



Genetic Improvement and Selective Breeding in Fish Aquaculture: Recent Advances

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Abstract

Aquaculture is one of the most rapidly expanding food production industries in the world, providing a growing share of animal protein in the world's diet. Sustaining this growth requires continuous improvements in productivity, resource-use efficiency, and resilience to environmental and disease-related challenges. Selective breeding has become an integral part of modern aquaculture and is a key method for achieving permanent and cumulative improvements in economically significant attributes such as growth rate, feed conversion ratio, resistance to disease and infection, reproductive capacity, product quality, and environmental adaptability. The use of marker-assisted selection, quantitative trait locus mapping, genome-wide association studies, genomic selection, and, more recently, genome editing, has revolutionized traditional breeding programs over the last ten years. These have significantly contributed to the more precise and efficient breeding programs and the faster genetic improvement in economically valuable fish species. This narrative review aims to summarize advances in genetic improvement and selective breeding in fish aquaculture, with a particular focus on genomic technologies and their applications in Atlantic salmon (*Salmo salar*), Nile tilapia (*Oreochromis niloticus*), common carp (*Cyprinus carpio*), and rainbow trout (*Oncorhynchus mykiss*). The review further covers current limitations, such as limited genetic diversity, infrastructure constraints, economic considerations, and ethical concerns with advanced breeding technologies. Lastly, key knowledge gaps and future opportunities are identified to develop sustainable, climate-resilient, and genetically better aquaculture systems for future global food needs.

Keywords: selective breeding, fish aquaculture, genetic improvement, genomic selection, marker-assisted selection, sustainable aquaculture

1. Introduction

Global fish demand has risen significantly during the last decades, due to population growth, urbanization, increased income, and awareness of fish and fishery products as a nutritious food source. Aquaculture is thus one of the fastest-growing food production industries in the world and now provides over 50% of the aquatic food consumed by people. However, expansion of aquaculture is still limited by biological, environmental, and economic issues, such as outbreaks of infectious diseases, suboptimal growth rates, lower feed conversion rates, environmental changes as a result of climate change, and rising costs of aquaculture production. In the past, these issues have increased the demand for sustainable production that both optimizes production efficiency and limits the use of chemical products and too many resource inputs (Gjedrem and Rye, 2018).

Of the variety of methods available, genetic improvement in aquaculture, through selective breeding, has proved one of the most effective and economic long-term methods of improving aquaculture productivity. In contrast, genetic gains, which rely on breeding, are cumulative and passed on through the generations, so that desirable traits can be carried forward through the generations. In recent decades, breeding programs have been established as part of commercial aquaculture, and have been successful in making continuous gains in the growth performance, feed conversion, reproduction, carcase quality, stress tolerance, and disease resistance of fish (Gjedrem and Rye, 2018). Phenotypic selection and pedigree selection have been largely used in traditional selection of fish; selection of broodstock based on observable traits and the performance of their ancestors. Considerable progress has been made in many cultured species, such as Atlantic salmon (*Salmo salar*), Nile tilapia (*Oreochromis niloticus*), common carp (*Cyprinus carpio*), rainbow trout (*Oncorhynchus mykiss*), and other marine finfish species, using these traditional methods. The large potential for genetic selection breeding to enhance the efficiency and profitability of aquaculture has been seen in several economically important production traits, such as annual genetic gains of around 10–15% (Gjedrem et al., 2012, Nguyen, 2016).

Traditional breeding has been revolutionized by the advent of molecular genetics and next-generation sequencing technologies, which make breeding more genomics-assisted. Breeders have been able to identify genomic regions with desirable traits with unprecedented accuracy using advances in high-throughput DNA sequencing, single nucleotide polymorphism (SNP) genotyping, quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), and marker-assisted selection (MAS). Recently, the use of genome-wide marker information in breeding has been revolutionized by the development of genomic selection, which relies on the ability to estimate the genetic merit of breeding candidates using information from genome-wide markers. In comparison with pedigree selection,

genomic selection significantly boosts the accuracy of prediction, especially for complex QTs influenced by many genes, such as disease resistance, feed efficiency, thermal tolerance, and environmental adaptation (Yáñez et al., 2015, Houston et al., 2020).

These genomic techniques have already been successfully applied to some commercially bred species such as Atlantic salmon, rainbow trout, and Nile tilapia, and have proven successful in increasing resistance to bacterial and viral diseases, growth rate, and production efficiency (Tsai et al., 2015, Correa et al., 2017, Kriaridou et al., 2020). Additionally, the improvement of bioinformatics, genome sequencing, transcriptomics, and the new technologies of genome editing like clustered regularly interspaced short palindromic repeats (CRISPR)-associated proteins are opening new areas of potential genetic progress and of strain development with improved environmental adaptation of fish (Houston et al., 2020, Yang et al., 2025).

Despite these remarkable advances, several practical and scientific hurdles continue to limit the widespread adoption of advanced genetic technologies. However, there are still several aquaculture species where the development of genomic resources is still incomplete, and a considerable investment of financial, human, and computational resources is needed to implement genomic breeding programs. Moreover, genetic diversity, avoiding high inbreeding levels, animal welfare, and ethical and regulatory issues related to genome editing are relevant aspects of sustainable breeding programs (Dhillon et al., 2025, Houston et al., 2020).

This narrative review critically synthesizes recent advances in genetic improvement and selective breeding in fish aquaculture, integrating evidence from conventional breeding programs and emerging genomic technologies. Special attention is given to the use of selective breeding strategies, molecular breeding tools, genomic selection, genome-wide association studies, and genome-editing technologies in the major cultured fish species. Current challenges and key gaps in knowledge are also discussed, along with future research priorities to facilitate sustainable, efficient, and climate-resilient aquaculture production systems.

2. Genetic Improvement in Fish Aquaculture Principles

Genetic improvement refers to the systematic selection and breeding of cultured populations towards higher frequencies of desirable alleles. In aquaculture, breeding programs aim to improve economically important characteristics, while ensuring that enough genetic variation is maintained to ensure the sustainability of the operation over time. Genetic improvement, in contrast to improvements made through nutrition or health management or agricultural practices, offers cumulative and permanent improvements since better genetic traits are passed on to future generations (Gjedrem et al., 2012). Thus, the concept of selective breeding has been a major focus for the development of sustainable aquaculture production systems, which lead to higher production rates, lower production costs, and enhanced resilience of the aquaculture fish.

The success of any breeding programme relies on the availability of genetic variation in the population that is being bred. The heritable variation allows breeders to select those with superior phenotypes for use as broodstock for the next generation. The four main factors influencing the rate of genetic gain are selection intensity, selection accuracy, genetic variation, and generation interval (Meuwissen et al., 2001). Breeding programmes can take advantage of this to ensure that there is continuous improvement in the commercially desirable traits and that undesirable characteristics are not allowed to build up.

The breeding goals in aquaculture have changed significantly in the last 30 years. The emphasis of early programmes was basically on body weight and growth rate, because these would directly affect production efficiency and market value. While growth remains the key objective, modern breeding programmes are more and more focused on simultaneously improving a range of other economically important traits such as feed conversion efficiency, carcass quality, age at first breeding, fillet production, egg and meat production, environmental stress, and resistance to bacterial, viral, and parasitic diseases (Nguyen, 2016, Gjedrem and Rye, 2018). Multi-trait selection allows for a balanced genetic improvement and minimizes the chances of adverse correlated responses that can be seen when a single characteristic is bred for.

In aquaculture, several approaches have been implemented in selective breeding, each with its own advantages and disadvantages. Mass selection is the most basic method, where the selection of breeding stock is based entirely on the performance of individuals in the population. This is an inexpensive and easy-to-use method that works best for those traits that have a high degree of heritability, like body weight. Its efficiency is, however, reduced for complex traits which are strongly affected by environment, such as disease resistance and reproductive performance (Gjedrem and Rye, 2018).

Many of these limitations can be overcome by family selection, which draws in pedigree information and considers the performance of relatives. Family records allow better estimation of breeding values and help to minimize the influence of environmental variations. Family selection can be especially useful for resistance to infectious diseases, which cannot be directly assessed in breeding candidates and can be assessed on representative siblings instead of potential broodstock. It has been adopted globally in Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhynchus mykiss*), and various other widely cultured fish species and has resulted in considerable gains in growth and survival (Houston et al., 2020).

Crossbreeding has also been used to take advantage of heterosis or hybrid vigour, which is the ability of a crossbred or hybrid offspring to perform better than either of the two parent breeds. Hybridization has benefited growth, stress resistance, reproductive performance, and environmental adaptability in several species raised in aquaculture.

However, due to the risk of losing genetic integrity and therefore affecting the breeding goals in the long term, crossbreeding must be carefully managed; otherwise, the result may be a loss of genetic value with too much introgression or uncontrolled hybridization (Teletchea and Fontaine, 2014).

Preservation of genetic diversity is an essential criterion for sustainable breeding programmes. Increasing inbreeding risk due to continuous selection without proper management leads to decreased reproductive performance, growth rate, survival, and adaptability. To control inbreeding and to maximise long-term genetic gain, effective breeding programmes utilise a combination of the following: Rotation mating systems, optimum contribution selection, large effective breeding populations, and pedigree or genomic information (Meuwissen et al., 2001, Houston et al., 2020). Such methods are especially significant for species that have small founder populations or large intensive commercial breeding systems.

Conventional breeding has also been reinforced by the development of molecular genetics, which has now allowed for the increased accuracy of the identification of genetically superior individuals. Molecular markers offer information that adds to that available in the phenotyping and pedigree, allowing breeders to separate the genetic component from the environment. In addition, marker-assisted selection has been most useful for major genes, and genome-wide marker information has enabled the development of genomic selection approaches that more accurately predict breeding values for complex quantitative traits than traditional approaches (Yáñez et al., 2015).

Commercial breeding programmes implemented over the past two decades clearly demonstrate the effectiveness of these principles. In species like the Atlantic salmon, the Nile tilapia (*Oreochromis niloticus*), the common carp (*Cyprinus carpio*), and the rainbow trout, the annual genetic gains of species under long-term selection programmes have been around 10-15%. Similar improvement has been noted for disease resistance and feed efficiency, which indicates that the careful design of breeding programmes produces cumulative gains that will drive profitability and limit production risk (Nguyen, 2016, Gjedrem et al., 2012).

In general, the concept of genetic improvement has progressed from the traditional phenotypic selection to an integrated breeding system (IBS), which involves the application of quantitative genetics, pedigree analysis, and molecular data. This change has paved the way for the development of modern genomic breeding programmes where the speed of genetic improvement is improving without reducing the genetic diversity of stocks and providing support to environmentally sustainable aquaculture production. The evolution of fish breeding from traditional family-based selection methods to modern methods using genomics and precision breeding is clearly indicated in Table 1, which depicts constant improvements in selection and breeding techniques.

Table 1: Major Milestones in Genetic Improvement of Fish Aquaculture

Period	Major Advancement	Significance	Key Reference
1970s–1980s	Introduction of family-based selective breeding	Established systematic genetic improvement programmes	Gjedrem et al. (2012)
1990s	Pedigree recording and quantitative genetic evaluation	Improved estimation of breeding values	Meuwissen et al. (2001)
2000–2010	Marker-assisted selection (MAS)	Enabled DNA-assisted selection for major traits	Yáñez et al. (2015)
2010–2015	Genome-wide association studies (GWAS)	Identified loci controlling economically important traits	Tsai et al. (2015)
2015–Present	Genomic selection (GS)	Improved prediction accuracy for complex traits	Houston et al. (2020)
2020–Present	Genome editing and AI-assisted breeding	Emerging technologies for precision aquaculture	Yue & Wang (2020)

3. Recent Advances in Selective Breeding

The process of selective breeding has grown from classic "phenotype" selection to a more comprehensive field that includes the tools of quantitative genetics, molecular biology, and computational genomics (Table 2). Previous breeding programmes were mainly based on performance and pedigree records, but recent advances have improved the accuracy and efficiency of assessing superior broodstock. These advances have now made it possible to produce the genetic gains needed for economically important traits more quickly and sustain long-term production of breeding stocks (Houston et al., 2020).

Refinement of family-based breeding programmes has been one of the most important developments. Family selection estimates breeding value based on family performance in addition to individual performance, as compared to mass selection, which only uses individual performance. This is especially useful for characteristics that are difficult to measure in breeding candidates, like resistance to infectious diseases, or if they must be measured, then destructive sampling is required, such as carcass characteristics. Breeding programs can accurately identify genetically superior parents, while not sacrificing valuable broodstock, by evaluating representative siblings. Family-based selection has been successfully implemented in commercial breeding programmes to enhance growth, survival and production

performance of Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhynchus mykiss*) and Nile tilapia (*Oreochromis niloticus*) (Gjedrem and Rye, 2018).

The first great integration of molecular genetics into aquaculture breeding was with Marker-assisted selection (MAS). MAS can identify favourable alleles for a gene or quantitative trait locus (QTL) controlling an economically important characteristic at an early stage of development. MAS is more efficient than phenotypic selection because it minimizes the influence of the environment and allows the selection of desirable genotypes at an early stage. The technique has worked well with single or a few major gene traits, such as resistance to particular pathogens and some reproductive traits. However, it has not proven to be as effective for polygenetic traits, in which many genes have small effects on the phenotype (Yáñez et al., 2015).

Recent developments in high-throughput sequencing and dense single nucleotide polymorphism (SNP) genotyping have paved the way to move from marker-assisted selection to genomic selection (GS). Genomic selection uses thousands of markers spread throughout the genome to estimate GBVs, as opposed to relying on a small number of genetic markers. This genome-wide approach takes into account both large and small genetic effects, and can therefore capture a much larger proportion of the total genetic variation in complex, quantitative traits like growth rate, feed conversion efficiency, disease resistance, thermal tolerance, and stress resilience, and lead to much better prediction accuracy (Meuwissen et al., 2001).

Another recent addition to modern fish breeding programmes is genome-wide association studies (GWAS). GWAS is based on statistical correlations between genetic markers and economically relevant traits and identifies genomic regions that are highly correlated with phenotypic variation. Many of the genes of commercially important fish species responsible for resistance to diseases, body weight, flesh quality, sexual maturity, and adaptation to the environment have been identified. GWAS can not only be used to gain biological insight into the architecture of a trait but also yield useful candidate markers for use in breeding programmes (Tsai et al., 2015, Robledo et al., 2018).

Infectious diseases are still a major cause of losses in aquaculture, and resistance against them has become one of the main goals of the modern selection process. Antimicrobial resistance, environmental contamination, and consumer safety are all concerns raised by the use of traditional disease control methods, such as antibiotics and chemical treatments. Therefore, it is possible to breed genetically resistant fish as a sustainable option. In Atlantic salmon, rainbow trout, and other farmed fish, genomic prediction models have shown significant benefits in terms of disease resistance against bacterial, viral, and parasitic diseases, minimizing fish deaths and decreasing reliance on therapeutic measures (Correa et al., 2017).

Selective breeding has also expanded beyond production traits to include characteristics directly related to sustainability. With the use of intensively farmed systems, feed costs are the largest operating expense, and feed conversion efficiency (FCE) is becoming more significant. Selecting for improved feed efficiency not only lowers production costs but also helps lower nutrient levels in the environment around the aquaculture facility. Likewise, breeding programmes are becoming more focused on tolerance to high water temperatures, hypoxia, and other environmental stressors to combat the escalating pressures of climate change on aquaculture production globally (Yue and Wang, 2017).

In addition to the developments in the wild, breeding programs have recently been aided by advances in the technology of genotyping-by-sequencing (GBS) that have enabled the discovery of genome-wide markers for both model and non-model species at an affordable cost. GBS can be compared and contrasted to conventional SNP arrays, which do not give the same flexibility for species with limited genomic resources, and also have the potential to speed the development of genomic tools for emerging aquaculture species. These technologies have enhanced the ability to identify genomic regions for growth and disease resistance, reproductive performance, and environmental adaptability, and have lowered the financial costs for implementing genomic breeding programmes (Robledo et al., 2018).

These developments have not put the modern technologies of selective breeding to ease of use, but several issues remain to be addressed. Other barriers include high costs of genotyping, small reference genome libraries for many cultured species, small breeding programmes in developing countries, and a lack of skilled staff. Moreover, breeding goals should be based on a compromise between productivity and the maintenance of genetic diversity since strong selection pressures may lead to higher inbreeding levels and lower adaptive capacities of the cultured populations. As such, sustainable breeding of these fish will demand proper management of broodstock, regular genetic diversity assessments, and periodic replenishment of new genetic resources, as necessary (Correa et al., 2017).

As a whole, in recent years, fish farming has undergone a revolution from being a primarily phenotype-driven undertaking to being a genomics-driven production system that can provide a quick and consistent genetic gain. Modern quantitative genetics is still the key to successful breeding programmes, but has been combined with molecular markers, GWAS, genomic prediction and high-throughput sequencing to greatly improve selection accuracy and breeding efficiency. These advances have set the groundwork for the potential acceleration of genetic improvement in future aquaculture systems with the application of emerging technologies such as advanced sequencing, multi-omics integration, and genome editing.

Table 2: Comparison of Selective Breeding Approaches Used in Fish Aquaculture

Breeding Method	Principle	Advantages	Limitations	Example Species
Mass selection	Selection based on phenotype	Simple and inexpensive	Low accuracy for complex traits	Oreochromis niloticus
Family selection	Uses pedigree information	Higher selection accuracy	Higher operational cost	Salmo salar
Marker-assisted selection	Selection using DNA markers	Effective for major genes	Limited to polygenic traits	Oncorhynchus mykiss
Genomic selection	Genome-wide SNP prediction	Highest prediction accuracy	Requires genomic infrastructure	Salmo salar
Genome editing	Targeted DNA modification	Potential rapid genetic gain	Regulatory and ethical concerns	Experimental species

4. Emerging Genomic Technologies in Fish Aquaculture

In aquaculture, breeding programmes have been transformed by the speed of their development of genomic technologies. While the traditional selection methods used by phenotypic traits and pedigree information are still valuable, they are becoming supplemented by molecular methods, which are more accurate at selecting and have shortened breeding cycles. With the aid of next-generation sequencing (NGS), high-density genotyping, bioinformatics, and genome analysis, breeders are able to detect genetic variants linked to economically important traits more efficiently than ever before. The technologies are helping to shift from traditional breeding to precision aquaculture, where selection decisions are more and more made based on information from the whole genome rather than only the phenotype (Houston et al., 2020)

4.1 Marker-Assisted Selection and Quantitative Trait Locus Mapping

Marker-assisted selection (MAS) is one of the first genomic tools to be used in aquaculture breeding programmes. The method involves using markers of the DNA which are highly associated with genes or quantitative trait loci (QTLs) that affect desirable traits. The validation of these associations would allow breeders to select superior animals at an early developmental stage while avoiding the need for expression of these traits to be attained, decreasing generation intervals and improving selection efficiency (Yáñez et al., 2015).

QTL mapping has been extensively used to detect genomic segments associated with pertinent traits such as growth, disease resistance, flesh quality, reproductive capacity, and stress tolerance, which are of economic value. In some of the species being cultured, major QTLs have been identified that have led to more focused breeding programmes, especially in Atlantic salmon (*Salmo salar*) and the rainbow trout (*Oncorhynchus mykiss*). However, many of the commercially important ones are polygenic, meaning that they are influenced by many genes and have relatively small effects. Therefore, QTL-based selection is often only a fraction of the genetic variation observed, and thus genome-wide approaches are needed (Tsai et al., 2015).

4.2 Genomic Selection

In the last decade, Genomic Selection (GS) has been one of the greatest advancements in aquaculture genetics. GS differs from MAS because it considers thousands of single nucleotide polymorphism (SNP) markers spread throughout the genome, rather than a few markers of interest. This approach also helps to capture both the major and minor genetic effects, which are especially useful for traits with differing measurements like feed efficiency, disease resistance, environmental tolerance, and reproductive performance (Meuwissen et al., 2001).

Genomic selection has been shown to be better than pedigree-based selection for many traits in commercial breeding programmes, especially for those that have low to moderate heritability. The increased predictability means that breeders can select better-quality broodstock at an earlier age, which can shorten generation intervals and speed up ongoing genetic improvement. In the Atlantic salmon, rainbow trout, and Nile tilapia, the results have been promising with significant increases in resistance against bacterial, viral, and parasitic diseases and improvements in growth rate and production efficiency (Kriaridou et al., 2020; Correa et al., 2017).

An added benefit of genomic selection is that it can enhance traits that are not easily measured, costly, or even not available on breeding candidates. For instance, disease challenge tests may involve sacrificing experimental fish, or otherwise infecting them with disease under experimental conditions. Using genomic data from healthy relatives to estimate disease resistance is a process that breeders can use to preserve valuable broodstock and still have high selection accuracy, which is called genomic prediction (Houston et al., 2020).

4.3 High-Throughput Sequencing and Multi-Omics Approaches

Next-generation sequencing technologies has greatly increased the amount of genomic information available for aquaculture species. High quality reference genomes have been generated for numerous commercially important fish using whole genome sequencing, which allows genes linked to economically important traits to be discovered. Meanwhile, the increasing availability of sequencing has enabled genome analysis to become more widely used in breeding programs across both the aquaculture sector and emerging industries. At the same time, the reduction in

sequencing costs has made genome analysis more readily available in aquaculture industry breeding programmes and emerging aquaculture industries (Yue and Wang, 2017).

In addition to genomics, the other omics technologies such as transcriptomics, proteomics, metabolomics and epigenomes offer complementary information on the expression of genes, the function of proteins, metabolic pathways and regulation. Transcriptomic analyses can be used to identify genes that are differently expressed in response to disease infection, thermal stress, and salinity adaptation or in response to rapid growth, providing potential genes for future breeding programmes. In addition to this, proteomic and metabolomic analyses have enhanced our understanding of how the environment affects physiology, and epigenetic studies have shown that the environment can affect the expression of genes without changing the DNA sequence (Houston et al., 2020). Combining these data sets allows a better understanding of biological characteristics than genomic data alone. The use of multi-omics approaches is thus a step towards precision breeding where genomic, physiological, and environmental data can be considered at the same time.

4.4 Genome Editing

Genome editing has garnered significant interest as a means to enhance genetic improvement in aquaculture, especially through the use of the CRISPR/Cas system (Boudry et al., 2021, Zenger et al., 2019). Unlike traditional breeding, which uses the naturally occurring variation in the population, genome editing allows for accurate targeting of specific DNA sequences involved in desired traits. Improved disease resistance, growth performance, environmental stress and tolerance, and resistance to emerging pathogens are potential applications.

Experimental work has shown that gene editing using the CRISPR system is possible in multiple fish species, and can be used to speed up breeding programmes beyond the rate of traditional selection. However, despite these developments, there are also technical, regulatory, consumer, and ethical issues that delay the commercialization of genetically edited food animals. Thus genome editing should be considered as an auxiliary technology at this stage, and not a substitute for existing selective breeding programmes (Houston et al., 2020).

4.5 Artificial Intelligence and Digital Breeding

There are new opportunities through recent developments in artificial intelligence (AI), machine learning and high performance computing for genomic breeding. Combining AI algorithms with massive genetic data, phenotypic and environmental as well as management data can enhance prediction precision and reveal complex interactions that are not captured by traditional statistical modeling (Boudry et al., 2021). The use of AI in conjunction with genomic selection can be used to enhance broodstock selection, to forecast breeding outcomes and make better decisions in commercial breeding programmes.

In addition, digital phenotyping approaches can be used to complement genome-based data, such as computer vision and automated imaging systems, and sensor-based monitoring which allows continuous, non-invasive assessment of growth, behaviour, health status, and welfare. Such technologies collect high quality phenotypic information which enhances the genomic prediction model and can improve the estimation of breeding values under commercial production environments. While the penetration is still in its early stages, with infrastructure challenges and implementation costs limiting use, digital breeding platforms will play more and more of a role in the future of aquaculture as it transitions to precision production systems.

4.6 Future Prospects of Genomic Breeding

Genetic improvement in aquaculture in the future is anticipated to rely on the use of genome-wide molecular data along with conventional quantitative genetics, multi-omics approaches, bioinformatics, and artificial intelligence (Zenger et al., 2019). In other words, these new technologies serve as supplements to current selection programs through increased accuracy of predictions, reduction of breeding costs in the long run, and acceleration of genetic gains.

Despite significant progress, there is still a wide gap between aquaculture in the developing countries and in the developed world in terms of genomic infrastructure, expertise, and funding. Making genomic tools accessible, developing reference genomes for understudied species, forming international collaborations for breeding programs, and building up bioinformatics capacities are crucial for making sure that the innovations in genomics are available to the entire aquaculture industry.

Overall, the development of genomics techniques will revolutionize the process of fish breeding to become more empirical and based on data and precision. The continued use of such techniques in breeding programs in the future will ensure increased productivity, disease resistance, adaptation to environments and efficient resource utilization.

5. Applications of Genetic Improvement in Major Cultured Fish Species

Most aquaculture species differ in how effective selective breeding and genomic technologies have been in their implementation, and this is due to differences in aquaculture systems, production goal, biology and genomic resources. Commercial breeding programmes have concentrated on high value species, in which there has been a sustained investment in breeding, leading to measurable gains in growth, disease resistance, feed efficiency and product quality. The lessons learnt from these species could serve as good examples for the application of the advanced methodologies of breeding to emerging aquaculture species (Table 3).

5.1 Atlantic Salmon (*Salmo salar*)

Atlantic salmon is one of the best case studies in long-term genetic improvements in aquaculture. The commercial breeding programmes started several decades ago have resulted in ever-improving growth rate, harvest weight, feed

utilization, fillet quality and resistance to infectious diseases. Selecting salmon on family basis is the basis for salmon breeding, but the use of genomic selection has greatly improved the accuracy of prediction of complex traits.

Disease resistance has been given special focus as it is a major economic challenge to the salmon farming industry due to infectious salmon anaemia, sea lice, pancreas disease and bacterial pathogens. Several chromosomal regions have been identified for resistance to sea lice and various infectious diseases as part of GWAS, which can be used to build a genome-based prediction model to better select broodstock (Tsai et al., 2015). Furthermore, Correa et al. (2017) showed that genomic selection (GS) significantly improved prediction accuracy for growth and disease resistance, which would allow better breeding programmes and a decrease in losses due to disease (Correa et al., 2017).

The Atlantic salmon industry is a further example of where quantitative genetics plays a crucial role in the integration of genomic technologies. In recent years, pedigree data, high-density SNP genotyping, and powerful statistical models have been used in tandem in a breeding programme to maximize genetic gain while controlling inbreeding. These methods have set Atlantic salmon as a model for aquaculture genomic breeding and offer insights to guide breeding programs for other cultured fish species (Houston et al., 2020).

5.2 Nile tilapia (*Oreochromis niloticus*)

Nile tilapia is one of the most popular freshwater fish in the world because of its fast growth, large brood size, tolerance to various environmental factors, and acceptability by consumers. The productivity of tilapia has been greatly enhanced by selective breeding, including those for body weight, feed conversion efficiency, survival, and harvest performance.

Although the traditional selection method based on family has yielded great genetic improvement in growth rate over several generations, recent advances in genomic technologies have further enhanced breeding efficiency. Marker-assisted selection and genomic prediction are currently becoming an important part of commercial breeding programs for disease resistance and environmental adaptability. The value of these technologies is especially significant as tilapia culture is moving into areas with shifting water temperature, bad water quality, and emerging diseases (Nguyen, 2016).

With the growing number of available genomic resources, such as high-density SNP panels and reference genome assemblies, the identification of genomic regions correlated with economically important traits has been sped up. These improvements will help enhance breeding accuracy and climate-resilient tilapia strains that can sustain productivity in dynamic environmental conditions are expected to develop (Yue and Wang, 2017).

5.3 Common Carp (*Cyprinus carpio*)

Common carp is one of the most ancient domesticated species of aquaculture production and still plays an important role in the production of freshwater aquaculture in Asia and Eastern Europe. In the past, selective breeding was directed toward a superior growth rate, body conformation, survival, and adaptation to local production environments. Recently, resistance to disease, feed efficiency and environmental stress have become additional emphasis points in breeding.

The advancement of genomic breeding in common carp is less developed than in Atlantic salmon and tilapia, but has developed rapidly in recent years since the development of marker discovery and the advancement of sequencing technologies. The use of genotyping-by-sequencing and genome-wide marker analyses has helped to identify genetic variants linked to economically important traits and has lowered the cost of genome-wide marker analyses for breeding programmes (Robledo et al., 2018).

Continued development of carp genomic resources is anticipated to enhance the accuracy of selection and help in better management of genetic diversity to strengthen carp breeding. Common carp is one of the most important freshwater fish species for aquaculture worldwide, and there is a great potential for improving production efficiency and for preserving the adaptability of locally important strains through an expansion of genomic breeding programmes.

5.4 Rainbow Trout (*Oncorhynchus mykiss*)

Another species for which progress in selective breeding and molecular genetics has been significant is another trout species, the rainbow trout. Commercial breeding programmes started with growth rate and harvestability traits and have gradually moved on to disease resistance, reproductive efficiency, carcass quality, and environmental tolerance. The use of genomic technologies to enhance resistance to bacterial and viral diseases that are important in trout production has been especially useful. Genome-wide association studies and genomic prediction models have led to the identification of genomic regions associated with disease resistance, which can be used to select the broodstock with higher accuracy, avoiding the burdensome disease challenge testing (Robledo et al., 2018; Zenger et al., 2019). These methods lower the death rate, help maintain a healthy environment for the fish, and minimize the need for antibiotics and other chemical products.

Apart from disease resistance, genomic selection has improved growth rate and feed use efficiency, which adds to the economic efficiency and sustainability. With the cost of sequencing continually dropping, genomic technologies will be increasingly available to trout breeding programmes of varying production sizes.

5.5 Comparative Perspective across Cultured Species

While the breeding programs vary between species, there are some similarities among contemporary aquaculture breeding programs. First, breeding programmes have moved from just focusing on growth to those that incorporate a suite of economically and environmentally relevant traits, such as disease resistance, feed efficiency, stress tolerance, and product quality (Song et al., 2023). Second, the use of molecular technologies has been increasingly used to complement traditional quantitative genetics, not replace it. Successful breeding programmes consistently integrate

phenotypic records, pedigree information, and genomic information to maximize the accuracy of the prediction and long-term genetic improvement.

Third, genomic resources are still not available for all aquaculture species (Song et al., 2023). While high value species like Atlantic salmon have large and well-developed genomic databases, well developed breeding companies, and sophisticated bioinformatics infrastructure, many of the freshwater and marine species lack the same features, including reference genomes, high-density marker panels, and organized breeding programmes (Boudry et al., 2021). To increase access of the benefits of genomic breeding in the aquaculture industry worldwide, these disparities will need to be addressed.

Table 3: Applications of Genetic Improvement in Major Cultured Fish Species

Species	Primary Breeding Objective	Genomic Technology	Major Outcome	Reference
<i>Salmo salar</i>	Disease resistance, growth	GWAS, GS	Improved disease resistance and harvest performance	Houston et al. (2020)
<i>Oreochromis niloticus</i>	Growth, feed efficiency	MAS, GS	Higher growth rates and productivity	Nguyen (2016)
<i>Cyprinus carpio</i>	Growth and adaptability	GBS, SNP markers	Improved genetic diversity management	Robledo et al. (2018)
<i>Oncorhynchus mykiss</i>	Disease resistance	GWAS, GS	Reduced disease-related mortality	Palaiokostas et al. (2018)

6. Discussion and Synthesis

One of the most important technological developments in the history of aquaculture is the advances made in breeding fish, from traditional phenotypic selection to genomics-assisted breeding. Findings from the literature reviewed support the consistency of this evidence that selective breeding has led to continuous improvement in economically important traits such as growth, feed conversion ratio, resistance to disease, reproductive performance and product quality. Genetic gains are different from management interventions, which typically produce short-term gains, and are cumulative over generations and therefore represent a long-term approach to improving aquaculture productivity (Gjedrem et al., 2012, Gjedrem and Rye, 2018).

Molecular genetics have also greatly improved the accuracy of broodstock selection in breeding programmes. First practical use of molecular information in aquaculture was with marker assisted selection (MAS) for major gene controlled traits. Recently, however, the introduction of genome-wide marker information into breeding value prediction models has changed breeding approach as a result of the development of genomic selection. This method is useful in particular for complex polygenic quantitative traits such as disease resistance, feed efficiency, adaptation to altered climatic conditions, stress tolerance, and adaptation to elevated CO₂ (Houston et al., 2020).

The literature also suggests that in addition to technological innovation, the quality of phenotypic data is important for the success of genomic breeding. Accurate measurements of economically important traits continue to be valuable due to the need to calibrate the genomic prediction models using accurate phenotype–genotype relationships. Thus, together with genomic tools, enhanced digital phenotyping, automated monitoring and precision aquaculture technologies will enhance the data available for use in breeding programmes. Combining genomic information with production data, environmental factors and management will likely further increase prediction accuracy and aid in more efficient selection decisions.

Another important finding emerging from recent studies is the increasing emphasis on breeding for resilience rather than productivity alone. In the past, breeding programmes have focused mainly on speed of growth and harvest weight since these have direct economic implications. New breeding goals are much more diverse and are expanded to include resistance to infectious diseases, tolerance of temperature extremes, hypoxia tolerance, feed utilization efficiency, reproductive performance and animal welfare. This change reflects broader trend towards the importance of producing fish that can perform well in a more dynamic environment, which is essential for sustainable aquaculture.

Despite substantial progress, the adoption of advanced breeding technologies in the aquaculture industry is still not widespread. Genomics, bioinformatics and coordinated breeding programmes have been continued and have helped high-value industries, particularly Atlantic salmon production. However, many species grown in freshwater and marine species in developing countries are still largely dependent on conventional selection, due to the lack of genomic resources, limited infrastructure and financial resources (Dhillon et al., 2025). This technology gap needs to be addressed with more international cooperation, capacity development, and the development of cost-effective genomic tools applicable to many different aquaculture systems.

Overall, the reviewed evidence demonstrates that sustainable genetic improvement requires an integrated approach combining quantitative genetics, molecular biology, advanced bioinformatics and informed broodstock management. Genomic technologies are not a replacement for traditional methods of breeding, but complement existing breeding

programmes by enabling more accurate selection and the maintenance of genetic diversity over the long-term. This comprehensive system is the way forward in fish breeding and it's a great solution to increase productivity, profitability and reduce environmental impact in global aquaculture.

7. Research Gaps and Future Directions

While considerable progress has been made in fish genetic improvement, there are still some key areas of research that need to be addressed. However, there are not yet genomic resources available or complete for many commercially important and emerging fish species that are suitable for aquaculture. While research on Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhynchus mykiss*), and Nile tilapia (*Oreochromis niloticus*) has been concentrated on these three species, many native and locally significant fish species are currently underrepresented in genomic studies. Therefore high-quality reference genomes, dense SNP panels and comprehensive databases of phenotypical traits should be developed as a research priority for these species.

Second, more attention should be placed on creating climate resilient breeds. While the majority of existing breeding programmes are oriented towards production traits, there is a lower number of studies on tolerance to increased water temperature, hypoxia, salinity changes, ocean acidification, and other environmental changes due to climate change. The long-term sustainability of aquaculture production systems will be enhanced by the addition of resilience traits to breeding programmes to make production systems more resilient to environmental shocks.

Third, there is limited integration of multi-omics technologies such as transcriptomics, proteomics, metabolomics and epigenomics into commercial breeding programmes. The potential of these complementary approaches to enhance our understanding of the complex biological pathways and discovery of new markers linked to economically important traits is not insignificant. Ideally, multi-omics data with the breeding models based on genomic prediction should be integrated into future breeding strategies for increased selection accuracy and biological interpretation.

One of the other key research areas is the use of Artificial Intelligence and Machine Learning for Genomic Prediction. Advanced computational methods can analyze large sets of genomic and phenotypic data simultaneously, which can increase the precision of the prediction of complex quantitative traits. In the near future, the integration of AI into precision aquaculture systems, such as automated imaging systems, biosensors, and environmental monitoring in real-time, can significantly improve the efficiency of breeding programs.

Genome editing technologies like CRISPR/Cas are also tools of great promise for future genetic improvement. More research is needed before a large-scale commercial application will be possible, however, to assess long-term ecological effects, food safety issues, animal welfare concerns, and public acceptance. The establishment of transparent regulatory frameworks will be key to responsible use of these technologies.

Lastly, future breeding programmes need to be more focused on conserving genetic diversity and continuously improving it. The selection intensity could also rise and inbreeding could be enhanced, leading to a reduction in adaptive capacity and limiting long-term breeding success. To ensure conservation of genetic resources while maintaining productivity, sustainable breeding programmes should consider the following additional parameters: genomic monitoring, optimum contribution selection, and effective broodstock management strategies.

8. Conclusion

Genetic improvement and selective breeding have become integral parts of current fish farming practices due to their ability to deliver sustained and permanent improvements in growth performance, feed efficiency, health, reproduction, and adaptability to the environment. The use of quantitative genetics coupled with molecular breeding methods, including genomic selection, genome-wide association studies, and next-generation sequencing, has greatly enhanced breeding programmes in terms of their efficiency and effectiveness.

Data analyzed within this study show that genomic techniques are contributing to an increased genetic gain among commercially valuable species, such as Atlantic salmon (*Salmo salar*), Nile tilapia (*Oreochromis niloticus*), common carp (*Cyprinus carpio*), and rainbow trout (*Oncorhynchus mykiss*). However, the wide implementation of such technologies is still limited by economic, technological, infrastructure, and other barriers, which are especially pronounced in the case of developing aquaculture sectors. Overcoming these constraints by means of international collaboration and cooperation and development of affordable breeding techniques would help overcome inequities in genetic advancement.

The future breeding programmes would require the application of integrated approaches that include the use of conventional quantitative genetics, genomic prediction, multi-omics, artificial intelligence, and responsible genome editing while protecting genetic diversity and animal welfare. These multidisciplinary approaches will contribute to improving the resilience, sustainability, and productivity of the aquaculture industry, thus supporting global food security and satisfying the increased need for animal proteins from aquatic environments.

Acknowledgement

The authors would like to thank the researchers and institutes whose work in literature helped in preparing this narrative review. The study did not receive any external financial support.

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