control, and predict their movements.

Environmental DNA (eDNA): Molecular Fingerprints

The Lag Phase is the most important period during which the management cannot see the population, which is already evolving. Environmental DNA (eDNA) entails the sampling of water and sequencing of genetic content that is released by organisms (through the skin, mucus, or waste). This enables detection at early stages with a level of sensitivity that is much higher than in the case of netting or visual survey. The Quantitative PCR (qPCR) Approach: Management can be given a chance to compute the relative abundance of an invader before it becomes a nuisance by targeting specific barcoding genes such as COI (Cytochrome c oxidase subunit I).

Gene Drives and CRISPR: Self-Limiting Populations

The technology of CRISPR-Cas9 can be used to produce so-called Gene Drives that avoid the normal genes passing on through Mendelian inheritance. An invasive population can have a self-limiting gene (e.g., making all offspring males) inserted into it. The Shift of the Inheritance: In nature, there is a 50% chance of either a trait being inherited. This is driven up to close to 100% with a Gene Drive. The Outcome: Within the span of a number of generations, the population loses its reproductive females, all the local invading stock is effectively put out of business by the local population, and no one has to resort to the use of chemicals.

Genomic Modeling for Climate Resilience

Due to the increase in ocean temperatures, the thermal niche of invading species changes. Genomic Landscape Modeling gives scientists the capabilities to superimpose temperature-tolerance genes of a species on climate projection maps of the future. This gives an idea of the fisheries that will be the most susceptible to new Lessepsian or tropical migrants in 2050.

Conclusion

This model confirms molecular evolution as the tipping point to the success of invasive aquatic species. Instead of being lifeless biological dangers, these invaders are dynamical systems able to rewire their gene expression either by epigenetic plasticity or by hybridizing through genetic bottlenecks. As a countermeasure to this developing threat, international policy should be changed in order to drop the olden customary physical checks in favor of a strong "Genomic Biosecurity" program. It encompasses the compulsory introduction of environmental DNA (eDNA) screening of international shipping and the introduction of genetic risk assessment to determine the potential of species used in aquaculture, the so-called evolutionary rescue. Nonetheless, there are still considerable gaps in knowledge, and one of them is the absence of Whole-Genome Sequencing (WGS) on high-risk species. The study emphasizes that merging environmental DNA (eDNA) surveillance with genomic biosecurity frameworks is essential to counter the "Trojan horse" effect, where rapid epigenetic adaptation and hybridization allow invasive taxa to bypass traditional ecological bottlenecks and decimate commercial aquaculture stocks. The absence of these genomic maps paralyses the creation of precision tools such as CRISPR-based gene drives or high-sensitivity eDNA primers. These gaps need to be closed in order to pursue a predictive and not a reactive management approach that can safeguard the future of the world's fisheries and aquaculture in the age of fast-changing climates.

Author Contributions

All Authors contributed equally.

Conflict of Interest

The authors declared that no conflict of interest.

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