Vol-4 Issue-1 2026
Scientific Research Journal of Science, Engineering and Technology
ISSN: 2584-0584, Peer Reviewed Journal

Enhancement of Fish Stocks through Aquaculture Genetics

Michel Murwanashyaka 1,2, Lihua Jiang*1, Xiaojun Yan1

*Correspondance: mikeshyaka@gmail.com (M. Michel)

florencejiang@126.com (L. Jiang)

xjyan@zjou.edu.cn (X. Yan)

Abstract

The growing demand for fish globally underscores the necessity for advancements in aquaculture, where genetics plays a pivotal role. This study investigates how aquaculture genetics can enhance growth rates, disease resistance, and the productivity of key fish species. Genetic improvement programs, including genomic selection, marker-assisted selection, and selective breeding, are essential for accelerating these developments. By leveraging the genetic diversity present in fish populations, these programs aim to promote desirable traits, thereby enhancing the overall quality of fish stocks. Selective breeding, a cornerstore of genetic enhancement, has demonstrated significant potential in increasing growth rates and feed efficiency. Marker-assisted selection enhances this process by identifying specific genetic markers associated with beneficial traits, thus expediting the breeding cycle. At the forefront of these approaches is genomic selection, which utilizes genome-wide data to identify and select individuals with superior genetic potential, yielding unprecedented precision in breeding outcomes. Furthermore, genetic techniques are vital for improving disease resistance in aquaculture. By identifying and disseminating immunity-related alleles, the industry can mitigate the impacts of prevalent diseases, ensuring sustainable fish production. Advances in CRISPR-Cas9 and other gene-editing technologies may further accelerate the development of robust fish strains through targeted genetic modifications. These genetic strategies not only increase production but also promote sustainability by reducing the environmental impact of fish farming and reliance on wild fish populations. This research underscores the necessity of integrating cutting-edge genetic technologies with traditional breeding methods, positioning aquaculture genetics as the foundation for the future of sustainable fish farming.

Keywords: Aquaculture Genetics, disease resistance, genetic improvement, genetic markers, fish productivity.

1. National Engineering Research Center of Marine Facilities Aquaculture, Zhejiang Ocean University, No. 1 Haida South Road, Dinghai District, Zhoushan, Zhejiang Province, 316022, China.
2. Kibogora Polytechnic University, Department of Sciences, PO. BOX 50 Nyamasheke,

   Rwanda.

Introduction

The global aquaculture sector has undergone rapid expansion over the past few decades, emerging as a major supplier of protein to the world's growing population (FAO, 2016). With over 600 fish species raised (FAO, 2022), the industry is incredibly diverse, yet only a handful of species, approximately 20–30, dominate global production (FAO, 2022). However, as the aquaculture sector expands to meet the needs of a growing human population, it faces multiple challenges ranging from environmental sustainability to production efficiency (Naylor et al., 2021). The strategic application of genetics to enhance fish populations has emerged as a pivotal approach to address these challenges and ensure long-term sustainability of aquaculture operations (Herkenhoff, 2025). A critical analysis of existing research reveals that genetic improvement initiatives are essential for increasing the productivity, disease resistance, and growth rates of key fish species. Traditional methods, such as selective breeding and hybridization, have been instrumental in achieving significant gains in species like carp and tilapia, with long-term improvements in feed efficiency and growth rates (T. Gjedrem, 2010). Furthermore, hybridization has been shown to produce species with enhanced environmental tolerance, growth rates, and disease resistance as exemplified by hybrid catfish, which outperform their parent species in these areas (R. A. Dunham, 2011).

The advent of modern biotechnology techniques has revolutionized aquaculture genetic improvement, with genomic selection and gene editing technologies offering unprecedented opportunities for enhancing fish stocks (J. M. Yáñez, Houston, & Newman, 2014). Genomic selection, which uses genetic markers to identify the best breeders, has significantly accelerated genetic gain in aquaculture species, as evident in the substantial advancements made in Atlantic salmon (J. M. Yáñez, Houston, R. D., and Newman, S. , 2014). Moreover, gene editing technologies, such as CRISPR-Cas9, enable targeted and precise genome alterations, allowing for the introduction of desirable traits, such as enhanced growth rates, disease resistance, and environmental tolerance (Grunwald, 2002). The impact of these genetic enhancement initiatives on production is substantial, with improved growth rates and feed efficiency contributing to reduced production cycles and lower feed costs, thereby increasing the economic and environmental sustainability of aquaculture operations. For instance, selectively bred Nile tilapia strains have demonstrated growth rates 20–30% higher than non-improved strains, resulting in a notable increase in productivity (El-Sayed, 2019). Furthermore, genetic enhancement has made notable strides in disease resistance, with selectively bred strains of Atlantic salmon exhibiting increased resistance to sea lice, leading to reduced infection rate and mortality (T. Gjedrem, & Baranski, M., 2009).

This review aims to critically analyse the current state of the art in aquaculture genetics, highlighting the gaps in knowledge and proposing novel insights that can meaningfully advance the field. By examining the interplay between traditional and modern biotechnology techniques, this synthesis seeks to provide a comprehensive framework for understanding the transformative potential of genetics in enhancing fish stocks for sustainable aquaculture. Ultimately, this research endeavours to contribute to the development of innovative solutions that can help address the complex challenges facing the aquaculture industry, ensuring a more sustainable and food-secure future for generations to come.

Importance of Aquaculture Genetics

Aquaculture genetics may play a key role in sustaining genetic resources and biodiversity for a sustainable future while simultaneously boosting productivity and quality (Sonesson et al., 2023). Planning the potential applications of gene transfer technologies, such as transgenesis, for the future benefit of aquaculture and its international social and economic context, as well as assuring their success, requires a solid understanding of genetics (Shakweer, Krivoruchko, Dessouki, & Khattab, 2023). There is a need for applied genetic research and a greater knowledge of how this research may be used for the responsible management of genetic resources due to the increased production and usage of genetically defined stocks, strains, and breeds in aquaculture. Aquaculture genetics has historically been weak in the area of understanding the genetic basis of features and the expected implications of selecting for those traits, which is necessary for the careful and informed use of genetic technology. To do this, local breeds or species may be selectively bred for desired qualities, taking into account the effects this will have on the genetic diversity and make-up as a whole. It can also be accomplished through the creation of genetically modified species or breeds; this strategy is debatable due to its possible negative effects on genetic resources.

The possibilities for sustainable development are diminished, and aquaculture is more susceptible to disease outbreaks and environmental changes when genetic diversity is lost (Henriksson et al., 2021). In contrast to these detrimental effects of intensification, genetic technology may eventually be used to boost the quantity and caliber of high-performing strains while preserving genetic variety and resources. Analogous patterns have been noted in aquaculture, where native strains and breeds are routinely supplanted by foreign or exotic strains, frequently leading to the genetic eradication of the native strains. As aquaculture becomes a more significant consumer of new genetic technology, it must work to prevent situations where genetic resources are compromised for the sake of temporary financial gain. For example, as the demand for food, originating from animals, has increased, the number of agricultural animal breeds, such as cattle, pigs, and poultry, has rapidly declined. Even while many breeds may be well adapted to the local environment, many of them are nevertheless in danger of going extinct, and some have even completely disappeared. It is imperative to strike a balance between the preservation of biodiversity and increased output while also taking into account the potential consequences of intensification on genetic resources. By displacing native breeds or species with a small number of high-performing strains in aquaculture and terrestrial livestock, intensification creates competition for land usage and puts genetic resources at risk. To improve aquaculture's quality and production efficiency, modern aquaculture genetics may play a key role. The challenge for aquaculture is to reduce its environmental impact while simultaneously expanding production to fulfil the growing global demand for fishery products.

Genetic Improvement Programs

Selective Breeding Programs

The implementation of selective breeding paradigms is assuming an increasingly prominent role in the realm of aquaculture production, as evidenced by the burgeoning application of cumulative genetic enhancement strategies in well-managed breeding programs (Boudry et al., 2021). The deliberate selection and mating of individuals exhibiting desirable traits facilitates the creation of offspring with improved attributes, including growth rate, disease resistance, production, and quality (Kashyap et al., 2024). The initiation of this process typically involves the identification of individuals exhibiting the requisite attributes, which may encompass characteristics such as increased milk yield in dairy animals, quicker growth in chickens and fish, or bigger fruit on plants. The subsequent coupling of individuals with complementary desirable traits through regulated mating protocols serves to augment the likelihood of offspring inheriting these advantageous features. The specific methodologies employed in breeding programs, including inbreeding, line breeding, or out-crossing, are contingent upon the program’s objectives and the level of genetic heterogeneity within the population. The iterative selection of offspring with desirable qualities as parents for the subsequent generations, simultaneous with the elimination of individuals with undesirable traits, progressively increases the frequency of desired characteristics within the population.

In the Asian subcontinent, the International Centre for Living Aquatic Research Management (ICLARAM) pioneered the implementation of selective breeding for aquaculture species in 1988, with a focus on the genetic improvement of farmed tilapia (A. Eknath et al., 1998). The relative ease of breeding of Tilapia, attributed to its prolific reproductive capacity, renders it an exemplary species for selective breeding initiatives. The notable success of Genetically Improved Farmed Tilapia (Gift) strain, which exhibits a 100% increase in growth rate relative to its base population and demonstrates adaptability to a wide range of environmental conditions, has contributed substantially to enhanced productivity and income for fish farmers in numerous developing countries in Asia. The selection of Nile Tilapia as a model species for aquaculture was motivated by its popularity, short generation time (approximately 6 months), innate tolerance to variable water quality, and robust disease resistance. Following five generations of selective breeding (A. Eknath et al., 1998), a more nuanced understanding of the genetic basis of production traits has emerged, which may serve to clarify the contradictory results observed in the previous selective breeding study. The efficacy of selective breeding programs can be further enhanced through the implementation of individual and family selection, as evidenced by the dramatic reduction in genetic variation achieved in a long-term selection program for Coho salmon. A better knowledge of the genetic basis of production traits may help to understand the contradictory results about selective breeding that have been observed in the past, as everything indicates that there should be genetic variation for growth rate in the common carp, but selection for growth rate has never been proven to be efficient (Vandeputte, 2003). Moreover, the evaluation of juveniles' trait can play a crucial role in the assessment of maternal traits in natural populations, while indirect selection methodologies can be employed to improve feed efficiency (Growth) in aquaculture species (Kashyap et al., 2024). The continued development of selective breeding programs is essential for the creation of more efficient and effective breeding strategies, which can lead to improved genetic quality, enhanced productivity, and reduced disease incidence. Furthermore, the prioritization of traits such as climate resilience will be critical for mitigating the environmental impact on aquaculture production and ensuring the long-term sustainability of this industry in the face of climate change.

Genetic Markers and DNA Analysis

The application of marker-assisted selection (MAS), also referred to as marker-aided breeding (MAB) or marker-aided selection, has emerged as a pivotal technique in the realm of genetic enhancement, distinct from genetic alternative selection (GAS) (Lal et al., 2024). This approach leverages a diverse array of molecular markers, including amplified fragment length polymorphisms (AFLPs), restriction fragment length polymorphisms (RFLPs), microsatellites, simple sequence repeats (SSRs), random amplified polymorphic DNA (RAPD), and single-nucleotide polymorphisms (SNPs). The efficiency of MAS is particularly pronounced for traits exhibiting low heritability, wherein a substantial proportion of the additive genetic variance is associated with the marker loci. In large populations, MAS has been demonstrated to be more effective than reliance on phenotypic selection alone (Xu et al., 2015). The establishment of molecular genetic markers is a prerequisite for stock structure analysis, and these markers can be broadly categorized into two groups based on their evolutionary dynamics and route of transmission: (i) protein markers, encompassing generic proteins and allozymes, and (ii) DNA markers, including nuclear DNA markers such as RAPDs and VNTRs, mitochondrial DNA, and chloroplast DNA (Hatanaka, 2003). Mutations, which introduce genetic variability, are ubiquitous among species. For geneticists to exploit this variation, it must be heritable and marked. The identification of a gene's location, its corresponding phenotypic manifestation, and its DNA sequence facilitates research into the inheritance of traits or genes.

The genetic markers, defined as unique DNA sequences or alterations in the genome associated with particular traits or characteristics, are essential for identifying individuals with desired traits for breeding purposes, particularly in regards to performance attributes in animals, cattle, and aquaculture species (Williamson, 2001); (Zaid, 1999). Single-nucleotide polymorphism (SNPs), resulting from a single-nucleotide mutation at a specific position in the DNA sequence, represent the most common type of genetic diversity in the genome. Genome-wide association studies (GWAS) or candidate gene approaches can be employed to identify SNPs associated with performance attributes. Microsatellites, characterized as short tandem repeat sequences present in all regions of the genome, can serve as genetic markers to assess genetic diversity and population organization due to their high polymorphism. Although their application in modern breeding programs has decreased, micro-satellites still maintain utility in certain contexts. Quantitative trait loci (QTLs), defined as discrete genetic regions associated with variation in quantitative traits such as growth, disease resistance, and yield, can be identified using QTL mapping methods. By leveraging marker-assisted selection (MAS), researchers can select individuals with the desired QTL alleles for breeding purposes. MAS is an indirect selection process, involves the selection of a trait of interest based on a linked marker (morphological, biochemical, or DNA/RNA variation), rather than the trait itself. This approach has been extensively researched and recommended for the breeding of plants and animals. For instance, the identification of a marker allele associated with disease resistance enables the selection of individuals with disease resistance, rather than solely focusing on the degree of disease resistance. Microsatellite markers have been developed for association with disease resistance in tilapia lines, allowing for the prediction of offspring survival prior to pathogen challenge and facilitating non-lethal and effective selection (Chen et al., 2022). The application of MAS has been demonstrated in various studies, including an investigation on Atlantic salmon (Salmo salar), wherein MAS was utilized to select individuals with improved growth rates, disease resistance, and flesh quality (R. D. Houston et al., 2012). The results of this study highlighted the efficacy of MAS in enhancing the efficiency of selection for multiple traits in aquatic species. Furthermore, (Yu et al., 2018) identified significant correlations between mutations in the coding region of the FST gene and growth traits in large yellow croaker using single-nucleotide polymorphism (SNP) screening, providing molecular evidence for the development of candidate markers.

Genetic linkage, or the chromosomal closeness between the marker locus and the locus determining disease resistance, is posited to be the underlying cause of the marker's high frequency of association with the gene or quantitative trait locus (QTL) of interest. Amplification fragment length polymorphisms and microsatellite markers represent two of the most widely used genetic markers in aquaculture, serving as reflections of specific DNA segments used to monitor particular genomic locations. The genetic markers are distributed throughout the organism’s DNA and are inherited from parent to offspring, facilitating the establishment of parentage and identification of regions conferring performance advantages. The utilization of marker-assisted selection enables selective breeding based on the presence of a particular marker consistently associated with a desired trait, such as resistance to a cold-water bacterial disease, without the need for a rigorously controlled challenge trial. However, the high expense of conventional techniques relying on physical assessment of an organism's characteristics and concerns regarding disease transmission must be considered when employing marker-assisted selection.

Hybridization and Cross-breeding

The strategic exploitation of hybridization or crossbreeding techniques has emerged as a vital approach for optimizing the genetic architecture of performance traits in aquaculture species. By facilitating the controlled mating of individuals from distinct strains or species, these methodologies enable the synergistic combination of desirable attributes from both parent lines, frequently yielding offspring that exhibit superior performance traits. A noteworthy example of this phenomenon is the hybridization of the blue catfish (*Ictalurus furcatus*) and the channel catfish (*Ictalurus punctatus*), which consistently produces offspring that display heterosis, or enhanced characteristics relative to their parents (R. A. Dunham, 2011). The resultant channel-blue hybrid catfish has been extensively researched and applied in the United States, demonstrating superior growth rate, disease resistance, and survival rates compared to pure-bred channel catfish. This finding has significant implications for commercial aquaculture, as the concomitant enhancement of growth efficiency and disease resistance directly translates to increased revenue and output. Similarly, hybridizing different tilapia species, such as Mozambique tilapia (*Oreochromis mossambicus*) and Nile tilapia (*Oreochromis niloticus*), has yielded hybrids that capitalize on the rapid growth rates of Nile tilapia and the salt tolerance of Mozambique tilapia (Hussain, 2003). These hybrids are particularly valuable in environments characterized by variable water salinity, as they can thrive in conditions that would be challenging for pure-bred lines. The success of hybridization and cross-breeding in aquaculture is contingent upon a profound understanding of the genetic and phenotypic characteristics of the parent species, enabling breeders to predict the outcomes of specific crossing and select the most promising pairings to generate high-achieving progeny. The efficacy of these breeding programs is increased by advances in genetic technology, such as genomic selection and molecular markers, which enable more precise parent line selection and hybrid performance prediction (Bentsen, 2012).

A vast array of aquaculture species, including salmon (Glover et al., 2009), tilapia (Ponzoni et al., 2011), catfish (R. A. M. Dunham, M.P, , 2012), shrimps (Z. Zhang, Lu, Lin, You, & Yang, 2023), and Asian seabass (Yue et al., 2009), exhibit rich genetic diversity, rendering them ideal candidates for hybridization and crossbreeding techniques. For instance, hybridization in tilapia has been demonstrated to improve growth rates by 20% over original lines (Ponzoni et al., 2011), highlighting their potential to transform the industry. In Asian seabass, three distinct lines were bred for enhanced growth, disease resistance (Yue et al., 2009), and increased omega-3 content (Yue et al., 2009), further underscoring the efficacy of these techniques. While hybridization and cross-breeding have benefits, they also pose potential drawbacks, such as reduced reproductive performance in hybrids, emphasizing the need to maintain genetic diversity in breeding populations. Current research is focused on developing management practices and breeding procedures that optimize the performance characteristics of hybrid lines while preserving their long-term survival (Bartley D, 2001). The recent advancements in genetic breeding are poised to further enhance genetic improvement in both cross and hybrid breeding, offering a new avenue for the optimization of aquaculture species. By harnessing the power of hybridization and crossbreeding, aquaculture can unlock the full potential of its species, driving innovation and sustainability in the industry.

Gene editing technologies

The advent of gene editing technologies has revolutionized the field of aquaculture, providing precise tools to manipulate an organism's genetic makeup. By leveraging these technologies, it is possible to add, remove, or modify specific genes, thereby significantly enhancing desirable characteristics in fish species, including growth rates, resistance to disease, and environmental tolerance. Among the most prominent gene editing tools is CRISPR-Cas9, a technique inspired by the bacterial immune system, which targets a specific DNA sequence with a guide RNA and then employs the Cas9 enzyme to induce a double-strand break at the target location. This enables the insertion, removal, or replacement of DNA at the break site, thus modifying the cell's natural repair mechanisms. The accuracy and efficacy of this technology have far-reaching implications for aquaculture genetics (Hsu, 2014). The application of CRISPR-Cas9 has yielded promising outcomes in aquaculture. For instance, researchers have utilized this technique to enhance fish disease resistance. A seminar study on zebra fish demonstrated that the deletion of the gene responsible for susceptibility to a particular disease significantly improved the fish's capacity to withstand infection (Grunwald, 2002). This approach can be applied to commercially significant species, such as salmon and tilapia, potentially mitigating the impacts of diseases that regularly strike aquaculture facilities. Furthermore, the use of CRISPR-Cas9 to improve fish growth rates has been explored. By targeting genes that regulate the synthesis of growth hormone, scientists can produce fish strains with enhanced growth rates and efficiency. A notable study on channel catfish successfully modified the myostatin gene, a negative regulator of muscle growth, resulting in fish with increased muscle mass and faster growth rates (Kang et al, 2009). This genetic modification can lead to shorter production cycles and higher yields, benefiting both farmers and consumers. In addition to CRISPR-Cas9, other gene editing technologies, including ZFNs (Zinc Finger Nucleases) and TALENs (Transcription Activator-including Effector Nucleases), have been employed in aquaculture. Although these methods are generally more complex and less efficient than CRISPR-Cas9, they still enable targeted modification to the genome and are utilized in the development of genetically modified fish. For example, TALENs have been used to eliminate specific genes from tilapia, resulting in strains with improved growth rates and disease tolerance (Ansai, 2014). The potential benefits of gene editing in aquaculture are substantial, as it can facilitate the creation of genetically superior strains with enhanced growth rates, disease resistance, and environmental tolerance, thereby promoting more sustainable and efficient fish farming practices.

However, gene editing in aquaculture also presents several challenges and ethical concerns. One of the primary concerns is the potential impact of genetically modified organisms (GMOs) on natural ecosystems. The unintended ecological consequences of genetically modified fish escaping into the wild and out-competing or interbreeding with natural populations are a significant concern (A. R. Kapuscinski, and D.J. Brister., 2001). To mitigate these risks, researchers are developing inhibition strategies and examining the behaviour and fitness of genetically edited fish in controlled settings. Additionally, public opinion and regulatory approval pose significant hurdles, as some consumers have expressed concerns about the safety and ethics of GMOs in food production. The regulatory frameworks governing gene editing in aquaculture vary widely between countries, and obtaining approval for genetically modified fish can be a protracted and challenging process (Van Eenennaam & Muir, 2011). Open communication and rigorous safety testing are essential to address these concerns and gather public and regulatory support. Despite these challenges, the transformative potential of gene editing technologies in aquaculture is undeniable.

Recent reviews highlighted the promise of CRISPR-Cas9 for efficiency, precision, and predictability in fish aquaculture (Ye, Zhu, & Sun, 2015) ; (Zhu & Ge, 2018). Other studies have explored the application of genome editing and RNAi therapeutic tools for combating pathogens in aquaculture (Gotesman, Menanteau-Ledouble, Saleh, Bergmann, & El-Matbouli, 2018); (Elaswad A, 2018). They also highlight the possibility for knock-in (KI) procedures and the benefits of the combination of genome editing and selective breeding. The increased speed of technology development within the genome) Sequencing has aided the rapid development of genome editing technologies. (R. D. Houston & Macqueen, 2019) reviewed the exploitation possibilities from sequencing and annotation of the Atlantic salmon genome. They build on (Lien et al., 2016), which was part of the Salmon Genome Project and had a special focus on the ecology, physiology and evolution of the salmon genome, as well as highlighting further possibilities by genome editing. The capacity to precisely alter fish genetic composition will facilitate the creation of strains more adapted to the needs of contemporary aquaculture as research and techniques evolve. This will enhance the sustainability and productivity of fish farming while also promoting economic growth and food security in areas where aquaculture is a major sector.

Genomic selection

Genomic selection is mostly employed in aquaculture breeding programs for features that are not directly measurable on the broodstock fish. These characteristics include things like disease resistance, processing yields, and product quality, which are assessed on both full and half-sibs of the broodstock fish. Based on genotype and phenotype data collected on their siblings and other relatives (referred to as a reference population), genomic selection estimates the genomic breeding values of genotyped selection candidates using genome-wide DNA marker information, usually single-nucleotide polymorphisms (SNPs). Alternative methods to assess the genetic merit of breeding individuals with various features have been investigated as a result of the awareness that traditional breeding programs for traits other than growth are challenging to implement. In particular, breeders are using genetic marker technology in the form of marker-assisted selection (MAS) to support animal selection as a result of the quick advancements in genomics and quantitative analytical techniques. The application of MAS to improve complex qualities governed by numerous genes with smaller effects is limited, even though this technique can be helpful for some traits where quantitative trait loci (QTL) of substantial effect have been identified. Only with increasingly sophisticated genomic-based techniques, where it is now feasible to precisely forecast genome-wide molecular breeding values for enhanced animal selection, can genetic improvement in these qualities be attained. This method, known as genomic selection, was initially put forth by (Meuwissen TH, 2001) and has become widely used in the plant and animal breeding industries.

The foundation of genomic selection is the hypothesis that most quantitative trait loci will be in significant linkage disequilibrium with at least one marker if there are a sufficient number of loci spread throughout the genome (Meuwissen TH, 2001). Thus, genomic selection yields precise estimates of genetic merit for a trait while concurrently estimating the total genetic influence of every pertinent QTL. Additionally, the genomic relationship matrix (GRM) is directly computed from genome-wide markers. Utilizing genomic best linear unbiased prediction methods (i.e., GBLUP, (VanRaden, 2008), the GRM can then be used to compute genomic estimated breeding values (GEBVs). When compared to estimates based solely on pedigree information, GRM, even on a smaller subset of markers, can accurately estimate the percentage of the genome shared by related individuals and, as a result, provide a higher accuracy of breeding value estimation (Habier, 2011). Aquaculture breeding programs' genetic responsiveness can be greatly enhanced by applying genomic selection. According to preliminary theoretical studies on genomic selection in aquatic species, compared to traditional selection, higher rates of genetic gain (up to 10% for body weight) and selection accuracy can be attained (Campos-Montes G. R., 2013). Reducing the generation interval and choosing candidates early in life based on their genomic breeding value can also result in additional increases in the rate of genetic gain (Campos-Montes G. R., 2013). Additionally, compared to conventional selection methods, genomic selection can lower rates of inbreeding by as much as 81% (Vandeputte M., 2014). This is especially crucial for aquaculture species because of the possibility of extraordinarily high fecundity, which could limit the effective population size (Ne) on the farm and cause inbreeding or a loss of diversity (Dupont-Nivet M., 2006). Genomic selection in aquaculture has the profound potential to shift the breeding structure from communal rearing environments with single-line mating systems to multifamily breeding programs, thereby reducing the need for infrastructure and possibly optimizing genetic gain and diversity (Fernandes Junior, 2016).

Impact on Fish Productivity

Enhanced Growth Rates

In farmed fish, selective breeding for better growth performance results in quicker growth rates and more effective feed conversion, which raises productivity and lessens environmental impact. Faster-growing strains produce less waste and use fewer resources because they require less feed. Using genetic data, selective breeding methods have proven to be quite successful in choosing broodstock with desired characteristics, including increased growth rate. The potential for genetic improvement is demonstrated by the notable gains in growth rates and feed efficiency that have resulted from genetic selection in tilapia (T. Gjedrem, & Baranski, M., 2009). Furthermore, faster and more accurate genetic gains are made possible by developments in genomic methods like marker-assisted selection (MAS) and genomic selection. Research on Atlantic salmon has demonstrated that by focusing on particular genetic markers linked to quicker growth, MAS can accelerate growth rates (Sonesson AK, 2005). By increasing growth rates and overall production, precision breeding makes aquaculture more productive, sustainable, and efficient. Adding biotechnological techniques like CRISPR/Cas9 gene editing increases the possibility of making genetic advancements even further. Studies have indicated that the process of gene editing can increase fish growth rates through the modification of genes that are directly related to growth and metabolism (Y. Zhang, Ding, Y., Guo, F., & Wang, X. , 2020). These developments demonstrate how important aquaculture genetics is to maintaining the productivity and expansion of fish stocks and guaranteeing the industry's long-term viability. Selective breeding and sophisticated genetic procedures have produced enhanced strains, which consistently exhibit better growth rates than non-improved strains. As to (A. E. Eknath, et al. , 2007), strains of Nile tilapia (*O. niloticus*) that have undergone selective breeding have exhibited growth rates that can surpass those of wild-type or non-selected strains by up to 30 to 40%. Likewise, strains of genetically enhanced farmed tilapia (GIFT) grow substantially quicker than non-improved strains, resulting in shorter production cycles and higher yields. Tilapia (*O. niloticus*), for instance, has exhibited growth rate gains of 60–70% in studies comparing GIFT tilapia with non-improved strains, thus increasing overall production efficiency (Gupta, 2004). The advantages of genetic improvement in commercial aquaculture have been demonstrated by selectively produced strains of Atlantic salmon (*Salmo salar*), which have demonstrated up to 20–30% higher growth rates and increased FCR when compared to wild-type strains (T. Gjedrem, 2000).

Improved Disease Resistance

Advances in genetic technology combined with selective breeding programs have produced fish strains that exhibit increased resistance against common diseases. These initiatives assist in lowering the frequency and intensity of disease outbreaks by locating and selecting for genetic markers linked to disease resistance. For instance, strains of rainbow trout (*Oncorhynchus mykiss*) with considerably reduced susceptibility to illnesses like bacterial cold water disease and viral haemorrhagic septicaemia have been produced by selective breeding for resistance to bacterial and viral infections (Silverstein J. T, 2008). In aquaculture populations, decreased death rates are closely correlated with improved disease resistance. Less disease-related mortality occurs in genetically resistant breeds, resulting in more stable and fruitful stocks. Research on Atlantic salmon (*Salmo salar*) has demonstrated that selective breeding for resistance to infectious pancreatic necrosis (IPN) has led to a considerable decrease in death rates, hence improving the overall survival of the stock (T. Gjedrem, & Baranski, M., 2009). The need for chemical therapies like antibiotics and anti-parasitic medicines decreases as disease resistance increases. This decreases production costs while also lessening the chance of drug-resistant microorganisms emerging and mitigating environmental effects. By increasing resistance to illnesses like *Streptococcus iniae* and *Francisella*, selective breeding operations in tilapia (*O. niloticus*) have shown reduced dependence on chemical treatments (Shoemaker, 2006). Strain GIFT (Genetically Improved Farmed Tilapia) demonstrates resistance against many diseases, such as Streptococcus species. Rainbow trout (*O. mykiss*) strains chosen for resistance to bacterial cold water illness and infectious hematopoietic necrosis virus (IHNV) have demonstrated significantly decreased mortality rates, lowering disease-related losses (Gupta, 2004). (Silverstein J. T, 2008). and Salmo salar, the Atlantic salmon: In aquaculture systems, selective breeding of strains for resistance to sea lice and other diseases has reduced illness incidence and enhanced general health (Gjøen, 1997).

Increased Reproductive Performance

According to a recent review paper published in Nature Reviews Genetics, many fish and shellfish species have been domesticated relatively recently in comparison to other livestock species. As a result, they offer varied gene pools with significant potential for selective breeding. There are opportunities to unleash that potential, according to academics, through the creation of tools to learn more about the genetics of these species and use those tools for breeding and management. The majority of aquaculture species have a high reproductive rate, and large populations with better genetics may be grown fast for increased productivity. As far as seafood is concerned, farmed fish is expected to surpass wild fish in the near future. Consequently, there is a great need for genetic tools and knowledge to improve the sustainability and efficiency of aquaculture systems, which presently mostly rely on unselected stocks. Understanding a species' genome can aid with the careful selection of a farming population with desired qualities, and as farm populations grow, tracking genomic variation will support the preservation of genetic diversity. When compared to non-improved strains, fish strains with genetic improvements grow noticeably quicker. For instance, strains of Nile tilapia (*O. niloticus*) that grow up to 30–50% quicker than wild forms are the product of selective breeding (A. E. Eknath, et al. , 2007).

In aquaculture operations, this quick growth results in better yields and biomass. Enhancing feed conversion ratios (FCR) is the main goal of selective breeding programs because it enables fish to convert feed into body mass more effectively. Research on Atlantic salmon (*S. salar*) has demonstrated that genetic advancements can result in feed efficiency gains of 10–15%, which can be translated into reduced feed expenses and improved growth performance (Thodesen, 1999). The combination of enhanced growth rates and improved feed efficiency results in shorter production cycles, allowing fish to reach market size more quickly. This reduces the overall time and resources needed for aquaculture production. For instance, improved strains of tilapia, such as the GIFT (Genetically Improved Farmed Tilapia), not only grow faster but also require less feed, leading to significant cost savings and higher profitability (Gupta, 2004). By reducing the time to market and feed expenses, these genetic improvements provide substantial economic benefits to aquaculture producers.

Future Perspectives and Challenges

Sustainable Genetic Management

The future of genetic advancements in aquaculture is likely to be shaped by the integration of cutting-edge genomic techniques, including whole-genome sequencing, CRISPR/Cas9 gene editing, and bioinformatics. According to a recent study by (Y. Zhang, Ding, Y., Guo, F., & Wang, X. , 2020), these technologies can precisely modify traits such as feed efficiency, growth rates, and disease resistance, thereby accelerating genetic improvement. The availability of extensive genomic datasets for various fish species will facilitate the identification of beneficial genes and genetic markers, which can be leveraged to enhance genomic selection techniques and selective breeding operations (R. D. e. a. Houston, 2020). However, it is crucial to prioritize sustainable breeding strategies that preserve genetic diversity and avoid inbreeding, which can be achieved through the creation of genetic libraries and implementation of rotational breeding programs (T. Gjedrem, Robinson, N., and Rye, M. , 2012). One of the major challenges in genetic enhancement efforts is ensuring that the genetic diversity required for fish populations to be resilient and adaptable is not compromised. The loss of genetic variation can render stocks more vulnerable to diseases and environmental changes (Liu, 2019). Furthermore, the use of genetic modification technologies raises concerns about ecology and ethics. It is essential to address public concerns over genetic engineering in aquaculture and assess the ecological impacts of releasing genetically modified organisms into the wild (Muir, 2002a). The establishment of comprehensive regulatory and policy frameworks is necessary to oversee genetic management practices in aquaculture, including guidelines for the application of genetic technologies, tracking genetic diversity, and guaranteeing genetically modified stock traceability (Ajmone M. P, 2023).

The genetic management and development of aquaculture species lag behind that of terrestrial agriculture, presenting a significant opportunity to enhance genetic management to capture and conserve the high levels of genetic diversity present in wild and domesticated genetic resources (Sonesson et al., 2023). A unique feature of farmed aquatic genetic resources (AqGR) is the presence of the wild counterparts, which constitute a larger reservoir of genetic diversity that can be utilized for starting selective breeding programs. These programs can be powerful tools for improving the performance of the aquaculture sector, with genetic gains typically being larger for aquaculture species compared to terrestrial populations. However, the importance of this wild genetic resource also underscores the responsibility to manage the total (wild and farmed) genetic resources of the species sustainably, both technologically and in terms of policies and regulations (Sonesson et al., 2023). In recognition of the critical importance of the effective management of genetic resources to the future of aquaculture development, the Food and Agriculture Organization of the United Nations (FAO) recently adopted a Global Plan of Action for the Conservation and Sustainable Use of AqGR for Food and Agriculture (FAO., 2022). This plan identified strategic priorities and recommended actions for the enhancement of genetic resource management. Typically, the genetic status of domesticated farmed types and the potential for genetic improvement are only considered when an aquaculture species sector reaches a certain scale and value. Unfortunately, many poorly managed aquaculture breeding populations suffer from inbreeding and genetic erosion (e.g., (Evans, Bartlett, Sweijd, Cook, & Elliott, 2004); (Li, Xu, & Yu, 2007); (Yue et al., 2009), which can be attributed to the high fecundity of aquatic species and the lack of managerial competencies in genetic management. In these cases, it is often possible to supplement genetic variation in farmed types by returning to wild relative stocks, although this approach can dilute the benefits of domestication selection for traits that enable farmed types to adapt and thrive in aquaculture systems (Janssen, Berentsen, & Komen, 2015). Therefore, the sustainable use in the context of AqGR should emphasize the effective genetic management of farmed types during and after the domestication process, regardless of whether genetic improvement is prioritized. Unfortunately, the genetic status of most farmed types of species under domestication is unknown and is not monitored, which can lead to speculation about the genetic status when adverse production events occur (Sonesson et al., 2023).

Ethical Considerations

Natural ecosystems are at risk when genetically modified (GM) fish are released into the wild or escape from captivity. The stability of ecosystems may be impacted by genetic contamination and loss of genetic variety resulting from the possible interbreeding of genetically modified fish with wild populations (A. R. H. Kapuscinski, E.M. , 1991). Maintaining genetic variety and improving production through genetics must coexist in harmony. Plans need to be created to keep fish populations, both farmed and wild, robust and healthy, while preventing the genetic base from becoming smaller (Lorenzen, 2012). Selective breeding may unintentionally result in welfare problems, such as increased susceptibility to stress or malformations, even though its goal is to promote good features. Fish welfare should be the top priority in ethical breeding methods to prevent genetic advancements from jeopardizing fish health and well-being (Huntingford, 2005). Advanced genetic editing techniques like CRISPR pose moral dilemmas regarding the appropriateness of human genome modification of animals. Guidelines are required to guarantee that genetic interventions are carried out ethically and openly (Van Eenennaam, 2017). Cultural and societal acceptance of genetically modified organisms (GMOs) varies greatly. To allay fears, give correct information, and foster public confidence in genetic technology employed in aquaculture, open communication and public involvement are essential (Marris, 2001). For the sake of equity, it is crucial to guarantee that small-scale and subsistence fish farmers profit from advances in aquaculture genetics. It is important to ensure equitable distribution of benefits among various populations and areas by providing equitable access to improved strains and technologies (Brummett, 2000).

Integration of Genomic Technologies

The strategic application of genomic selection, which involves utilizing data from the entirety of individual's genome to predict their breeding value, has revolutionized the field of aquaculture. This innovative approach enables the precise identification and selection of broodstock with desired qualities, such as growth rate, disease resistance, and feed efficiency, thereby facilitating more effective breeding programs (Meuwissen TH, 2001). Notably, research conducted on Atlantic salmon has demonstrated that genomic selection can accelerate genetic gains by 20–30% compared to conventional methods (Sonesson AK, 2005). The comprehensive information afforded by whole-genome sequencing provides invaluable insights into genetic diversity within and between populations, which is essential for maintaining genetic diversity and identifying genes associated with significant traits (R. D. e. a. Houston, 2020). The importance of preserving genetic diversity in aquaculture populations cannot be overstated, as it enables fish stocks to develop resistance and adaptability to environmental changes and disease outbreaks. The precise editing of fish genomes using CRISPR/Cas9 technology has emerged as a powerful tool for enhancing desirable traits such as disease resistance. For instance, Researchers have successfully employed CRISPR to generate tilapia lines with enhanced disease resistance by targeting specific genes involved in immune responses (Li L, 2019). This not only improves overall fish health but also reduces the need for antibiotics. The integration of genomic technology into breeding programs has been shown to increase cost-effectiveness, streamline the breeding process, and accelerate the development of superior fish strains through the use of marker-assisted selection (MAS) and genomic selection (T. Gjedrem, Robinson, N., and Rye, M. , 2012).

The advent of whole-genome sequencing (WGS) has also facilitated the application of genome-wide association studies (GWAS) to livestock and aquaculture species, enabling the identification of potential causal variants (Fraslin, Houston, & Robledo, 2022). However, despite the availability of WGS data, identifying genuine causal variants remains a significant challenge due to their small effects and the presence of linkage disequilibrium among nearby variants (VanRaden, Tooker, O'Connell, Cole, & Bickhart, 2017). To address this issue, pre-selection of genetic variants based on raw GWAS results has been proposed for livestock species, resulting in moderate improvements in the prediction accuracy of complex traits. Furthermore, the combination of GWAS and transcriptome analysis offers a powerful approach for identifying SNPs and candidate genes, with the potential to develop molecular markers for plant breeding (Zhou et al., 2022). In addition to genetic factors, Epigenetic modifications such as DNA methylation and histone modifications regulate gene expression, which is highly responsive to environmental factors such as temperature, nutrition, and stress. These modifications can have transgenerational effects, potentially influencing the adaptability and resilience of offspring without changing the underlying DNA sequence (Youngson & Whitelaw, 2008). The development of epigenetic research in aquaculture has the potential to revolutionize our understanding of the complex interactions between genetic and environmental factors and their impacts on fish development and productivity. As such, further research in this area is warranted to fully elucidate the mechanisms underlying epigenetic modification and their implications for aquaculture breeding programs.

Conclusion

The maintenance of sustainable practices and the satiation of burgeoning global demand for fish necessitate the pivotal role of aquaculture genetics in increasing fish populations. The advent of genetic principles has triggered a typical shift in aquaculture, facilitating the production of fish stocks with improved growth rates, disease resistance, and reproductive efficiency. The improvement of fish stocks' productivity and quality is largely dependent on aquaculture genetics. Scientists can create superior breeds of fish that grow quickly, resist sickness better, and reproduce more effectively by comprehending and modifying genetic features. This genetic advancement is essential to guaranteeing a consistent and dependable supply of fish that is fit for human consumption. Aquaculture's genetic advancement has been largely dependent on selective breeding initiatives. In these systems, the top performers are selected based on certain desired features, and they are then bred across multiple generations. By gradually enhancing these features in the population, this strategy improves overall performance, growth rates, and resilience to disease. Selective breeding has been transformed by the application of genetic markers and DNA analysis, which allows for more accurate breeding stock selection. With the aid of these instruments, it is possible to identify particular genes linked to desired characteristics, making it easier to choose people who possess these genes. Breeding programs are more accurate, and the breeding process moves more quickly thanks to this genomic information. Techniques like hybridization and cross-breeding are used to combine advantageous features from various strains or species. Aquaculturists can generate fish with improved traits, like faster growth and increased resilience to environmental stressors, by breeding hybrids. The genetic variety and adaptability of aquaculture organisms are increased by these techniques. Advancements in genome editing technologies, such as CRISPR-Cas9, present previously unheard-of possibilities to directly alter fish genetic composition. Compared to conventional breeding approaches, these technologies are more accurate and effective at producing fish with specified features because they can add, remove, or modify specific genes. Aquaculture could benefit greatly from focused and quick genetic advancements thanks to gene editing. Whole-genome data is used by genomic selection to forecast an individual's breeding value. By using the complete genetic data, this method chooses the most suitable candidates for reproduction, increasing the precision and effectiveness of genetic enhancement initiatives. Genomic selection works especially well for complex traits with multiple gene influences.

The production of fish has been greatly affected by the incorporation of these genetic approaches. Higher yields and faster production cycles are made possible by improved growth rates. Better disease resistance results in healthier stocks by lowering death rates and the requirement for medical interventions. A steady supply of fry and fingerlings is ensured by increased reproductive performance, which supports viable aquaculture operations. In the future, maintaining genetic improvement while taking ethical and ecological factors into account would require sustainable genetic management. To avoid inbreeding and guarantee the long-term sustainability of fish stocks, genetic diversity must be preserved. It is important to carefully analyse the ethical implications of gene editing and any potential ecological effects. For aquaculture to remain sustainable in the future, integrating genomic technology into standard operating procedures will necessitate large infrastructural and training investments.

Acknowledgements

This is to thank Kibogora Polytechnic University, Department of Sciences, PO. BOX 50 Nyamasheke, Rwanda, with its partnership with the National Engineering Research Center of Marine Facilities Aquaculture, Zhejiang Ocean University, Zhoushan, 316022, China.

Declaration of Competing Interest

No conflict of interest in the paper

Funding

This work is supported by the Aquaculture Breeding and Seedling Technology Innovation Center Project of Zhoushan (2025Y001-1), National Key Research and Development Program of China Grants (2023YFD2401900), National Key Research and Development Program of China (2023YFD2401905)

Data availability

Enquiries about data availability should be directed to the authors.

Authors contribution

Murwanashyaka Michel: Writing original draft, writing review & editing.

Lihua Jiang: Supervision, writing review & editing.

Xiaojun Yan: Supervision, funding acquisition.

ORCID

Murwanashyaka Michel https://orcid.org/0009-0001-1482-548X

References

Ajmone M. P, B. P., Licia C, Johanes A.L, . (2023). Genomic characterization of animal genetic resources - Practical guide. *Reasearchgate*. doi:https://doi.org/10.4060/cc3079en

Ansai, S., Kinoshita, M. . (2014). Targeted mutagenesis using CRISPR/Cas system in medaka. . *Biology Open, 3(5)*, 362–371. doi:https://doi.org/10.1242/bio.20148177

Bartley D, R. K., Immink A . . (2001). The use of inter-specific hybrids in aquaculture and fisheries. *Review in Fish Biology*.

Bentsen, H. B., Gjerde, B., Nguyen, N.H., Rye, M., Ponzoni, R.W., Palada de Vera, M.S., Bolivar, H.L., Velasco, R.R., Danting, J.C., Dionisio, E.E., Longalong, F.M., Reyes, R.A., Abella, T.A., Tayamen, M.M., Eknath, A.E., . (2012). Genetic improvement of farmed tilapias: Genetic parameters for body weight at harvest in Nile tilapia (Oreochromis niloticus) during five generations of testing in multiple environments. . *Aquaculture*, 338–341, 356–365. doi:https://doi.org/10.1016/j.aquaculture.2012.01.027

Boudry, P., Allal, F., Aslam, M. L., Bargelloni, L., Bean, T. P., Brard-Fudulea, S., . . . Houston, R. D. (2021). Current status and potential of genomic selection to improve selective breeding in the main aquaculture species of International Council for the Exploration of the Sea (ICES) member countries. *Aquaculture Reports, 20*, 100700. doi:https://doi.org/10.1016/j.aqrep.2021.100700

Brummett, R. E. a. M. J. W. (2000). The evolution of aquaculture in African rural and economic development. *Ecological Economics, 33*, 193–203. doi:https://doi.org/10.1016/S0921-8009(99)00142-1

Campos-Montes G. R., M. H. H., Martínez-Ortega A., Jiménez A. M., Castillo-Juárez H. . (2013). Genetic parameters for growth and survival traits in Pacific white shrimp Penaeus

(Litopenaeus vannamei) from a nucleus population undergoing a two-stage selection program. doi:https://doi.org/10.1007/s10499-012-9553-1

Chen, C.-C., Huang, C.-W., Lin, C.-Y., Ho, C.-H., Pham, H. N., Hsu, T.-H., . . . Gong, H.-Y. (2022). Development of Disease-Resistance-Associated Microsatellite DNA Markers for Selective Breeding of Tilapia (Oreochromis spp.) Farmed in Taiwan. *Genes, 13*(1), 99. doi:https://doi.org/10.3390/genes13010099

Dunham, R. A. (2011). Aquaculture and fisheries biotechnology: genetic approaches. 2nd Edition. *Aquaculture and Fisheries Biotechnology:* , pp 240–277.

Dunham, R. A. M., M.P, . (2012). Production of Hybrid Catfish. *Southern Regional Aquaculture Center: Stoneville, MS, USA, 436*, 1–7.

Dupont-Nivet M., V. M., Haffray P., Chevassus B. . (2006). Effect of different mating designs on inbreeding, genetic variance and response to selection when applying individual selection in fish breeding programs. *Aquaculture*. doi:https://doi.org/10.1016/j.aquaculture.2005.07.005

Eknath, A., Dey, M., Rye, M., Gjerde, B., Abella, T. A., Sevilleja, R., . . . Bentsen, H. (1998). Selective Breeding of Nile Tilapia for Asia. *6th World Congress on Genetics Applied to Livestock Production, 27*, 89–96.

Eknath, A. E., et al. . (2007). Genetic improvement of farmed tilapias: the growth performance of eight strains of Oreochromis niloticus tested in different farm environments. *Aquaculture, 228(1-4)*, 105–116. doi:https://doi.org/10.1016/0044-8486(93)90035-W

El-Sayed, A.-F. (2019). Tilapia Culture. 2nd ed. . *Elsevier/Academic*, 1–20. doi:https://doi.org/10.1016/B978-0-12-816509-6.00001-X

Elaswad A, D. R. (2018). Disease reduction in aquaculture with genetic and genomic technology: current and future aproaches. *Rev Aquacul, 10(4)*, 876– 898. doi: https://doi.org/10.1111/raq.12205

Evans, B., Bartlett, J., Sweijd, N., Cook, P., & Elliott, N. G. (2004). Loss of genetic variation at microsatellite loci in hatchery produced abalone in Australia (Haliotis rubra) and South Africa (Haliotis midae). *Aquaculture, 233*(1), 109–127. doi:https://doi.org/10.1016/j.aquaculture.2003.09.037

FAO. (2016). The state of world fisheries and aquaculture. *Food and Agriculture Organization of the United Nations. , Rome, 2016.*

FAO. (2022). The state of world fisheries and aquaculture Towards Blue Transformation. Rome.

FAO. (2022). Global plan of action for the conservation, sustainable use and development of aquatic genetic resources for food and agriculture. *Commission on Genetic Resources for Food and Agriculture*.

Fernandes Junior, G. A. (2016). Genomic prediction of breeding values for carcass traits in Nellore cattle. Genetics, selection,. *Genomic Selection and Evolution, 48*, p.7. doi:https://doi.org/10.1186/s12711-016-0188-y

Fraslin, C., Houston, R. D., & Robledo, D. (2022). Chapter 6 - Methods for mapping genomic variants associated with production traits in aquaculture species. In I. F. Monzón & J. M. O. Fernandes (Eds.), *Cellular and Molecular Approaches in Fish Biology* (pp. 193–220): Academic Press.

Gjedrem, T. (2000). Genetic improvement of cold-water fish species. . *Aquaculture Research, 31(1)*, 25–33. doi:https://doi.org/10.1046/j.1365-2109.2000.00389.x

Gjedrem, T. (2010). The First Family-Based Breeding Program in Aquaculture. . *Reviews in Aquaculture*. doi:https://doi.org/10.1111/j.1753-5131.2010.01011.x

Gjedrem, T., & Baranski, M. (2009). Selective Breeding in Aquaculture: An Introduction. . *Springer*. doi:https://doi.org/10.1007/978-90-481-2773-3

Gjedrem, T., Robinson, N., and Rye, M. . (2012). The importance of selective breeding in aquaculture to meet future demands for animal protein: A review. *Aquaculture*. doi:https://doi.org/10.1016/j.aquaculture.2012.04.008

Gjøen, H. M., & Bentsen, H. B. . (1997). Past, present, and future of genetic improvement in salmon aquaculture. . *ICES Journal of Marine Science, , 54(6)*, 1009–1014. doi:https://doi.org/10.1016/S1054-3139(97)80005-7

Glover, K. A., Otterå, H., Olsen, R. E., Slinde, E., Taranger, G. L., & Skaala, Ø. (2009). A comparison of farmed, wild and hybrid Atlantic salmon (Salmo salar L.) reared under farming conditions. *Aquaculture, 286*(3), 203–210. doi:https://doi.org/10.1016/j.aquaculture.2008.09.023

Gotesman, M., Menanteau-Ledouble, S., Saleh, M., Bergmann, S. M., & El-Matbouli, M. (2018). A new age in AquaMedicine: unconventional approach in studying aquatic diseases. *BMC Veterinary Research, 14*(1), 178. doi:https://doi.org/10.1186/s12917-018-1501-5

Grunwald, D. J., Eisen, J. S. . (2002). Headwaters of the zebrafish—emergence of a new model vertebrate. . *Nature Reviews Genetics, 3(9)* 717–724.

Gupta, M. V., & Acosta, B. O. . (2004). From drawing board to dining table: The success story of the GIFT project. . *NAGA, WorldFish Center Quarterly, 27(3-4)*, 4–14.

Habier, D., R. L. Fernando, K. Kizilkaya, and D. Garrick. . (2011). Extension of the Bayesian alphabet for genomic selection. . *BMC Bioinformatics, 12*, 186. doi:https://doi.org/10.1186/1471-2105-12-186

Hatanaka, T. a. G., Jr P.M. . (2003). RAPD markers indicate the occurrence of structured populations in a migratory freshwater fish species. . *Genetics and Molecular Biology 26*, 19–25.

Henriksson, P. J. G., Troell, M., Banks, L. K., Belton, B., Beveridge, M. C. M., Klinger, D. H., . . . Tran, N. (2021). Interventions for improving the productivity and environmental performance of global aquaculture for future food security. *One Earth, 4*(9), 1220–1232. doi:https://doi.org/10.1016/j.oneear.2021.08.009

Herkenhoff, M. E. (2025). Perspectives of Population Genetics in the Genetic Improvement and Biodiversity Conservation of Fish Species. In R. T. Maia, P. T. Felix, & M. D. A. Campos (Eds.), *Advances and Trends in Population Genetics Studies*. London: IntechOpen.

Houston, R. D., Davey, J. W., Bishop, S. C., Lowe, N. R., Mota-Velasco, J. C., Hamilton, A., . . . Taggart, J. B. (2012). Characterisation of QTL-linked and genome-wide restriction site-associated DNA (RAD) markers in farmed Atlantic salmon. *BMC Genomics, 13*, 244. doi:https://doi.org/10.1186/1471-2164-13-244

Houston, R. D., & Macqueen, D. J. (2019). Atlantic salmon (Salmo salar L.) genetics in the 21st century: taking leaps forward in aquaculture and biological understanding. *Anim Genet, 50*(1), 3–14. doi:https://doi.org/10.1111/age.12748

Houston, R. D. e. a. (2020). Harnessing genomics to fast-track genetic improvement in 668 aquaculture. . *Nature Reviews Genetics. Nature Research*, pp. 389–409. doi:https://doi.org/10.1038/s41576- 669 020-0227-y.

Hsu, P. D., Lander, E. S., & Zhang, F. . (2014). Development and applications of CRISPR-Cas9 for genome engineering. *Cell, 157(6)*, 1262–1278. doi:https://doi.org/10.1016/j.cell.2014.05.010

Huntingford, F. A. A., C. E. . (2005). Behavioural syndromes in farmed fish: implications for production welfare. . *Behaviour, 142*, 1207–1221. doi:https://doi.org/10.1163/156853905774539382

Hussain, M. G. a. A. H. M. K. (2003). Breeding, monosex male tilapia seed production and culture technologies of BFRI super tilapia. . *Bangladesh Fisheries Research Institute, Mymensingh, Extension manual No. 25*.

Janssen, K., Berentsen, P., & Komen, J. (2015). *Current status of selective breeding in European aquaculture*.

Kang et al. (2009). Introducing precise genetic modifications by CRISPR/Cas-mediated genome editing. *J Assist Reprod Genet*. doi:https://doi.org/10.1007/s10815-016-0710-8

Kapuscinski, A. R., and D.J. Brister. (2001). Genetic Impacts of Aquaculture. Environ mental Effects of Aquaculture.

Kapuscinski, A. R. H., E.M. . (1991). Implications of introduction of transgenic fish into natural ecosystems. . *Canadian Journal of Fisheries and Aquatic Science, 48 (suppl. 1)*, 99–107. doi:https://doi.org/10.1139/f91-308

Kashyap, N., Meher, P., Eswaran, S., Kathirvelpandian, A., Udit, U., Jaiswar, R., . . . Kashyap. (2024). A Review on Genetic Improvement in Aquaculture through Selective Breeding. *Journal of Advances in Biology & Biotechnology, 27*, 618–631. doi:https://doi.org/10.9734/jabb/2024/v27i71022

Lal, J., Vaishnav, A., Singh, S. K., Meena, D. K., Biswas, P., Mehta, N. K., & Priyadarshini, M. B. (2024). Biotechnological innovation in fish breeding: from marker assisted selection to genetic modification. *Discover Biotechnology, 1*(1), 7. doi:https://doi.org/10.1007/s44340-024-00007-6

Li L, L. Y., Huang T, Liang W, Chen M. . (2019). Development of an attenuated oral vaccine strain of tilapia group B streptococci serotype Iay gene knockout technology. . *Fish Shellfish Immunol. , 93*, 924– 933. doi:https://doi.org/10.1016/j.fsi.2019.07.081

Li, Q., Xu, K., & Yu, R. (2007). Genetic variation in Chinese hatchery populations of the Japanese scallop (Patinopecten yessoensis) inferred from microsatellite data. *Aquaculture, 269*(1), 211–219. doi:https://doi.org/10.1016/j.aquaculture.2007.04.017

Lien, S., Koop, B. F., Sandve, S. R., Miller, J. R., Kent, M. P., Nome, T., . . . Davidson, W. S. (2016). The Atlantic salmon genome provides insights into rediploidization. *Nature, 533*(7602), 200–205. doi:https://doi.org/10.1038/nature17164

Liu, W., Chen, L., Zhang, S., Hu, F., Wang, Z., Lyu, J., et al. . (2019). Decrease of gene expression diversity during domestication of animals and plants. *BMC Evol. Biol. , 19*, 19. . doi:https://doi.org/10.1186/s12862-018- 1340-9

Lorenzen, K., M. C. Beveridge, and M. Mangel. . (2012). Cultured fish: integrative biology and management of domestication and interactions with wild fish. *Biological Reviews, 87*, 639–660. doi:https://doi.org/10.1111/j.1469-185X.2011.00215.x

Marris, C. (2001). Public perceptions of transgenic products: the influence of the behaviour of laboratory scientists. *In J.-P. Toutant and E. Balàzs (Eds.) Molecular Farming : Proceedings of the OECD Workshop held in La Grande Motte (France) September 3-6, 2000., INRA editions, Versailles.* , pp.289–305.

Meuwissen TH, H. B., Goddard ME (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics 157*, 1819–1829. doi:https://doi.org/10.1093/genetics/157.4.1819

Muir, W. M. a. R. D. H., . . (2002a). Assessment of possible ecological risks and hazards of transgenic fish with implications for other sexually reproducing organisms. *Transgenic Res*, pp. 355–384. doi:https://doi.org/10.1023/a:1015203812200.

Naylor, R. L., Hardy, R. W., Buschmann, A. H., Bush, S. R., Cao, L., Klinger, D. H., . . . Troell, M. (2021). A 20-year retrospective review of global aquaculture. *Nature, 591*(7851), 551–563. doi:https://doi.org/10.1038/s41586-021-03308-6

Ponzoni, R., Nguyen, N., Khaw, H. L., Hamzah, A., Abu-Bakar, K., & Yee, H. Y. (2011). Genetic improvement of Nile tilapia (Oreochromis niloticus) with special reference to the work conducted by the WorldFish Center with the GIFT strain. *Reviews in Aquaculture, 3*. doi:https://doi.org/10.1111/j.1753-5131.2010.01041.x

Shakweer, W. M. E., Krivoruchko, A. Y., Dessouki, S. M., & Khattab, A. A. (2023). A review of transgenic animal techniques and their applications. *J Genet Eng Biotechnol, 21*(1), 55. doi:https://doi.org/10.1186/s43141-023-00502-z

Shoemaker, C. A., Klesius, P. H., & Evans, J. J. . (2006). Modified live Flavobacterium columnare vaccine: field safety and efficacy in tilapia. *Aquaculture, 261(2)*, 752–758.

Silverstein J. T, V. R. L., Palti Y, Leeds T. D, Rexroad C, E. III Welch, T. J, Wiens G, D. Ducrocq V. . (2008). Rainbow trout resistance to bacterial cold-water disease in moderately heritable and is not adversely correlated with growth. *Animal Science*. doi:https://doi.org/10.2527/jas.2008-1157

Sonesson, A., Hallerman, E., Humphries, F., Hilsdorf, A., Leskien, D., Rosendal, G. K., . . . Mair, G. (2023). Sustainable management and improvement of genetic resources for aquaculture. *Journal of the World Aquaculture Society, 54*, 364–396. doi:https://doi.org/10.1111/jwas.12968

Sonesson AK, G. B., Meuwissen (2005). Truncation selection for BLUP-EBV and phenotypic values in fish breeding schemes. *Aquaculture*. doi:https://doi.org/10.1016/j.aquaculture.2004.09.024

Thodesen, J., et al., . (1999). Genetic variation in feed intake, growth and feed utilization in Atlantic salmon (Salmo salar). *Aquaculture, 180(3-4)*, 237–246. doi:https://doi.org/10.1016/S0044-8486(00)00527-5

Van Eenennaam & Muir. (2011). Transgenic salmon: a final leap to the glocery shelf. *Nature Biotechnology*. doi:https://doi.org/10.1038/nbt.1938

Van Eenennaam, A. L. (2017). Genetic modification of food animals. . *Curr.Opin. Biotechnol, 44*, 27–34. doi:https://doi.org/10.1016/j.copbio.2016.10.007

Vandeputte, M. (2003). Selective breeding of quantitative traits in the common carp (Cyprinus carpio): a review. *Aquatic Living Resources, 16*(5), 399–407. doi:https://doi.org/10.1016/S0990-7440(03)00056-1

Vandeputte M., G. R., Dupont-Nivet M., Haffray P., Vergnet A., Chavanne H., et al. . (2014). Multi-site evaluation of the rearing performances of 5 wild populations of European sea bass (Dicentrarchus labrax). . *Aquaculture*. doi:https://doi.org/10.1016/j.aquaculture.2014.01.005

VanRaden, P. M. (2008). Efficient methods to compute genomic predictions. . *J. Dairy Sci, 91*, 4414–4423. doi:https://doi.org/10.3168/jds.2007-0980.

VanRaden, P. M., Tooker, M. E., O'Connell, J. R., Cole, J. B., & Bickhart, D. M. (2017). Selecting sequence variants to improve genomic predictions for dairy cattle. *Genet Sel Evol, 49*(1), 32. doi:https://doi.org/10.1186/s12711-017-0307-4

Williamson, J. H. (2001). Broodstock management for imperilled and other fishes. In: Fish hatchery management, (Ed. G. A. Wedemeyer),. *American Fisheries Society, Bethesda, Maryland, second edition*, 397–482.

Xu, K., Duan, W., Xiao, J., Tao, M., Zhang, C., Liu, Y., & Liu, S. (2015). Development and application of biological technologies in fish genetic breeding. *Science China Life Sciences, 58*(2), 187–201. doi:https://doi.org/10.1007/s11427-015-4798-3

Yáñez, J. M., Houston, R. D., & Newman, S. (2014). Genetics and genomics of disease resistance in salmonid species. *Frontiers in Genetics, Volume 5 - 2014*. doi:https://doi.org/10.3389/fgene.2014.00415

Yáñez, J. M., Houston, R. D., and Newman, S. . (2014). Genetics and genomics of disease resistance in salmonid species. . *Front Genetics*. doi:https://doi.org/10.3389/fgene.2014.00415.

Ye, D., Zhu, Z., & Sun, Y. (2015). Fish genome manipulation and directional breeding. *Sci China Life Sci, 58*(2), 170–177. doi:https://doi.org/10.1007/s11427-015-4806-7

Youngson, N. A., & Whitelaw, E. (2008). Transgenerational epigenetic effects. *Annu Rev Genomics Hum Genet, 9*, 233–257. doi:https://doi.org/10.1146/annurev.genom.9.081307.164445

Yu, Z., Mingxing, H. A. N., Mingyue, C. A. O., Yayun, Z., Juan, L. I., & Liangyi, X. U. E. (2018). SNP Detection of FST Gene and Its Association With Growth Traits in Larimichthys crocea. *Journal of Nuclear Agricultural Sciences, 32*(5), 883–891. doi:https://doi.org/10.11869/j.issn.100-8551.2018.05.0883

Yue, G. H., Zhu, Z. Y., Lo, L. C., Wang, C. M., Lin, G., Feng, F., . . . Orban, L. (2009). Genetic variation and population structure of Asian seabass (Lates calcarifer) in the Asia-Pacific region. *Aquaculture, 293*(1), 22–28. doi:https://doi.org/10.1016/j.aquaculture.2009.03.053

Zaid, A. H., H.G. Porceddu, E. and Nicholas, F. . (1999). Glossary of biotechnology and genetic engineering. FAO Research and Technology Paper. *No. 7, Rome, Italy.*

Zhang, Y., Ding, Y., Guo, F., & Wang, X. . (2020). Application of CRISPR/Cas9 technology in aquaculture species: advancements and prospects. . *Molecular Science*. doi:https://doi.org/10.3390/ijms25179299

Zhang, Z., Lu, C., Lin, K., You, W., & Yang, Z. (2023). Genetic Diversity and Genetic Structure among Four Selected Strains of Whiteleg Shrimp (Litopenaeus vannamei) Using SSR Markers. *Fishes, 8*(11), 544. doi:https://doi.org/10.3390/fishes8110544

Zhou, H., Xiao, X., Asjad, A., Han, D., Zheng, W., Xiao, G., . . . Zhou, Q. (2022). Integration of GWAS and transcriptome analyses to identify SNPs and candidate genes for aluminum tolerance in rapeseed (Brassica napus L.). *BMC Plant Biol, 22*(1), 130. doi:https://doi.org/10.1186/s12870-022-03508-w

Zhu, B., & Ge, W. (2018). Genome editing in fishes and their applications. *Gen Comp Endocrinol, 257*, 3–12. doi:https://doi.org/10.1016/j.ygcen.2017.09.011