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Genetic Improvements in Aquaculture

Su Ürünleri Yetiştiriciliğinde Genetik İlerlemeler

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ABSTRACT

Genetic enhancement plays a crucial role in product development in the shift from wild harvesting to agricultural production. The initial phase typically involves domestication, followed by further genetic modifications to improve production traits. Aquaculturists, like their terrestrial counterparts, prioritize traits such as rapid growth, increased efficiency, disease resistance, and high quality. Various tools are utilized to achieve these genetic enhancements. This article seeks to assess the present state and obstacles concerning the administration of farmed aquatic genetic resources while offering suggestions for enhancement.

Keywords: Aquaculturists, Aquatic genetic resources, Genetic enhancement, Disease resistance

ÖZ

Genetik iyileştirme, yabani hasattan tarımsal üretime geçişte ürün geliştirmede çok önemli bir rol oynamaktadır. Başlangıç aşaması, tipik olarak evcilleştirmeyi ve ardından üretim özelliklerini geliştirmek için daha fazla genetik modifikasyonu içermektedir. Su ürünleri yetiştiricileri de karasal ortamda yapılan yetiştiricilik türlerinde olduğu gibi hızlı büyüme, artan verim, hastalıklara dayanıklılık ve yüksek kalite özelliklerine öncelik vermektedir. Bu genetik iyileştirmeleri elde etmek için çeşitli araçlar kullanılır. Bu makale, yetiştiriciliği yapılan sucul genetik kaynakların yönetimine ilişkin mevcut durumu ve engelleri değerlendirmeyi ve iyileştirme önerileri sunmayı amaçlamaktadır

Anahtar Kelimeler: Su ürünleri yetiştiricileri, Sucul genetik kaynaklar, Genetik iyileştirme, Hastalık direnci

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1. Introduction

Genetic advancements in aquaculture aim to enhance specific traits in aquatic species like fish, shellfish, and crustaceans. These traits include growth rate, disease resistance, feed efficiency, and tolerance to environmental stressors. These improvements play a crucial role in sustainable aquaculture practices, as they help meet the growing global demand for seafood while minimizing the negative impact on the environment (Abdelrahman et al 2017).

The correlation between cultivated variants of cultured species and their wild counterparts will significantly impact the conservation, sustainable utilization, and advancement of Aquatic Genetic Resources. These interactions must be effectively managed, including proper management and conservation of wild resources, considering their current and potential future contributions to aquaculture and their preservation in their natural habitats (Allen et al. 2002)

When dealing with cultured genetic resources, whether they are from non-native species or farmed varieties of native Aquatic Genetic Resources that have the potential to become invasive, it is crucial to assess the possible harm they may cause to native wild genetic resources before any introduction or utilization in aquaculture. The competition for resources between the development of new species for aquaculture and the cultivation of existing species is a significant factor to consider. The costs involved in developing aquaculture for new species are not easily quantifiable, as it requires substantial research and development efforts and the establishment of a value chain and market for the product. Therefore, it is crucial to establish procedures for pre-evaluating new species before investing in their adaptation for aquaculture. In some cases, it may be more cost-effective to achieve the objectives of developing a new species by implementing a targeted breeding program for an existing cultured species, rather than introducing a completely new species. It's crucial to find an equilibrium between fostering species diversity and refining the cultivation and adaptation of existing species when devising aquaculture production plans. The increasing temperatures driven by climate change can impact the tolerance limits of currently farmed species. This challenge can be addressed by either identifying new species that are better suited for cultivation in such environments or by implementing breeding programs aimed at improving the heat tolerance and resilience to temperature fluctuations in existing aquaculture species (Yadav et al. 2024). It is crucial to evaluate the costs and benefits of both approaches. Therefore, countries need to adopt a strategic approach that considers specific target objectives and takes into account the existing and projected market demand for associated products.

While genetic technologies such as single nucleotide polymorphism (SNP) panels, including genotyping-in-Thousands by sequencing (GT-seq), are available, their accessibility and cost may be prohibitive for low-value aquaculture species in developing countries. Consequently, there is an urgent need to develop and promote affordable genetic tools that can be integrated across the seed production and supply chain to support sustainable aquaculture practices (Campbell et al. 2016). These tools are essential for monitoring the genetic status of key genetic resources within major species and production systems, thereby preserving genetic diversity and reducing the risk of inbreeding. To achieve this goal, several strategies can be implemented, including the creation of customized marker systems tailored to specific species and enhancing the infrastructure and capacities of developing and transitional economies. Strengthening technical expertise and improving access to relevant technologies will be vital for the effective execution of these genetic management strategies across different regions (Rasal et al. 2024). One potential approach could involve establishing national or regional mechanisms for quantitatively assessing genetic diversity within seed supply systems. This evaluation could be based on the analysis of environmental DNA (eDNA) samples, which contain aggregated DNA from various sources, using specifically designed marker systems to ensure accurate detection and monitoring.

Genetic advancements in aquaculture play a crucial role in increasing productivity, reducing production costs, and minimizing the environmental impact. However, it is important to carefully consider the potential ethical, environmental, and regulatory implications associated with these techniques. Effective management of the roughly 700 aquatic species cultivated globally is vital for aquaculture to meaningfully contribute to the United Nations' Sustainable Development Goals. However, the implementation of genetic improvement programs in aquaculture faces various constraints, including technological, economic, and infrastructural challenges. Addressing these issues is critical to optimizing genetic enhancement efforts and ensuring the sector's sustainability and growth. A significant challenge in the aquaculture sector is the insufficient knowledge regarding the genetic status of numerous farmed species. Characterizing these genetic resources and developing information systems to monitor both the cultivated varieties and their wild relatives is crucial. In recent years, advancements in genetics have become a major focus within the industry. However, aquaculture practices in developing countries largely depend on unimproved fish strains. Evidence supports the viability of genetic enhancement initiatives, with various selection methodologies available to improve these strains (Abdelrahman et al. 2017).

1.1. Domestication

Many of the aquatic species commonly cultivated have been partially domesticated, with some undergoing additional genetic enhancements. Just as terrestrial livestock and crops are bred for productivity and proximity to humans, aquatic organisms are now facing similar selection pressures. While the domestication of aquatic species may be in its early stages compared to terrestrial species, advancements in technology and tools are accelerating the process of domestication and genetic improvement Genetic diversity serves as a vast reserve that can be harnessed for the initiation of selective breeding programs, which are highly effective in enhancing the performance of the aquaculture industry. The transfer of training and technology between different sectors of aquaculture can have a significant impact, particularly for lower-value species (Abdelrahman et al. 2017).

1.2. Selective breeding

Selective breeding is a primary technique employed for genetic improvement in aquaculture. This process involves the strategic selection of individuals with the highest genetic merit to act as breeders for subsequent generations. To assess genetic value accurately, populations are cultivated in a controlled environment, allowing for any observed differences to be attributed solely to genetic factors, rather than environmental influences. This method enhances the effectiveness of breeding programs by ensuring that the traits being selected are indeed hereditary and not impacted by external conditions.

However, this process of selective breeding can be quite costly due to the need for specialized facilities to maintain a standardized environment, ensure consistent rearing practices, and measure numerous groups of animals. Only the top-performing individuals are chosen for breeding to produce subsequent generations with improved genetic traits (Alemu et al. 2024).

While the practice of selective breeding has been established since the early 20th century, it is important to recognize that the field has evolved significantly. Recent advancements in experimental design, tagging technologies for identifying specific individuals and groups, and the development of computational tools have greatly improved the precision and effectiveness of traditional selective breeding methods. These innovations have facilitated substantial genetic enhancements across various species, optimizing breeding outcomes and increasing overall productivity in aquaculture.

1.3. Genetic markers

Genetic markers are classified into various types, with amplification fragment length polymorphisms (AFLPs) and microsatellite markers being frequently employed in aquaculture. These markers serve as indicators of specific DNA regions, facilitating the identification of genomic locations. They are distributed throughout an organism's genome and are passed down from parents to offspring, making them valuable tools for studying genetic variation and improving breeding programs.

Genetic markers play a crucial role in determining parentage by sharing markers between offspring and their parents. Additionally, they hold promise in pinpointing DNA regions that offer performance advantages. Marker-assisted selection, where breeding decisions are based on the presence of specific markers, can streamline the process by eliminating the need for challenge trials in controlled environments. This approach proves particularly beneficial when direct trait measurements are costly or when elite performers in disease challenges cannot be used for breeding due to disease transmission concerns (Bishaw, and Turner, 2008).

1.4. Genetic engineering

Genetic engineering encompasses various techniques such as chromosome set manipulations and transgenesis. Chromosome set manipulation involves modifying sets of chromosomes in organisms, altering the typical two sets of chromosomes found in normal organisms.

Chromosome set manipulation can be used to create triploids, organisms with three sets of chromosomes, which are often sterile. This characteristic can be advantageous in scenarios where reproduction is undesirable. For example, in the United States, this technology has been employed to manage nonindigenous weed populations by inhibiting the reproduction of grass carp. Similarly, oysters have also been subjected to chromosomal manipulation to mitigate quality degradation during the spawning season (Alemu et al. 2024).

1.5. Transgenesis

Transgenesis is a biotechnological approach that involves the integration of genes into organisms, moving beyond traditional breeding methods. A notable example of transgenic crops is soybean plants engineered for herbicide resistance. By transferring a bacterial gene into these plants, the reliance on labor-intensive cultivation and weeding is significantly decreased. Another example is golden rice, which has been genetically modified to include three foreign genes from bacteria and daffodils, enabling the rice to synthesize vitamin A. These innovations illustrate the potential of transgenic technology in enhancing agricultural efficiency and nutritional content.

The introduction of transgenic organisms extends beyond crops to include aquatic organisms as well. The Glofish, a fluorescent zebrafish, was the first transgenic aquatic organism to be commercially available in the United States in 2004. The ability of these fish to fluoresce is due to transgenes derived from jellyfish and coral. It is important to note that the Glofish is not intended for consumption as food (Boudry et al. 2021).

The United States Food and Drug Administration (FDA) is currently evaluating genetically modified Atlantic salmon that has been engineered with a growth hormone gene from Chinook salmon and a promoter from the ocean pout. These salmon are under consideration for approval as a food source. Concurrently, research efforts are underway globally to develop additional aquatic transgenic organisms that could offer benefits such as enhanced disease resistance, improved nutritional profiles, and other desirable traits.

Genetic diversity represents a substantial resource that can be utilized to initiate selective breeding programs, which are proven to significantly improve the performance of the aquaculture sector. Facilitating the transfer of training and technology across different aquaculture sectors can greatly benefit lower-value species, enhancing their productivity and sustainability**.**

This review aims to evaluate the current status and challenges in managing genetic resources in farmed aquatic species by synthesizing information from a wide range of published studies. Additionally, it seeks to offer recommendations for enhancing genetic diversity within aquaculture practices moving forward. Genetic advancements in aquaculture.

2. Genetic Applications in Aquaculture

2.1. Selective Breeding: This method involves selecting individuals with desirable traits to be the parents of the next generation. Over time, this can lead to populations with improved traits. For example, by choosing fish with faster growth rates or higher disease resistance as parents, stocks with these traits can be developed.

Selective breeding in fish involves intentionally choosing individuals with desirable characteristics, such as rapid growth, strong disease resistance, and enhanced feed conversion efficiency, to act as parents for the next generation. This method is aimed at enhancing the overall performance and productivity of fish populations in aquaculture settings. Here is an overview of how selective breeding is implemented in fish (Boudry et al. 2021; Budhlakoti, 2022).

a. Trait Identification: The initial step in selective breeding is pinpointing the traits that hold the most significance for the specific aquaculture operation. These traits can vary based on factors like market demand, environmental conditions, and production objectives. Common traits focused on in fish selective breeding programs include growth rate, fillet quality, disease resistance, feed efficiency, and resilience to environmental stressors such as temperature fluctuations or low oxygen levels.

b. Establishment of Breeding Population: Once the desired traits are identified, a breeding population is established using individuals that display these traits. These founding individuals may be sourced from wild populations, commercial stocks, or existing breeding initiatives. It is essential to uphold genetic diversity within the breeding population to prevent inbreeding depression and ensure the sustained success of the breeding program (Budhlakoti, 2022).

c. Family Selection: Fish are typically bred in controlled settings like hatcheries, where parentage can be accurately traced. Families are created by mating chosen individuals based on their genetic suitability for the target traits. The offspring resulting from these pairings are then assessed for their performance in the traits of interest.

d. Performance Testing: The offspring from selected families are reared under standardized conditions, and their performance in target traits is assessed through regular measurements and observations. This process may involve monitoring growth rates, survival rates, disease resistance, and other pertinent parameters (Campbell et al. 2016).

e. Selection of Breeders: The breeders for the next generation are chosen based on the performance testing results, with a focus on individuals who possess the highest genetic merit for the desired traits. To identify the most genetically superior individuals, statistical methods are employed to estimate breeding values during the selection process.

f. Iterative Breeding Cycles: Selective reproduction is a repetitive procedure that includes multiple rounds of mating, performance evaluation, and selection across various generations. The goal of each reproduction cycle is to enhance the genetic quality of the population for specific traits. As time passes, the collective genetic advancements result in populations displaying notably improved performance and productivity (Doublet et al. 2020).

g. Record Keeping and Data Analysis: Maintaining precise records and conducting thorough data analysis are crucial aspects of selective breeding initiatives. Comprehensive documentation of breeding choices, performance test outcomes, pedigree details, and genetic evaluations is upheld to monitor genetic advancements and inform future breeding strategies.

Selective breeding has proven to be effective in enhancing various fish species in aquaculture, such as salmon, tilapia, trout, catfish, and shrimp. This has led to notable enhancements in traits like growth rate, disease resistance, and feed efficiency. These genetic improvements play a significant role in bolstering the profitability, sustainability, and competitiveness of aquaculture operations.

2.2. Marker-Assisted Selection (MAS): Marker-assisted selection (MAS) involves the identification of genetic markers associated with desirable traits, allowing for more efficient selection of individuals exhibiting those traits. This method accelerates the breeding process by enabling early selection based on genetic markers instead of waiting for the physical expression of traits. Consequently, MAS enhances the effectiveness of breeding programs, leading to improved genetic outcomes in various species.

Marker-assisted selection (MAS) is a breeding method that leverages genetic markers to effectively choose individuals exhibiting desired traits. Unlike traditional selective breeding, which depends on phenotypic assessments, MAS allows for the direct selection of individuals based on their genetic makeup. This approach enhances the efficiency and accuracy of breeding programs, facilitating the development of improved traits in various species here is how MAS operates:

a. Identification of Genetic Markers: The first step in Marker-Assisted Selection (MAS) is to identify genetic markers associated with the traits of interest. These markers may include DNA sequences like single nucleotide polymorphisms (SNPs), microsatellites, or other genetic variations linked to specific traits, typically established through genetic mapping studies or association analyses. By pinpointing these markers, breeders can more effectively select individuals that exhibit the desired characteristics.

b. Genotyping: Once the genetic markers associated with the target traits are identified, individuals in the breeding population undergo genotyping to determine their genotype at these marker loci. This process can be carried out using various molecular biology techniques, such as polymerase chain reaction (PCR) followed by DNA sequencing or high-throughput genotyping arrays (Dunham et al. 2000).

c. Association Analysis: Following genotyping, statistical analyses are conducted to evaluate the relationship between marker genotypes and phenotypic traits. This enables researchers to pinpoint which markers are closely linked to the target traits and possess the highest predictive capability.

d. Marker-Assisted Selection: Based on the outcomes of the association analysis, individuals with favorable marker genotypes linked to the desired traits are chosen as breeding candidates. These individuals may not necessarily display the trait phenotype themselves but are anticipated to pass on the desired alleles to their offspring.

e. Validation and Selection Efficiency: The effectiveness of Marker-Assisted Selection (MAS) is contingent upon the accuracy of the marker-trait associations and the heritability of the traits being targeted. To ensure the reliability of the selected markers, validation studies are performed to assess their predictive capabilities across diverse genetic backgrounds and environmental conditions. This validation process is crucial for confirming that the markers will consistently identify individuals with the desired traits in various contexts Continuous validation and improvement of marker panels enhance the efficiency and dependability of MAS over time (Gamage et al. 2023).

f. Integration with Traditional Breeding: MAS is frequently integrated with conventional selective breeding methods to enhance breeding efficiency and expedite genetic advancement. By combining genetic information obtained from markers with phenotypic evaluations, breeders can make more informed decisions and achieve faster genetic progress in target traits.

g. Application in Aquaculture: MAS has been applied in aquaculture species such as salmon, tilapia, shrimp, and catfish to enhance traits like growth rate, disease resistance, fillet quality, and stress tolerance. The utilization of MAS in aquaculture breeding programs has resulted in a more precise selection of breeding candidates, reduced generation intervals, and increased genetic gain per unit of time and resources.

MAS offers several advantages over traditional breeding methods, including the ability to select individuals at an early age before phenotypic traits are fully expressed, improved selection accuracy, and the potential to simultaneously select multiple traits. However, MAS also requires specialized infrastructure for genotyping and data analysis, as well as ongoing research to identify and validate informative genetic markers for target traits (Gjedrem and Baranski, 2010).

2.3. Genomic Selection

Genomic selection employs genomic data to enhance the accuracy of predicting individuals' breeding values. By examining the entire genome, which includes both marker and non-marker loci, this approach captures genetic variation more comprehensively. As a result, genomic selection facilitates more precise decision-making in the selection process, improving the overall effectiveness of breeding programs

Genomic Selection (GS) is a breeding approach that leverages genomic data to improve the accuracy of predicting an individual's breeding value. Unlike traditional breeding methods, which typically depend on phenotypic evaluations and pedigree information, GS utilizes data from the entire genome to assess the genetic potential of individuals for specific traits. This comprehensive analysis allows for a more precise estimation of genetic merit, enhancing the efficiency of breeding programs (. Gjedrem et al., 2012; Hallerman 2021). Here's an overview of how genomic selection works

a. Genotyping: The initial step in genomic selection involves genotyping individuals in the breeding population using advanced genotyping techniques like SNP arrays or next-generation sequencing. This process generates a comprehensive set of genetic markers spread across the genome (Hasan et al. 2021).

b. Phenotypic Data Collection: Simultaneously, phenotypic data is collected for the target traits of interest from the individuals in the breeding population. These traits may include growth rate, disease resistance, feed efficiency, and other economically significant traits relevant to the breeding objectives.

c. Genomic Prediction Model: A genomic prediction model is then developed using statistical methods to estimate the genetic relationship between marker genotypes and phenotypic traits. This model utilizes the information from the genetic markers to predict the breeding value of individuals for the target traits (Hely et al. 2013; Houston et al. 2020).

d. Training Population: The accuracy of the genomic prediction model depends on the availability of a training population comprising individuals with both genotypic and phenotypic data. This dataset is used to train the model and establish the relationship between marker genotypes and trait phenotypes.

e. Prediction of Breeding Values: Once the genomic prediction model is trained, it can be applied to individuals in the breeding population who have been genotyped but lack phenotypic data. The model predicts the breeding values of these individuals solely based on their marker genotypes (Jannink et al. 2010)

f. Breeding Candidate Selection: Breeding candidates for the next generation are chosen based on their high predicted breeding values for the desired traits. By utilizing genomic estimated breeding values (GEBVs), breeders can make more informed decisions and achieve faster genetic progress compared to traditional selection methods.

g. Validation and Enhancement: To ensure the accuracy and reliability of genomic prediction models in predicting breeding values in independent populations, validation is necessary. Continuous research and validation studies contribute to improving the models**,** enhancing their predictive capabilities, and making them applicable across various genetic backgrounds and environments

(Abdelrahman et al.2017).

Genomic selection offers several advantages over traditional breeding methods. It allows for the selection of individuals at a young age before phenotypic traits are fully expressed. It also increases the accuracy of selection and enables the simultaneous selection of multiple traits. Additionally, it helps capture genetic variation that may not be evident from pedigree information alone and accelerates the rate of genetic improvement in breeding programs. However, implementing genomic selection requires significant investment in genotyping and data analysis infrastructure. It also necessitates expertise in statistical genetics and bioinformatics (Lorenzen et al. 2012).

2. 4. Triploidy

Triploidy involves inducing an extra set of chromosomes in an organism, resulting in sterility. This can be advantageous in aquaculture as it prevents unintended breeding in cultured populations, reducing the risk of genetic pollution from escaped individuals. These various approaches to genetic improvements in aquaculture contribute to the development of sustainable practices that meet the increasing demand for seafood while minimizing environmental impact.

a. Genetic Engineering: Although genetic engineering techniques like transgenesis are not extensively used in aquaculture compared to other fields, they have the potential to introduce new traits into aquatic species. For instance, scientists have investigated the enhancement of disease resistance or improvement of growth rates through genetic modification (Manzoor et al.2024; Rasal et al. 2024)

b. Hybridization: The process of hybridization involves crossing individuals from different strains or species to create hybrids that possess desirable traits, such as disease resistance or tolerance to specific environmental conditions. Offspring resulting from hybrid vigor or heterosis may exhibit superior traits when compared to the parental lines.

c. Cryopreservation of Germplasm: Cryopreservation techniques allow for the long-term storage of genetic material, including sperm, eggs, or embryos. This preserves valuable genetic diversity for future breeding programs and research purposes (Rasal et al. 2024).

2. 5. Ongoing Challenges

Ongoing challenges persist in the realm of genetic improvement, with classical breeding techniques serving as the fundamental basis for future advancements. The continuous refinement of these techniques aims to enhance the rate of performance improvement. However, the integration of marker information into selective breeding poses a significant challenge, requiring the identification of marker-trait associations and the development of strategies to effectively incorporate this information (Regan et al. 2021).

A significant challenge in the aquaculture industry is the simultaneous enhancement of multiple traits in aquatic species, such as rapid growth, disease resistance, and product quality. The complex interactions among these traits are not well understood, largely due to the unclear definition of genetic values and the fact that multiple traits are often not assessed in the same individuals. While some genetic correlations between specific traits have been established, such as the observed negative relationship between growth rates and resistance to viral hemorrhagic septicemia in rainbow trout, further research is essential to address these complexities and refine genetic improvement strategies

The foundation of genetic improvement in the foreseeable future will continue to rely on classical breeding techniques. These techniques will be further refined to enhance the rate of improvement in performance. However, the integration of marker information into selective breeding presents several challenges, including the practical aspects of identifying associations between markers and traits, as well as determining the most effective ways to leverage this information in breeding programs. These challenges highlight the need for comprehensive strategies that ensure reliable marker-trait associations can be established and utilized effectively to enhance breeding outcomes (Shikuku et al. 2021).

In such scenarios, understanding the markers linked to disease resistance and obtaining more accurate estimates of genetic value for multiple traits can offer viable solutions. Recent advancements in genetic improvement techniques enable the identification and selection of relatively rare individuals that demonstrate superior performance across several traits of interest for breeding applications. These developments pave the way for enhanced breeding strategies that can address the complexities of trait interactions in aquaculture (Sinha et al. 2023; Sonesson et al. 2023).

3. Today's Challenges and Needs

The lack of information regarding the genetic resources in the majority of the world's aquaculture sectors highlights the urgent need for the development of information systems. By establishing robust information systems for these genetic resources and implementing targeted conservation and utilization strategies, we can effectively safeguard the future of our genetic resources. It is important to acknowledge that our current understanding of genetic management issues in aquaculture is still limited compared to the knowledge accumulated during the domestication of terrestrial species for agriculture. Therefore, the key to enhancing the conservation and sustainable use of genetic resources in aquaculture lies in gaining a comprehensive understanding and characterization of these resources, as well as implementing accessible information systems to facilitate their utilization (Abdelrahman et al. 2017; Varshney et al. 2021).

Sustainable use focuses on the cultivation of aquatic species that are currently under domestication. It is essential to recognize the opportunity for effective management and sustainable utilization of these resources, as well as the conservation of their genetic diversity before it is lost. Various strategies can be employed to manage genetic diversity throughout the domestication process of species intended for aquaculture, ensuring their resilience and long-term viability. The initial emphasis is often placed on resolving technical challenges in artificial breeding before expanding breeding systems to satisfy commercial seed production demands. However, genetic diversity is frequently overlooked during these early phases, as the primary focus tends to be on fulfilling quantity requirements rather than prioritizing quality. This oversight can have long-term implications for the sustainability and resilience of aquaculture species. A prevalent concern is the insufficient attention given to the genetic quality of base populations, which are essential as the genetic foundation for the initial domestication efforts. Moreover, these base populations often exist at inadequate sizes, both in terms of census and effective population sizes. This limitation can hinder the potential for long-term genetic improvement and resilience in aquaculture species (Xu et al. 2017; Wang et al. 2023).

Effective population size is a crucial factor in maintaining genetic variation within a population. It reflects the population's ability to preserve genetic diversity, which is influenced by the relationships among individuals and the number of breeding individuals contributing to the next generation. Both the overall population size and the number of breeding individuals play significant roles in determining effective population size. Effective population size is a crucial factor in maintaining genetic variation within a population. It reflects the population's ability to preserve genetic diversity, which is influenced by the relationships among individuals and the

Number of breeding individuals contributing to the next generation. Both the overall population size and the number of breeding individuals play significant roles in determining effective population size however, if not controlled, hybridization can result in species introgression, causing the loss of distinct species. Examples of this can be seen in Clarias catfishes Clarias macrocephalus and C. gariepinus, as well as in Chinese carp Hypophthalmichthys molitrix and Aristichthys nobilis (Yáñez et al. 2015).

In the conservation of wild relative genetic resources, it is essential to prioritize in situ conservation methods, such as habitat protection, restoration, effective management of aquatic protected areas, and sustainable fisheries management for species that are actively harvested. The genetic consequences of these conservation strategies are often not well understood, making it crucial to assess the genetic status of species conserved in situ and the size of the populations being fished. If in situ conservation is not feasible or could be complemented by ex-situ conservation efforts, this option should be considered, especially as new farmed varieties continue to emerge.

In situ conservation necessitates continuous monitoring and management of genetic diversity within the protected populations. It also requires long-term funding to be effective, which can make widespread implementation challenging. One significant obstacle in conserving aquatic genetic resources is the limited options available for ex-situ conservation, particularly for fish species. Currently, the primary method employed is the cryopreservation of male gametes, while attempts to cryopreserve fish oocytes or embryos have largely been unsuccessful. As a result, the potential role of ex-situ in vitro conservation remains limited until effective methods are developed for a broader range of aquatic species (Yáñez et al. 2015).

The sustainable use of Aquatic Genetic Resources revolves around implementing established knowledge and best practices to effectively manage genetic diversity and prevent inbreeding. Raising awareness about the implications of seed supply systems, particularly regarding the renewal of broodstock across generations, is essential. Both emerging and established aquaculture sectors must undergo a mindset shift to understand that the genetic quality of seed is as crucial as the quantity produced. Prioritizing genetic quality can lead to more sustainable aquaculture practices, ensuring that production systems are robust and resilient in the face of environmental challenges (Zhu et al., 2024).

When developing an aquaculture sector for a particular species, it is essential to prioritize genetic management from the initial implementation of seed supply systems, including the careful selection of source base populations. The management of effective population size should be adjusted based on the species' fecundity and generation time. Unfortunately, many aquaculture species globally have not received sufficient focus on broodstock genetic management, which jeopardizes the genetic integrity of farmed varieties. There is a considerable opportunity to design or adapt breeding and seed supply systems to meet not only the demand for seed quantity but also to safeguard genetic diversity (Hallerman et al. 2021).

Numerous successful aquaculture breeding programs effectively manage inbreeding using low-tech methods. These programs typically involve identifying families and tracking lineage through physical tagging and separate rearing of individuals until tagging is completed. While such practices improve production performance, they require careful management and appropriate infrastructure to ensure effective family management. However, this level of genetic diversity oversight is often lacking in aquaculture operations that do not have organized breeding programs in place.

To effectively enhance genetic management within current seed supply systems, it is essential to develop a cost-efficient method for assessing the genetic status of farmed varieties about their wild relatives, particularly the wild populations from which the cultivated types are derived. This approach would facilitate better monitoring and comparison of genetic diversity, aiding in the preservation of essential traits and overall genetic integrity (Gjedrem et al. 2012; Yáñez et al. 2015).

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