International Journal of Biological Reports 4(2) 77–108 2026

Role of bioinformatics and omics data integration in improving aquaculture production traits

Nahavandi R.[1*]; Pourmozaffar S.[2]; Abbaspour Anbi A.[3]; Khiabani A.R.[4]; Ebrahimi H.[5]; Masaeli Sh.[6]

Received: September 2025 Accepted: January 2026

Abstract

The rapid advancement of high-throughput biological data-generation technologies over the past two decades has driven the widespread adoption of omics approaches, including genomics, transcriptomics, proteomics, metabolomics, and metagenomics, in fisheries and aquaculture research. These technologies generate extensive molecular datasets that facilitate the identification of genetic and biochemical determinants underlying economically important production traits, such as growth performance, feed efficiency, disease resistance, flesh quality, survival, and environmental adaptability. However, the full value of these datasets depends on their effective processing, integration, and interpretation through advanced bioinformatics tools and analytical frameworks. Recent developments in bioinformatics and multi-omics integration have significantly enhanced the understanding of complex biological processes and accelerated genetic improvement programs in commercially important aquaculture species, including salmon, tilapia, and shrimp. The integration of genomic resources with transcriptomic, proteomic, and metabolomic analyses, together with genome-wide association studies, genomic selection, and genome-editing technologies, has improved the identification and validation of candidate genes and molecular pathways associated with key production traits. These advances have the potential to substantially increase breeding efficiency while providing deeper insights into polygenic architectures and gene–environment interactions. The strategic application of bioinformatics-driven multi-omics analyses offers a powerful framework for improving the sustainability, productivity, and profitability of modern aquaculture systems. Nevertheless, their successful implementation requires long-term investment in research infrastructure, computational resources, data management, and specialized human capacity. Collectively, these approaches provide promising opportunities for developing resilient aquatic stocks, reducing environmental impacts, and strengthening global food security.

Keywords: Bioinformatics, multi-omics integration, Genomics, Genomic selection, Genome-wide, Association studies (GWAS), Aquaculture breeding, Economic traits, Precision aquaculture

1-Animal Science Research Institute of Iran (ASRI), Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
2- Persian Gulf Mollusks Research Station, Persian Gulf and Oman Sea Ecology Research Center, Iranian Fisheries Sciences Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Bandar Lengeh, Iran
3-National Artemia Research Center, Iranian Fisheries Science Research Institute (IFSRI), Agricultural Research, Education and Extension Organization (AREEO), Urmia, Iran
4-Department of Agriculture & Natural Resources, University of Applied Science and Technology, Tehran, Iran
5-Persian Gulf Research Center, Persian Gulf University, Bushehr, Iran
6-Iranian Fisheries Sciences Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran
*Corresponding autho's Email: Rezanahavandi91@gmail.com

Introduction

Aquaculture has emerged as one of the most important sectors of animal protein production worldwide over recent decades, with its contribution to human food supply continuing to increase, particularly in developing countries. Rapid global population growth, increasing limitations on freshwater resources, escalating pressure on natural fish stocks, and the intensifying impacts of climate change have collectively heightened the need to improve the efficiency and sustainability of aquatic production systems. Under these circumstances, the enhancement of economically important traits, including rapid growth, feed utilization efficiency, disease resistance, tolerance to fluctuating salinity and temperature conditions, and superior product quality, has become a central objective of breeding and management programs in aquaculture. Over the past several decades, selective breeding efforts in many cultured aquatic species have primarily relied on conventional approaches based on phenotypic record-keeping and mass selection. Although these strategies have yielded measurable improvements in certain cases, they face substantial limitations when applied to complex traits governed by numerous genes of small individual effect and influenced by extensive environmental interactions. Furthermore, long production cycles in some aquaculture species, difficulties associated with accurate phenotypic recording under commercial farming conditions, and the high costs of challenge-testing procedures, such as experimental pathogen exposure for evaluating disease resistance, have constrained the rate of genetic improvement. Technological advances in DNA and RNA sequencing, molecular imaging, mass spectrometry, and other high-resolution analytical platforms have led to the emergence of a new generation of research methodologies collectively known as omics technologies. These approaches enable comprehensive and simultaneous investigation of the entire complement of genes (genomics), expressed RNA transcripts (transcriptomics), proteins (proteomics), and metabolites (metabolomics) within a biological system. In parallel, metagenomics-based analyses of the composition and functional dynamics of microbial communities associated with aquatic organisms and their culture environments have opened new avenues for understanding host–microbiome interactions and their implications for aquatic health, productivity, and environmental adaptation (Lau *et al*., 2025). A common characteristic of all omics technologies is their capacity to generate extraordinarily large and complex datasets that cannot be effectively utilized without advanced computational tools and analytical methodologies. It is within this context that bioinformatics assumes a pivotal role. Broadly defined, bioinformatics is the discipline concerned with the management, processing, analysis, and interpretation of biological data through the application of statistical, algorithmic, and computational approaches. In fisheries and aquaculture sciences, bioinformatics enables researchers to extract biologically meaningful patterns from vast quantities of raw data and translate them into molecular markers, predictive models, and candidate biological pathways that can be exploited for genetic improvement and management interventions aimed at enhancing economically important traits (Zhang *et al*., 2023). Despite the rapid expansion of omics-based research across a wide range of aquatic species, a substantial gap remains between molecular-level discoveries and their practical implementation in commercial aquaculture systems. This translational disconnect can be attributed, in part, to limitations in computational infrastructure and bioinformatics resources, as well as to economic constraints and insufficient integration among molecular biologists, bioinformaticians, and aquaculture practitioners. Consequently, a systematic synthesis of existing knowledge and the development of a clear conceptual framework for integrating omics-derived information with bioinformatics analyses are essential for bridging the divide between scientific discovery and field-level application. Against this backdrop, the present review aims to elucidate the role, capabilities, and emerging applications of bioinformatics and omics-based data analyses in the improvement of economically important traits in cultured aquatic species. By highlighting current advances, methodological frameworks, and future prospects, this review seeks to provide a comprehensive perspective on how these technologies can contribute to the development of more productive, resilient, and sustainable aquaculture systems (Rather *et al*., 2023).

Theoretical foundations of omics and bioinformatics in aquatic species

Definition and significance of omics

The term omics refers to a collection of comprehensive and high-throughput approaches that share the common objective of systematically investigating all components within a specific level of biological organization. For instance, genomics focuses on the study of the complete set of genes and DNA sequences, transcriptomics examines the entire repertoire of RNA transcripts, proteomics investigates the full complement of proteins, and metabolomics analyzes all small-molecule metabolites present within a cell, tissue, or organism. Unlike conventional reductionist studies that typically examine individual components in isolation, omics approaches adopt a genome-wide and systems-level perspective, emphasizing global biological patterns and interactions. In fisheries and aquaculture sciences, the application of omics technologies has expanded rapidly in recent years, particularly in commercially important groups such as cold-water and warm-water fish species, shrimp, and bivalve mollusks. These technologies provide opportunities to move beyond reliance on phenotypic observations alone and enable direct exploration of the genetic and molecular foundations underlying economically important traits. For example, transcriptomic analyses can identify gene expression patterns associated with immune responses to pathogens or adaptation to salinity stress, thereby facilitating the selection of families or breeding lines with superior adaptive capacity and production performance (Martínez-Espinosa, 2025).

Genomics in aquatic species

Genomics represents the foundation of many omics-based investigations and focuses on the characterization and analysis of genome structure, organization, and function. In aquatic species, genomic studies often face unique challenges arising from factors such as polyploidy, large genome sizes, and the abundance of repetitive DNA sequences, all of which complicate genome assembly and annotation processes. Nevertheless, advances in next-generation sequencing (NGS) technologies, coupled with sophisticated bioinformatics methodologies, have enabled the generation of high-quality draft genomes for numerous aquaculture species of economic importance. Within the field of genomics, several major areas of investigation can be distinguished:

Genome sequencing and assembly

This stage involves transforming raw sequencing reads into longer contiguous sequences (contig) through the application of assembly algorithms, followed by the reconstruction of chromosome-scale genomic architectures.

Accurate genome assembly

provides the essential framework for downstream genetic and functional analyses. Genome Annotation Genome annotation encompasses the identification and characterization of genes, regulatory elements, non-coding RNAs, and other functional genomic features. The accuracy of this process is strongly influenced by sequencing quality, assembly completeness, and the availability of comparative genomic information from phylogenetically related species.

Identification of genetic variation

Comparative analyses of genomes from different individuals within a species enable the detection of diverse forms of genetic variation, including single nucleotide polymorphisms (SNPs), insertion–deletion mutations (indel), and larger structural variants. These genetic polymorphisms constitute the foundation for the construction of genetic maps and the identification of genomic regions associated with economically important traits. The true value of genomics in aquaculture becomes particularly evident when genomic information is integrated with extensive phenotypic datasets within selective breeding programs. Such integration enables the implementation of advanced breeding strategies, including genomic selection, which has emerged as a powerful tool for accelerating genetic improvement and will be discussed in greater detail in subsequent sections (Wang *et al*., 2024).

Transcriptomics and gene expression analysis

Transcriptomics is concerned with the comprehensive analysis of the complete set of RNA transcripts expressed within a cell, tissue, or organism under a specific physiological or environmental condition. Because many economically important traits in aquatic species arise from subtle alterations in gene expression patterns in response to environmental factors, nutrition, and various stressors, transcriptomics has become an indispensable tool for elucidating the molecular mechanisms underlying these traits. Currently, RNA sequencing (RNA-Seq) represents the predominant methodology employed in transcriptomic studies. In this approach, extracted RNA molecules are first converted into complementary DNA (cDNA) and subsequently subjected to high-throughput sequencing. The resulting sequence reads are aligned to a reference genome or reference transcriptome using bioinformatics pipelines, allowing gene expression levels to be quantified through metrics such as Fragments Per Kilobase of Transcript per Million Mapped Reads (FPKM) or Transcripts Per Million (TPM). Comparative analyses among different experimental groups—for example, disease-resistant versus disease-susceptible fish populations—facilitate the identification of differentially expressed genes (DEGs) associated with specific phenotypic outcomes. Beyond differential expression analysis, transcriptomic datasets can be integrated with gene co-expression network analyses to identify coordinated expression patterns and functional gene modules associated with particular biological traits. Such information is highly valuable for the discovery of candidate genes and the development of molecular markers for selective breeding applications. Importantly, transcriptomics is not limited to the investigation of stress-response mechanisms. In aquaculture research, it has been extensively applied to the study of muscle growth, gonadal development, lipid metabolism, nutritional physiology, and responses to alternative dietary formulations. Consequently, transcriptomic analyses provide critical insights into the regulatory processes that govern productivity, adaptation, and overall performance in cultured aquatic species (Monzó *et al*., 2025).

Proteomics and metabolomics

Although genomic and transcriptomic analyses provide valuable insights into the genetic blueprint and gene expression landscape of an organism, the ultimate functional manifestations of genetic activity are largely reflected at the levels of proteins and metabolites. Proteomics and metabolomics therefore serve as essential links between genetic information and the observable phenotype. Proteomics focuses on the identification, quantification, structural characterization, and post-translational modification of proteins, whereas metabolomics investigates the complete repertoire of low-molecular-weight metabolites present within biological systems. Together, these disciplines offer a more direct representation of cellular function and physiological status than genomic information alone. In aquatic species, proteomic studies commonly employ methodologies such as two-dimensional gel electrophoresis (2-DE) and mass spectrometry (MS) for protein identification and quantification (Zambon *et al*., 2025). The resulting datasets are subsequently analyzed using specialized databases and bioinformatics platforms to assign protein identities and classify their biological functions. Bioinformatics analyses in proteomics typically involve peptide-spectrum matching, protein annotation, pathway enrichment analysis, and the reconstruction of protein–protein interaction networks, thereby providing a comprehensive understanding of the molecular processes underlying economically important traits. Similarly, metabolomics relies on advanced analytical techniques, including gas chromatography–mass spectrometry (GC–MS), liquid chromatography–mass spectrometry (LC–MS), and nuclear magnetic resonance (NMR) spectroscopy, to characterize metabolite profiles within biological samples. Multivariate statistical analyses of metabolomics data can reveal metabolic differences among groups exhibiting contrasting phenotypes, such as high-growth versus low-growth individuals or animals subjected to different nutritional regimes. These approaches facilitate the identification of metabolite biomarkers associated with feed efficiency, flesh quality, physiological condition, and overall health status. Consequently, metabolomics provides a powerful framework for understanding how genetic and environmental factors converge to influence economically important traits in aquaculture species and offers valuable opportunities for the development of precision breeding and management strategies (Tzec-Interián *et al*., 2025).

Metagenomics and the aquatic microbiome

In recent years, growing evidence has demonstrated that the performance and health of aquatic organisms are not determined solely by the host genome. Rather, symbiotic microbial communities inhabiting the gastrointestinal tract, skin, surrounding water, and pond sediments play critical roles in regulating growth, immune function, nutrient utilization, and overall physiological performance. Consequently, the concept of the aquatic organism as a holobiont, a biological unit comprising both the host and its associated microbiota—has gained increasing attention in aquaculture research. Metagenomics is a powerful culture-independent approach that enables the characterization of microbial community composition and functional potential through the direct sequencing of DNA extracted from environmental or biological samples. By eliminating the need for microbial isolation and cultivation, metagenomics provides a more comprehensive and accurate representation of microbial diversity and ecological interactions. In aquaculture studies, metagenomic investigations commonly employ sequencing of specific regions of the 16S ribosomal RNA (16S rRNA) gene for bacterial community profiling, or other taxonomic marker genes, through a strategy known as metabarcoding. At a broader level, shotgun metagenomic sequencing enables the comprehensive analysis of all genomic DNA present within a biological sample without the need for microorganism isolation, cultivation, or targeted amplification of specific genomic regions. This approach provides simultaneous information on both taxonomic composition and functional genetic capacity. The resulting datasets are analyzed using bioinformatics pipelines to determine microbial community structure, diversity patterns, taxonomic composition, and predicted metabolic functions. Findings from these studies have consistently demonstrated that alterations in gut microbiome composition are associated with economically important traits such as growth performance, feed conversion efficiency, and disease resistance. These discoveries have opened new opportunities for the targeted manipulation of microbial communities through the application of probiotics, prebiotics, and optimized culture-management strategies aimed at enhancing productivity and health in aquaculture systems (Yáñez *et al.*, 2022).

Bioinformatics: Transforming taw fata into sctionable knowledge

A defining characteristic of all omics technologies is their capacity to generate massive volumes of highly complex biological data. Without appropriate computational infrastructure, analytical algorithms, and specialized software platforms, these datasets possess limited practical value. Bioinformatics, as an interdisciplinary field integrating biology, computer science, statistics, and mathematics, provides the essential framework for transforming raw biological data into structured information and, ultimately, into actionable knowledge applicable to breeding programs and aquaculture management.

The analytical workflow for omics data generally encompasses several key stages:

- Quality control and data preprocessing, including the removal of low-quality reads, contaminants, sequencing artifacts, and technical errors.
- Sequence assembly and mapping, whereby sequencing reads are assembled or aligned to an appropriate reference genome, transcriptome, or database.
- Quantification and normalization, involving the estimation and standardization of gene expression levels, protein abundances, or metabolite concentrations to facilitate reliable comparisons among samples.
- nabling the detection of biologically relevant molecular signatures.

- Functional interpretation, including gene enrichment analyses, pathway-based investigations using resources such as the Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway Database, and the reconstruction of biological interaction networks to elucidate molecular mechanisms underlying observed phenotypes.

Predictive modeling and trait forecasting, in which extracted biological patterns are integrated into computational models for predicting economically important traits and supporting decision-making processes.

A major challenge in modern aquaculture lies in translating bioinformatics-derived findings into practical tools that can support production-oriented decisions. These applications include broodstock selection, feed formulation and optimization, health management, disease prevention, and the regulation of environmental conditions within production systems. The successful implementation of omics-assisted aquaculture therefore depends not only on technological advancements but also on effective collaboration among bioinformaticians, molecular biologists, quantitative geneticists, and aquaculture practitioners. Continuous interaction among these stakeholders is essential for ensuring that molecular discoveries are converted into tangible improvements in productivity, sustainability, and economic performance within commercial aquaculture operations (Nambiar and Banuru, 2025).

The tole of bioinformatics in the analysis of genomic data from aquatic species

Next-generation sequencing and its implications for aquatic genomics

The advent of next-generation sequencing (NGS) technologies has revolutionized genomic research by enabling access to genomic information even in species that had previously received limited scientific attention. Historically, whole-genome sequencing was feasible only for a small number of model organisms due to the substantial costs and technical constraints involved. However, continuous advances in sequencing technologies have dramatically reduced both the cost and time required for genome sequencing, thereby facilitating large-scale genomic investigations across a diverse range of aquatic species. In the field of aquaculture, this technological transformation has resulted in the availability of high-quality draft genome assemblies for numerous commercially important species. Nevertheless, from a bioinformatics perspective, sequencing outputs are not directly interpretable in their raw form. Instead, they are generated as collections of short or long sequence reads that must undergo a series of computational analyses before meaningful biological information can be extracted. Transforming raw sequencing data into biologically relevant insights requires a structured bioinformatics workflow encompassing data preprocessing, genome assembly, annotation, and variant discovery. The design of an appropriate analytical pipeline and the selection of suitable computational tools are therefore critical determinants of the accuracy and reliability of downstream analyses. Ultimately, these processes enable the conversion of genomic data into actionable information that can support the improvement of economically important traits in aquaculture species (Anderson *et al*., 2025).

Genome assembly and functional annotation

Genome assembly in aquatic species presents unique challenges arising from factors such as large genome sizes, high proportions of repetitive sequences, and, in certain taxa, polyploid genome structures. To overcome these complexities, modern assembly strategies often integrate short-read sequencing data with long-read technologies, complemented by auxiliary resources such as genetic linkage maps and chromosome-conformation information. Assembly algorithms reconstruct genomic sequences by identifying overlaps and sequence similarities among individual reads, thereby generating contiguous DNA sequences (*contigs*) and subsequently larger *scaffolds* composed of multiple linked contigs. These assembled genomic frameworks provide the foundation for subsequent functional characterization. Following genome assembly, the next critical step is genome annotation, which aims to identify and characterize genes, protein-coding regions, non-coding RNAs, regulatory elements, and other functional genomic features. Genome annotation typically relies on a combination of evidence-based approaches, including transcriptomic and proteomic datasets, and *ab initio* gene prediction algorithms. The accuracy and completeness of annotation play a decisive role in determining the extent to which genes and biological pathways associated with economically important traits can be reliably identified in downstream analyses. From an applied perspective, the availability of a well-assembled and comprehensively annotated reference genome constitutes a fundamental resource for a wide range of advanced genomic applications, including:

- Identification of candidate genes associated with rapid growth, disease resistance, and salinity adaptation;
- Development of molecular markers such as single nucleotide polymorphisms (SNPs) and microsatellites;
- Construction of high-resolution genetic linkage maps and refined physical maps for genomic analysis and selective breeding programs (Song *et al*., 2025).

Consequently, genome assembly and annotation serve as the essential foundation upon which modern genomic-assisted breeding strategies and precision aquaculture applications are built.

Identification of molecular markers and genetic diversity

One of the most significant outcomes of genomic data analysis is the identification of molecular markers that can be effectively incorporated into selective breeding programs. Among the various classes of molecular markers, single nucleotide polymorphisms (SNPs) have gained particular prominence in aquaculture due to their high abundance throughout the genome and their suitability for high-throughput genotyping platforms. Bioinformatics plays a central role in SNP discovery and characterization. Sequencing reads generated from multiple individuals are first aligned to a reference genome, after which nucleotide positions exhibiting sequence variation among individuals are identified. Subsequently, stringent quality-control filters are applied to eliminate sequencing artifacts and false-positive variants, ensuring that only high-confidence SNPs are retained for downstream analyses. In addition to SNPs, other forms of genetic variation, including microsatellites and structural variants such as deletions, insertions, duplications, and inversions, can also be detected from genomic datasets. However, the identification and characterization of these variants generally require more sophisticated computational approaches due to their structural complexity. The information derived from these genetic polymorphisms is invaluable for estimating key population genetic parameters, including genetic diversity, population structure, levels of inbreeding, and kinship relationships among individuals. Consequently, molecular marker datasets provide the foundation for the development of population-based breeding strategies and the effective management of genetic resources in aquaculture species.

Linkage mapping and identification of quantitative trait loci (QTL)

Following the identification of a sufficient number of molecular markers, the next step involves the construction of genetic linkage maps. These maps estimate the relative order and genetic distances among markers based on the frequency of recombination events occurring between them during inheritance.Genetic linkage maps constitute powerful tools for the identification of genomic regions associated with quantitative traits, commonly referred to as quantitative trait loci (QTLs). In QTL studies, phenotypic measurements, such as growth rate, feed efficiency, or disease resistance, are integrated with genotypic information across the genome. Through the application of statistical and bioinformatics methodologies, genomic regions exhibiting significant associations with phenotypic variation can be identified. These QTL regions may contain one or multiple genes influencing the trait of interest. Subsequent investigations employing advanced genetic and genomic approaches, including fine mapping and transcriptomic analyses, enable the progressive narrowing of broad genomic intervals and facilitate the identification of the specific genes or causal mutations underlying trait variation. The primary practical application of QTL analysis lies in the development of trait-associated molecular markers and their implementation in marker-assisted selection (MAS) programs. By incorporating genomic information into breeding decisions, selection can be performed at earlier developmental stages, or even before the full phenotypic expression of a trait, thereby enhancing selection efficiency and accelerating genetic gain relative to approaches that rely exclusively on phenotypic records (Ibrahim *et al*., 2025).

Applications of transcriptomics and bioinformatics analyses in economically important traits

Design of RNA-Seq studies in aquatic species

The value of transcriptomic investigations is highly dependent on the quality of experimental design. In studies focusing on economically important traits in aquaculture species, transcriptomic analyses commonly involve comparisons between two or more groups exhibiting clearly differentiated phenotypes. Examples include fast-growing versus slow-growing fish, disease-resistant versus disease-susceptible families, or individuals receiving alternative dietary treatments, such as standard and optimized feed formulations. Several experimental factors critically influence the success and biological relevance of RNA-Seq studies. These include the selection of appropriate target tissues—such as liver, muscle, intestine, or immune-related tissues—the timing of sample collection, and the number of biological replicates incorporated into the experimental design. Following the extraction of high-quality RNA and the preparation of sequencing libraries, the resulting raw sequencing data must undergo rigorous quality assessment and preprocessing procedures. After filtering and data refinement, sequencing reads are aligned to a reference genome or reference transcriptome, providing the foundation for subsequent analyses of gene expression patterns and molecular pathways associated with economically important traits in aquatic organisms (Lv *et al*., 2024).

Identification of differentially expressed genes and biological pathway analysis

Following sequence alignment and transcript quantification, the principal objective of transcriptomic analysis is to estimate gene expression levels and compare them across different experimental groups. To achieve this, a range of statistical approaches is employed to identify genes exhibiting significant expression differences between biological conditions. These genes, referred to as differentially expressed genes (DEGs), provide the first molecular insights into the mechanisms underlying observed phenotypic variation. However, a simple list of DEGs is often insufficient for a comprehensive biological interpretation. Consequently, downstream functional analyses are conducted to reveal the broader biological significance of expression changes. These analyses commonly include:

- Gene enrichment analysis, which identifies overrepresented biological processes, molecular functions, and cellular components among the differentially expressed genes
- Metabolic and signaling pathway analysis, which determines the biological pathways enriched with DEGs and highlights the cellular mechanisms most strongly affected under specific conditions
- Gene co-expression network analysis, which identifies clusters of genes displaying coordinated expression patterns and potentially participating in common regulatory or physiological processes.

Collectively, these approaches provide a systems-level understanding of molecular responses, enabling researchers to move beyond individual genes and obtain a more comprehensive view of how aquatic organisms respond to different environmental, nutritional, and management-related conditions (Liu and Naganuma, 2024).

Applications of transcriptomics in economically important traits transcriptomic

approaches have been widely applied across diverse areas of aquaculture research. Some of the most significant applications related to economically important traits are outlined below:

Growth and nutritional efficiency

Utilization Efficiency Comparative analyses of gene expression patterns in tissues such as muscle and liver from individuals exhibiting different growth performances can reveal genes and biological pathways involved in energy metabolism, protein synthesis, nutrient utilization, and lipid deposition. Such studies facilitate the identification of candidate genes associated with enhanced growth potential, which can subsequently be incorporated into selective breeding programs as molecular markers. Furthermore, transcriptomic insights can support the development of precision nutrition strategies by enabling the formulation of diets tailored to the metabolic requirements of specific breeding lines or production populations, thereby improving feed efficiency and overall production performance (Zhang *et al*., 2025).

Disease resistance

Disease outbreaks remain one of the most significant sources of economic loss in aquaculture production systems. Transcriptomic analyses comparing resistant and susceptible individuals following controlled pathogen challenge experiments have substantially advanced the understanding of host immune responses. By examining immune-related tissues, including the spleen and kidney, researchers can identify genes, signaling pathways, and regulatory networks associated with effective pathogen defense mechanisms. These findings contribute to the development of molecular markers for disease resistance, facilitate marker-assisted and genomic selection strategies, and provide valuable information for vaccine development and farm health-management programs (Macedo *et al*., 2024).

Adaptation to environmental stressors

Environmental variables such as temperature, salinity, dissolved oxygen concentration, and water quality exert profound influences on the physiological performance of aquatic organisms. Transcriptomic technologies provide a powerful means of investigating the molecular responses of fish and crustaceans to these environmental stressors. Studies in this area have identified key regulatory pathways involved in stress adaptation, including those associated with heat shock proteins, antioxidant defense systems, osmoregulatory mechanisms, and cellular stress signaling. Understanding these molecular responses can facilitate the selection of stress-tolerant breeding lines and support the optimization of environmental management practices within aquaculture facilities (Houston *et al*., 2022).

Flesh quality and body composition

In commercially important aquaculture species, flesh quality represents a critical economic trait influencing both market value and consumer acceptance. Transcriptomic investigations of muscle tissue under different nutritional and management conditions have enabled the identification of genes and biological pathways involved in lipid deposition, muscle fiber development, tissue structure, and fatty acid metabolism. These studies contribute to a deeper understanding of the molecular determinants of flesh texture, nutritional composition, and overall product quality. Consequently, transcriptomic information can be integrated into breeding and nutritional strategies aimed at improving both the sensory and nutritional attributes of aquaculture products (Power *et al*., 2023).

Proteomics and metabolomics: Bridging the gap between the genome and phenotype

The role of proteomics in aquatic species research

Proteomics, defined as the comprehensive study of proteins within a biological system, becomes particularly valuable when the objective is to understand how genetic variation and gene expression are translated into the actual functional activities of cells and tissues. While genomic and transcriptomic analyses provide insights into an organism's genetic blueprint and transcriptional landscape, proteins ultimately execute most biological functions and therefore represent a more direct reflection of phenotype. Fundamental physiological processes, including muscle contraction, immune responses, nutrient transport, cellular signaling, and metabolic regulation, are mediated by proteins. Moreover, post-translational modifications (PTMs), such as phosphorylation, glycosylation, acetylation, and ubiquitination, can profoundly influence protein activity, stability, localization, and interaction networks. These regulatory mechanisms cannot be fully elucidated through transcriptomic analyses alone, underscoring the importance of proteomics in functional biological investigations. In aquaculture research, proteomic studies typically combine protein separation techniques, such as two-dimensional gel electrophoresis (2-DE), with protein identification and quantification through mass spectrometry (MS)-based platforms. Following data acquisition, bioinformatics pipelines are employed to process spectral information, match peptide sequences to reference protein databases, and classify proteins according to their structural characteristics, molecular functions, and biological roles. This integrative approach provides valuable insights into the molecular mechanisms underlying economically important traits in aquatic species (Purcell *et al*., 2025).

Applications of proteomics in the improvement of economically important traits

Flesh quality and seafood product characteristics

Alterations in muscle protein composition and abundance can directly influence commercially important quality attributes, including texture, water-holding capacity, flavor, nutritional value, and post-harvest shelf life. Proteomic analyses enable the identification of key proteins associated with superior product quality, providing valuable targets for selective breeding programs and for optimizing post-harvest handling and processing practices (Jaiswal *et al*., 2023).

Responses to disease and environmental stress

Proteomic profiling of immune-related tissues and biological fluids, such as serum and mucus, facilitates the identification of defense proteins, inflammatory mediators, stress-response molecules, and signaling pathways involved in host protection. These investigations contribute to a more comprehensive understanding of the molecular mechanisms underlying disease resistance and environmental adaptation, thereby supporting the development of improved health-management strategies in aquaculture systems. Evaluation of Nutritional Interventions Proteomics also serves as a powerful tool for assessing the physiological effects of alternative dietary formulations. Changes in the abundance of metabolic proteins within the liver, intestine, and other nutritionally relevant tissues can reveal how different feed ingredients and nutritional regimes influence nutrient utilization, metabolic efficiency, and growth performance. Such information can be leveraged to formulate more efficient and sustainable aquafeeds that maximize production outcomes while minimizing costs and environmental impacts (Young *et al*., 2023).

Metabolomics and metabolic indicators of performance

Metabolomics focuses on the comprehensive analysis of small-molecule metabolites present within biological systems. Because metabolites represent the final or intermediate products of cellular biochemical pathways, metabolomic profiles provide one of the closest molecular representations of the observable phenotype. Furthermore, metabolite concentrations can respond rapidly to changes in nutritional status, physiological condition, environmental factors, and disease processes, making metabolomics a highly sensitive tool for assessing biological performance. In aquatic species, metabolomic investigations commonly employ advanced analytical platforms such as gas chromatography–mass spectrometry (GC–MS), liquid chromatography–mass spectrometry (LC–MS), and nuclear magnetic resonance (NMR) spectroscopy to characterize metabolite composition and abundance across diverse biological samples (Marhuenda-Egea and Sanchez-Jerez, 2025).

Bioinformatics analysis of metabolomic datasets generally involves several key steps:

- Signal processing, peak detection, alignment, and normalization to ensure data quality and comparability among samples;
- Metabolite identification and annotation through spectral matching against established reference databases;
- Application of multivariate statistical approaches, including principal component analysis (PCA), to discriminate among biological groups and identify major sources of variation;
- Mapping of significant metabolites onto biological pathways to elucidate their relationships with underlying metabolic processes and physiological functions.

The outcome of these analyses is often the identification of distinct metabolic signatures associated with specific biological states or performance traits. Examples include metabolic profiles linked to accelerated growth, superior feed efficiency, enhanced disease resilience, or tolerance to thermal stress.

Importantly, the predictive value of metabolomic data is substantially enhanced when integrated with genomic and transcriptomic information. Such multi-layered datasets provide a comprehensive systems-level perspective of biological function and offer powerful opportunities for the prediction, monitoring, and optimization of performance in aquaculture production systems. Consequently, metabolomics has emerged as a critical component of modern precision aquaculture and data-driven breeding strategies aimed at improving sustainability, productivity, and economic efficiency (Young *et al.*, 2024).

Metagenomics and the microbiome in enhancing the performance and health of aquatic organisms

The importance of the microbiome in aquaculture systems

The significance of the microbiome in aquaculture can be examined from two complementary perspectives:

- Its role in the health, physiology, and performance of aquatic organisms
- Its contribution to the sustainability, stability, and operational efficiency of aquaculture production systems.

Over the past decade, the perception of microorganisms within aquaculture environments has undergone a fundamental transformation. Rather than being viewed solely as potential pathogens, microbial communities are now increasingly recognized as functional partners of the host and key regulators of ecosystem processes. This paradigm shift has profound implications for the management and optimization of modern aquaculture systems.

The microbiome: The forgotten part of the aquatic ecosystem

Aquatic organisms inhabit highly dynamic environments characterized by continuous exposure to water and sediments containing vast and diverse microbial communities. Under such conditions, the boundary between the host and its surrounding microbial environment is inherently diffuse. Consequently, Fish or shrimp should be considered as a superorganism along with gut microbiome, skin, gills and water and substrate microbiome.

Several microbiome compartments are particularly relevant in aquaculture systems:

- The gut microbiome, comprising bacteria, fungi, and, in some cases, archaea, which contribute to digestion, nutrient metabolism, immune regulation, and host physiology;
- The skin and gill microbiomes, which serve as the first biological barrier against waterborne pathogens and play critical protective and regulatory roles;
- The water and sediment microbiomes, which influence water quality, nutrient cycling processes such as nitrogen and phosphorus turnover, and the ecological balance between beneficial and potentially harmful microorganisms.

Recognizing the microbiome as an integral component of the production system represents a crucial step toward the development of next-generation management strategies aimed at improving productivity, health, and environmental sustainability in aquaculture operations (Rajeev *et al*., 2024).

The tole of the hut microbiome in growth, feed conversion efficiency, and health

Among the various microbiome-associated functions, the contribution of the gut microbiota to nutrition and growth is of particular importance. Numerous symbiotic intestinal microorganisms actively participate in digestive and metabolic processes through several mechanisms:

- Production of digestive enzymes, including proteases, lipases, amylases, and cellulases, which enhance the breakdown and utilization of dietary nutrients;
- Biosynthesis of essential vitamins, particularly members of the vitamin B complex, as well as other biologically active compounds beneficial to host physiology;
- Generation of short-chain fatty acids (SCFAs), which provide additional energy sources for intestinal epithelial cells and contribute to the maintenance of gut integrity and mucosal health.

Collectively, these functions improve nutrient utilization efficiency, enhance feed conversion performance, and promote growth without necessarily increasing feed consumption. Given that feed costs typically represent the largest operational expense in aquaculture production, such improvements can yield substantial economic benefits. Beyond their nutritional functions, gut microbial communities play a pivotal role in immune regulation and disease resistance. The establishment and maintenance of a stable and balanced population of beneficial microorganisms can enhance host health through several complementary mechanisms:

- It suppresses pathogenic bacteria by competing for space and nutrients
- Production of antimicrobial compounds, including bacteriocins, organic acids, and other inhibitory metabolites that exert selective pressure against opportunistic pathogens;
- Stimulation and modulation of both local and systemic immune responses, thereby strengthening host immune preparedness and resilience against infectious challenges.

Through these interconnected mechanisms, the gut microbiome acts as a critical determinant of health, productivity, and disease resistance, reinforcing its importance as a target for innovative management interventions aimed at improving aquaculture performance and sustainability (Hossieni *et al*., 2024).

Water and sediment microbiomes as regulators of aquaculture environmental quality

Water quality is among the most critical determinants of success in aquaculture production systems. A substantial proportion of the biological and biogeochemical processes governing water quality are regulated by microbial communities inhabiting the water column and pond sediments. These environmental microbiomes perform essential ecosystem functions that directly influence animal health, productivity, and system stability.

The principal roles of environmental microbial communities include:

- Nitrogen cycling: Nitrifying and denitrifying microorganisms play indispensable roles in the transformation of toxic nitrogenous compounds. Through sequential biochemical processes, ammonia and nitrite are converted into less harmful forms, thereby preventing the accumulation of toxic metabolites within culture systems. Disruptions in these microbial communities may result in elevated ammonia and nitrite concentrations, leading to physiological stress, impaired growth, and increased mortality.

- Decomposition of organic matter: Uneaten feed, fecal waste, and other organic residues continuously accumulate in aquaculture environments. If not efficiently degraded, these materials can deteriorate water quality and promote the development of anaerobic conditions within sediments. Decomposer microorganisms contribute to ecological stability by converting complex organic compounds into simpler forms that can be recycled within the ecosystem.
- Competition with opportunistic pathogens: The presence of a diverse and balanced community of non-pathogenic microorganisms limits the ecological niches available for pathogenic species. Through competitive interactions, beneficial microbial populations can suppress the establishment and proliferation of opportunistic pathogens, thereby contributing to disease prevention and environmental resilience (Liu *et al*., 2024).

Microbiome management: From disease control to sustainable production

Historically, health management strategies in aquaculture were primarily focused on the elimination or suppression of pathogens through the extensive use of disinfectants and antimicrobial agents. As understanding of microbial ecology has advanced, this perspective has shifted toward the active management of microbial communities. Rather than attempting to eradicate microorganisms indiscriminately, contemporary approaches seek to guide the composition and functionality of the microbiome toward desirable and stable ecological states.

Several key strategies have emerged for microbiome-based management:

- Probiotics: The supplementation of beneficial bacteria and yeasts through feed or water with the objective of enhancing the gut microbiome and improving the microbial balance of the culture environment.
- Prebiotics and synbiotics: The use of substrates that selectively stimulate the growth and activity of beneficial microorganisms, or the combined application of probiotics and prebiotics to maximize synergistic effects on host health and performance.
- Optimization of feeding practices and stocking density: Adjustments in feed quantity, feed composition, stocking density, and water-exchange regimes can substantially influence microbial community structure and

functionality, thereby affecting both environmental quality and animal performance.

- Polyculture and Integrated Multi-Trophic Aquaculture (IMTA) systems: The co-cultivation of species occupying different trophic levels—such as fish, macroalgae, and mollusks—can promote nutrient recycling and ecological balance. By creating complementary nutrient pathways, IMTA systems contribute to the stabilization and diversification of microbial communities while enhancing overall system sustainability.

This ecosystem-based approach shifts the focus from reactive crisis management to proactive prevention through the establishment of resilient and self-regulating production environments. Over the long term, microbiome-centered management strategies have the potential to reduce production costs, mitigate biological risks, improve animal welfare, and enhance the environmental sustainability of aquaculture operations (Amillano-Cisneros *et al*., 2025).

The microbiome, sntibiotics, and food safety concerns

The extensive and often indiscriminate use of antibiotics in aquaculture has raised significant concerns regarding both animal and public health. Beyond promoting the emergence and dissemination of antimicrobial resistance, antibiotic exposure can profoundly disrupt the structure and functionality of microbial communities associated with both cultured organisms and their surrounding environments.Among the most important consequences of microbiome disruption are:

- Reduction in the abundance and diversity of beneficial microbial populations
- Creation of ecological niches that facilitate the proliferation of opportunistic and antibiotic-resistant microorganisms
- Increased potential for the horizontal transfer of antimicrobial resistance genes among microbial communities, including pathogenic bacteria.

Such disturbances extend beyond their immediate effects on cultured stocks. Alterations in microbial community dynamics can compromise animal health and production performance while simultaneously posing risks to consumers and to surrounding natural ecosystems through the dissemination of resistant microorganisms and resistance determinants.

In contrast, the promotion and maintenance of beneficial microbiomes have emerged as promising complementary or alternative strategies to reduce reliance on antimicrobial agents. By enhancing microbial stability and resilience, microbiome-based interventions can improve host health, strengthen disease resistance, and contribute to the production of safer aquaculture products that better satisfy the increasingly stringent requirements of domestic and international markets regarding food safety and environmental sustainability (Caballero *et al*., 2024).

Future perspectives: The microbiome as a precision management tool

Recent advances in metagenomic technologies and bioinformatics have dramatically improved the ability to characterize microbial community structure and function with high resolution across temporal and environmental gradients. As a result, the microbiome is increasingly being viewed not merely as a biological component of aquaculture systems but as a valuable source of actionable information for precision management. In the near future, several transformative applications are likely to emerge:

- Gut and environmental microbiome profiles may serve as sensitive biomarkers of animal health status and early indicators of disease risk
- Nutritional and management strategies may be customized according to the unique microbial signatures of individual farms and production systems
- Selective breeding programs may incorporate host–microbiome interactions as an additional criterion for the improvement of economically important traits

Within this emerging framework, the microbiome is expected to evolve from a largely hidden biological factor into an active and strategically managed component of aquaculture production. Such a transition has the potential to enhance productivity, reduce biological and environmental risks, and accelerate the development of more sustainable and environmentally responsible aquaculture systems (Vanden Bussche and Verdegem, 2023).

Metagenomic approaches and bioinformatics analyses

Metagenomic investigations in aquaculture generally employ two principal methodological approaches:

- Metabarcoding, which involves sequencing taxonomic marker genes, most commonly the 16S ribosomal RNA (16S rRNA) gene, to characterize bacterial community composition at the genus or species level
- Shotgun metagenomic sequencing, in which all DNA present within an environmental or biological sample is randomly fragmented and sequenced. This approach provides a far more comprehensive representation of microbial diversity and functional potential, enabling simultaneous assessment of taxonomic composition and metabolic capabilities.
- The large-scale datasets generated through these methodologies require extensive bioinformatics processing, including quality filtering, sequence alignment, taxonomic classification, assembly, functional annotation, and the calculation of ecological diversity indices. To support these analyses, numerous specialized software

platforms and curated databases have been developed, enabling researchers to identify dominant microbial taxa, predict metabolic pathways, and investigate the relationships between microbiome structure and host performance.

These analytical frameworks provide critical insights into the ecological and functional dynamics of aquaculture-associated microbial communities and form the foundation for microbiome-informed management strategies (Usyk *et al*., 2023).

Applications of metagenomics in economically important traits and health

Multiple studies have demonstrated that shifts in microbiome composition can be associated with economically important traits such as growth, feed-use efficiency, and disease resistance. For example, an increased relative abundance of certain short-chain fatty-acid–producing bacteria in the intestine may correlate with improved digestive efficiency and enhanced growth, whereas a relative decline in pathogenic taxa in response to probiotic administration can reduce health risks. Bioinformatics enables the following:

- Identification of microbial signatures associated with desirable performance.
- Evaluation of the effects of dietary additives (probiotics, prebiotics, synbiotics) on the microbiome.
- Design of targeted microbiome-modulation strategies to improve economically important traits (Coskuner-Weber *et al*., 2025).

From omics data to breeding programs and practical aquaculture management

Marker-assisted selection (MAS)

Marker-assisted selection (MAS) was among the earliest approaches to incorporate molecular information into selective breeding programs. As an indirect selection strategy, MAS utilizes molecular markers that are closely linked to quantitative trait loci (QTLs) controlling economically important traits, thereby facilitating the selection of superior broodstock and breeding families.

A major advantage of MAS is that selection decisions can be made at early developmental stages, often before the target phenotype is fully expressed, thereby reducing the need for prolonged phenotypic recording and accelerating the breeding process.

The successful implementation of MAS depends on several key prerequisites:

- Identification of QTLs with relatively large and consistent effects on target traits
- Development of molecular markers exhibiting strong and stable linkage with these QTLs
- Validation of marker–trait associations across multiple populations and production environments to ensure robustness and transferability.

When these conditions are met, MAS can significantly improve selection efficiency and enhance genetic progress in aquaculture breeding programs (Wang and Wu, 2025).

Genomic selection (GS)

Genomic selection (GS) represents a major advancement beyond traditional marker-assisted selection. Rather than focusing on a limited number of QTLs, GS exploits genome-wide information derived from thousands to millions of single nucleotide polymorphisms (SNPs) distributed throughout the genome to predict the genomic breeding values of individuals. In this approach, a reference population possessing both extensive phenotypic records and high-density genotypic information is used to estimate marker effects and construct predictive models. These models are subsequently applied to candidate populations for which only genotypic information is available, enabling the estimation of genomic breeding values without the need for direct phenotypic assessment.Genomic selection is particularly valuable in aquaculture for traits that:

- Are expensive or difficult to phenotype, such as resistance to specific diseases
- Are expressed late in the production cycle, including traits related to sexual maturation, reproductive performance, and flesh quality.
- By enabling early and more accurate selection decisions, GS has the potential to accelerate genetic gain while reducing the costs and logistical constraints associated with conventional breeding programs.

The bioinformatics framework supporting genomic selection involves the management of large-scale genomic datasets, implementation of sophisticated statistical and quantitative genetic models, and evaluation of predictive performance under diverse breeding and environmental scenarios (Kang *et al*., 2025).

Integration of multi-omics data in trait modeling

The rapid expansion of genomic, transcriptomic, proteomic, and metabolomic datasets has generated a critical question in modern biological research: how can these multiple layers of biological information be integrated to improve the prediction and understanding of economically important traits? In recent years, a variety of multi-omics integration strategies have been proposed to address this challenge. These approaches seek to combine gene regulatory networks, biological pathways, molecular interactions, and metabolic signatures into unified predictive frameworks capable of capturing the complexity of phenotype determination. At this level, bioinformatics functions as an integrative bridge that connects disparate datasets into coherent biological models. Effective multi-omics integration generally requires:

- Normalization and standardization of data generated from heterogeneous analytical platforms
- Application of machine learning algorithms, network-based approaches, and advanced computational modeling techniques
- Assessment of model robustness and transferability across genetically distinct populations and diverse environmental conditions.

Although this field remains under active development, its potential applications are considerable. Multi-omics models are expected to improve the accuracy of genetic evaluations and facilitate the implementation of precision aquaculture strategies, including genotype-specific nutritional programs and management practices tailored to the physiological and metabolic characteristics of individual production stocks (Yu *et al*., 2025).

Translating omics data into practical farm management

One of the most significant challenges facing contemporary aquaculture research is the effective translation of laboratory-based discoveries into practical applications under commercial farming conditions. The true value of omics technologies can only be realized when molecular insights are converted into tools that support routine management decisions. To facilitate this transition, several requirements must be addressed:

- Research findings should be translated into user-friendly and operationally relevant tools, such as diagnostic kits, genotyping panels, nutritional guidelines, and management protocols
- The costs and technical complexity associated with these technologies must remain economically feasible for commercial producers
- Strong and sustained collaboration should be established among research institutions, breeding companies, hatcheries, and aquaculture producers to promote knowledge transfer and technology adoption.

In this context, the development of integrated software systems and digital management platforms capable of simultaneously storing, processing, and analyzing molecular, phenotypic, and environmental data will play a pivotal role in transforming bioinformatics-derived knowledge into practical decision-support tools.Such platforms are expected to form the foundation of next-generation precision aquaculture systems, enabling data-driven management strategies that improve productivity, sustainability, and economic efficiency across the aquaculture value chain (Veroli *et al*., 2025).

Challenges and limitations in the application of bioinformatics and omics technologies in aquaculture

Technical and infrastructural challenges

The successful implementation of omics-based research and breeding programs requires access to robust computational and data-storage infrastructures. The enormous volume of genomic, transcriptomic, proteomic, and metabolomic data generated by high-throughput technologies necessitates the availability of high-performance computing systems, dedicated servers, and scalable data-storage platforms. In many countries and research institutions, limitations in computational infrastructure constrain the scope and depth of bioinformatics analyses, often resulting in incomplete data processing or increased reliance on external facilities and international collaborations. Furthermore, the rapid evolution of analytical methodologies and bioinformatics software demands continuous updating of technical expertise and computational competencies among research personnel. Another important challenge is the lack of universally adopted standards for data storage, annotation, and sharing. Inconsistent data formats and metadata structures can hinder interoperability among studies, thereby limiting opportunities for large-scale meta-analyses and cross-study integration of omics datasets (Bouras *et al*., 2023).

Economic and structural constraints

Although the costs associated with omics technologies have declined substantially over the past decade, their implementation remains financially demanding, particularly during the establishment phase. Investment in sequencing platforms, laboratory infrastructure, high-quality consumables, computational resources, and specialized analytical services can impose significant financial burdens. For small- and medium-scale aquaculture enterprises, the direct adoption of these technologies may not always be economically feasible unless supported through national breeding initiatives, cooperative frameworks, public–private partnerships, or collaborations with larger commercial enterprises. In addition, the fragmented ownership structures and heterogeneous management practices that characterize many aquaculture sectors present substantial obstacles to the large-scale implementation of genomics-based breeding programs. The absence of comprehensive systems for recording phenotypic performance, pedigree information, and production data further limits the effective utilization of molecular information and reduces the potential impact of advanced breeding strategies (Yáñez *et al*., 2022).

Shortage of interdisciplinary expertise

Bioinformatics operates at the intersection of multiple scientific disciplines, including genetics, molecular biology, fisheries science, statistics, mathematics, and computer science. Consequently, the success of omics-driven research depends on effective collaboration among specialists from these diverse fields. In many instances, research teams possess strong expertise in one domain while lacking sufficient capacity in others. Moreover, communication gaps frequently exist between academic researchers and aquaculture practitioners, limiting the translation of scientific discoveries into practical applications. As a result, valuable biological datasets may remain underutilized or fail to generate outcomes with direct relevance to production systems. Addressing this challenge requires sustained investment in interdisciplinary education and workforce development, both through formal university programs and through specialized professional training initiatives designed for researchers and industry personnel (Ovchinnikova and Shi, 2023).

Bridging the gap between research and farm-level application

A considerable proportion of omics-based studies are conducted under controlled laboratory conditions and on relatively limited experimental scales. Translating these findings into commercial aquaculture environments is considerably more complex due to the dynamic, multifactorial, and economically constrained nature of production systems. Successful implementation requires extensive validation under field conditions, adaptation to operational realities, and a thorough understanding of producers' needs and priorities. In some cases, a strong emphasis on academic publication outputs may inadvertently reduce long-term engagement with industry stakeholders and limit the practical evaluation of research outcomes. To narrow this research-to-application gap, projects should be designed from the outset with the active participation of multiple stakeholders, including researchers, breeding companies, producers, and policymakers. Furthermore, economic feasibility assessments and implementation strategies should be incorporated as integral components of project planning and evaluation rather than being considered only after scientific objectives have been achieved.

Ethical and policy considerations

The increasing use of genomic information and advanced breeding technologies raises important ethical, legal, and policy-related questions that must be addressed to ensure responsible and equitable implementation. Key issues include:

- Intellectual property rights associated with genetically improved strains and breeding resources;
- Equitable access to emerging genomic technologies for small-scale and resource-limited producers;
- Potential ecological consequences arising from the unintended release of genetically selected or improved stocks into natural ecosystems.

These concerns highlight the need for comprehensive legal and ethical frameworks governing the generation, ownership, sharing, and application of genomic data and breeding technologies. Policymakers must develop regulatory strategies that simultaneously encourage innovation and technological advancement while safeguarding biodiversity, ecosystem integrity, and the interests of small-scale producers. A balanced governance framework will be essential for ensuring that the benefits of bioinformatics and omics technologies contribute to the long-term sustainability, competitiveness, and resilience of the aquaculture sector without compromising environmental stewardship or social equity (Liu *et al*., 2022).

Future perspectives and emerging directions

Multi-omics integration and systems-level understanding of aquatic organisms

The future trajectory of omics research is increasingly directed toward the integration of multiple layers of biological information and the development of systems-level models capable of describing organismal function in a holistic manner. In aquaculture, the convergence of genomic, transcriptomic, proteomic, metabolomic, and metagenomic datasets is expected to provide a more comprehensive understanding of the complex interactions among genotype, environment, and phenotype.Such integrative frameworks offer unprecedented opportunities to elucidate the molecular mechanisms underlying economically important traits and to reveal the dynamic biological networks that govern growth, health, adaptation, and productivity. By capturing these multidimensional interactions, systems-based models can support the development of more coordinated and efficient breeding, nutritional, and management strategies tailored to the biological characteristics of cultured species.

The expanding role of artificial intelligence and machine learning

As biological datasets continue to increase in both volume and complexity, conventional statistical approaches are often insufficient to fully exploit the information they contain. Consequently, artificial intelligence (AI) and machine learning (ML) methodologies are becoming increasingly important for the analysis of large-scale biological data and the identification of complex, non-linear patterns that may otherwise remain undetected. Within aquaculture systems, AI- and ML-based approaches can be applied to:

- Predict growth performance, health status, and production outcomes using integrated genomic and environmental datasets;
- Identify optimal dietary formulations tailored to specific genotypes and production objectives;
- Continuously analyze information generated by environmental sensors, monitoring systems, and production records to support real-time decision-making.

The integration of these computational approaches with omics-derived information is expected to accelerate the development of intelligent decision-support systems capable of enhancing production efficiency, animal welfare, and resource utilization across aquaculture operations (Vo *et al*., 2021).

Precision and smart aquaculture

A major trend across modern agriculture and animal production is the transition toward precision-based management, whereby production decisions are adapted to the real-time status of individual production units or even individual organisms. Aquaculture is increasingly embracing this paradigm through the adoption of precision aquaculture technologies. In precision aquaculture systems, data generated from environmental sensors, imaging technologies, automated weighing systems, and other monitoring platforms are integrated with genetic and molecular information to provide a comprehensive representation of stock performance and environmental conditions. Within this framework, bioinformatics and omics analyses extend far beyond their traditional role as research tools. Instead, they become integral components of the farm's digital infrastructure, contributing directly to operational decision-making and production management. When effectively implemented, precision aquaculture has the potential to improve productivity, reduce operational costs, enhance resource-use efficiency, and minimize environmental impacts, thereby contributing to the long-term sustainability and resilience of aquaculture production systems (Islam, 2023).

Opportunities for developing countries

At first glance, omics technologies and bioinformatics may appear to be accessible primarily to countries with substantial financial and technological resources. However, the continuous decline in sequencing costs, coupled with the expansion of outsourcing services and international collaborative networks, has significantly lowered barriers to participation for developing nations.

The critical factor is not necessarily the scale of investment but rather the strategic prioritization of resources toward species and traits of greatest economic and national importance. For example, a national aquaculture genomics initiative may adopt a phased approach by:

- Establishing high-quality genomic resources and characterizing genetic diversity in a limited number of strategically important species;
- Focusing initially on a small set of high-priority traits, such as growth performance and resistance to major diseases;
- Gradually expanding both the range of target traits and the number of species included as technical capacity and infrastructure develop.

Effective collaboration among universities, research institutes, private-sector stakeholders, breeding companies, and governmental agencies, supported by coherent policy frameworks, will be essential for maximizing the benefits of these technologies and ensuring their successful implementation within developing aquaculture sectors (Ashraf Rather *et al*., 2024).

Conclusion

The integration of omics technologies with advanced bioinformatics methodologies has opened a new frontier in fisheries science and aquaculture. By enabling the investigation of biological systems across multiple molecular dimensions, from the genome and transcriptome to proteins, metabolites, and associated microbial communities, these approaches provide powerful tools for deciphering the complex mechanisms underlying economically important traits. Through the application of these technologies, it is now possible to identify genes, molecular pathways, biomarkers, and regulatory networks associated with growth performance, feed efficiency, disease resistance, environmental stress tolerance, and product quality. Such knowledge can be effectively incorporated into selective breeding programs, health management strategies, nutritional optimization, and precision production systems. Despite their considerable promise, the full realization of omics- and bioinformatics-driven aquaculture remains contingent upon overcoming several important challenges, including limitations in computational infrastructure, high initial implementation costs, shortages of interdisciplinary expertise, and the persistent gap between scientific research and practical farm-level application. Strategic investment in infrastructure, education, and technological capacity, combined with long-term planning, strengthened national and international collaborations, and careful consideration of ethical, regulatory, and policy-related issues, will be essential for unlocking the full potential of these technologies. Ultimately, the continued integration of bioinformatics and multi-omics approaches into aquaculture research and production systems is expected to play a transformative role in enhancing productivity, sustainability, resilience, and global competitiveness, thereby contributing significantly to the future development of a more efficient and environmentally responsible fisheries and aquaculture sector.

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