



# Genome-Based Prediction of Traits in Aquaculture Populations

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## DESCRIPTION

Aquaculture has grown rapidly as a major source of animal protein for global consumption, emphasizing the need for efficient and sustainable breeding strategies. Traditional selective breeding has improved growth rates, disease resistance, and feed efficiency in many species. However, advancements in genomic technologies have introduced new approaches to breeding that rely on genetic information, enabling more precise and accelerated selection. Genomic selection, which uses genome-wide markers to predict the breeding value of individuals, has become an increasingly important tool in modern aquaculture programs.

Genomic selection differs from conventional breeding in its use of dense marker data to estimate the genetic potential of breeding candidates. While traditional methods rely on phenotypic evaluation and pedigree information, genomic approaches consider the entire genome, capturing both additive and non-additive genetic effects. This allows for more accurate predictions of traits that are difficult to measure directly, such as disease resistance, feed conversion efficiency, or stress tolerance. The integration of genomic information into breeding programs has demonstrated improved selection accuracy and reduced generation intervals.

Several models have been developed to analyze genomic data for aquaculture breeding. The Genomic Best Linear Unbiased Prediction (GBLUP) model is widely used due to its simplicity and computational efficiency. GBLUP treats the effects of all markers as random and assumes that they contribute equally to the trait of interest. Alternative models, such as Bayesian approaches, allow for variable effects across markers and can accommodate traits controlled by few genes of large effect alongside polygenic traits. These models provide flexibility in analyzing complex traits and can improve prediction accuracy in populations with diverse genetic architectures.

Tools for genomic selection continue to evolve, improving both data collection and analysis. Advances in sequencing technologies have reduced costs and increased throughput,

enabling the genotyping of thousands of individuals across hundreds of thousands of loci. Bioinformatic pipelines allow for efficient processing, quality control, and annotation of genomic data. Additionally, software platforms for genomic prediction integrate statistical models, visualization, and cross-validation tools to assess prediction accuracy and optimize selection strategies. These resources have made genomic selection increasingly accessible to aquaculture programs worldwide.

Environmental variation also affects the accuracy of genomic selection. Aquaculture species are grown in diverse conditions, including freshwater, brackish, and marine environments, with varying temperatures, water quality, and management practices. Genotype-by-environment interactions can influence trait expression, potentially reducing the transferability of genomic predictions across locations. Strategies to manage these effects include developing environment-specific prediction models or incorporating environmental covariates into genomic analyses. These approaches allow for more accurate selection in heterogeneous production systems.

Cost considerations remain an important factor for implementing genomic selection. While genotyping costs have decreased, they still represent a significant investment, particularly for small-scale operations. Integrating genomic selection with existing breeding programs requires balancing genotyping, phenotyping, and operational expenses. However, studies have shown that the long-term benefits of increased selection accuracy, faster genetic gain, and reduced generation intervals can outweigh initial costs, particularly for high-value species. Strategic planning and collaboration among breeding organizations can further improve cost efficiency.

Genomic selection can support the improvement of multiple traits simultaneously, which is particularly valuable in aquaculture where production efficiency, health, and product quality are all economically significant. Multi-trait selection allows for balanced genetic progress, avoiding unintended consequences of focusing on a single trait. For example, selection for rapid growth alone may compromise disease resistance or flesh quality. Genomic tools provide the resolution

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to monitor multiple traits and predict correlated responses, enabling breeders to optimize overall population performance.

Integration of genomic selection with other technologies offers additional opportunities. Marker-assisted selection, genomic-enabled breeding programs, and gene editing are complementary approaches that can enhance genetic improvement. While gene editing remains subject to regulatory and ethical considerations, its combination with genomic selection could accelerate gains for traits that are otherwise difficult to improve. Similarly, high-throughput phenotyping and automated monitoring systems provide additional data streams that strengthen predictive models and support real-time decision-making.

The adoption of genomic selection also has implications for sustainability. By increasing the efficiency of breeding programs, genomic approaches can reduce the number of animals required to achieve production goals, minimizing resource use and environmental impact. Improved disease resistance reduces reliance on therapeutics, decreasing chemical inputs and

supporting animal welfare. Optimized feed efficiency reduces waste output, improving water quality and reducing nutrient loading in aquatic systems. These benefits align with broader objectives for environmentally responsible aquaculture development.

In conclusion, genomic selection represents a transformative tool for aquaculture breeding, offering precise, efficient, and multi-trait improvement compared with traditional methods. By integrating genome-wide markers, statistical models, and bioinformatic tools, breeders can predict the genetic potential of individuals more accurately, accelerating genetic gain and supporting sustainable production. Challenges remain, including phenotyping, environmental variation, cost, and expertise, but advances in technology and collaborative approaches are helping overcome these limitations. Continued investment in genomic research, training, and infrastructure will support the broader adoption of these methods, enabling aquaculture to meet global food demands while maintaining environmental and economic sustainability.