



Multi-Omics Approaches in Fish Health Management

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Multi-omics has emerged as a powerful tool that enable comprehensive research in fish health management by studying biological processes at molecular levels. Multi-omics. It comprises genomics, transcriptomics, proteomics and metabolomics, that provide insights on host-pathogen interactions, immune regulation, disease progression and physiological adaptation in host. Genomic tools are required for accurate identification and characterization of pathogen, while transcriptomics study reveals the differential gene expression, proteomics investigates protein function and its regulation and metabolomics provides information related to metabolic alterations associated with disease conditions. The integration of these technologies can help in the discovery of biomarkers, novel therapeutic targets and disease resistance mechanisms. Additionally, multi-omics offers advanced diagnostics, vaccine development, immunostimulant discovery and precision disease management, thereby contributing to sustainable aquaculture.

Introduction

Aquaculture is one of the fastest-growing food production sectors in the world and contributes significantly to global food security and economic development. With advancements in the intensive aquaculture practices, incidences of infectious and non-infectious diseases has also been increasing, that leads to substantial production and economic loss. Fish health is influenced by a highly complex and dynamic interplay among host genetics, pathogen virulence, environmental factors, nutritional status and associated microbial communities. Disease management in aquaculture farms are one of the major challenges faced by farmers (Assefa and Abunna, 2018). To understand the biological mechanisms underlying host-pathogen interactions rather than relying solely on symptom-based interventions advanced technologies are required.

Recent advances such as high-throughput omics technologies have transformed fish health research by aiding comprehensive analysis of biological systems at molecular level. Omics approaches such as genomics, transcriptomics, proteomics and metabolomics allow detailed study of genetic variation, gene expression patterns, protein abundance and metabolite dynamics, respectively, during health and disease conditions (Karczewski and Snyder, 2018). These approaches have become powerful tools for exploring the interactions between fish immune systems and invading pathogens.

Genomics

Genomics is a molecular tool that focuses on the study of an organism's complete genetic composition, including genome structure, organization, function and variation (Olyman et al., 2024). The genomic workflow begins with the extraction and purification of high-quality DNA, followed by library preparation and high-throughput sequencing after preprocessing steps such as DNA fragmentation and amplification. The generated sequencing datasets undergo quality assessment, assembly, integration and downstream bioinformatic analyses to derive biologically meaningful information through genome annotation and data mining. It enables comprehensive analysis of pathogen genomes with high resolution and accuracy.

Among the genomic tools, whole-genome sequencing (WGS) is used to provide complete sequence of pathogen genomes and reveal all its genetic information. By comparing genomic sequences with reference databases, WGS facilitates precise identification of pathogens at species and strain levels. Genomic analyses support the discovery of virulence-associated genes and other genomic determinants involved in pathogenicity and host adaptation. Comparative pathogenomics further enable genome-level comparisons among pathogenic strains and allow to investigate evolutionary relationships, genetic diversity, adaptation strategies and transmission dynamics. Genomic information also plays an important role in epidemiological studies by integrating genomic data with geographic information to trace pathogen movement, identify sources of outbreaks and understand transmission pathways. Such analyses can help in the development of targeted biosecurity and disease management strategies by identification of novel vaccine candidates, therapeutic targets and molecular markers associated with disease resistance.

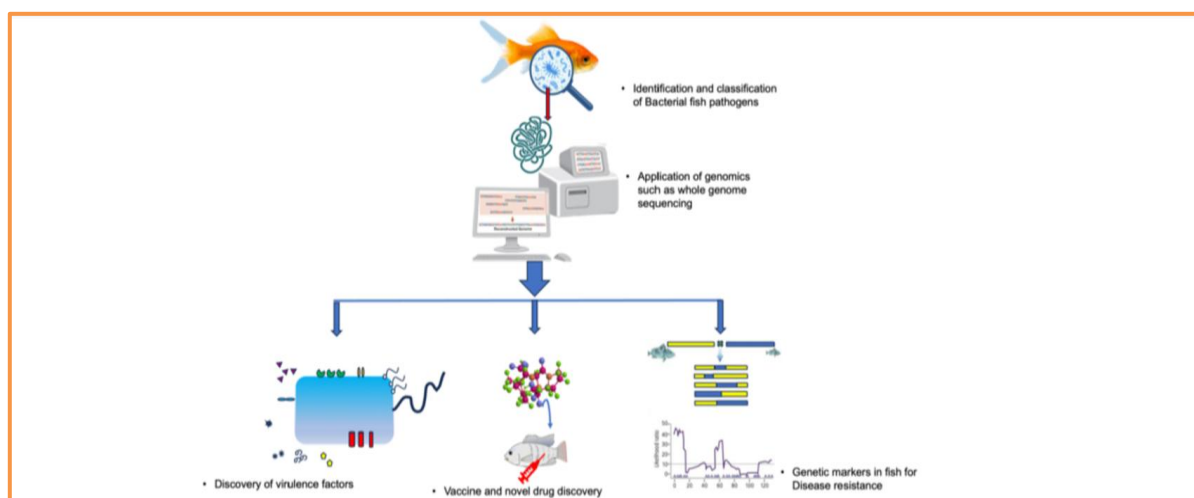


Figure 1. Genomics applications in fish health management (Source: Olyman *et al.*, 2024)

Table 1. Common omics approaches and analytical tools used in fish health research

Omics Approach	Major Tools / Platforms	Primary Function
Genomics	Next Generation Sequencing (NGS)	High-throughput genome sequencing
	SPAdes, SOAPdenovo	Genome assembly
	BLAST	Sequence similarity analysis
	Prokka	Genome annotation
	VFDB	Virulence factor identification
	CARD	Antimicrobial resistance analysis
	MEGA	Phylogenetic and evolutionary analysis
Transcriptomics	Microarray	Gene expression
	RNA-seq	Whole transcriptome profiling
	HISAT2	RNA sequence alignment
	StringTie	Transcript assembly and quantification
Proteomics	SDS-PAGE	Protein separation
	2D-GE	Separation of complex protein mixtures
	LC-MS/MS	Protein identification and quantification
	MALDI-TOF MS	Protein mass analysis
	iTRAQ	Relative protein quantification
	SWISS-MODEL	Protein structure prediction
	STRING	Protein-protein interaction analysis
Metabolomics	PyMOL	Protein visualization
	GC-MS	Metabolite separation and identification
	LC-MS	Detection of metabolites
	NMR	Metabolite characterization
	KEGG	Metabolic pathway mapping

Transcriptomics

Transcriptomics refers to the comprehensive analysis of the entire set of RNA molecules expressed within a cell, tissue, or organism at a specific physiological or developmental stage. The transcriptome includes multiple classes of RNA, such as messenger RNAs (mRNAs), transfer RNAs (tRNAs), ribosomal RNAs (rRNAs) and various non-coding RNAs (ncRNAs) (Li et al., 2025). This provides information on dynamic changes in gene activity and reveals how organisms respond to internal and external stimuli. By studying the variations in transcriptional profiles across tissues, developmental stages and stress conditions, differentially expressed genes and regulatory pathways involved in physiological adaptation and pathological processes can be identified. Currently, transcriptomics involves two principal technologies, i.e., microarray hybridization and RNA sequencing (RNA-seq). In microarray technology chips are fluorescently labeled with cDNA probes to hybridize with target sequences for simultaneous measurement of known gene expression patterns. RNA-seq involves the conversion of RNA into complementary DNA libraries followed by high-throughput sequencing to generate quantitative and qualitative information on transcript abundance. This approach enables comprehensive detection of protein-coding transcripts, small regulatory RNAs and uncharacterized non-coding RNAs.

Proteomics

Proteomics is defined as large-scale study of the complete set of proteins (proteome) expressed in a cell, tissue, organ or organism under specific physiological and environmental conditions. The proteome is highly dynamic and changes continuously in response to developmental stages, environmental stimuli, disease conditions, stress and cellular signalling events. As proteins act as the primary functional molecules within biological systems, proteomic analysis provides direct insights into cellular activities and physiological responses. Modern proteomics is beyond the identification and quantification of proteins and encompasses the investigation of protein localization, post-translational modifications, structural organization, molecular interactions, enzymatic activity and biological functions (Aslam et al., 2025). Proteomics is generally categorized into three major domains: expression proteomics, structural proteomics and functional proteomics. Expression proteomics focuses on analysing quantitative differences in protein abundance across biological conditions. Structural proteomics determines the three-dimensional organization and architecture of proteins and protein complexes within specific cellular environments. Structural proteomic contribute to revealing how proteins assemble, interact and regulate cellular processes under defined physiological conditions. Functional proteomics represents an advanced area of proteomic research that investigates the spatial and temporal dynamics of protein interactions and signalling pathways and examines how proteins collectively regulate cellular responses.

Metabolomics

Metabolomics is an advanced approach used for quantitative profiling of the complete repertoire of metabolites and their dynamic concentrations within a biological system. Variations in metabolite abundance reflect alterations in cellular metabolism and provide valuable information regarding physiological adaptation, immune activation, environmental stress responses and disease progression. The metabolomics workflow generally involves metabolite extraction followed by identification and quantification using advanced techniques such as mass spectrometry (MS) and nuclear magnetic resonance (NMR) spectroscopy. Subsequent data processing and bioinformatic analyses enable the identification of metabolic pathways and the interpretation of biological responses. Differentially accumulated metabolites may act as potential biomarkers for disease diagnosis and prognosis and can reveal pathways involved in immune activation and pathogen resistance (Megha et al., 2021).

Conclusion

Disease outbreaks continue to be one of the major challenges in aquaculture, resulting in high mortality and economic loss. To address these challenges, advanced omics technologies have emerged to understand disease progression, pathogenic mechanisms and complex host-pathogen interactions. The multi-omics technique provides comprehensive insights into disease-associated genes, differential gene expression, proteins, metabolites, immune responses and molecular biomarkers. Such approaches support targeted disease control, accurate disease diagnosis and improved fish health management. In future, continued advancements in omics technologies and bioinformatics is expected to play an important role in developing sustainable and precision based disease management strategies in aquaculture.

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