



Review Paper

Advancing Aquaculture Genetics through Omics Technologies: A Review

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Abstract

Aquaculture plays a pivotal role in meeting global food demands, contributing 59% of the 223.2 million tonnes of fisheries and aquaculture production in 2022. The integration of omics technologies, genomics, transcriptomics, proteomics, and metabolomics has revolutionized aquaculture genetics, enabling comprehensive insights into the molecular mechanisms governing fish growth, disease resistance, and environmental adaptability. This review explores the application of these omics disciplines in advancing aquaculture research and production. Genomics facilitates genome sequencing and genetic marker identification, enhancing selective breeding and disease resistance through techniques like QTL mapping and CRISPR/Cas9. Transcriptomics reveals gene expression profiles, elucidating responses to environmental stressors and phenotypic plasticity. Proteomics provides a detailed understanding of protein dynamics, aiding in biomarker discovery and food quality assessment. Metabolomics uncovers metabolic pathways and biomarkers, offering insights into fish health and nutrition under varying conditions. Integrated multi-omics approaches, despite challenges like limited genomic data, promise a holistic understanding of fish physiology, paving the way for sustainable aquaculture practices and improved global food security.

1. Introduction

In 2022, global fisheries and aquaculture production rose significantly to 223.2 million tonnes, including 185.4 million tonnes of aquatic animals. That year, aquaculture alone accounted for 130.9 million tonnes, representing 59% of total fisheries and aquaculture output, with an estimated value of USD 312.8 billion (SOFIA, 2024). The increasing global demand for food presents challenges, as expanding land-based food production raises environmental and health concerns (Yadav et al., 2024; Yadav et al., 2025). Seafood, with its rich nutritional profile and lower environmental impact compared to terrestrial food production, is well-positioned to support global food supply and future food and nutrition security (Costello et al., 2020; Lal et al., 2024).

Over the past decade, technological advancements have accelerated fish genome sequencing, enabling the development of protocols and

methods to study global changes in gene, protein, and metabolite expression levels (Zampiga et al., 2018). While genes primarily function at the protein level, responses to stress are often regulated at the transcriptional stage.

Consequently, analyzing transcriptional profiles has become crucial in understanding how genes coordinate responses to various physiological and pathological factors (Prieto-Álamo et al., 2012). Traditionally, it was believed that genes govern all cellular and organismal processes by directing the hierarchical synthesis of proteins, mRNA, and metabolites when activated (Alfaro and Young, 2018). However, this view has evolved with the recognition that many metabolic processes are governed by intricate regulatory networks and feedback mechanisms, including post-translational protein modifications and metabolite fluxes, which operate independently of gene expression (Saroglia and Liu, 2012; Chubukov et al.,

2013; Feussner and Polle, 2015). Rather than identifying individual gene products separately, modern technological advancements now enable the use of non-targeted "omics" approaches to examine the complete set of gene products including transcripts, proteins, and metabolites within a biological sample. Due to their exploratory nature, these methods often lead to the formulation of new theories rather than merely validating existing ones. One of the key advantages of "omics" techniques is their ability to uncover unexpected insights, driving significant innovation and discovery in a highly efficient manner. Omics technology is playing a crucial role in modern aquaculture and its related research. Various omics disciplines such as genomics, proteomics, transcriptomics, epigenomics, lipidomics, glycomics, and metabolomics are paving the way for advancements in fisheries research and sectoral development (Tripathi et al., 2022). As a collection of advanced technologies, omics enables the exploration of functions, mechanisms, interactions, and relationships among genes, transcripts, proteins, lipids, and other biomolecules within a biological sample in an unbiased and non-targeted manner (Horgan et al., 2011). The foundation for expanding these techniques is rooted in the central dogma of biology, encompassing DNA replication, mRNA transcription, and protein translation (Power et al., 2023). High-throughput screening technologies provide a comprehensive view of various biological molecules at different levels, including genes (genomics), mRNA (transcriptomics), proteins (proteomics), lipids (lipidomics), and metabolites (metabolomics), all of which are essential for cellular function and maintenance (Westerhoff et al., 2004; Horgan et al., 2011). Additionally, omics technologies have proven highly valuable in assessing the quality of perishable food products. They facilitate the detection of pathogenic and spoilage bacteria, as well as the evaluation of how processing and storage impact proteins, carbohydrates, and fats in different food products (Carrera et al., 2013; Ferri et al., 2015). When integrated with other omics platforms, proteomics offers a comprehensive view of the molecular composition of a biological sample in an unbiased and non-targeted manner (Hasin et al., 2017). Proteomics emerged to address the need for a more complete understanding of cellular processes by analyzing the entire proteome (the complete set of proteins) within a specific tissue or fluid, rather than focusing on individual proteins. This approach provides valuable insights into an organism's physiological state at a given time, offering a holistic perspective of the subject under study (Rodrigues et al., 2012; Almeida et al., 2014). Despite growing interest in proteomics technologies, their application in aquaculture remains relatively new. Proteomics only began gaining traction in this field in the 21st century, with a noticeable increase in related research publications over the past decade (Eckersall et al., 2012; Rodrigues et al., 2012, 2018; Almeida et al., 2014).

The integration of biological data from multiple omics platforms, known as systems biology, provides a more

comprehensive understanding of an organism's information flow compared to studies focusing on a single omics type. This approach enables hypothesis-driven various experiments that have significantly advanced our knowledge of physiological processes in fishes (Horgan & Kenny, 2011). Genomics, the study of an organism's genome, can complement proteomic research by validating proteome data or correlating findings at the transcript level (Raposo de Magalhães et al., 2020). While gene expression profiles are traditionally examined using cDNA microarrays, real-time quantitative reverse transcription polymerase chain reaction (qRT-PCR) is now identified as the most accurate and reliable technique for validating proteomic data. This method offers rapid analysis with high sensitivity, accuracy, and reproducibility for assessing the relative mRNA expression of target genes (Mallona et al., 2010; Kozera & Rapacz, 2013). Metabolomics, the most recent addition to systems biology strategies, is widely applied across various aquaculture research areas, including studies on fish stress and their mechanism (Melis et al., 2014; Mushtaq et al., 2014; Jin et al., 2015; Ma et al., 2015; Castejón et al., 2016; Sheedy et al., 2016; Young et al., 2016; Alfaro & Young, 2018). Despite the existing research gap in proteomics within the aquaculture sector, an integrated omics approach presents vast opportunities for enhancing fish production, which is essential for ensuring global food security (Jaiswal et al., 2023). In Figure 1 shows schematic representation of the molecular biology pipeline, illustrating the flow from genomics to transcriptomics, proteomics, and metabolomics, culminating in phenotypic variations.

2. Role of genomics in aquaculture

2.1 Genome sequencing

The primary objective of genome sequencing is to decipher structural and functional similarities between organisms. Whole genome sequencing provides critical insights into the structural, functional, evolutionary, and organismal aspects of species or species groups (Randhawa & Pawar, 2021). Genomic selection relies on collecting genome-wide genotype data from a large number of individuals, a process that requires significant financial investment (Kriaridou et al., 2020). Recent genome sequencing projects in various fish species have enhanced our understanding of the molecular and genetic mechanisms that influence their responses to environmental stressors (Schartl et al., 2013; Chen et al., 2014). Comparative genome analysis between distantly related species offers valuable information, particularly through the accumulation of neutral mutations in nonfunctional regions (Crollius & Weissenbach, 2005). Whole genome shotgun (WGS) strategy has been used to generate extensive genomic data, including 412.8 Gb (350X genome coverage), 74.2 Gb (66X genome coverage), and 71.4 Gb (63X genome coverage) using Illumina paired-end, 2-8 kb, and 2-10 kb mate-pair libraries, respectively in Pikeperch (*Sander lucioperca*) (Nguinkal et al., 2019). Additionally, RNA sequencing has been employed to identify single nucleotide

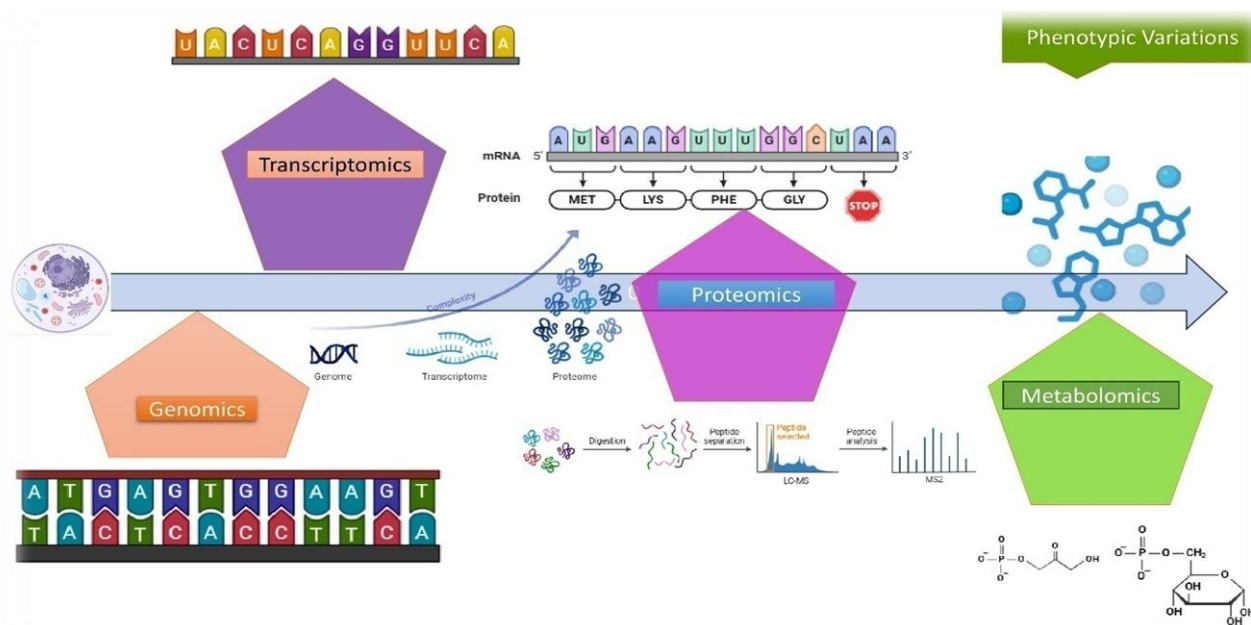


Figure 1: Integrated overview of genomics, transcriptomics, proteomics, and metabolomics in relation to phenotypic variation

polymorphism (SNP) markers associated with growth traits in Rainbow Trout, aiding in the detection of genes linked to genetic variation in growth (Salem et al., 2012). Similarly, transcriptome analysis has been utilized to identify growth-related genes and explore their functions in compensatory growth in Mandarin Fish (*Siniperca chuatsi*) (Liu et al., 2020).

Infectious diseases pose a significant challenge to the sustainable growth of fish farming. Various genetic approaches, including quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS), have been employed to analyze the genetic architecture of disease resistance. Additionally, transcriptomics and functional assays help link a fish's genetic makeup to the molecular mechanisms involved in pathogen interactions (Fraslin et al., 2020). QTL mapping plays a crucial role in unraveling these complex interactions by identifying the genetic factors that determine host resistance. This approach helps pinpoint genetic variations and mechanisms that influence whether a fish is resistant or susceptible to disease (Houston et al., 2020). A GWAS based on genome sequencing was conducted to identify loci associated with resistance to rotten body disease in large yellow croaker (*Larimichthys crocea*). The study identified 2,019,067 single nucleotide polymorphisms (SNPs), with 14 SNPs ultimately linked to disease resistance, accounting for phenotypic variance between 5.4% and 9.2% (Zhang et al., 2022). Similarly, restriction site-associated DNA sequencing (RAD-seq) has been used to identify genetic markers related to disease resistance in rainbow trout (*Oncorhynchus mykiss*) (Campbell et al., 2014).

2.2 Genetic markers and QTL mapping

Genetic markers commonly used in aquaculture research include simple sequence repeats (SSRs or microsatellites), restriction fragment length polymorphism (RFLP), randomly amplified polymorphic DNA (RAPD), single nucleotide polymorphism (SNP), amplified fragment length polymorphism (AFLP), and expressed sequence tags (ESTs) (Ramya and Behera, 2023). These nuclear DNA markers have significantly contributed to the assessment of genetic variability, inbreeding analysis, parentage assignments, species and strain identification, and the development of high-resolution genetic linkage maps for aquaculture species (Wenne, 2023).

Marker-assisted selection (MAS) utilizes genetic markers linked to desirable traits to inform breeding decisions, playing a crucial role in improving agricultural species. MAS has proven highly effective in developing animal and plant strains with significantly enhanced traits (Han et al., 1997; Serraj et al., 2005). Quantitative trait locus (QTL) mapping is essential for understanding the genetic basis of complex traits, such as growth and sex determination in aquaculture species. This technique helps identify specific genomic regions associated with these traits, supporting MAS-based breeding programs. Advances in high-throughput sequencing technologies have greatly facilitated marker discovery and genotyping (Liu et al., 2020). Linkage maps of high-density, form the foundation of QTL mappings, serve as valuable tools for studying genomic biology and evolutionary genetics. They allow researchers to quantify recombination rates, linkage disequilibrium, and chromosomal rearrangements across chromosomes, sexes, and populations (Hillier et al., 2007). A QTL mapping study in *Epinephelus fuscoguttatus*, *Epinephelus tukula*, and their hybrid

progeny successfully constructed genetic maps and identified 45 QTLs, comprising 318 SNPs linked to growth traits. Additionally, 56 candidate genes associated with growth, metabolism, bone formation, and neural regulation were identified (Chen et al., 2022).

The CRISPR/Cas9 genome editing technology has shown great success in improving desirable traits in fish species, including growth rate, muscle quality, disease resistance, and pigmentation. This technology allows for precise and targeted DNA modifications, leading to enhancements in key characteristics (Zhu et al., 2024). By enabling accurate genome editing, CRISPR/Cas9 plays a crucial role in boosting traits like growth performance (e.g., higher body weight, length, and muscle fiber development), muscle quality, disease resistance, and even sex determination. (Li et al., 2014; Khalil et al., 2017; Zhang et al., 2020; Potts et al., 2021; Nagahama et al., 2021; Kamachi et al., 2023; Wu et al., 2023). Technology has been successfully used to enhance growth rates in economically significant species like tilapia and common carp, helping improve the efficiency of aquaculture production systems (Li et al., 2021; Zhu et al., 2024). CRISPR/Cas9 is also commonly employed to target and modify specific genes, resulting in a range of beneficial outcomes. For instance, it has been applied to alter pigmentation pathways, enhancing coloration in ornamental fish such as goldfish and common carp (Chen et al., 2019; Li et al., 2024). More importantly, genetic modifications using this technology have significantly improved disease resistance by enhancing immune responses in species like Atlantic salmon and rainbow trout, reducing mortality caused by common aquaculture pathogens (Edvardsen et al., 2014). Additionally, CRISPR/Cas9 has demonstrated potential in improving feed conversion efficiency, as seen in medaka, helping to lower production costs and reduce environmental impact (Yeh et al., 2017). These advancements highlight the transformative role of genome editing in aquaculture, paving the way for more sustainable and efficient fish farming practices.

2.3 Critical Synthesis

Aquaculture genomics has entered a powerful new phase, moving beyond simple gene maps to an integrated view of polygenic networks, host-microbiome interactions, and precision gene editing with clear commercial promise. Yet, this progress is constrained by persistent gaps between genomic data and real-world phenotypes, environmental and epigenetic unpredictability, high technical and economic barriers, unresolved ecological risks, and fragmented global regulations. Bridging these biological, technological, and governance challenges will be essential for translating molecular breeding innovations into resilient, ethical, and widely accessible aquaculture systems.

3. Application of transcriptomics in aquaculture

3.1 RNA sequencing

Animal populations can alter their phenotypes in response to environmental changes through two main mechanisms: plasticity and genetic adaptation. Plasticity refers to a genotype's ability to produce different phenotypes depending on environmental conditions, which shifts the trait phenotype along a "norm of reaction" defined by the genotype (Bradshaw, 1965; Woltereck, 1909). Over the past decade, transcriptomics- the study of all gene expressions has been used to explore the relationships between environment, genotype, and phenotype in natural populations (Oomen and Hutchings, 2017). Recent advancements in high-throughput sequencing, particularly deep RNA-seq, have revolutionized transcriptomics. RNA-seq is a rapid and cost-effective method that enables researchers to determine the full set of genes expressed in a specific environment, including their sequences with single base-pair resolution and their relative abundances with unprecedented precision compared to older techniques (Wang et al., 2009). A study using RNA-sequencing (RNA-Seq) on the brain tissues of male and female golden mahseer (*Tor putitora*) revealed substantial sequencing data, with 20.6 million reads from male brains and 21.5 million reads from female brains. The study uncovered distinct gene expression profiles between sexes, providing valuable insights that could aid in developing reproductive manipulation strategies for this species (Shahi et al., 2023). Another RNA-seq study focused on the differential gene expression in the brains of juvenile rainbow trout (*Oncorhynchus mykiss*), specifically examining migratory and resident behaviors. The analysis identified 533 differentially expressed genes (1.9%) between different crosses and between smolt and resident samples. This research contributes a list of candidate genes and pathways for future studies on migration in rainbow trout and potentially other migratory species (Hale et al., 2016). In zebrafish, a growth association study utilized gene expression and single nucleotide polymorphism (SNP) identification to explore potential markers for growth. The identified genes are considered good candidates for further growth studies in fish, especially regarding SNPs that might be associated with varying growth rates in response to a plant protein-based diet (Ullao et al., 2015).

3.2 Critical synthesis

Transcriptomics has become a cornerstone of modern aquaculture research, bridging the gap between an organism's genetic potential and its actual physical response to the environment. By analyzing the complete

Table 1: Summary of transcriptomic studies conducted in various fish species

Fish Species	Infection	Methods used	Organ	Key findings	Reference
Grass carp (<i>Ctenopharyngodon idella</i>)	<i>Aeromonas hydrophila</i>	RNA-Seq, Illumina NextSeq™ 500	Spleen	Complement C1q subcomponent subunit C (C1QC), complement component 8 subunit beta (C8B) and the complement component factor B (CFB), coagulation factor II (thrombin) receptor (F2R) were significantly up-regulated, while fibrinogen gamma chain (FGG) was down-regulated, and lysosomal acid lipase/cholesterol ester hydrolase (LIPA) remained unaffected, exhibiting complex temporal patterns.	Dang <i>et al.</i> (2016)
Atlantic salmon (<i>Salmo salar</i>)	<i>Piscirickettsia salmonis</i>	Microarray	Head kidney	Atlantic salmon families with different susceptibilities to <i>P. salmonis</i> infection were analyzed for gene expression. Low-susceptibility families showed iron-depletion mechanisms as a defense strategy, which was supported by finding iron acquisition genes in <i>P. salmonis</i> that respond to low-iron conditions.	Pulgar <i>et al.</i> (2015)
Tilapia (<i>Oreochromis niloticus</i>)	<i>Streptococcus agalactiae</i>	RNA-Seq, Illumina HiSeq™ 2000	Spleen and Kidney	Gene expression analysis revealed 1,399 differentially expressed genes, including 65 immune-related genes across 17 pathways. The study confirmed changes in six genes' expression involved in toll-like receptor signaling, providing insights into tilapia's immune response to this pathogen.	Zhang <i>et al.</i> (2013)
Grass carp (<i>Ctenopharyngodon idella</i>)	Grass Carp Reo Virus (GCRV)	RNA-Seq, Illumina HiSeq™ 2000	Spleen, Gill, Liver and Intestine	RNA-seq analysis showed GCRV triggered immune responses across all tested tissues rather than targeting specific organs. The infection disrupted lipid and carbohydrate metabolism, with complement and cellular immunity playing key roles in the disease progression.	Shi <i>et al.</i> (2014)
Zebrafish (<i>Danio rerio</i>)	Response to fulvic acid	DNBseq	Gill	Upregulation of xenobiotic metabolism (<i>cyp1a3</i> , <i>cyp1b1</i> , <i>pik3r6</i>), immune response (<i>rgs2</i> , <i>dll1</i> , <i>ccl19</i> , <i>acod1</i>), and mucosal glycoprotein expression (<i>muc2</i> , <i>prg4</i>)	Lieke <i>et al.</i> (2025)
Zebrafish (<i>Danio rerio</i>)	Effects of probiotics (<i>Lactococcus lactis</i> WFLU12) on neurotransmission and stress alleviation	RNA-Seq	Liver	Genes related to neurotransmission, (<i>htr3a</i> , <i>mao</i> , <i>ddc</i> , <i>ntsr1</i> , and <i>gfra2</i>), stress (<i>hsp70</i> , <i>hsp90b1</i> , <i>hspE1</i> , <i>prdx1</i> , and <i>gss</i>) and transcriptional regulators (<i>fos</i> , <i>dusp1</i> , and <i>dusp2</i>) were upregulated.	Lee <i>et al.</i> (2023)
Zebrafish (<i>Danio rerio</i>)	Effect of 17 α -ethinylestradiol on male larvae during gonadal differentiation	RNA Seq	Gonads	While EE2 affected some key genes involved in sex differentiation (e.g., <i>cldn19</i> , <i>ctbp1</i> , <i>hsd17b4</i>), it didn't alter the expression of all expected genes (e.g., <i>wnt4b</i>).	Abdelmoneim <i>et al.</i> (2019)
Zebrafish (<i>Danio rerio</i>)	Effects of 17 α -ethinyl estradiol	RNA Seq, Illumina	Whole brain	Alters brain gene expression in a sex-specific manner, impacting hundreds of	Saaristo <i>et al.</i> (2017)

		seq (Mi Seq and Hi Seq)		transcripts and confirming changes in genes related to transposable elements, neuroserpin, and heat shock protein, providing insights into EE2's feminizing brain effects.	
Catfish (<i>Clarias batrachus</i>)	Comparative testicular transcriptome analysis from different reproductive phases	Illumina paired-end sequencing	Testis	Revealed varying numbers of transcripts (105-123k) and reads (42-62M). Most functional categories peaked during spawning. Involved in cell proliferation, cytoskeleton organization, and responses to vitamin A and hypoxia. Some genes showed significant differential expression related to spermatogenesis, steroidogenesis, sperm development, and sperm motility.	Roy et al. (2017)
Zebrafish (<i>Danio rerio</i>)	Identification of key genes expressed in the gonads	RNA-Seq, Illumina Seq	Gonads (ovaries and testes)	Ovaries showed high expression of stem cell maintenance genes, while testes expressed high levels of reproductive receptor and hormone-related genes. In the purified testicular cell fraction, genes associated with post-meiotic germ cells were particularly abundant.	Bar et al. (2016)

Table 2: Summary of proteomics studies conducted in various fish species

Species	Parameter	Key findings	Reference
<i>Cyprinus carpio</i>	Seminal plasma protein	Identification of 137 proteins in semen plasma, in which transferrin, serine proteinase inhibitors, complement C3 and Wap65 were abundant.	Dietrich et al. (2014)
	Blood plasma protein	Macroglobulins and immunoglobulins were major protein identified.	Dietrich et al. (2014)
<i>Cyprinus carpio</i>	Semen freezability	Sperm exhibiting poor freezability were related to protein involved in innate immune response, while protein involved in maintenance of sperm membrane integrity and antioxidative protection were associated with higher freezability of sperm.	Dietrich et al. (2017)
<i>Sparus auratus</i>	Stress biomarkers in skin mucus	Shotgun proteomics identified 2166 proteins in skin mucus. Hypoxia and repeated net handling majorly affected fish skin mucus proteome, proving candidacy of 28 skin mucus in future management protocol as biomarkers.	De Magalhães et al. (2023)
<i>Oncorhynchus kisutch</i>	Growth	Proteomics studies of growth hormone transgenesis and selective breeding for growth showed focused upregulation of system, driving protein synthesis and, diverse changes justifying complex modification in metabolic and cellular pathways, respectively.	Causey et al. (2018)
<i>Scorpaena plumieri</i>	Protein composition and biological activities of skin mucus and venom	Protein showing toxicity was present in both venom and skin mucus extract. Both extracts showed proteolytic as well as anti-microbial activities.	Borges et al. (2018)
<i>Paralichthys olivaceus</i>	Immunity against <i>Streptococcus parauberis</i>	In whole kidney, a sum of 82 proteins were differentially expressed, among which those involved in mediating immune responses (cathepsins, goose-type lysozyme, heat-shock protein and, complement components) and,	Cha et al. (2012)

		in cellular recovery and glycoprotein synthesis (cell division cycle 48 and calreticulin) were expressed most dramatically. Besides, proteins unrelated to immunity were not expressing themselves.	
<i>Sander lucioperca</i>	Ovarian fluid and egg protein	96 ovarian fluid proteins were identified. Abundant proteins in ovarian fluid showed involvement in egg immunological defense, restoration of immune homeostasis after inflammation, free radical scavenging and, sperm performance enhancement during fertilization.	Nynca et al. (2021)
<i>Oncorhynchus mykiss</i>	Skeletal deformities in diploid and triploid larvae	Among diploid larvae, creatine kinase was reported to be upregulated, and apo-lipo-protein A-I-2, apo-lipo-protein A-II were downregulated. In heat shock induced triploid larvae, apo-lipo-protein A-I-2, apo-lipo-protein A-II, parvalbumin, myosin light chain 1-1 and nucleoside diphosphate kinase were decreased.	Babaheydari et al. (2016)
<i>Oncorhynchus mykiss</i>	Heat stress	The study identified 3,362 proteins, including 152 differentially expressed proteins (DEPs). Of these, 37 were specifically expressed in the heat stress group, with 42 proteins upregulated and 38 downregulated. Most proteins were in the cytoplasm, nucleus, and extracellular matrix, involved in functions like enzyme facilitation and protein binding. Besides, significant changes in various biological processes, particularly in the estrogen signaling pathway, platelet activation, and complement and coagulation cascades due to high temperature stress.	Kang et al. (2019)
<i>Oncorhynchus mykiss</i>	<i>Yersinia ruckeri</i> infection in head kidney and spleen	Upon infection, 85 and 34 proteins were differentially expressed in spleen and head kidney, respectively, which included metalloproteinase, lysosomal, tetraspanin, antioxidant, metalloproteinase, c-type lectin receptor proteins, cytoskeleton and, cathepsin B.	Kumar et al. (2018)
<i>Acipenser persicus</i>	Ova	73 different proteins were identified, which were classified into 11 groups in context of their chief known function involving metabolism and energy production, cell structure, transcription, protein synthesis, translation, transport, cell signaling, cell division, cell defense, vitellogenin, unclassified and unknown function.	Keyvanshokoo and Vaziri (2007)

set of RNA transcripts, researchers can distinguish between genetic adaptation and phenotypic plasticity, the latter being a genotype's ability to produce varying phenotypes across a "norm of reaction" (Bradshaw, 1965). The advent of deep RNA-sequencing (RNA-seq) has revolutionized this field, offering a high-resolution, cost-effective tool to quantify gene expression with single base-pair precision, far surpassing the capabilities of older technologies.

4. Role of proteomics in aquaculture

4.1 Protein identification and quantification

Proteomics is the study of proteins aimed at understanding the structure, function, and regulation of biological systems (Bludau and Aebersold, 2020).

This includes proteins that are directly synthesized based on genetic instructions, as well as those that result from post-translational modifications (Monti et al., 2019). It offers a more comprehensive view of an organism's phenotype, as metabolites, being highly sensitive to environmental changes, provide insights into the actual metabolic and physiological processes occurring within the organism (Betz, 2020). High-throughput genomic and proteomic studies have been conducted on molecular signaling cascades, including the effects of neurotransmitter and nuclear receptor agonists and antagonists (Martyniuk et al., 2012). In addition to transcriptomics, investigating the neuro-proteome is crucial for toxicology and physiology research, as fish share orthologs with human genes that serve as drug targets (Gunnarsson et al., 2008), and are expected to exhibit conserved molecular responses to neuroactive compounds. Previous studies identified

unique proteins in the hypothalamus of largemouth bass (LMB), goldfish, and fathead minnow (FHM) telencephalon. These proteins were functionally annotated using tools like AgBase-Goanna to further understand their roles (McCarthy et al., 2006; Martyniuk et al., 2010; Popesku et al., 2010).

Aquaculture faces significant challenges in providing high-quality farmed fish through sustainable production systems. To address these challenges, new management strategies and advanced technologies, such as proteomics, are being used to study factors such as welfare, safety, nutrition, and disease, all of which directly impact the quality of the final product (Rodrigues et al., 2018). Proteomics offers powerful tools to assess food quality and safety and has contributed significantly to biomarker discovery, particularly for food authentication. Research has explored the most effective methods for assessing fish identity, emphasizing the crucial role of proteomics in verifying fish species and processed products' authenticity (Mazzeo and Siciliano, 2016). Proteomics also aids in the identification and detection of pathogens such as Anisakids, using techniques like parallel reaction monitoring (PRM) mass spectrometry. This method, coupled with the purification of thermostable proteins and trypsin digestion, allows for the fast monitoring of peptide markers (Carrera et al., 2016). Furthermore, proteomics is applied to fish otoliths using qualitative shotgun proteomics strategies for protein expression profiling. Liquid chromatography coupled with an electrospray ionization-orbitrap tandem mass spectrometer has uncovered diverse roles of proteins in otoliths, revealing valuable life history information that could help in understanding fish biology and population ecology (Rideout et al., 2023).

4.2 Functional proteomics

Proteomics has vast potential in human and animal research (Almeida et al., 2015), yet its application in fisheries science, particularly for economically significant species, remains limited. While some proteomic studies have been conducted in model fish species, comprehensive proteomic analyses of aquaculture species are still rare (Piñeiro and Martinez, 2012). One such study focused on organ-based protein profiling of *Labeo rohita*, a key aquaculture species. This research aimed to analyze tissue-specific protein expression and identify global post-translational modifications (PTMs) such as acetylation, methylation, and phosphorylation across various tissues. By mapping these modifications, the study provided a valuable proteome resource that can advance both basic and applied research in aquaculture, addressing the critical challenge of meeting global food and nutritional security demands (Nissa et al., 2021).

Sustainability challenges in aquaculture are also a significant concern, especially with the industry's dependence on marine-derived ingredients, which are finite (FAO, 2022). In response, proteomics and

phosphoproteomics analyses have been applied to understand the impacts of alternative diets on fish health. A study on large yellow croakers (*Larimichthys crocea*) fed a soybean oil-based diet identified immune protein markers in the liver. This research highlighted the effects of high soybean oil inclusion, showing that it upregulated NF- κ B signaling-related proteins and activated the MAPK pathway, promoting immune cell migration. These findings could help develop strategies to alleviate health issues linked to soybean oil-based diets, contributing to more sustainable aquaculture practices (Zhu et al., 2023).

4.3 Critical synthesis

Proteomics has deepened fisheries research by revealing phenotype-level complexity beyond genomics, capturing post-translational regulation, neurotoxicological responses, and diet-induced immune pathways relevant to sustainability. However, its broader application is constrained by limited species-specific datasets, high costs, and demanding bioinformatics requirements. Key challenges remain in translating functional proteomic insights into standardized, scalable tools for aquaculture management, food security, and welfare monitoring across diverse production systems.

5. Role of Metabolomics in Aquaculture

5.1 Metabolite Profiling

Metabolomics, a promising new 'omics' approach, focuses on using metabolite profiles to identify biomarkers that reflect the physiological responses of living samples—such as whole organisms, tissues, or cells—to environmental or culture conditions (Alfaro and Young, 2018). This approach provides valuable insights into fish metabolism by analyzing a wide range of metabolites in biofluids or tissues through non-targeted methods. Factors like nutrition and environmental stress can significantly influence fish metabolism, making metabolomics a powerful tool for understanding these impacts (Roques et al., 2020). While metabolomics was initially developed for human health applications, it has recently expanded to include livestock animals and, more recently, fish (Wishart 2008; Brennan 2013; Goldansaz et al. 2017). Metabolomic research is increasingly applied in aquaculture to study metabolic changes and the end products of gene expression, offering a deeper understanding of fish health, nutrition, and environmental interactions (Lulijwa et al., 2022). The field utilizes several analytical platforms, including mass spectrometry (MS), nuclear magnetic resonance (NMR), and vibrational-based techniques like Raman and infrared spectroscopy (Sidira et al., 2024). These methods help characterize complex metabolic changes in response to various conditions. In fish, metabolomic studies have been utilized in areas such as environmental metabolomics, health monitoring, and fish nutrition (Samuelsson and Larsson 2008; Alfaro and Young 2018). Unlike targeted approaches, the holistic nature of metabolomics allows researchers to capture the broader metabolic shifts that occur when a biological system is

exposed to specific environmental conditions, such as different diets or stressors (Brennan et al., 2015; Sébédio 2017; Alfaro & Young 2018). The above studies provide comprehensive view of how fish respond to their environment, making it a valuable tool for advancing aquaculture research, improving fish nutrition, and optimizing environmental conditions for better fish health.

5.2 Identifying Biomarkers

Fingerprinting and profiling are complementary approaches used to study the effects of environmental factors on metabolism. These methods, when combined, provide insights into how organisms adapt to different environmental conditions, particularly in aquaculture. For example, a study on fasted gilthead sea bream (*Sparus aurata*) used both fingerprinting and profiling to identify nutritional biomarkers and the metabolic adaptations that occur under specific conditions (Gil-Solsona et al., 2017). Similarly, nuclear magnetic resonance (NMR) spectroscopy has been utilized in *Sparus aurata* to enhance the traceability of the species by providing detailed metabolic and lipid profile data (Badaoui et al., 2024). Metabolomics techniques, like Gas Chromatography-Mass Spectrometry (GC-MS), have also been applied to study the metabolic profile of *Siniperca chuatsi* (Mandarin fish) when farmed in a recirculating aquaculture system (RAS) versus traditional pond farming methods. The results suggested that RAS could enhance certain metabolic processes that are beneficial for fish growth and health (Xiao et al., 2020). Temperature variations significantly influence fish growth and development. A study on juvenile European seabass (*Dicentrarchus labrax*) used metabolomics to investigate how different temperatures impacted the fish over 60 days. This research identified potential marker metabolites, such as L-cysteine and taurocholic acid, which could provide insights into the metabolic mechanisms by which temperature influences growth and development (Zhang et al., 2021). In the context of aquaculture, metabolomics is also used to understand the effects of diet, such as oxidized fish oil, on fish health. For instance, a study on juvenile hybrid grouper (*Epinephelus fuscoguttatus* and *Epinephelus lanceolatus*) fed oxidized fish oil showed that it inhibited growth performance and induced oxidative stress in the liver. This was marked by reduced antioxidant enzyme activity and increased malondialdehyde levels (Long et al., 2021). Other studies have explored similar effects of oxidized fish oil on various species, including the Pond loach (*Misgurnus anguillicaudatus*) and Yellow catfish (*Ameiurus natalis*), using metabolomics and transcriptomic approaches (Yin et al., 2019; Zhang et al., 2017, 2019, 2021). Metabolomics, as an emerging discipline, complements genomics, transcriptomics, and proteomics to offer a holistic understanding of biological

systems and improve aquaculture practices (Adav and Wang, 2021).

5.3 Understanding Metabolic Pathways

Proteomics has been widely used in fish research to study hepatic metabolism and stress responses to various environmental and nutritional factors (Gandar et al., 2017; Pédrón et al., 2017; Zhang et al., 2017; Causey et al., 2018; Naderi et al., 2018; Ghisaura et al., 2019; Raposo de Magalhães et al., 2021; Quan et al., 2021). This approach focuses on understanding protein expression and post-translational modifications in fish, offering valuable insights into how the liver responds to different stressors, such as environmental changes or disease. While proteomics is well-established, untargeted metabolomics has become increasingly relevant in fish stress research in recent years, though it has been explored less extensively (Ziarrusta et al., 2018; Jiao et al., 2020; Alfaro et al., 2021). Metabolomics, which focuses on profiling a wide variety of metabolites, is a powerful tool for understanding the metabolic responses of fish to various stressors.

Integrated multiomics approaches, combining genomics, transcriptomics, proteomics, and metabolomics, have emerged as promising methods for gaining a more comprehensive understanding of the interrelationships between biomolecules and their functions (Raposo de Magalhães et al., 2020). However, the full potential of multiomics is still limited in fish and aquaculture research due to challenges such as insufficient genomic data, a lack of advanced analytical tools, and gaps in comprehensive databases. Despite these challenges, recent studies have provided valuable insights into how fish respond to nutritional stress, environmental changes, and pathogens, using multiomics approaches (Wei et al., 2021; Zhu et al., 2019; Wen et al., 2019; Colás-Ruiz et al., 2022; Dale et al., 2020).

5.4 Critical synthesis

Metabolomics has emerged as a powerful tool for decoding real-time physiological responses in fish, linking environmental conditions, nutrition, and culture systems directly to growth and health outcomes. However, its application in aquaculture is still constrained by limited databases, technical complexity, and uneven infrastructure, while the promise of fully integrated multi-omics remains largely unrealized. Advancing toward holistic, predictive models that work across species and region-specific environments will be essential to translate metabolomic insights into practical, scalable aquaculture management strategies.

Table 3: Summary of metabolomics studies conducted in various fish species

Species	Parameter	Result	Reference
<i>Cyprinus carpio</i>	Gill metabolome	Metabolomic analysis exhibited 96 metabolites in fish gills (involved in amino acid, lipid and carbohydrate metabolism, and are considerably supplemented in tricarboxylic acid (TCA) cycle), decreased to 90, post 7 days recovery period of silver nanoparticle exposure.	Xiang et al. (2021)
<i>Sparus aurata</i>	Clotted serum metabolome	Replacing fish-based feed with plant-based ingredients significantly altered the metabolic profile, with over 50 mainly lipid-related metabolites showing differential expression. These changes, including shifts in N-acyl taurine, cytidine, and other nucleoside-related compounds, indicate impacts on lipid metabolism, tissue repair, and DNA turnover.	Gil-Solsona et al. (2018)
<i>Megalobrama amblycephala</i>	Plasma metabolic profile for fish maturation	A whole of 29 metabolites were recognized as differential biomarkers linked with female maturation level.	Zhou et al. (2017)
<i>Thunnus thynnus</i>	Sex dependent health condition	Differential metabolic disturbance between male and female were reported, mainly involved in energy, lipid and amino acid metabolism. In male tuna, ketogenesis and fatty acids biosynthesis were activated.	Cappello et al. (2018)
<i>Salvelinus alpinus</i>	Liver, muscle and plasma metabolic profile	Fish fed with test diet (decontaminated fishmeal, <i>Mytilus edulis</i> and <i>Saccharomyces cerevisiae</i>) had lower level of trimethyl-amine-N-oxide (TMAO), aromatic amino acids and higher level of betaine, in plasma or tissue.	Cheng et al. (2017)
<i>Salvelinus alpinus</i>	Effect of <i>Rhodotorula toruloides</i> on metabolism	No significant changes were observed in metabolites of liver. In plasma, metabolites involved in energy pathway for instance, serine, choline, 3-hydroxy-butyrate, alanine, and betaine were significantly higher in experimental treatment group.	Brunel et al. (2022)
<i>Oncorhynchus mykiss</i>	Amino acid metabolism	Different soluble chemical compounds were exhibited between diets (fish oil based, plant based and control) upon proton nuclear magnetic resonance (H-NMR) based metabolomics analysis. In relation to fish meal-based diet, plant-based diet fed fish showed higher plasma amino acid content.	Deborde et al. (2021)
<i>Epinephelus coioides</i>	Metabolic Effect of Dietary Taurine Supplementation	In the taurine-supplemented feed group, key metabolites associated with energy metabolism, amino acid absorption, and glycol-phospholipid pathways were reduced, indicating a downregulation of glycolysis–gluconeogenesis, protein digestion and absorption, and membrane lipid metabolism.	Shen et al. (2019)
<i>Brachymystax lenok</i>	Intestinal metabolic profile in response to heat stress	Under heat stress, 51 metabolites were differentially expressed (34 in positive and 17 in negative ion mode), reflecting major metabolic disruption. These changes involved glycolysis, fatty acid β -oxidation, reduced glycerophospholipid metabolites, and broad alterations in amino acid profiles, indicating impaired energy balance and protein metabolism.	Chen et al. (2022)

Table 4: Summary of use of integrated omics techniques use in aquaculture

Fish species	Technology Used	Study	Key findings	References
Black tiger shrimp (<i>Penaeus monodon</i>)	Microbiomics, Transcriptomics and Metabolomics	To investigate the intestinal microbiota, host gene expression, and metabolites of black tiger shrimp (<i>Penaeus monodon</i>) with varying growth performance.	Gut bacterial community structure was similar between top- and bottom-weight shrimp, clear differences emerged at the functional level. Top-weight shrimp showed enhanced expression of genes linked to nutrient metabolism and immunity, along with higher levels of amino acids and energy-related metabolites, indicating more efficient nutrient utilization and superior growth performance.	Uengwetwanit et al. (2020)
Pearl gentian grouper <i>Epinephelus fuscoguttatus</i> ♀ × <i>Epinephelus lanceolatus</i> ♂	Microbiomics, Transcriptomics and Metabolomics	Examination of marine fish enteritis caused by soybean meal in juvenile pearl gentian groupers, <i>Epinephelus fuscoguttatus</i> ♀ × <i>Epinephelus lanceolatus</i> ♂.	Soybean meal-induced enteritis in juvenile pearl gentian groupers disrupted gut microbial balance, suppressing beneficial bacteria while promoting pathogenic species.	Zhang et al. (2021)
Grass carp (<i>Ctenopharyngodon idellus</i>)	Transcriptomics and Metabolomics	Viral Susceptibility in Grass Carp Dependent on Age.	Juvenile grass carp were more vulnerable to viral infections than older fish, a pattern linked to weaker immune readiness. Reduced expression of interferons and cytokines in younger fish, together with lower levels of energy metabolites essential for immune defense, explains their heightened susceptibility, while older individuals exhibit more robust antiviral and metabolic responses.	He et al. (2021)
<i>Salmo salar</i>	Metabolomics, Transcriptomics and Proteomics	Important Components and Mechanisms of Atlantic Salmon's (<i>Salmo salar</i>) Physiological Response to Chemotherapeutic-Induced Oxidative Stress.	Integrated metabolomic, transcriptomic, and proteomic analyses showed that chemotherapeutic exposure induces oxidative stress in salmon, triggering strong antioxidant responses, especially in the liver and gills. The depletion of metabolites such as glutathione highlights metabolic reprogramming to counter stress, revealing key molecular pathways underlying stress resilience and the impacts of chemotherapeutic treatments.	Lazado et al. (2021)
Grouper (<i>Epinephelus coioides</i>), Orange-spotted grouper	Transcriptomics and Proteomics Analysis	Examining orange-spotted grouper larvae infected with the nervous necrosis virus reveals elevated collagen synthesis and adhesion molecules in the persistent state.	NNV-infected orange-spotted grouper larvae exhibited a persistent infection marked by enhanced collagen production and elevated adhesion molecules. Concordant transcriptomic and proteomic evidence points to intensified extracellular matrix remodeling and	Ge et al. (2020)

			cell adhesion as host strategies to preserve tissue integrity, which may inadvertently facilitate long-term viral persistence.	
Common carp <i>Cyprinus carpio</i>	Genomics and Metabolomics	To examine how exposure to nanosilver affects fish gill damage and recovery.	Nanosilver exposure induced severe gill damage and oxidative stress in common carp, accompanied by activation of stress-response genes and disruption of antioxidant and energy metabolism. Although partial recovery occurred after exposure ceased, persistent metabolic alterations in gill tissue suggest lasting adverse effects of nanosilver toxicity on fish health.	Xiang et al. (2021)
GIFT Tilapia (<i>Oreochromis niloticus</i>)	Transcriptomics, Metabolomics	To investigate the response mechanism for glycolipid metabolism in the liver of genetically modified farmed tilapia (GIFT, <i>Oreochromis niloticus</i>) under hypoxic stress.	Hypoxic stress in GIFT tilapia triggered marked shifts in liver glycolipid metabolism, with enhanced glycolysis and lipid synthesis supporting short-term energy homeostasis under low oxygen. However, sustained hypoxia disrupted liver function, ultimately compromising growth and overall fish health.	Ma et al. (2021)
<i>Scylla paramamosain</i> (Crab)	Transcriptomics and Proteomics	To investigate osmoconformation and osmoregulation on crab <i>Scylla paramamosain</i> .	<i>Scylla paramamosain</i> demonstrates strong salinity tolerance through coordinated molecular adaptations. The upregulation of ion transport and stress-response genes, together with elevated osmoregulatory proteins such as Na ⁺ /K ⁺ -ATPase, enables effective osmotic balance and supports survival across fluctuating estuarine environments.	Niu et al. (2020)
Grass carp (<i>Ctenopharyngodon idellus</i> C.et V)	Proteomics and metabolomics	To investigate the texture of crisp grass carp (<i>Ctenopharyngodon idellus</i> C.et V) fed a natural dietary pro-oxidant.	Dietary pro-oxidants in crisp grass carp enhanced muscle firmness by upregulating structural muscle proteins, as revealed by proteomics. However, metabolomic evidence of increased oxidative stress and depleted antioxidants indicates a trade-off, where improved texture may come at the cost of fish health unless antioxidant balance is carefully managed.	Yu et al. (2020)
<i>Pavona minuta</i>	Transcriptomics & Metabolomics (using Ultra-Performance Liquid Chromatography Tandem Mass Spectrometry (UPLC-MS))	Exposing the host metabolism and symbiotic microorganism response patterns to temperature stresses in Scleractinian Coral (<i>Pavona minuta</i>).	Temperature stress in <i>Pavona minuta</i> disrupted host metabolism and symbiotic stability, suppressing genes linked to photosynthesis and nutrient exchange and reducing key sugars and amino acids. Concurrent shifts in symbiotic microbial communities weakened host-symbiont interactions, driving coral bleaching and lowering resilience to thermal stress.	Liang et al. (2021)
Crucian carp (<i>Carassius</i>)	Genomics and Proteomics	The first report on the crucian carp	<i>Rahnella aquatilis</i> KCL-5 was identified as an emerging pathogen	Liang et al. (2020)

<i>auratus</i>)	analyses	pathogenic <i>Rahnella aquatilis</i> KCL-5 characterization.	in crucian carp, causing hemorrhages and internal organ damage. Genomic and proteomic evidence confirmed the presence and expression of virulence factors linked to adhesion and toxin production, underscoring the importance of surveillance and biosecurity measures to prevent its spread in aquaculture systems.	
Hybrid Striped Bass (HSB) (striped bass x white bass)	Transcriptomics and Metabolomics	Method for comprehending the regulation of white muscle growth in hybrid striped bass aquaculture.	Hybrid striped bass exhibited enhanced white muscle growth under optimized aquaculture conditions. Transcriptomic analysis showed upregulation of genes involved in myogenesis and protein synthesis, while metabolomic profiles indicated increased levels of amino acids and energy metabolites. These findings suggest that dietary and environmental factors can be manipulated to promote muscle development and improve yield.	Nguyen and Alfaro, (2020)
<i>Tenualosa ilisha</i>	Transcriptomics, Metabolomics	Research on <i>Tenualosa ilisha</i> , an anadromous clupeid, to better understand how habitat affects nutritional composition.	Habitat strongly shaped the nutritional profile of <i>Tenualosa ilisha</i> . Marine environments promoted higher expression of lipid metabolism genes and elevated omega-3 fatty acid levels, demonstrating how environmental conditions directly influence the nutritional quality of this species.	Gangult et al. (2020)
Mud crab (<i>Scylla paramamosain</i>)	Transcriptomics and Metabolomics	Elucidation of metabolic responses in mud crab <i>Scylla paramamosain</i> challenged to WSSV infection.	WSSV infection in <i>Scylla paramamosain</i> induced pronounced metabolic reprogramming, marked by activation of immune and energy metabolism genes and elevated amino acid levels. However, the concurrent depletion of energy reserves points to metabolic exhaustion, which likely underlies the high mortality associated with infection.	Kong et al. (2020)
Kuruma shrimp (<i>Marsupenaeus japonicus</i>)	Transcriptomics and Metabolomics	Research on how the hepatopancreas of kuruma shrimp (<i>Marsupenaeus japonicus</i>) reacts to cold stress.	Cold stress in kuruma shrimp triggered molecular adjustments in the hepatopancreas, including activation of stress-response and lipid metabolism pathways.	Ren et al. (2020)
Yellow drum (<i>Nibea albiflora</i>)	Transcriptomics and Metabolomics	The yellow drum's (<i>Nibea albiflora</i>) liver's physiological reactions to cold and starvation stressors.	Combined cold and starvation stress in yellow drum led to pronounced liver dysfunction, characterized by suppressed metabolic gene expression and activation of stress-response pathways.	Jiao et al. (2020)
Pearl oyster (<i>Pinctada fucata martensii</i>)	Metabolomics and Transcriptomics	to investigate the pearl oyster's (<i>Pinctada fucata martensii</i>) larval metamorphosis.	Larval metamorphosis in <i>Pinctada fucata martensii</i> is driven by coordinated molecular remodeling, with enhanced expression of shell formation and hormone-signaling	Zhang et al. (2021)

			genes alongside elevated amino acids and energy metabolites.	
turbot (<i>Scophthalmus maximus</i>)	Metabolome and Transcriptome	Heat stress effects on juvenile turbot <i>Scophthalmus maximus</i> for lipid metabolism.	Heat stress disrupted lipid metabolism in juvenile turbot. Transcriptomic analysis showed downregulation of lipid synthesis genes and upregulation of oxidative stress pathways, while metabolomic profiles indicated reduced levels of fatty acids and increased oxidative stress markers.	Zhao et al. (2021)
Manila clam, <i>Ruditapes philippinarum</i>	Transcriptomics and Metabolomics	Benzo[a]pyrene increases the toxicity of mercury to the Manila clam, <i>Ruditapes philippinarum</i> .	Combined exposure to benzo[a]pyrene and mercury significantly increased toxicity in Manila clams. Transcriptomic analysis revealed upregulation of detoxification and stress response genes, while metabolomic profiles showed altered levels of antioxidants and energy metabolites. These changes indicate synergistic toxic effects, leading to impaired growth and survival.	Jiang et al. (2021)
<i>Exopalaemon carinicauda</i>	Transcriptomics and Proteomics Analysis	Research on the responses of <i>Exopalaemon carinicauda</i> to alkalinity stress.	Alkalinity stress in <i>Exopalaemon carinicauda</i> triggered significant physiological responses. Transcriptomic analysis showed upregulation of ion transport and stress response genes, while proteomic data confirmed increased levels of stress-related proteins. These adaptations help the shrimp cope with high alkalinity but may reduce growth and reproductive success under chronic exposure.	Qin et al. (2021)
Oyster Parasite (<i>Perkinsus marinus</i>)	Transcriptional and Metabolic	Investigation of Lipid Deprivation in <i>Perkinsus marinus</i> , an Oyster Parasite.	Lipid deprivation in <i>Perkinsus marinus</i> disrupted its metabolic and reproductive processes. Transcriptomic analysis revealed downregulation of lipid metabolism genes, while metabolomic profiles showed reduced levels of fatty acids essential for growth. These findings suggest that targeting lipid metabolism could be a strategy to control this oyster parasite.	Noell & Pitula, (2021)
Juvenile largemouth bass (<i>Micropterus salmoides</i>)	Metabolomics and Transcriptomics	To investigate how new proteins affect the intestinal health of young largemouth bass (<i>Micropterus salmoides</i>) when they are fed in a different way.	Novel protein diets (e.g., plant-based or insect-based) altered intestinal health in juvenile largemouth bass. Transcriptomic analysis showed differential expression of immune and digestive genes, while metabolomic profiles indicated changes in amino acid and lipid metabolism. Optimized protein diets improved gut health and growth, but unsuitable proteins caused inflammation and reduced nutrient absorption.	Li et al. (2023)

Crucian carp (<i>Carassius auratus</i>)	Metabolomics and Transcriptomics	Physiological reactions of crucian carp (<i>Carassius auratus</i>) gills to saline-alkaline stress.	Saline-alkaline stress caused significant gill damage in crucian carp. Transcriptomic analysis revealed upregulation of ion transport and stress response genes, while metabolomic profiles showed altered levels of osmoregulatory metabolites.	Liu et al. (2022)
Hybrid sturgeon	Metabolomics transcriptomics	Mechanism of hybrid sturgeon liver metabolism under ship noise stress.	Ship noise stress disrupted liver metabolism in hybrid sturgeon. Transcriptomic analysis showed downregulation of metabolic genes and upregulation of stress response pathways, while metabolomic profiles indicated reduced levels of energy metabolites and increased oxidative stress markers.	Zhang et al. (2022)
Different fish species and seafood species	Transcriptomics, Proteomics, Microbiomics, and Metabolomics	To evaluate the toxicity of microplastics and nanoplastics to fish and seafood.	Multi-omics studies show that micro- and nanoplastics disrupt fish and shellfish health at multiple biological levels. Transcriptomic changes drive oxidative stress and immune dysfunction, while proteomic and metabolomic shifts reveal disturbed lipid and energy metabolism; gut microbiome dysbiosis further amplifies inflammation and pathogen risk.	Bhagat et al. (2022)
<i>Tetraodon Nigroviridis</i>	Transcriptomics, Proteomics	<i>Exogenous vibrio</i> Parahaemolyticus Infection on molecular mechanism of <i>Tetraodon nigroviridis</i> .	C3 was strongly upregulated at gene and protein levels due to downregulation of C3-targeting miRNAs, activating complement, chemokine, and JAK-STAT pathways. The results confirm <i>V. parahaemolyticus</i> as a blood-borne extracellular pathogen targeting the liver, with miR-29b linked to liver steatosis.	Jiang et al. (2022)
<i>Pelteobagrus vachelli</i>	Transcriptome, miRNAome, Proteome, and Metabolome	Environmental Hypoxia Response on muscle of <i>Pelteobagrus vachelli</i> .	Hypoxia (4 h, 0.7 mg/L O ₂) altered HIF-1 signaling, energy metabolism, and muscle function. Significant changes included inhibited oxidative phosphorylation, increased anaerobic glycolysis, and muscle damage. Discrete tissue-specific responses showed muscles suffered more damage than liver.	Li et al. (2022)
<i>Cyprinus carpio</i>	Metabolomics, transcriptomics	Impact of dietary proanthocyanidins on common carp intestinal microbiota, muscle nutrients, lipid metabolism, and antioxidant capacity.	Pro supplementation (0.8 g/kg) enhanced antioxidant capacity, increased muscle n-3 and n-6 PUFA levels, and improved gut microbial diversity, notably <i>Cetobacterium</i> and <i>Pirellula</i> . Transcriptomic changes indicated enhanced lipid turnover and reduced cholesterol absorption in the intestine.	Jia et al. (2023)
<i>Oncorhynchus tshawytscha</i>	Proteome, and Metabolome	Forecasting Fish Performance-Based Features and Feed	Liver and muscle proteomic, metabolomic, and lipid profiles were key predictors of feed efficiency (FE).	Young et al. (2023)

		Efficiency.	Efficient fish showed enhanced protein synthesis, whereas inefficient fish exhibited greater protein degradation, with multi-omics models explaining 30.4% of FE variation.	
<i>Pelteobagrus vachelli</i>	Transcriptome, miRNAome, Proteome, and Metabolome	Investigation of the effects of energy metabolism on brain dysfunction in <i>Pelteobagrus vachelli</i> under hypoxic stress.	Hypoxia (0.7 mg/L, 4 h) inhibited energy metabolism (oxidative phosphorylation, carbohydrate/protein metabolism), causing blood-brain barrier injury, neurodegenerative, and autoimmune diseases. Brain damage was milder than in muscle due to blood redistribution. Key pathways included HIF-1 signaling, with tissue-specific responses noted.	Li et al. (2023)
Sea bream (<i>Sparus aurata</i>)	Transcriptomic and Metabolomics	Research on gilt-head sea bream (<i>Sparus aurata</i>) subjected to sulisobenzene, a UV filter.	After 22 days of exposure (10 µg/L), 371 liver genes were differentially expressed, impacting oxidative phosphorylation and lipid metabolism. Metabolomics identified 123 altered plasma and 118 liver metabolites, indicating oxidative stress and lipid peroxidation. Multi-omics integration confirmed BP-4 as a potential endocrine disruptor, with energy depletion and metabolic stress.	Colás-Ruiz et al. (2022)
Red seabream (<i>Pagrus major</i>)	Transcriptomic and Metabolomics	Research on red seabream (<i>Pagrus major</i>) hepatopancreas fed a diet consisting of soybean meal.	8-week soybean meal-based diet in <i>Pagrus major</i> impaired growth and hepatopancreas condition, reducing cholesterol levels and causing hepatocyte atrophy. Integrated transcriptomic and metabolomic analyses revealed disrupted cholesterol, bile acid, amino acid, lipid, and energy metabolism, driving metabolic stress and tissue degeneration.	Yoshinaga et al. (2023)
Golden pompano (<i>Trachinotus ovatus</i>)	Metagenomics and Transcriptomics	Investigation of zinc exposure regulation mechanisms in the intestine-liver axis of golden pompano <i>Trachinotus ovatus</i> .	Low dietary zinc (134.6 mg/kg) promoted growth, enriched gut bacteria diversity, and activated liver growth hormone metabolism. While, in high dietary zinc (161.4 mg/kg) reduced growth, caused gut bacteria imbalance (dysbiosis), activated bacterial competition systems (T6SS), and triggered liver stress (oxidative stress, immune/antiviral responses).	Ma et al. (2022)
Crucian carp (<i>Carassius auratus</i>)	Transcriptomic, Proteomics	Skin immune response to <i>Aeromonas hydrophila</i> infection in crucian carp <i>Carassius auratus</i> revealed by multi-omics analysis.	Proteomic-transcriptomic analysis showed that <i>Aeromonas hydrophila</i> infection rapidly activates crucian carp skin immunity, with widespread changes in metabolic, stress, cytoskeletal, and immune proteins. Key immune factors such as lysozyme, complement C3, DNAJC8, and AIF1L were strongly upregulated, confirming a robust early defense	Li et al. (2022)

			response.	
Rainbow trout (<i>Oncorhynchus mykiss</i>)	Metagenomic, Metabolomics	Variations in rainbow trout (<i>Oncorhynchus mykiss</i>) probiotic and synbiotic additives.	Probiotic and synbiotic feed additives in rainbow trout (<i>Oncorhynchus mykiss</i>) reduced <i>Candidatus Mycoplasma salmoninae</i> in the gut, altered microbial metabolic pathways (e.g., arginine and terpenoid synthesis), and shifted intestinal metabolites (lipids, amino acids, bile acids).	Rasmussen et al. (2022)
Pacific oysters (<i>Crassostrea gigas</i>)	Transcriptomics, Proteomics, and metabolomics	Investigating bioinformatics methods to evaluate Pacific oysters' (<i>Crassostrea gigas</i>) tolerance mechanisms and response to salt stress during depuration.	High salinity (38 g/L) upregulated glycolysis genes and proteins but reduced lipid metabolism and citric acid cycle activity. Salinity fluctuations of $\pm 10\%$ preserved oyster quality, while $\pm 20\%$ caused metabolic and protein disruptions. Optimal depuration salinity should align within $\pm 10\%$ of production area salinity.	Chen et al. (2023)
<i>Pelteobagrus fulvidraco</i>	Transcriptomics and Proteomics	The IL17 signaling pathway was found to be a putative signaling mechanism that mediates inflammation and gill hyperplasia during ammonia nitrogen stress.	Transcriptomics and proteomics revealed upregulated IL-17-related genes and proteins, driving immune responses and oxidative stress. Gill hyperplasia impaired respiratory function, highlighting IL-17 as a key mechanism in ammonia-induced damage.	Zhang et al. (2023)
Common Carp (<i>Cyprinus carpio</i>)	Genomics, Transcriptomics and Epigenomics	Research on Genes Associated with Amino Acids in the Common Carp (<i>Cyprinus carpio</i>).	Integrated GWAS, transcriptomic, and epigenomic analyses identified key genes and pathways controlling essential and flavor-related amino acids in carp. The overlap between genetic variants, differential expression, and promoter methylation highlights promising molecular targets for improving nutritional quality.	Zhang et al. (2022)
Rainbow trout (<i>Oncorhynchus mykiss</i>)	Genomics and Transcriptomics	Finding, categorizing, and describing the functions of HSP70s in rainbow trout (<i>Oncorhynchus mykiss</i>).	Rainbow trout possess 23 HSP70 genes grouped into seven evolutionary clades. Groups 3 and 6 show distinct stress responses—group 3 to <i>Ichthyophthirius multifiliis</i> infection and group 6 to thermal stress. TFBS variation drives expression differences, while HSP70a isoforms respond strongly to hypoxia, heat, and crowding, underscoring HSP70s as key stress biomarkers in aquaculture.	Roh et al. (2022)
Grass carp (<i>Ctenopharyngodon idellus</i>)	Transcriptomics and Proteomics	Investigation of the regulatory mechanisms behind the impacts of artificial feed and grass feeding on grass carp (<i>Ctenopharyngodon idellus</i>) growth and	Comparative transcriptomic and proteomic analyses showed that artificial feed accelerates grass carp growth but compromises muscle texture, while grass feeding enhances muscle quality at the cost of growth rate. Differential regulation	Zhao et al. (2023)

		muscle quality.	of lipid metabolism and protein synthesis pathways underlies these effects, offering targets for feed optimization.	
Common carp (<i>Cyprinus carpio</i>)	Transcriptomics and metabolomics	Research on the molecular mechanisms behind the variations in muscle quality in common carp (<i>Cyprinus carpio</i>) raised in two aquaculture systems.	Integrated transcriptomic and metabolomic analyses revealed system-specific regulation of carp muscle quality. Pond culture enhanced lipid biosynthesis linked to firmness and flavor, while flow-through systems favored protein metabolism, highlighting aquaculture system-dependent effects on muscle quality.	Want et al. (2024)
Yellow catfish (<i>Pelteobagrus fulvidraco</i>)	Transcriptomics and metabolomics	Study on liver metabolism in yellow catfish (<i>Pelteobagrus fulvidraco</i>) under hypoxic stress.	Transcriptomic and metabolomic analyses showed that hypoxic stress reshapes liver metabolism in yellow catfish, suppressing aerobic pathways while enhancing lipid and carbohydrate remodeling. Elevated lactate and stress-response gene expression indicate a shift toward anaerobic metabolism, revealing adaptive mechanisms underlying hypoxia tolerance in aquaculture species.	Want et al. (2024)
<i>Sparus aurata</i>	Genomics, Transcriptomics and metabolomics, Proteomics	The hepatic response of <i>Sparus aurata</i> to various aquaculture Challenges.	Examined hepatic responses to aquaculture challenges using genomics, transcriptomics, proteomics, and metabolomics. Stressors (e.g., crowding, diet) altered liver gene expression and protein profiles. Metabolic pathways like lipid oxidation were disrupted, affecting fish health. Integrated omics revealed biomarkers for stress resilience in sea bream.	Raposo de Magalhães et al. (2024)
<i>Thamnaconus septentrionalis</i>	Transcriptomics and metabolomics	Molecular processes of <i>Thamnaconus septentrionalis</i> negative responses to H ₂ O ₂ .	Integrated transcriptomic and metabolomic analyses revealed that H ₂ O ₂ stress activates oxidative-stress genes and disrupts amino acid metabolism. Reduced glutathione levels indicate compromised antioxidant defenses, clarifying mechanisms of oxidative damage and stress adaptation.	Li et al. (2024)
Grass carp (<i>Ctenopharyngodon idella</i>)	Metagenomics and Transcriptomics	Study on gut microbiome of grass carp.	Metagenomic and transcriptomic analyses revealed diet-driven shifts in the grass carp gut microbiome, with Firmicutes associated with enhanced nutrient absorption. Corresponding upregulation of host digestive and immune genes highlights microbiota-host interactions that can guide probiotic strategies to improve gut health and growth.	Li et al. (2024)

greater amberjack (<i>Seriola dumerili</i>)	Genomics and Transcriptomics	Sex-related research in greater amberjack (<i>Seriola dumerili</i>) includes sex-specific marker development, sex-biased expression analysis, and gene identification.	Genomic and transcriptomic analyses identified sex-biased genes underlying gonad development and reproduction in amberjack. Males showed elevated metabolic gene expression, while females exhibited immune-related upregulation, supporting sex-specific breeding strategies in aquaculture.	Li et al. (2025)
Crucian carp (<i>Carassius auratus</i>)	Genomics and Transcriptomics	Investigation of miRNA-mediated alterations in crucian carp intestinal microbiota <i>Rahnella aquatilis</i> infected <i>Carassius auratus</i> .	Transcriptomic analysis revealed miRNA-mediated regulation of immune and metabolic genes during <i>Rahnella aquatilis</i> infection, leading to shifts in gut microbiota and loss of beneficial bacteria. These findings highlight miRNAs as key modulators of host-microbe interactions and disease resistance.	Huo et al. (2024)
Rockfish	Transcriptomics and Metabolomics	Effect of toxic fibrous and fragmented microplastic exposure to juvenile rockfish.	Integrated transcriptomic and metabolomic analyses showed that fibrous microplastic exposure activates stress and detoxification pathways while reducing amino acid levels, indicating metabolic disruption. These results elucidate microplastic toxicity mechanisms affecting juvenile rockfish health.	Choi et al. (2024)
Lateo <i>labrax japonicus</i>	Metagenomics and Transcriptomics	Investigating the metabolome and gut microbiota of Lateo (<i>Labrax japonicus</i>).	Investigated gut microbiota and metabolome interactions in sea bass via metagenomics and transcriptomics. Diet shifts altered microbial composition, affecting lipid and carbohydrate metabolism. Host genes for digestion and immunity correlated with specific bacteria. Results guide dietary interventions for enhanced gut health and growth.	Zhou et al. (2025)
Yellow catfish (<i>Pelteobagrus fulvidraco</i>)	Transcriptome, Proteome and Metabolome	Study on yellow catfish's (<i>Pelteobagrus fulvidraco</i>) brain sex-specific reactions to prolonged hypoxia.	Multi-omics analyses revealed sex-specific brain responses to prolonged hypoxia in catfish, with males showing elevated stress-related gene expression and females exhibiting metabolic downregulation. Altered metabolites such as GABA indicate distinct neural adaptation and hypoxia tolerance mechanisms.	Yin & Zhao, (2025).
Groupers (<i>Epinephelus lanceolatus</i>)	Transcriptomics and Metabolomics	Research on fish iridovirus-induced liver metabolic reprogramming and alpha-linolenic acid's antiviral properties.	Researched liver metabolic reprogramming during fish iridovirus infection. Transcriptomics and metabolomics showed upregulated antiviral and lipid metabolism genes. Alpha-linolenic acid reduced viral load by modulating metabolic pathways. Results suggest dietary interventions for viral disease management.	Liu et al. (2024)
<i>Salmo trutta</i>	Metagenomics and Metabolomics	Investigation of the regulatory mechanisms of several probiotics on	Investigated probiotic effects on growth and gut health using metagenomics and metabolomics.	Chen et al. (2024)

		<i>Salmo trutta</i> growth performance and intestinal health.	Probiotics increased beneficial bacteria, enhancing nutrient absorption. Metabolites like short-chain fatty acids rose, supporting gut integrity. Findings promote probiotic use for improved trout performance.	
<i>Carassius auratus</i>	Metabolomics and Proteomics	How <i>Auxenochlorella pyrenoidosa</i> Protein Extract Works to Replace Fetal Bovine Serum in Fish Muscle Cell Culture.	Explored <i>Auxenochlorella pyrenoidosa</i> protein as a fetal bovine serum alternative in fish cell culture. Metabolomics and proteomics showed comparable cell growth and protein profiles. Key metabolic pathways remained stable, supporting serum replacement. Results advance sustainable fish muscle cell culture techniques.	Dong et al. (2024)
(<i>Cyprinus carpio</i> var. <i>baisensis</i>)	Transcriptomics and Metabolomics	Mechanisms underlying the common strain black carp's (<i>Cyprinus carpio</i> var. <i>baisensis</i>) escape response.	Transcriptomic and metabolomic analyses revealed that escape responses in black carp are supported by rapid activation of muscle contraction and energy metabolism pathways. Elevated lactate levels reflect acute energy demand, providing molecular insights that can inform selective breeding for stress resilience and performance.	Xu et al. (2024)
<i>Penaeus monodon</i>	Transcriptomic and Metabolomic Analyses	Study on <i>Penaeus monodon</i> based on immunological and physiological reactions to ammonia-N stress.	Investigated ammonia-N stress responses using transcriptomic and metabolomic analyses. Stress upregulated immune and detoxification genes in shrimp. Metabolites like amino acids decreased, indicating metabolic strain. Results inform stress mitigation strategies for shrimp aquaculture.	Luo et al. (2024)
<i>Cynoglossus semilaevis</i>	Transcriptomics, Proteomics and Ubiquitinated Proteomic Analyses	Study on <i>Cynoglossus semilaevis</i> pseudomales.	Studied pseudomale development using transcriptomics, proteomics, and ubiquitinated proteomic analyses. Sex-reversal genes and ubiquitinated proteins regulated gonad differentiation. Metabolic and immune pathways differed between sexes. Findings elucidate molecular mechanisms of sex determination in flatfish.	Zhang et al. (2024)
Adult razor clam (<i>Sinonovacula constricta</i>)	Transcriptome and Metabolome	Razor clam (<i>Sinonovacula constricta</i>) ammonia nitrogen tolerance physiological reaction mechanism.	Researched ammonia nitrogen tolerance mechanisms using transcriptomics and metabolomics. Stress upregulated detoxification and antioxidant genes. Metabolites like taurine increased, supporting osmoregulation. Results reveal adaptive strategies for ammonia tolerance in clams.	Sun et al. (2024)

<i>Pelteobagrus fulvidraco</i>	Transcriptome , Proteome, and Metabolome	Research on <i>Pelteobagrus fulvidraco</i> based on ovarian and testicular failure brought on by persistent hypoxia.	Investigated gonadal failure under persistent hypoxia using transcriptomics, proteomics, and metabolomics. Hypoxia downregulated reproductive genes and altered steroid metabolism. Metabolites like testosterone decreased, impairing gonad function. Findings highlight hypoxia's reproductive impacts in catfish.	Zhao et al. (2024)
American shad (<i>Alosa sapidissima</i>)	Transcriptomics, Proteomics, and Metabolomics	Understanding the molecular regulation of the American shad (<i>Alosa sapidissima</i>) exposure to high temperatures.	Studied molecular responses to high temperatures using transcriptomics, proteomics, and metabolomics. Heat stress upregulated chaperone and antioxidant proteins. Metabolites like glucose altered, indicating metabolic shifts. Results inform thermal tolerance mechanisms for shad conservation.	Luo et al. (2024)
<i>Mylopharyngodon piceus</i>	Integrated Transcriptomics and Metabolomics analysis	Mechanism of hepatotoxicity of diclofenac and/or nanoplastyrene in <i>Mylopharyngodon piceus</i> .	Explored hepatotoxicity of diclofenac and nanoplastyrene using transcriptomics and metabolomics. Toxins upregulated liver stress and detoxification genes. Metabolites like bile acids decreased, reflecting liver damage. Findings reveal synergistic toxic effects on black carp liver.	Chen et al. (2024)
<i>Macrobrachium rosenbergii</i>	Transcriptomics, Proteomics and Metabolomics	Mechanism of Acute Low-Salinity Stress in <i>Macrobrachium rosenbergii</i> Larval Stages.	Investigated low-salinity stress in larvae using transcriptomics, proteomics, and metabolomics. Stress altered osmoregulatory and immune gene expression. Metabolites like glycine increased, supporting salinity adaptation. Results guide salinity management in shrimp larval culture.	Li et al. (2024)
Nile Tilapia	Transcriptome and Metabolome	Chronic Microcystin-LR Exposure and Its Toxic Effects on the Liver of Nile Tilapia.	Studied chronic microcystin-LR exposure effects on liver using transcriptomics and metabolomics. Toxin upregulated detoxification and oxidative stress genes. Metabolites like glutathione decreased, indicating liver damage. Findings highlight molecular mechanisms of cyanotoxin toxicity in tilapia.	Li et al. (2024)
Juvenile Rockfish	Transcriptomics and Metabolomics	Impact of Fibrous and Fragmented Microplastics of Polyethylene Terephthalate on Juvenile Rockfish.	Examined polyethylene terephthalate microplastic effects using transcriptomics and metabolomics. Microplastics disrupted metabolic and immune pathways. Metabolites like amino acids decreased, reflecting toxicity. Results underscore microplastic risks to juvenile fish health.	Choi et al. (2024)
Yellow catfish (<i>Pelteobagrus fulvidraco</i>)	Transcriptomics, Metabolomics and	Finding hepatic protein-metabolite networks unique to each sex in yellow	Multi-omics analyses revealed sex-specific hepatic adaptations to long-term hypoxia in catfish, with males exhibiting stronger antioxidant	Zhao et al. (2024)

	Proteomics	catfish (<i>Pelteobagrus fulvidraco</i>) exposed to long-term hypoxia.	responses and females showing altered lipid metabolism. Changes in metabolites such as NAD ⁺ highlight distinct regulatory networks underlying hypoxia resilience.	
<i>Takifugu rubripes</i>	Transcriptomic and Metabolomic Analyses	The physiological reactions of <i>Takifugu rubripes</i> larvae to varying temperatures in their liver.	Investigated larval liver responses to temperature changes using transcriptomic and metabolomic analyses. Temperature shifts altered metabolic and developmental genes. Metabolites like lipids fluctuated, affecting growth. Results inform optimal rearing conditions for pufferfish larvae.	Zhou et al. (2025)
Golden pompano (<i>Trachinotus ovatus</i>)	Transcriptomics and Metabolomics Analyses	Investigating the fundamental processes by which enteritis affects golden pompano (<i>Trachinotus ovatus</i>).	Studied enteritis effects using transcriptomics and metabolomics analyses. Enteritis upregulated inflammatory and immune genes in the gut. Metabolites like short-chain fatty acids decreased, impairing gut health. Findings elucidate molecular mechanisms of enteritis for disease management.	Yuan et al. (2024)
Atlantic Salmon (<i>Salmo salar</i>)	Metabolomics analyses	Identification of Possible Plasma Biomarkers in Atlantic Salmon Infected with PRV-1.	Identified plasma biomarkers for PRV-1 infection using metabolomics analyses. Infection altered lipid and amino acid metabolites in plasma. Key biomarkers included ceramides, indicating immune activation. Results support non-invasive diagnostics for salmon viral infections.	Ivanova et al. (2024)
Crucian Carp (<i>Carassius auratus</i>)	Transcriptomics and Metabolomics Analyses	Examining Differences in Triploid and Diploid Crucian Carp's (<i>Carassius auratus</i>) gill physiological reactions to habitat stress caused by NaHCO ₃ .	Compared triploid vs. diploid gill responses to NaHCO ₃ stress using transcriptomics and metabolomics. Triploids showed higher stress gene expression and metabolic resilience. Metabolites like taurine increased, supporting osmoregulation. Findings highlight ploidy effects on stress adaptation in carp.	Han et al. (2024)
<i>Macrobrachium rosenbergii</i>	Transcriptomics and Metabolomics	Research on the variations in the growth of female <i>Macrobrachium rosenbergii</i> gigantic freshwater prawns.	Researched growth variations in female prawns using transcriptomics and metabolomics. Larger females upregulated growth and reproductive genes. Metabolites like amino acids increased, supporting tissue development. Results inform selective breeding for enhanced prawn growth.	Zhao et al. (2025)
Grass carp (<i>Ctenopharyngodon idellus</i>)	Metabolomics	The regulatory mechanism that underlies the impact of homologous <i>Bacillus tequilensis</i> (GCB-3) on grass carp (<i>Ctenopharyngodon idellus</i>) growth performance.	Metabolomic analysis showed that <i>Bacillus tequilensis</i> (GCB-3) supplementation increases beneficial metabolites, including short-chain fatty acids, enhancing nutrient absorption and growth performance. These results support probiotic application in grass carp aquaculture.	Wang et al. (2024)

Zebrafish	Transcriptomics and Metabolomics	Research on how exposure to ammonia-enhanced <i>Microcystis aeruginosa</i> causes zebrafish to lose muscle nutrients and accumulate liver fat.	Investigated ammonia-enhanced <i>Microcystis aeruginosa</i> effects using transcriptomics and metabolomics. Exposure caused muscle nutrient loss and liver fat accumulation. Genes for lipid metabolism and stress were upregulated. Results reveal synergistic toxicity mechanisms in zebrafish.	Ou-Yang et al. (2024)
Yellowfin tuna (<i>Thunnus albacares</i>)	Transcriptomics and Metabolomics	Research on how adult and juvenile yellowfin tuna (<i>Thunnus albacares</i>) differ in their intestinal lipid metabolism.	Integrated transcriptomic and metabolomic analyses revealed life-stage differences in intestinal lipid metabolism in tuna, with adults showing higher lipid absorption gene expression and altered triglyceride profiles. These findings inform age-specific dietary strategies in aquaculture.	Zou et al. (2024)
Sea Bass (<i>Dicentrarchus Labrax</i>)	Proteomics, Lipidomics, Metabolomics Characterization and Metagenomics Analysis	Sea Bass (<i>Dicentrarchus Labrax</i>) Freshness Estimation and Illicit Conservation Treatment Detection.	Multi-omics analyses linked sea bass freshness to distinct protein and lipid profiles, while illicit treatments produced characteristic microbial and metabolite signatures. These results demonstrate the value of integrated omics for seafood freshness assessment and quality control.	Benedetto et al. (2024)

6. Role of integrating omics technologies in aquaculture

6.1 Systems biology approach

The development of molecular biology technologies has led to a significant shift in biological research. While single-omics approaches (such as genomics, proteomics, and metabolomics) have provided valuable insights, the complexity of biological systems demands a more holistic view. Multi-omics approaches, which integrate data from multiple biomolecular disciplines, have emerged as a powerful tool for systems biology, offering a comprehensive perspective on molecular responses in living systems (Nam et al., 2023). Multi-omics encompasses a range of scientific fields, including genomics, epigenomics, transcriptomics, proteomics, phosphoproteomics, metabolomics, lipidomics, and microbiomics. By combining these disciplines, researchers can gain insights into the complex interactions between various biomolecules and understand how they contribute to biological processes (Kim and Kim, 2021). In aquaculture, multi-omics has been instrumental in improving our understanding of various biological mechanisms, from DNA variations (genomics) to gene expression (transcriptomics) and protein function (proteomics), as well as metabolic and chemical processes (metabolomics) (Alfaro and Young, 2016; Chandhini and Rejish Kumar, 2018; Ye et al., 2018). In particular, the application of multi-omics in environmental

toxicology has proven to be valuable, as it allows for the integration of multiple layers of molecular data to understand the complex responses of biological systems to external stressors (Augustyn et al., 2021). In aquaculture research, this integrative approach has been used to address various challenges, such as understanding the molecular responses of fish to temperature changes and saline-alkaline stress. For instance, studies on low-temperature tolerance in *Takifugu fasciatus* (fugu) used a combination of mRNA-seq and metabolomics to identify differentially expressed metabolites and genes involved in cold tolerance (Wen et al., 2019). Similarly, a multi-omics study on the gills of crucian carp exposed to saline-alkaline stress provided insights into the physiological responses to changes in carbonate alkalinity (Liu et al., 2022). Additionally, the use of integrated multi-omics technologies has been applied to study the epithelial tissue and mucus secreted by fish, aiming to better understand mucosal immunity and functionality in teleost species (Reyes-López et al., 2020). By combining transcriptomics, metabolomics, and biochemical assays, multi-omics provides a more comprehensive understanding of biological systems, facilitating the development of more sustainable and efficient practices

in aquaculture. For example, an integrated approach combining metabolomics and transcriptomics was used to evaluate the effects of different diets on the metabolism and gene expression of rainbow trout (*Oncorhynchus mykiss*), providing valuable insights into how diet influences fish health and growth (Cao et al., 2022).

6.2 Predictive modeling

Recent advancements in sequencing and high-throughput technologies have led to the generation of a wide range of omics data, such as genomics, epigenomics, transcriptomics, proteomics, metabolomics, lipidomics, glycomics, cytomics, microbiomics, metagenomics, radiomics, interactomics, and chemical genomics (Hasin et al., 2017). While genomics and epigenomics data focus on genetic makeup and microbiomics, metagenomics, and chemical genomics provide insight into environmental factors, most other omics data uncover the molecular details of distinct endophenotypes at various levels (Wu and Xie, 2024). These datasets are essential for linking genetic information to phenotypic traits and predicting how phenotypes will respond to environmental changes (Guo and Li, 2023). For instance, transcriptomics analysis helps identify which genes are upregulated or downregulated due to genetic variations or environmental influences (Shang et al., 2022).

7. Applications of omics technologies in aquaculture

Aquaculture, which involves the farming of aquatic organisms, is essential for fulfilling the increasing global demand for seafood. Despite its importance, the industry encounters several challenges, such as disease outbreaks, environmental degradation, and the need for sustainable practices. Omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, offer valuable solutions to these challenges by providing a detailed understanding of the molecular processes behind various biological functions. These technologies are transforming breeding programs, improving disease management strategies, and optimizing nutrition in aquaculture.

7.1 Breeding and genetic improvement

Marker-Assisted Selection (MAS) uses genetic markers linked to desirable traits to identify superior broodstock, speeding up genetic improvement by allowing breeders to select individuals with desired genes without solely relying on phenotypic traits. For example, in Atlantic salmon, MAS has been used to select for resistance to the infectious pancreatic necrosis virus (IPNV), a disease that can cause substantial economic losses (Moen et al., 2009). Genomic selection (GS) advances MAS by analyzing the entire genome to predict an individual's breeding value, offering higher accuracy in predicting complex traits, which results in faster genetic progress and more

efficient selection. GS has been successfully applied in various aquaculture species, such as Atlantic salmon (Ødegård et al., 2014) and rainbow trout (Vallejo et al., 2017), improving growth rates and disease resistance. Omics technologies help unravel the genetic makeup of complex traits like disease resistance and stress tolerance. By identifying genes and pathways tied to these traits, researchers can breed more resilient aquaculture species capable of withstanding environmental stress and disease. For instance, transcriptomic studies have highlighted genes related to Nile tilapia's response to salinity stress, offering insights into the species' osmoregulatory mechanisms (Magdeldin et al., 2014).

7.2 Disease management

Rapid and accurate disease diagnostics are essential for effective disease management in aquaculture. Omics technologies provide powerful tools for pathogen identification and characterization, allowing for early detection and targeted treatment. For instance, metagenomics has been utilized to uncover novel viruses in shrimp, broadening our understanding of the viral diversity linked to shrimp diseases (Zhang et al., 2019).

The development of effective vaccines is crucial for preventing disease outbreaks and reducing economic losses in aquaculture. Transcriptomics and proteomics can help identify potential vaccine targets by uncovering the molecular mechanisms of host-pathogen interactions. For example, proteomics has been applied to identify immunogenic proteins in the bacterial pathogen *Vibrio anguillarum*, which could serve as potential vaccine candidates to protect fish from vibriosis (Sun et al., 2012).

Breeding disease-resistant strains offers a sustainable solution for disease management in aquaculture. Omics technologies can pinpoint genetic markers associated with disease resistance, aiding in the selection of broodstock with enhanced immunity. For example, genomics has been used to identify quantitative trait loci (QTL) related to resistance against white spot syndrome virus (WSSV) in shrimp, which can be leveraged for breeding programs aimed at improving WSSV resistance (Yu et al., 2015).

7.3 Nutrition and feed development

Optimizing nutrition is essential for promoting growth and health in aquaculture species. Omics technologies play a pivotal role in identifying the specific nutritional needs of various species at different life stages, allowing for customized diets that meet these needs. For instance, transcriptomics has been used to explore the nutritional requirements of Atlantic salmon during early development, revealing insights into the genes and pathways involved in nutrient metabolism and utilization (Morais et al., 2012).

Creating cost-effective and sustainable feeds presents a

significant challenge in aquaculture. Transcriptomics and metabolomics can evaluate how different feed ingredients impact fish metabolism and growth, helping formulate feeds that enhance nutrient efficiency and reduce environmental impacts. For example, metabolomics has been applied to assess the influence of various dietary protein sources on rainbow trout, offering insights into how different proteins affect metabolic profiles and growth (Jónsdóttir et al., 2013).

Functional feeds, which include bioactive compounds that support fish health and resistance to disease, are gaining traction. Omics technologies can identify these bioactive compounds and clarify their mechanisms of action, leading to the development of functional feeds that promote health while reducing antibiotic dependence. For example, transcriptomics has been used to identify genes involved in the immune response of Atlantic salmon to dietary prebiotics, showcasing the potential of prebiotics to boost immune function and improve disease resistance (Torrecillas et al., 2014).

7.4 Stress response and environmental adaptation

Aquaculture species are frequently exposed to various stressors, including temperature fluctuations, salinity changes, and low oxygen levels. Omics technologies can pinpoint genes and pathways that play a role in stress responses, offering valuable insights into the molecular mechanisms behind stress tolerance. This information can be used to breed more resilient strains capable of withstanding environmental challenges. For instance, transcriptomics has been employed to investigate the response of Pacific oysters to heat stress, uncovering the genes and pathways involved in cellular protection and repair (Lang et al., 2015).

Aquaculture species also thrive under different environmental conditions. Omics technologies can help unravel the molecular mechanisms of adaptation to factors like salinity, temperature, and oxygen availability. This knowledge can inform the selection of species or strains that are best suited for specific aquaculture environments, ensuring optimal growth and survival. For example, genomics has been utilized to explore the adaptation of Atlantic salmon to varying salinity levels, shedding light on the genetic underpinnings of osmoregulation and salinity tolerance (Larsen et al., 2016).

7.5 Reproduction and development

Understanding the reproductive biology of aquaculture species is essential for optimizing breeding programs and ensuring successful reproduction. Omics technologies offer valuable insights into the molecular mechanisms behind sex determination, gametogenesis, and spawning. For example, transcriptomics has been applied to study sex differentiation in Nile tilapia, identifying the genes and pathways involved in gonad development and sex determination (Tao et al., 2013).

The early life stages of aquatic organisms are often the most vulnerable. Omics technologies can track gene expression patterns during early development, providing a detailed understanding of the molecular processes that influence larval development and survival. This knowledge can help improve hatchery practices and boost larval survival rates. For instance, transcriptomics has been used to study the development of European sea bass larvae, uncovering the genes and pathways involved in organogenesis and metamorphosis (Saavedra et al., 2014).

8. Conclusion and future prospects

Omics technologies are reshaping the aquaculture landscape by providing powerful and precise tools for genetic improvement, disease prevention, nutritional optimization, and environmental adaptation. Their application holds immense potential for enhancing aquaculture productivity, ensuring animal welfare, and promoting long-term sustainability. As these technologies become more refined and cost-effective, their widespread adoption will play a pivotal role in advancing global food security and fostering economic resilience in aquaculture-dependent regions.

The integration of genomics, transcriptomics, proteomics, and metabolomics—collectively known as multi-omics—offers a comprehensive understanding of the complex biological systems that govern aquatic life. This holistic approach enables more accurate phenotype predictions, improved selective breeding programs, targeted nutritional formulations, and enhanced strategies for disease control. Such integrative insights are critical for building a more efficient and sustainable aquaculture sector.

Emerging advancements in sequencing technologies, particularly long-read and single-cell sequencing, are expected to further revolutionize omics applications in aquaculture. Long-read sequencing enables the characterization of full-length transcripts and complex genomic regions, while single-cell sequencing unveils cellular heterogeneity and dynamic gene expression at the individual cell level. These tools will deepen our understanding of gene regulatory networks and organismal responses to stressors and pathogens.

As omics platforms generate increasingly large and complex datasets, the need for sophisticated computational tools continues to grow. Artificial intelligence and machine learning algorithms are poised to play a crucial role in extracting actionable insights, enabling pattern recognition, phenotype prediction, and the development of data-driven management strategies in aquaculture systems.

Additionally, the integration of gene-editing technologies such as CRISPR-Cas9 with omics data holds great promise for the precise development of strains with desirable traits, including enhanced growth, stress tolerance, and disease resistance. Omics-guided genome editing ensures not only the efficiency of trait

improvement but also the biological safety and ethical viability of such interventions. In the broader context of sustainability, omics technologies contribute by identifying genetic markers linked to feed efficiency, waste reduction, and resilience to environmental challenges. This enables the design of eco-friendly practices that reduce the ecological footprint of aquaculture operations while safeguarding animal welfare through stress monitoring and early disease diagnostics.

In conclusion, the future of aquaculture lies in the continued advancement and integration of omics technologies. With responsible application and interdisciplinary collaboration, these tools will drive innovation, sustainability, and resilience in global aquaculture systems, paving the way for a more secure and ethical blue economy.

9. Statement of Declarations

Conflict of Interest: The authors declare no competing interests.

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References

- Abdelmoneim, A., Abdu, A., Chen, S., Sepúlveda, M. S. (2019). Molecular signaling pathways elicited by 17 α -ethinylestradiol in Japanese medaka male larvae undergoing gonadal differentiation. *Aquatic Toxicology*, 208, 187–195. <https://doi.org/10.1016/j.aquatox.2019.01.013>
- Adav, S. S., Wang, Y. (2021). Metabolomics signatures of aging: recent advances. *Aging and Disease*, 12, 646–661.
- Afzaal, M., Saeed, F., Hussain, M., Shahid, F., Siddeeg, A., Al-Farga, A. (2022). Proteomics as a promising biomarker in food authentication, quality and safety: a review. *Food Science & Nutrition*, 10, 2333–2346.
- Agarwal, D., Shanmugam, S. A., Kathirvelpandian, A., Eswaran, S., Rather, M. A., Rakkannan, G. (2024). Unraveling the impact of climate change on fish physiology: a focus on temperature and salinity dynamics. *Journal of Applied Ichthyology*, 2024, 5782274.
- Ahmed, F., Kumar, G., Soliman, F. M., Adly, M. A., Soliman, H. A., El-Matbouli, M., Saleh, M. (2019). Proteomics for understanding pathogenesis, immune modulation and host pathogen interactions in aquaculture. *Comparative Biochemistry and Physiology Part D*, 32, 100625.
- Ai, C. H., Zhu, Z. X., Huang, D. D., Yang, G., De Liu, T., Bai, Y., Xia, J. H. (2023). Identification of SNPs and candidate genes associated with early growth in orange-spotted grouper (*Epinephelus coioides*) by a genome-wide association study. *Aquaculture*, 565, 739129.
- Alfaro, A. C., Nguyen, T. V., Venter, L., Ericson, J. A., Sharma, S., Ragg, N. L., Mundy, C. (2021). The effects of live transport on metabolism and stress responses of abalone (*Haliotis iris*). *Metabolites*, 11, 748.
- Alfaro, A. C., Young, T. (2018). Showcasing metabolomic applications in aquaculture: a review. *Reviews in Aquaculture*, 10, 135–152.
- Almeida, A. M. D., Bassols, A., Bendixen, E., Bhide, M., Cecilian, F., Cristobal, S., Turk, R. (2015). Animal board invited review: advances in proteomics for animal and food sciences. *Animal*, 9, 1–17.
- Augustyn, D. R., Wyciślik, Ł., Mrozek, D. (2021). Perspectives of using Cloud computing in integrative analysis of multi-omics data. *Briefings in Functional Genomics*, 20, 198–206.
- Babaheydari, S. B., Keyvanshokoo, S., Dorafshan, S., Johari, S. A. (2016). Proteomic analysis of skeletal deformity in diploid and triploid rainbow trout (*Oncorhynchus mykiss*) larvae. *Comparative Biochemistry and Physiology Part D*, 19, 1–7. <https://doi.org/10.1016/j.cbd.2016.05.001>
- Badaoui, W., Marhuenda-Egea, F. C., Valero-Rodriguez, J. M., Sanchez-Jerez, P., Arechavala-Lopez, P., Toledo-Guedes, K. (2024). Metabolomic and lipidomic tools for tracing fish escapes from aquaculture facilities. *ACS Food Science & Technology*, 4, 871–879.
- Bar, I., Cummins, S., Elizur, A. (2016). Transcriptome analysis reveals differentially expressed genes associated with germ cell and gonad development in the Southern bluefin tuna (*Thunnus maccoyii*). *BMC Genomics*, 17, 1–14. <https://doi.org/10.1186/s12864-016-2397-8>
- Benedetto, A., Robotti, E., Belay, M. H., Ghignone, A., Fabbris, A., Goggi, E., et al. (2024). Multi-omics approaches for freshness estimation and detection of illicit conservation treatments in sea bass (*Dicentrarchus labrax*): data fusion applications. *International Journal of Molecular Sciences*, 25(3), 1509.
- Betz, A. (2020). Improving analysis and interpretation of transcriptomics and proteomics in environmental sciences. Doctoral dissertation, ETH Zurich.
- Bhagat, J., Zang, L., Nishimura, N., Shimada, Y. (2022). Application of omics approaches for assessing microplastic and nanoplastic toxicity in fish and seafood species. *TrAC Trends in Analytical Chemistry*, 154, 116674.
- Bludau, I., Aebersold, R. (2020). Proteomic and interactomic insights into the molecular basis of cell functional diversity. *Nature Reviews Molecular Cell Biology*, 21, 327–340.
- Bohara, K., Joshi, P., Acharya, K. P., Ramena, G. (2024). Emerging technologies revolutionising disease diagnosis and monitoring in aquatic animal health. *Reviews in Aquaculture*, 16, 836–854.
- Borges, M. H., Andrich, F., Lemos, P. H., Soares, T. G., Menezes, T. N., Campos, F. V., et al. (2018). Combined proteomic and functional analysis reveals rich sources of protein diversity in skin mucus and venom from *Scorpaena plumieri*. *Journal of Proteomics*, 187, 200–211. <https://doi.org/10.1016/j.jprot.2018.08.002>
- Bradshaw, A. D. (1965). Evolutionary significance of phenotypic plasticity in plants. *Advances in Genetics*, 13, 115–155.
- Brennan, L. (2013). Metabolomics in nutrition research: current status and perspectives. *Biochemical Society Transactions*, 41, 670–673.
- Brennan, L., Gibbons, H., O’Gorman, A. (2015). An overview of the role of metabolomics in the identification of dietary biomarkers. *Current Nutrition Reports*, 4, 304–312.
- Brunel, M., Burkina, V., Pickova, J., Sampels, S., Moazzami, A. A. (2022). Oleaginous yeast *Rhodotorula toruloides* biomass effect on the metabolism of Arctic char (*Salvelinus alpinus*). *Frontiers in Molecular Biosciences*, 9, 931946. <https://doi.org/10.3389/fmolb.2022.931946>
- Campbell, N. R., LaPatra, S. E., Overturf, K., Towner, R., Narum, S. R. (2014). Association mapping of disease resistance traits in rainbow trout using restriction site associated DNA sequencing. *G3 (Bethesda)*, 4, 2473–2481.

- Cao, Y., Gao, Q., Li, X., Zhou, Y., Dong, S., Wang, Y., et al. (2022). Integrated analysis of metabolomics and transcriptomics for assessing effects of fish meal and fish oil replacement on the metabolism of rainbow trout (*Oncorhynchus mykiss*). *Frontiers in Marine Science*, 9, 843637.
- Cappello, T., Giannetto, A., Parrino, V., De Marco, G., Mauceri, A., Maisano, M. (2018). Food safety using NMR-based metabolomics: assessment of the Atlantic bluefin tuna, *Thunnus thynnus*, from the Mediterranean Sea. *Food and Chemical Toxicology*, 115, 391–397. <https://doi.org/10.1016/j.fct.2018.03.038>
- Carrera, M., Cañas, B., Gallardo, J. M. (2013). Proteomics for the assessment of quality and safety of fishery products. *Food Research International*, 54, 972–979.
- Carrera, M., Gallardo, J. M., Pascual, S., González, Á. F., Medina, I. (2016). Protein biomarker discovery and fast monitoring for the identification and detection of Anisakids by parallel reaction monitoring (PRM) mass spectrometry. *Journal of Proteomics*, 142, 130–137.
- Castejón, D., García-Segura, J. M., Herrera, A., Cambero, M. I. (2016). NMR-detection of methylamine compounds in Atlantic salmon (*Salmo salar*) subjected to E-beam irradiation. *Food Control*, 60, 455–460.
- Causey, D. R., Kim, J., Stead, D. A., Martin, S. A., Devlin, R. H., Macqueen, D. J. (2018). Proteomic comparison of selective breeding and growth hormone transgenesis in fish: unique pathways to enhanced growth. *Journal of Proteomics*, 192, 114–124. <https://doi.org/10.1016/j.jprot.2018.08.013>
- Causey, D. R., Pohl, M. A., Stead, D. A., Martin, S. A., Secombes, C. J., Macqueen, D. J. (2018). High-throughput proteomic profiling of the fish liver following bacterial infection. *BMC Genomics*, 19, 1–17.
- Cha, I., Kwon, J., Park, S., Nho, S., Jang, H., Park, S., et al. (2012). Kidney proteome responses in the teleost fish *Paralichthys olivaceus* indicate a putative immune response against *Streptococcus parauberis*. *Journal of Proteomics*, 75, 5166–5175. <https://doi.org/10.1016/j.jprot.2012.05.046>
- Chandhini, S., Rejish Kumar, V. J. (2019). Transcriptomics in aquaculture: current status and applications. *Reviews in Aquaculture*, 11, 1379–1397.
- Chen, H., Wang, J., Du, J., Si, Z., Yang, H., Xu, X., et al. (2019). ASIP disruption via CRISPR/Cas9 system induces black patches dispersion in Oujiang color common carp. *Aquaculture*, 498, 230–235.
- Chen, L., Zhang, H., Shi, H., Li, Z., Xue, C. (2023). Application of multi-omics combined with bioinformatics techniques to assess salinity stress response and tolerance mechanisms of Pacific oyster (*Crassostrea gigas*) during depuration. *Fish & Shellfish Immunology*, 137, 108779.
- Chen, M., Wang, Z., He, H., He, W., Zhang, Z., Sun, S., et al. (2024). Multi-omics analysis reveals the regulatory mechanism of different probiotics on growth performance and intestinal health of *Salmo trutta*. *Microorganisms*, 12(7), 1410.
- Chen, S., Tian, Y., Li, Z., Li, Z., Liu, Y., Wang, L., et al. (2022). Construction of a high-density genetic linkage map and QTL mapping for growth traits in hybrid *Epinephelus fuscoguttatus* (♀) and *Epinephelus tukula* (♂) progeny. *Aquaculture*, 551, 737921.
- Chen, S., Zhang, G., Shao, C., Huang, Q., Liu, G., Zhang, P., et al. (2014). Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. *Nature Genetics*, 46, 253–260.
- Chen, T., Jiang, H., He, Y., Shen, Y., Fang, J., Huang, Z., et al. (2024). Histopathological, physiological, and multi-omics insights into the hepatotoxicity mechanism of nanopolystyrene and/or diclofenac in *Mylopharyngodon piceus*. *Environmental Pollution*, 341, 122894.
- Chen, Y., Liu, Y., Bai, Y., Xu, S., Yang, X., Cheng, B. (2022). Intestinal metabolomics of juvenile lenok (*Brachymystax lenok*) in response to heat stress. *Fish Physiology and Biochemistry*, 48, 1389–1400. <https://doi.org/10.1007/s10695-022-01128-7>
- Cheng, K., Müllner, E., Moazzami, A. A., Carlberg, H., Brännäs, E., Pickova, J. (2017). Metabolomics approach to evaluate a Baltic Sea sourced diet for cultured Arctic char (*Salvelinus alpinus* L.). *Journal of Agricultural and Food Chemistry*, 65, 5083–5090. <https://doi.org/10.1021/acs.jafc.7b00994>
- Choi, K. M., Mun, S. H., Shin, D., Kim, C. H., Kim, T. H., Jung, J. H. (2024). The adverse effects of exposure to fibrous and fragmented polyethylene terephthalate microplastic in juvenile rockfish based on two omics approach. *SSRN*, 4705176.
- Choi, K. M., Mun, S. H., Shin, D., Kim, C. H., Kim, T. H., Jung, J. H. (2024). The toxic effects of exposure to fibrous and fragmented microplastic in juvenile rockfish based on two omics approach. *Chemosphere*, 367, 143541.
- Chubukov, V., Uhr, M., Le Chat, L., Kleijn, R. J., Jules, M., Link, H., et al. (2013). Transcriptional regulation is insufficient to explain substrate-induced flux changes in *Bacillus subtilis*. *Molecular Systems Biology*, 9, 709.
- Colás-Ruiz, N. R., Ramirez, G., Courant, F., Gomez, E., Hampel, M., Lara-Martín, P. A. (2022). Multi-omic approach to evaluate the response of gilt-head sea bream (*Sparus aurata*) exposed to the UV filter sulisobenzene. *Science of the Total Environment*, 803, 150080.
- Combe, M., Reverter, M., Caruso, D., Pepey, E., Gozlan, R. E. (2023). Impact of global warming on the severity of viral diseases: a potentially alarming threat to sustainable aquaculture worldwide. *Microorganisms*, 11, 1049.
- Costello, C., Cao, L., Gelcich, S., Cisneros-Mata, M. Á., Free, C. M., Froehlich, H. E., et al. (2020). The future of food from the sea. *Nature*, 588, 95–100.
- Crollius, H. R., Weissenbach, J. (2005). Fish genomics and biology. *Genome Research*, 15, 1675–1682.
- Cui, M., Cheng, C., Zhang, L. (2022). High-throughput proteomics: a methodological mini-review. *Laboratory Investigation*, 102, 1170–1181.
- Dai, X., Shen, L. (2022). Advances and trends in omics technology development. *Frontiers in Medicine*, 9, 911861.
- Dale, K., Yadete, F., Müller, M. B., Pampanin, D. M., Gilabert, A., Zhang, X., et al. (2020). Proteomics and lipidomics analyses reveal modulation of lipid metabolism by perfluoroalkyl substances in liver of Atlantic cod (*Gadus morhua*). *Aquatic Toxicology*, 227, 105590.
- Dang, Y., Xu, X., Shen, Y., Hu, M., Zhang, M., Li, L., et al. (2016). Transcriptome analysis of the innate immunity-related complement system in spleen tissue of *Ctenopharyngodon idella* infected with *Aeromonas hydrophila*. *PLoS ONE*, 11, e0157413. <https://doi.org/10.1371/journal.pone.0157413>
- Dayon, L., Cominetti, O., Affolter, M. (2022). Proteomics of human biological fluids for biomarker discoveries: technical advances and recent applications. *Expert Review of Proteomics*, 19, 131–151.
- De Magalhães, C. R., Farinha, A. P., Carrilho, R., Schrama, D., Cerqueira, M., Rodrigues, P. M. (2023). A new window into fish welfare: a proteomic discovery study of stress biomarkers in the skin mucus of gilthead seabream (*Sparus aurata*). *Journal of Proteomics*, 281, 104904. <https://doi.org/10.1016/j.jprot.2023.104904>

- De Mori, G., Cipriani, G. (2023). Marker-assisted selection in breeding for fruit trait improvement: a review. *International Journal of Molecular Sciences*, 24, 8984.
- Deborde, C., Hounoum, B. M., Moing, A., Maucourt, M., Jacob, D., Corraze, G., et al. (2021). Putative imbalanced amino acid metabolism in rainbow trout long term fed a plant-based diet as revealed by ¹H-NMR metabolomics. *Journal of Nutritional Science*, 10, e3. <https://doi.org/10.1017/jns.2021.3>
- Deshpande, D., Chhugani, K., Chang, Y., Karlsberg, A., Loeffler, C., Zhang, J., et al. (2023). RNA-seq data science: from raw data to effective interpretation. *Frontiers in Genetics*, 14, 997383.
- Dietrich, M. A., Arnold, G. J., Nynca, J., Fröhlich, T., Otte, K., Ciereszko, A. (2014). Characterization of carp seminal plasma proteome in relation to blood plasma. *Journal of Proteomics*, 98, 218–232. <https://doi.org/10.1016/j.jprot.2014.01.005>
- Dietrich, M. A., Irnazarow, I., Ciereszko, A. (2017). Proteomic identification of seminal plasma proteins related to the freezability of carp semen. *Journal of Proteomics*, 162, 52–61. <https://doi.org/10.1016/j.jprot.2017.04.015>
- Dong, N., Jiang, B., Chang, Y., Wang, Y., Xue, C. (2024). Integrated omics approach: revealing the mechanism of *Auxenochlorella pyrenoidosa* protein extract replacing fetal bovine serum for fish muscle cell culture. *Journal of Agricultural and Food Chemistry*, 72(11), 6064–6076.
- Eckersall, P. D., de Almeida, A. M., Miller, I. (2012). Proteomics, a new tool for farm animal science. *Journal of Proteomics*, 75, 4187–4189.
- Edvardsen, R. B., Leininger, S., Kleppe, L., Skaftnesmo, K. O., Wargelius, A. (2014). Targeted mutagenesis in Atlantic salmon (*Salmo salar* L.) using the CRISPR/Cas9 system induces complete knockout individuals in the F0 generation. *PLoS ONE*, 9, e108622.
- FAO. (2022). The state of world fisheries and aquaculture 2022: towards blue transformation. Rome: Food and Agriculture Organization of the United Nations.
- FAO. (2024). The state of world fisheries and aquaculture 2024. Rome: Food and Agriculture Organization of the United Nations. <https://doi.org/10.4060/cd0683en>
- Faught, E., Schaaf, M. J. (2024). Molecular mechanisms of the stress-induced regulation of the inflammatory response in fish. *General and Comparative Endocrinology*, 345, 114387.
- Ferri, E., Galimberti, A., Casiraghi, M., Airolidi, C., Ciaramelli, C., Palmioli, A., et al. (2015). Towards a universal approach based on omics technologies for the quality control of food. *BioMed Research International*, 2015, 365794.
- Feussner, I., Polle, A. (2015). What the transcriptome does not tell—proteomics and metabolomics are closer to the plants' patho-phenotype. *Current Opinion in Plant Biology*, 26, 26–31.
- Fontagné-Dicharry, S., Larroquet, L., Dias, K., Cluzeaud, M., Heraud, C., Corlay, D. (2018). Effects of dietary oxidized fish oil supplementation on oxidative stress and antioxidant defense system in juvenile rainbow trout (*Oncorhynchus mykiss*). *Fish & Shellfish Immunology*, 74, 43–51.
- Fraslin, C., Quillet, E., Rochat, T., Dechamp, N., Bernardet, J. F., Collet, B., et al. (2020). Combining multiple approaches and models to dissect the genetic architecture of resistance to infections in fish. *Frontiers in Genetics*, 11, 677.
- Gandar, A., Laffaille, P., Marty-Gasset, N., Viala, D., Molette, C., Jean, S. (2017). Proteome response of fish under multiple stress exposure: effects of pesticide mixtures and temperature increase. *Aquatic Toxicology*, 184, 61–77.
- Ganguly, S., Mitra, T., Mahanty, A., Mohanty, S., Mohanty, B. P. (2020). A comparative metabolomics study on anadromous clupeid *Tenualosa ilisha* for better understanding the influence of habitat on nutritional composition. *Metabolomics*, 16, 1–14.
- Ge, H., Lin, K., Zhou, C., Lin, Q., Zhang, Z., Wu, J., et al. (2020). A multi-omic analysis of orange-spotted grouper larvae infected with nervous necrosis virus identifies increased adhesion molecules and collagen synthesis in the persistent state. *Fish Shellfish Immunology*, 98, 595–604.
- Ghini, V., Meoni, G., Vignoli, A., Di Cesare, F., Tenori, L., Turano, P., et al. (2023). Fingerprinting and profiling in metabolomics of biosamples. *Progress in Nuclear Magnetic Resonance Spectroscopy*, 138–139, 1–22.
- Ghisaura, S., Pagnozzi, D., Melis, R., Biosa, G., Slawski, H., Uzzau, S., et al. (2019). Liver proteomics of gilthead sea bream (*Sparus aurata*) exposed to cold stress. *Journal of Thermal Biology*, 82, 234–241.
- Gilmour, K. M., Daley, M. A., Egginton, S., Kelber, A., McHenry, M. J., Patek, S. N., et al. (2023). Through the looking glass: attempting to predict future opportunities and challenges in experimental biology. *Journal of Experimental Biology*, 226, jeb245336.
- Gil-Solsona, R., Caldach-Giner, J. A., Nacher-Mestre, J., Lacalle-Bergeron, L., Sancho, J. V., Hernández, F., et al. (2018). Contributions of MS metabolomics to gilthead sea bream (*Sparus aurata*) nutrition: serum fingerprinting of fish fed low fish meal and fish oil diets. *Aquaculture*, 498, 503–512. <https://doi.org/10.1016/j.aquaculture.2018.08.080>
- Gil-Solsona, R., Nacher-Mestre, J., Lacalle-Bergeron, L., Sancho, J. V., Caldach-Giner, J. A., Hernández, F., Pérez-Sánchez, J. (2017). Untargeted metabolomics approach for unraveling robust biomarkers of nutritional status in fasted gilthead sea bream (*Sparus aurata*). *PeerJ*, 5, e2920.
- Goldansaz, S. A., Guo, A. C., Sajed, T., Steele, M. A., Plastow, G. S., Wishart, D. S. (2017). Livestock metabolomics and the livestock metabolome: a systematic review. *PLoS ONE*, 12, e0177675.
- Gunnarsson, L., Jauhiainen, A., Kristiansson, E., Nerman, O., Larsson, D. G. J. (2008). Evolutionary conservation of human drug targets in organisms used for environmental risk assessments. *Environmental Science & Technology*, 42, 5807–5813.
- Guo, J., Wang, A., Mao, S., Xu, X., Li, J., Shen, Y. (2022). Construction of high-density genetic linkage map and QTL mapping for growth performance in black carp (*Mylopharyngodon piceus*). *Aquaculture*, 549, 737799.
- Guo, T., Li, X. (2023). Machine learning for predicting phenotype from genotype and environment. *Current Opinion in Biotechnology*, 79, 102853.
- Gutierrez Reyes, C. D., Alejo-Jacuinde, G., Perez Sanchez, B., Chavez Reyes, J., Onigbinde, S., et al. (2024). Multi omics applications in biological systems. *Current Issues in Molecular Biology*, 46, 5777–5793.
- Hale, M. C., McKinney, G. J., Thrower, F. P., Nichols, K. M. (2016). RNA-seq reveals differential gene expression in the brains of juvenile resident and migratory smolt rainbow trout (*Oncorhynchus mykiss*). *Comparative Biochemistry and Physiology Part D*, 20, 136–150.
- Han, F., Romagosa, I., Ullrich, S. E., Jones, B. L., Hayes, P. M., Wesenberg, D. M. (1997). Molecular marker-assisted selection for malting quality traits in barley. *Molecular Breeding*, 3, 427–437.
- Han, S., Han, L., Yuan, F., Liu, W., Wang, J., Jin, X., et al. (2025). Exploring disparities in gill physiological responses to NaHCO₃-induced habitat stress in triploid

- and diploid crucian carp (*Carassius auratus*): a comprehensive investigation through multi-omics and biochemical analyses. *Metabolites*, 15(1), 5.
- Hasin, Y., Seldin, M., Lusi, A. (2017). Multi-omics approaches to disease. *Genome Biology*, 18, 83.
- Hayes, C. N., Nakahara, H., Ono, A., Tsuge, M., Oka, S. (2024). From omics to multi-omics: a review of advantages and tradeoffs. *Genes*, 15, 1551.
- He, L., Zhu, D., Liang, X., Li, Y., Liao, L., Yang, C., et al. (2021). Multi-omics sequencing provides insights into age-dependent susceptibility of grass carp (*Ctenopharyngodon idellus*) to reovirus. *Frontiers in Immunology*, 12, 694965.
- Helal, M., Hany, N., Maged, M., Abdelaziz, M., Osama, N., Younan, Y. W., et al. (2022). Candidate genes for marker-assisted selection for growth, carcass and meat quality traits in rabbits. *Animal Biotechnology*, 33, 1691–1710.
- Hillier, L. W., Miller, R. D., Baird, S. E., Chinwalla, A., Fulton, L. A., Koboldt, D. C., et al. (2007). Comparison of *C. elegans* and *C. briggsae* genome sequences reveals extensive conservation of chromosome organization and synteny. *PLoS Biology*, 5, e167.
- Horgan, R. P., Kenny, L. C. (2011). 'Omic' technologies: genomics, transcriptomics, proteomics and metabolomics. *Obstetrics & Gynaecology*, 13, 189–195.
- Houston, R. D., Bean, T. P., Macqueen, D. J., Gundappa, M. K., Jin, Y. H., Jenkins, T. L., et al. (2020). Harnessing genomics to fast-track genetic improvement in aquaculture. *Nature Reviews Genetics*, 21, 389–409.
- Huang, Y., Li, Z., Li, M., Zhang, X., Shi, Q., Xu, Z. (2025). Fish genomics and its application in disease-resistance breeding. *Reviews in Aquaculture*, 17, e12973.
- Huo, J., Li, X., Hu, X., Lv, A. (2024). Multi-omics analysis of miRNA-mediated intestinal microflora changes in crucian carp *Carassius auratus* infected with *Rahnella aquatilis*. *Frontiers in Immunology*, 15, 1335602.
- Jackson, T. K., Rhode, C. (2024). A high-density genetic linkage map and QTL identification for growth traits in dusky kob (*Argyrosomus japonicus*). *Aquaculture*, 586, 740786.
- Jaiswal, S., Rasal, K. D., Chandra, T., Prabha, R., Iquebal, M. A., Rai, A., et al. (2023). Proteomics in fish health and aquaculture productivity management: status and future perspectives. *Aquaculture*, 566, 739159.
- Jia, R., Hou, Y., Feng, W., Li, B., Zhu, J. (2022). Alterations at biochemical, proteomic and transcriptomic levels in liver of tilapia (*Oreochromis niloticus*) under chronic exposure to environmentally relevant level of glyphosate. *Chemosphere*, 294, 133818.
- Jia, R., Hou, Y., Feng, W., Nomingere, M., Li, B., Zhu, J., et al. (2023). Multi-omics analysis to understand the effects of dietary proanthocyanidins on antioxidant capacity, muscle nutrients, lipid metabolism, and intestinal microbiota in *Cyprinus carpio*. *Antioxidants*, 12(12), 2095.
- Jiang, S., Fu, L., Gao, Z., Deng, H., Zhang, Y., You, X., et al. (2022). Multi-omics study on the molecular mechanisms of *Tetraodon nigroviridis* resistance to exogenous *Vibrio parahaemolyticus* infection. *Frontiers in Marine Science*, 9, 914028.
- Jiang, W., Fang, J., Du, M., Gao, Y., Fang, J., Jiang, Z. (2021). Integrated transcriptomics and metabolomics analyses reveal benzo[a]pyrene enhances the toxicity of mercury to the Manila clam, *Ruditapes philippinarum*. *Ecotoxicology and Environmental Safety*, 213, 112038.
- Jiao, S., Nie, M., Song, H., Xu, D., You, F. (2020). Physiological responses to cold and starvation stresses in the liver of yellow drum (*Nibea albiflora*) revealed by LC-MS metabolomics. *Science of the Total Environment*, 715, 136940.
- Jin, Y., Tian, L. X., Xie, S. W., Guo, D. Q., Yang, H. J., Liang, G. Y., et al. (2015). Interactions between dietary protein levels, growth performance, feed utilization, gene expression and metabolic products in juvenile grass carp (*Ctenopharyngodon idella*). *Aquaculture*, 437, 75–83.
- Johnston, I. A., Kent, M. P., Boudinot, P., Looseley, M., Bargelloni, L., Faggion, S., et al. (2024). Advancing fish breeding in aquaculture through genome functional annotation. *Aquaculture*, 740589.
- Kamachi, Y., Kawahara, A. (2023). CRISPR-Cas9-mediated genome modifications in zebrafish. *Methods in Molecular Biology*, 2637, 313–324.
- Kang, Y., Liu, Z., Shi, H., Wang, J., Huang, J., Li, Y., et al. (2019). Label-free quantification of protein expression in the rainbow trout (*Oncorhynchus mykiss*) in response to short-term exposure to heat stress. *Comparative Biochemistry and Physiology Part D*, 30, 158–168. <https://doi.org/10.1016/j.cbd.2019.02.009>
- Keyvanshokoo, S., Vaziri, B. (2007). Proteome analysis of Persian sturgeon (*Acipenser persicus*) ova. *Animal Reproduction Science*, 109, 287–297. <https://doi.org/10.1016/j.anireprosci.2007.10.008>
- Khalil, K., Elayat, M., Khalifa, E., Daghash, S., Elasad, A., Miller, M., et al. (2017). Generation of myostatin gene-edited channel catfish (*Ictalurus punctatus*) via zygote injection of CRISPR/Cas9 system. *Scientific Reports*, 7, 7301.
- Kim, D. Y., Kim, J. M. (2021). Multi-omics integration strategies for animal epigenetic studies—a review. *Animal Bioscience*, 34, 1271–1282.
- Kong, T., Ren, X., Lin, S., Li, S., Gong, Y. (2020). Elucidation of metabolic responses in mud crab *Scylla paramamosain* challenged to WSSV infection by integration of metabolomics and transcriptomics. *Developmental & Comparative Immunology*, 113, 103799.
- Kozera, B., Rapacz, M. (2013). Reference genes in real-time PCR. *Journal of Applied Genetics*, 54, 391–406.
- Kriaridou, C., Tsairidou, S., Houston, R. D., Robledo, D. (2020). Genomic prediction using low density marker panels in aquaculture: performance across species, traits, and genotyping platforms. *Frontiers in Genetics*, 11, 124.
- Kumar, G., Hummel, K., Noebauer, K., Welch, T. J., Razzazi-Fazeli, E., El-Matbouli, M. (2018). Proteome analysis reveals a role of rainbow trout lymphoid organs during *Yersinia ruckeri* infection process. *Scientific Reports*, 8, 13998. <https://doi.org/10.1038/s41598-018-31982-6>
- Lal, J., Deb, S., Singh, S. K., Biswas, P., Debbarma, R., Yadav, N. K., Debbarma, S., Vaishnav, A., Meena, D. K., Waikhom, G., Patel, A. B. (2024). Diverse uses of valuable seafood processing industry waste for sustainability: a review. *Environmental Science and Pollution Research*, 31, 62249–62263. <https://doi.org/10.1007/s11356-023-28890-2>
- Lazado, C. C., Timmerhaus, G., Breiland, M. W., Pittman, K., Hytterød, S. (2021). Multiomics provide insights into the key molecules and pathways involved in the physiological adaptation of Atlantic salmon (*Salmo salar*) to chemotherapeutic-induced oxidative stress. *Antioxidants*, 10(12), 1931.
- Lee, Y., Nguyen, T. L., Roh, H., Kim, A., Park, J., Lee, J., et al. (2023). Mechanisms underlying probiotic effects on neurotransmission and stress resilience in fish via transcriptomic profiling. *Fish & Shellfish Immunology*, 141, 109063.
- Leeuwis, R. H., Gamperl, A. K. (2022). Adaptations and plastic phenotypic responses of marine animals to the environmental challenges of the high intertidal zone.

- Oceanography and Marine Biology, 60, 625–679.
- Li, C., Zhang, X., Zhao, L., Liu, S. (2024). Multi-omics profiling reveals the molecular mechanisms of H₂O₂-induced detrimental effects on *Thamnaconus septentrionalis*. BMC Genomics, 25(1), 984.
- Li, D., Zeng, L., Zhang, W., Wang, Q., Wu, J., Zhu, C., et al. (2025). Multi-omics study of sex in greater amberjack (*Seriola dumerili*): identifying related genes, analyzing sex-biased expression, and developing sex-specific markers. Comparative Biochemistry and Physiology Part D, 53, 101364.
- Li, H., Wang, X., Zhang, R., Liu, L., Zhu, H. (2024). Generation of golden goldfish *Carassius auratus* via tyrosinase gene targeting by CRISPR/Cas9. Aquaculture, 583, 740594.
- Li, J. N., Zhao, Y. T., Cao, S. L., Wang, H., Zhang, J. J. (2020). Integrated transcriptomic and proteomic analyses of grass carp intestines after vaccination with a double-targeted DNA vaccine of *Vibrio mimicus*. Fish & Shellfish Immunology, 98, 641–652.
- Li, J., Yang, Z., Yan, J., Zhang, K., Ning, X., Wang, T., et al. (2023). Multi-omics analysis revealed the brain dysfunction induced by energy metabolism in *Pelteobagrus vachelli* under hypoxia stress. Ecotoxicology and Environmental Safety, 254, 114749.
- Li, J., Zhang, G., Yin, D., Li, Y., Zhang, Y., Cheng, J., et al. (2022). Integrated application of multiomics strategies provides insights into the environmental hypoxia response in *Pelteobagrus vachelli* muscle. Molecular & Cellular Proteomics, 21(3), 100206.
- Li, L., Wang, Y., Huang, Y., Wang, C. (2023). Multi-omics approach to study the dual effects of novel proteins on the intestinal health of juvenile largemouth bass (*Micropterus salmoides*) under an alternate feeding strategy. Frontiers in Immunology, 14, 1110696.
- Li, M., Dai, S., Liu, X., Xiao, H., Wang, D. (2021). A detailed procedure for CRISPR/Cas9-mediated gene editing in tilapia. Hydrobiologia, 848, 3865–3881.
- Li, M., Liang, H., Yang, H. (2024). Deciphering the gut microbiome of grass carp through multi-omics approach. Microbiome, 12, 2.
- Li, M., Yang, H., Zhao, J., Fang, L., Shi, H., Li, M., Wang, D. (2014). Efficient and heritable gene targeting in tilapia by CRISPR/Cas9. Genetics, 197, 591–599.
- Li, P., Guo, M., Sun, B. (2019). Integration of multi-omics data to mine cancer-related gene modules. Journal of Bioinformatics and Computational Biology, 17, 1950038.
- Li, X., Hu, X., Lv, A., Guan, Z. (2022). Skin immune response to *Aeromonas hydrophila* infection in crucian carp *Carassius auratus* revealed by multi-omics analysis. Fish & Shellfish Immunology, 127, 866–875.
- Li, X., Xu, B., Shen, P., Cheng, H., Fan, Y., Gao, Q. (2024). Regulation and response mechanism of acute low-salinity stress during larval stages in *Macrobrachium rosenbergii* based on multi-omics analysis. International Journal of Molecular Sciences, 25(12), 6809.
- Li, Y., Yang, H., Fu, B., Kaneko, G., Li, H., Tian, J., et al. (2024). Integration of multi-omics, histological, and biochemical analysis reveals the toxic responses of Nile tilapia liver to chronic microcystin-LR exposure. Toxins, 16(3), 149.
- Liang, J., Hu, X., Lü, A., Sun, J. (2020). First report on the characterization of pathogenic *Rahnella aquatilis* KCL-5 from crucian carp: revealed by genomic and proteomic analyses. Journal of Fish Diseases, 43(8), 889–914.
- Liang, J., Luo, W., Yu, K., Xu, Y., Chen, J., Deng, C., et al. (2021). Multi-omics revealing the response patterns of symbiotic microorganisms and host metabolism in coral *Pavona minuta* to temperature stresses. Metabolites, 12(1), 18.
- Lieke, T., Jung-Schroers, V., Rebl, A. (2025). Freshwater browning as a hidden threat – transcriptomic responses in fish gills exposed to fulvic acid. Journal of Hazardous Materials, 488, 137260. <https://doi.org/10.1016/j.jhazmat.2025.137260>
- Lin, H., Zhou, S., Li, X., Liu, Y., Luo, W., Zhao, Y., et al. (2024). Effects of oxidized fish oil diet supplemented with tea polyphenols on intestinal health and liver metabolism of spotted sea bass (*Lateolabrax maculatus*). Aquaculture Reports, 37, 102201.
- Lin, X., Tan, J., Shen, Y., Yang, B., Zhang, Y., Liao, Y., et al. (2022). A high-density genetic linkage map and QTL mapping for sex in *Clarias fuscus*. Aquaculture, 561, 738723.
- Liu, H., Luo, Q., Ou, M., Zhu, X., Zhao, J., Chen, K. (2020). High-density genetic linkage map and QTL fine mapping of growth and sex in snakehead (*Channa argus*). Aquaculture, 519, 734760.
- Liu, L., Zhang, Y., Yuan, M. D., Xiao, D. M., Xu, W. H., Zheng, Q., et al. (2024). Integrated multi-omics analysis reveals liver metabolic reprogramming by fish iridovirus and antiviral function of alpha-linolenic acid. Zoological Research, 45(3), 520.
- Liu, X., Zeng, S., Liu, S., Wang, G., Lai, H., Zhao, X., et al. (2020). Identifying the related genes of muscle growth and exploring the functions by compensatory growth in mandarin fish (*Siniperca chuatsi*). Frontiers in Physiology, 11, 553563.
- Liu, Y., Yao, M., Li, S., Wei, X., Ding, L., Han, S., et al. (2022). Integrated application of multi-omics approach and biochemical assays provides insights into physiological responses to saline-alkaline stress in the gills of crucian carp (*Carassius auratus*). Science of the Total Environment, 822, 153622.
- Liu, Z., Zhou, T., Gao, D. (2022). Genetic and epigenetic regulation of growth, reproduction, disease resistance and stress responses in aquaculture. Frontiers in Genetics, 13, 994471.
- Long, M., Zhao, J., Li, T., Tafalla, C., Zhang, Q., Wang, X., et al. (2015). Transcriptomic and proteomic analyses of splenic immune mechanisms of rainbow trout (*Oncorhynchus mykiss*) infected by *Aeromonas salmonicida* subsp. *salmonicida*. Journal of Proteomics, 122, 41–54.
- Long, S., Dong, X., Tan, B., Zhang, S., Xie, S., Yang, Q., et al. (2021). Growth performance, antioxidant ability, biochemical index in serum, liver histology and hepatic metabolomics analysis of juvenile hybrid grouper fed with oxidized fish oil. Aquaculture, 545, 737261.
- Lulijwa, R., Alfaro, A. C., Young, T. (2022). Metabolomics in salmonid aquaculture research: applications and future perspectives. Reviews in Aquaculture, 14, 547–577.
- Luo, M., Zhu, W., Liang, Z., Feng, B., Xie, X., Li, Y., et al. (2024). High-temperature stress response: insights into the molecular regulation of American shad (*Alosa sapidissima*) using a multi-omics approach. Science of the Total Environment, 916, 170329.
- Luo, Z., Zhou, F., Jiang, S., Huang, J., Yang, L., Yang, Q., et al. (2024). Immune and physiological responses in *Penaes monodon* to ammonia-N stress: a multi-omics approach. Frontiers in Immunology, 15, 1510887.
- Ma, J. L., Qiang, J., Tao, Y. F., Bao, J. W., Zhu, H. J., Li, L. G., et al. (2021). Multi-omics analysis reveals the glycolipid metabolism response mechanism in the liver of genetically improved farmed tilapia (GIFT, *Oreochromis niloticus*) under hypoxia stress. BMC Genomics, 22, 1–16.
- Ma, S., Shu, X., Wang, W. X. (2022). Multi-omics reveals the

- regulatory mechanisms of zinc exposure on the intestine–liver axis of golden pompano *Trachinotus ovatus*. *Science of the Total Environment*, 816, 151497.
- Ma, Y. M., Yang, M. J., Wang, S., Li, H., Peng, X. X. (2015). Liver functional metabolomics discloses an action of L-leucine against *Streptococcus iniae* infection in tilapias. *Fish & Shellfish Immunology*, 45, 414–421.
- Mallona, I., Lischewski, S., Weiss, J., Hause, B., Egea-Cortines, M. (2010). Validation of reference genes for quantitative real-time PCR during leaf and flower development in *Petunia hybrida*. *BMC Plant Biology*, 10, 4.
- Manso, S. C., Garcia, B. F., Mastrochirico-Filho, V. A., Porto-Foresti, F., Yáñez, J. M., Hashimoto, D. T. (2024). Genomic predictions for resistance to *Aeromonas hydrophila* in pacu (*Piaractus mesopotamicus*). *Aquaculture*, 582, 740553.
- Martyniuk, C. J. (2022). Omics-driven insight into physiological responses of species in aquaculture. *Comparative Biochemistry and Physiology Part D*, 43, 101013.
- Martyniuk, C. J., Kroll, K. J., Doperalski, N. J., Barber, D. S., Denslow, N. D. (2010). Environmentally relevant exposure to 17 α -ethinylestradiol affects the telencephalic proteome of male fathead minnows. *Aquatic Toxicology*, 98, 344–353.
- Martyniuk, C. J., Kroll, K. J., Doperalski, N. J., Barber, D. S., Denslow, N. D. (2010). Genomic and proteomic responses to environmentally relevant exposures to dielrin: indicators of neurodegeneration? *Toxicological Sciences*, 117, 190–199.
- Martyniuk, C. J., Popescu, J. T., Chown, B., Denslow, N. D., Trudeau, V. L. (2012). Quantitative proteomics in teleost fish: insights and challenges for neuroendocrine and neurotoxicology research. *General and Comparative Endocrinology*, 176, 314–320.
- Mazzeo, M. F., Siciliano, R. A. (2016). Proteomics for the authentication of fish species. *Journal of Proteomics*, 147, 119–124.
- McCarthy, F. M., Wang, N., Magee, G. B., Nanduri, B., Lawrence, M. L., Camon, E. B., et al. (2006). AgBase: a functional genomics resource for agriculture. *BMC Genomics*, 7, 229.
- Melis, R., Cappuccinelli, R., Roggio, T., Anedda, R. (2014). Addressing marketplace gilthead sea bream (*Sparus aurata* L.) differentiation by ¹H NMR-based lipid fingerprinting. *Food Research International*, 63, 258–264.
- Mendoza-Porras, O., Rusu, A. G., Stratford, C., Wade, N. M. (2024). Rapid detection of heat stress biomarkers in Atlantic salmon (*Salmo salar*) liver using targeted proteomics. *Aquaculture and Fisheries*, 4, e147.
- Moen, T., Baranski, M., Sonesson, A. K., Kjølglum, S. (2009). Confirmation and fine-mapping of a major QTL for resistance to infectious pancreatic necrosis in Atlantic salmon (*Salmo salar*): population-level associations between markers and trait. *BMC Genomics*, 10, 368.
- Monisha, G., Sowndarya, K. (2024). RNA-SEQ: a high-revolution view of the transcriptome. *Biotechnology and Biological Sciences*, 73, 1–10.
- Monti, C., Zilocchi, M., Colugnat, I., Alberio, T. (2019). Proteomics turns functional. *Journal of Proteomics*, 198, 36–44.
- Mukherjee, A., Abraham, S., Singh, A., Balaji, S., Mukunthan, K. S. (2024). From data to cure: a comprehensive exploration of multi-omics data analysis for targeted therapies. *Molecular Biotechnology*, 66, 1–21.
- Mushtaq, M. Y., Marçal, R. M., Champagne, D. L., Van Der Kooy, F., Verpoorte, R., Choi, Y. H. (2014). Effect of acute stresses on zebrafish (*Danio rerio*) metabolome measured by NMR-based metabolomics. *Planta Medica*, 80, 1227–1233.
- Naderi, M., Keyvanshokoo, S., Ghaedi, A., Salati, A. P. (2018). Effect of acute crowding stress on rainbow trout (*Oncorhynchus mykiss*): a proteomics study. *Aquaculture*, 495, 106–114.
- Nagahama, Y., Chakraborty, T., Paul-Prasanth, B., Ohta, K., Nakamura, M. (2021). Sex determination, gonadal sex differentiation, and plasticity in vertebrate species. *Physiological Reviews*, 101, 1497–1525.
- Nam, S. E., Bae, D. Y., Ki, J. S., Ahn, C. Y., Rhee, J. S. (2023). The importance of multi-omics approaches for the health assessment of freshwater ecosystems. *Molecular & Cellular Toxicology*, 19, 3–11.
- Napier, J. D., Heckman, R. W., Juenger, T. E. (2023). Gene-by-environment interactions in plants: molecular mechanisms, environmental drivers, and adaptive plasticity. *The Plant Cell*, 35, 109–124.
- Nguinkal, J. A., Brunner, R. M., Verleih, M., Rebl, A., de Los Ríos-Pérez, L., Schäfer, N., et al. (2019). The first highly contiguous genome assembly of pikeperch (*Sander lucioperca*), an emerging aquaculture species in Europe. *Genes*, 10, 708.
- Nguyen, N. H. (2024). Genetics and genomics of infectious diseases in key aquaculture species. *Biology*, 13, 29.
- Nguyen, T. V., Alfaro, A. C. (2020). Applications of omics to investigate responses of bivalve haemocytes to pathogen infections and environmental stress. *Aquaculture*, 518, 734488.
- Nguyen, T. V., Alfaro, A. C. (2020). Metabolomics investigation of summer mortality in New Zealand Greenshell™ mussels (*Perna canaliculus*). *Fish & Shellfish Immunology*, 106, 783–791.
- Nissa, M. U., Banerjee, A., Goswami, M., Srivastava, S. (2022). Comprehensive data and workflow for mapping global proteome and post-translational modifications in Indian major carp, *Labeo rohita*. *Data in Brief*, 45, 108746.
- Nissa, M. U., Pinto, N., Mukherjee, A., Reddy, P. J., Ghosh, B., Sun, Z., et al. (2021). Organ-based proteome and post-translational modification profiling of a widely cultivated tropical water fish, *Labeo rohita*. *Journal of Proteome Research*, 21, 420–437.
- Niu, J., Hu, X. L., Ip, J. C., Ma, K. Y., Tang, Y., Wang, Y., et al. (2020). Multi-omic approach provides insights into osmoregulation and osmoconformation of the crab *Scylla paramamosain*. *Scientific Reports*, 10(1), 21771.
- Noell, K., Pitula, J. S. (2021). A dual omics approach to evaluate transcriptional and metabolic responses during lipid deprivation in an oyster parasite, *Perkinsus marinus*. *OMICS: A Journal of Integrative Biology*, 25(2), 93–101.
- Nynca, J., Żarski, D., Fröhlich, T., Köster, M., Bobe, J., Ciereszko, A. (2021). Comparative proteomic analysis reveals the importance of the protective role of ovarian fluid over eggs during the reproduction of pikeperch. *Aquaculture*, 548, 737656. <https://doi.org/10.1016/j.aquaculture.2021.737656>
- Ødegård, J., Moen, T., Santi, N., Korsvoll, S. A., Kjølglum, S., Meuwissen, T. H. (2014). Genomic prediction in an admixed population of Atlantic salmon (*Salmo salar*). *Frontiers in Genetics*, 5, 402.
- Oikonomou, S., Kazlari, Z., Papapetrou, M., Papanna, K., Papaharisis, L., Manousaki, T., et al. (2022). Genome wide association (GWAS) analysis and genomic heritability for parasite resistance and growth in European seabass. *Aquaculture Reports*, 24, 101178.
- Oomen, R. A., Hutchings, J. A. (2017). Transcriptomic responses to environmental change in fishes: insights from RNA sequencing. *Facets*, 2, 610–641.

- Othman, R., Elabd, H., Pratiwy, F. M., Barzkar, N., Lim, L. S., Rodrigues, K. F. (2024). Biosecurity in aquaculture: nurturing health and ensuring sustainability. In: *Essentials of Aquaculture Practices*. Singapore: Springer; pp. 139–182.
- Ou-Yang, K., Kuang, Y., Yang, H., He, Y., Wang, L., Wang, X., et al. (2024). Multi-omics analysis reveals the toxic mechanism of ammonia-enhanced *Microcystis aeruginosa* exposure causing liver fat deposition and muscle nutrient loss in zebrafish. *Journal of Hazardous Materials*, 461, 132631.
- Palomba, M., Ruggetti, A., Mignogna, G., Castrignanò, T., Rahimi, H., Masuelli, L., et al. (2023). Proteomic characterization of extracellular vesicles released by third stage larvae of the zoonotic parasite *Anisakis pegreffii* (Nematoda: Anisakidae). *Frontiers in Cellular and Infection Microbiology*, 13, 1079991.
- Pasandideh, R., Mohammadabadi, M., Pasandideh, M. (2022). The application of genomic selection in improvement of molecular breeding programs in aquaculture. *Agricultural Biotechnology Journal*, 14, 133–156.
- Pédrón, N., Artigaud, S., Infante, J. L. Z., Le Bayon, N., Charrier, G., Pichereau, V., et al. (2017). Proteomic responses of European flounder to temperature and hypoxia as interacting stressors: differential sensitivities of populations. *Science of the Total Environment*, 586, 890–899.
- Perkons, I., Varunjikar, M. S., Rasinger, J. D. (2023). Unveiling the potential of proteomics in addressing food and feed safety challenges. *EFSA Journal*, 21, e211013.
- Piñeiro, C., Martinez, I. (2012). Evaluation of fish quality and safety by proteomics techniques. In: *Proteomics in Foods: Principles and Applications*. Boston: Springer; pp. 161–180.
- Popesku, J. T., Martyniuk, C. J., Denslow, N. D., Trudeau, V. L. (2010). Rapid dopaminergic modulation of the fish hypothalamic transcriptome and proteome. *PLoS ONE*, 5, e12338.
- Potts, R. W., Gutierrez, A. P., Penaloza, C. S., Regan, T., Bean, T. P., Houston, R. D. (2021). Potential of genomic technologies to improve disease resistance in molluscan aquaculture. *Philosophical Transactions of the Royal Society B*, 376, 20200168.
- Power, D. M., Taoukis, P., Houhoula, D., Tsironi, T., Flemetakis, E. (2023). Integrating omics technologies for improved quality and safety of seafood products. *Aquaculture and Fisheries*, 8, 457–462.
- Prieto-Álamo, M. J., Osuna-Jiménez, I., Abril, N., Alhama, J., Pueyo, C., López-Barea, J. (2012). Omics methodologies: new tools in aquaculture studies. *IntechOpen*.
- Pulgar, R., Hödar, C., Travisany, D., Zuñiga, A., Domínguez, C., Maass, A., et al. (2015). Transcriptional response of Atlantic salmon families to *Piscirickettsia salmonis* infection highlights the relevance of the iron-deprivation defence system. *BMC Genomics*, 16, 495. <https://doi.org/10.1186/s12864-015-1716-9>
- Puthumana, J., Chandrababu, A., Sarasan, M., Joseph, V., Singh, I. B. (2024). Genetic improvement in edible fish: status, constraints, and prospects on CRISPR-based genome engineering. *3 Biotech*, 14, 44.
- Qi, S., Wang, J., Zhang, Y., Naz, M., Afzal, M. R., Du, D., et al. (2023). Omics approaches in invasion biology: understanding mechanisms and impacts on ecological health. *Plants*, 12, 1860.
- Qin, Z., Ge, Q., Wang, J., Li, M., Liu, P., Li, J., et al. (2021). Comparative transcriptomic and proteomic analysis of *Exopalaemon carinicauda* in response to alkalinity stress. *Frontiers in Marine Science*, 8, 759923.
- Quan, J., Kang, Y., Li, L., Zhao, G., Sun, J., Liu, Z. (2021). Proteome analysis of rainbow trout (*Oncorhynchus mykiss*) liver responses to chronic heat stress using DIA/SWATH. *Journal of Proteomics*, 233, 104079.
- Ramya, V. L., Behera, B. K. (2023). Molecular markers and their application in fisheries and aquaculture. In: *Biotechnological Tools in Fisheries and Aquatic Health Management*. Singapore: Springer; pp. 115–150.
- Randhawa, S. S., Pawar, R. (2021). Fish genomes: sequencing trends, taxonomy and influence of taxonomy on genome attributes. *Journal of Applied Ichthyology*, 37, 553–562.
- Raposo de Magalhães, C. S. F., Cerqueira, M. A. C., Schrama, D., Moreira, M. J. V., Boonanuntanasarn, S., Rodrigues, P. M. L. (2020). A proteomics and other omics approach in the context of farmed fish welfare and biomarker discovery. *Reviews in Aquaculture*, 12, 122–144.
- Raposo de Magalhães, C., Sandoval, K., Kagan, F., McCormack, G., Schrama, D., Carrilho, R., et al. (2024). Transcriptomic changes behind *Sparus aurata* hepatic response to different aquaculture challenges: an RNA-seq study and multiomics integration. *PLoS ONE*, 19(3), e0300472.
- Raposo de Magalhães, C., Schrama, D., Farinha, A. P., Revets, D., Kuehn, A., Planchon, S., et al. (2020). Protein changes as robust signatures of fish chronic stress: a proteomics approach to fish welfare research. *BMC Genomics*, 21, 309.
- Raposo de Magalhães, C., Schrama, D., Nakharuthai, C., Boonanuntanasarn, S., Revets, D., Planchon, S., et al. (2021). Metabolic plasticity of gilthead seabream under different stressors: analysis of the stress responsive hepatic proteome and gene expression. *Frontiers in Marine Science*, 8, 676189.
- Rasmussen, J. A., Villumsen, K. R., Ernst, M., Hansen, M., Forberg, T., Gopalakrishnan, S., et al. (2022). A multi-omics approach unravels metagenomic and metabolic alterations of a probiotic and synbiotic additive in rainbow trout (*Oncorhynchus mykiss*). *Microbiome*, 10(1), 21.
- Reid, J. M., Acker, P. (2022). Properties of phenotypic plasticity in discrete threshold traits. *Evolution*, 76, 190–206.
- Ren, X., Yu, Z., Xu, Y., Zhang, Y., Mu, C., Liu, P., et al. (2020). Integrated transcriptomic and metabolomic responses in the hepatopancreas of kuruma shrimp (*Marsupenaeus japonicus*) under cold stress. *Ecotoxicology and Environmental Safety*, 206, 111360.
- Reyes-López, F. E., Ibarz, A., Ordóñez-Grande, B., Vallejos-Vidal, E., Andree, K. B., Balasch, J. C., et al. (2020). Skin multi-omics-based interactome analysis: integrating the tissue and mucus exuded layer for a comprehensive understanding of the teleost mucosa functionality as model of study. *Frontiers in Immunology*, 11, 613824.
- Rideout, R. M., Youssef, T. N., Adamack, A. T., John, R., Cohen, A. M., Fridgen, T. D., et al. (2023). Qualitative shotgun proteomics strategy for protein expression profiling of fish otoliths. *BioChem*, 3, 102–117.
- Rodrigues, K. F., Biun, H., Yong, W. T. L., Chin, G. J. W. L., Ching, F. F., Othman, R. (2023). The application of molecular markers in fish breeding and aquaculture. In: *Marine Biotechnology: Applications in Food, Drugs and Energy*. Singapore: Springer; pp. 73–101.
- Rodrigues, P. M., Martin, S. A., Silva, T. S., Boonanuntanasarn, S., Schrama, D., Moreira, M., Raposo, C. (2018). Proteomics in fish and aquaculture research. In: *Proteomics in Domestic Animals: From Farm to Systems Biology*. Cham: Springer; pp. 311–338.
- Rodrigues, P. M., Silva, T. S., Dias, J., Jessen, F. (2012). Proteomics in aquaculture: applications and trends.

- Journal of Proteomics, 75, 4325–4345.
- Roh, H., Kim, D. H. (2022). Identification, classification and functional characterization of HSP70s in rainbow trout (*Oncorhynchus mykiss*) through multi-omics approaches. *Fish & Shellfish Immunology*, 121, 205–214.
- Roques, S., Deborde, C., Richard, N., Skiba-Cassy, S., Moing, A., Fauconneau, B. (2020). Metabolomics and fish nutrition: a review in the context of sustainable feed development. *Reviews in Aquaculture*, 12, 261–282.
- Roy, A., Basak, R., Rai, U. (2017). De novo sequencing and comparative analysis of testicular transcriptome from different reproductive phases in freshwater spotted snakehead *Channa punctatus*. *PLoS ONE*, 12, e0173178.
<https://doi.org/10.1371/journal.pone.0173178>
- Saaristo, M., Wong, B. B. M., Mincarelli, L., Craig, A., Johnstone, C. P., Allinson, M., et al. (2017). Characterisation of the transcriptome of male and female wild-type guppy brains with RNA-Seq and consequences of exposure to the pharmaceutical pollutant, 17 α -ethinyl estradiol. *Aquatic Toxicology*, 186, 28–39.
<https://doi.org/10.1016/j.aquatox.2017.02.016>
- Salem, M., Vallejo, R. L., Leeds, T. D., Palti, Y., Liu, S., Sabbagh, A., et al. (2012). RNA-Seq identifies SNP markers for growth traits in rainbow trout. *PLoS ONE*, 7, e36264.
- Samuelsson, L. M., Larsson, D. G. J. (2008). Contributions from metabolomics to fish research. *Molecular BioSystems*, 4, 974–979.
- Sanches, P. H. G., de Melo, N. C., Porcari, A. M., de Carvalho, L. M. (2024). Integrating molecular perspectives: strategies for comprehensive multi-omics integrative data analysis and machine learning applications in transcriptomics, proteomics, and metabolomics. *Biology*, 13, 848.
- Saroglia, M., Liu, Z. (Eds.). (2012). *Functional genomics in aquaculture*. Wiley-Blackwell.
- Schartl, M., Walter, R. B., Shen, Y., Garcia, T., Catchen, J., Amores, A., et al. (2013). The genome of the platyfish, *Xiphophorus maculatus*, provides insights into evolutionary adaptation and several complex traits. *Nature Genetics*, 45, 567–572.
- Schwartz, T. S. (2020). The promises and the challenges of integrating multi-omics and systems biology in comparative stress biology. *Integrative and Comparative Biology*, 60, 89–97.
- Sébédo, J. L. (2017). Metabolomics, nutrition, and potential biomarkers of food quality, intake, and health status. *Advances in Food and Nutrition Research*, 82, 83–116.
- Serraj, R., Hash, C. T., Rizvi, S. M. H., Sharma, A., Yadav, R. S., Bidinger, F. R. (2005). Recent advances in marker-assisted selection for drought tolerance in pearl millet. *Plant Production Science*, 8, 334–337.
- Shahi, N., Singh, B., Mallik, S. K., Sarma, D., Surachetpong, W. (2023). RNA-Seq reveals differential gene expression patterns related to reproduction in the golden mahseer. *Fishes*, 8, 352.
- Shang, F., Lu, Y., Li, Y., Han, B., Wei, R., Liu, S., et al. (2022). Transcriptome analysis identifies key metabolic changes in the brain of *Takifugu rubripes* in response to chronic hypoxia. *Genes*, 13, 1347.
- Shao, L., Dong, Y., Chen, S., Sheng, J., Cai, L., Xu, X., et al. (2024). Revealing extracellular protein profile and excavating spoilage-related proteases of *Aeromonas salmonicida* based on multi-omics investigation. *International Journal of Biological Macromolecules*, 265, 130916.
- Sharma, P., Doultani, S., Hadiya, K. K., George, L. B., Highland, H. N. (2024). Overview of marker-assisted selection in animal breeding. *Journal of Advances in Biology & Biotechnology*, 27, 303–318.
- Sheedy, J. R., Lachambre, S., Gardner, D. K., Day, R. W. (2016). ¹H-NMR metabolite profiling of abalone digestive gland in response to short-term starvation. *Aquaculture International*, 24, 503–521.
- Shen, G., Wang, S., Dong, J., Feng, J., Xu, J., Xia, F., et al. (2019). Metabolic effect of dietary taurine supplementation on grouper (*Epinephelus coioides*): a ¹H-NMR-based metabolomics study. *Molecules*, 24, 2253. <https://doi.org/10.3390/molecules24122253>
- Shen, X., Niu, Y. C., Uichanco, J. A. V., Phua, N., Bhandare, P., Thevasagayam, N. M., et al. (2023). Mapping of a major QTL for increased robustness and detection of genome assembly errors in Asian seabass (*Lates calcarifer*). *BMC Genomics*, 24, 449.
- Shi, M., Huang, R., Du, F., Pei, Y., Liao, L., Zhu, Z., Wang, Y. (2014). RNA-seq profiles from grass carp tissues after reovirus (GCRV) infection based on singular and modular enrichment analyses. *Molecular Immunology*, 61, 44–53.
<https://doi.org/10.1016/j.molimm.2014.05.004>
- Sidira, M., Agriopoulou, S., Smaoui, S., Varzakas, T. (2024). Omics-integrated approach (metabolomics, proteomics and lipidomics) to assess the quality control of aquatic and seafood products. *Applied Sciences*, 14, 10755.
- Sun, G., Lv, L., Yao, H., Lin, Z., Xu, N., Dong, Y. (2024). Integrated application of multi-omics and biochemical analysis revealed the physiological response mechanism of ammonia nitrogen tolerance in the razor clam (*Sinonovacula constricta*). *Frontiers in Marine Science*, 11, 1444929.
- Thakur, K., Sharma, D., Chauhan, D., Mahajan, D., Choudhary, K., Brar, B., et al. (2023). A systems biology approach in fisheries science. In: *Systems Biology, Bioinformatics and Livestock Science*; pp. 76–97.
- Tharun, P. S., Talekar, N., Akkati, V. R. (2024). Applications of molecular marker implementation for enhanced oilseed breeding through marker-assisted selection (MAS). *Journal of Experimental Agriculture International*, 46, 865–876.
- Tripathi, A. K. (2022). Applications of omics technology in deciphering microbial mechanisms in environmental waste management. *South Dakota School of Mines and Technology*.
- Tripathy, P. S., Khatei, A., Parhi, J. (2022). Omics in aquaculture. In: *Advances in Fisheries Biotechnology*. Singapore: Springer; pp. 83–94.
- Uengwetwanit, T., Uawisetwathana, U., Arayamethakorn, S., Khudet, J., Chaipayechara, S., Karoonuthaisiri, N., et al. (2020). Multi-omics analysis to examine microbiota, host gene expression and metabolites in the intestine of black tiger shrimp (*Penaeus monodon*) with different growth performance. *PeerJ*, 8, e9646.
- Ulloa, P. E., Rincón, G., Islas-Trejo, A., Araneda, C., Iturra, P., Neira, R., et al. (2015). RNA sequencing to study gene expression and SNP variations associated with growth in zebrafish fed a plant protein-based diet. *Marine Biotechnology*, 17, 353–363.
- Vahabi, N., Michailidis, G. (2022). Unsupervised multi-omics data integration methods: a comprehensive review. *Frontiers in Genetics*, 13, 854752.
- Vallejo, R. L., Leeds, T. D., Gao, G., Parsons, J. E., Martin, K. E., Evenhuis, J. P., et al. (2017). Genomic selection models double the accuracy of predicted breeding values for bacterial cold water disease resistance compared to a traditional pedigree-based model in rainbow trout aquaculture. *Genetics Selection Evolution*, 49, 17.
- Vela-Avitúa, S., LaFrentz, B. R., Lozano, C. A., Shoemaker, C.

- A., Ospina-Arango, J. F., Beck, B. H., et al. (2023). Genome-wide association study for *Streptococcus iniae* in Nile tilapia (*Oreochromis niloticus*) identifies a significant QTL for disease resistance. *Frontiers in Genetics*, 14, 1078381.
- Verdegem, M., Buschmann, A. H., Latt, U. W., Dalsgaard, A. J., Lovatelli, A. (2023). The contribution of aquaculture systems to global aquaculture production. *Journal of the World Aquaculture Society*, 54, 206–250.
- Villarreal, F., Burguener, G. F., Sosa, E. J., Stocchi, N., Somoza, G. M., Turjanski, A. G., et al. (2024). Genome sequencing and analysis of black flounder (*Paralichthys orbignyanus*) reveals new insights into *Pleuronectiformes* genomic size and structure. *BMC Genomics*, 25, 297.
- Wang, J., Yu, X., Wu, S., Jin, C., Wang, M., Ding, H., et al. (2024). Identification of candidate SNPs and genes associated with resistance to nervous necrosis virus in leopard coral grouper (*Plectropomus leopardus*) using GWAS. *Fish & Shellfish Immunology*, 144, 109295.
- Wang, L., Liu, C., Wang, L., Xu, J., Zheng, J., Xu, Y., et al. (2025). Multi-omics integrative analysis reveals the molecular mechanisms of muscle adaptive changes in largemouth bass (*Micropterus salmoides*) under water flow stress in recirculating aquaculture. *Aquaculture*, 742172.
- Wang, L., Sun, F., Yang, Z., Lee, M., Yeo, S., Wong, J., et al. (2024). Mapping the genetic basis for sex determination and growth in hybrid tilapia (*Oreochromis mossambicus* × *O. niloticus*). *Aquaculture*, 593, 741310.
- Wang, L., Wang, L., Liu, C., Ma, F., Huang, J., Jin, Z., et al. (2024). Multi-omics reveals the molecular mechanism of muscle quality changes in common carp (*Cyprinus carpio*) under two aquaculture systems. *Comparative Biochemistry and Physiology Part D*, 52, 101290.
- Wang, M., Zhao, S., Wang, J., Nie, L., Li, L., Zhu, X., et al. (2024). Multi-omics analysis provides insight into liver metabolism in yellow catfish (*Pelteobagrus fulvidraco*) under hypoxic stress. *Aquaculture*, 583, 740531.
- Wang, X., Zhang, D. M., Zhang, X., Lei, X., Li, Y., Huang, Q., et al. (2024). Integrated multiple-omics reveals the regulatory mechanism underlying the effects of homologous *Bacillus tequilensis* (GCB-3) on growth performance of grass carp (*Ctenopharyngodon idellus*). *Aquaculture Reports*, 36, 102138.
- Wang, Z., Gerstein, M., Snyder, M. (2009). RNA-Seq: a revolutionary tool for transcriptomics. *Nature Reviews Genetics*, 10, 57–63.
- Wei, S., Yun, B., Liu, S., Ding, T. (2022). Multiomics technology approaches in blue foods. *Current Opinion in Food Science*, 45, 100833.
- Wei, Y., Li, B., Xu, H., Liang, M. (2021). Liver metabolome and proteome response of turbot (*Scophthalmus maximus*) to lysine and leucine in free and dipeptide forms. *Frontiers in Marine Science*, 8, 694404.
- Wen, X., Hu, Y., Zhang, X., Wei, X., Wang, T., Yin, S. (2019). Integrated application of multi-omics provides insights into cold stress responses in pufferfish *Takifugu fasciatus*. *BMC Genomics*, 20, 557.
- Wenne, R. (2023). Microsatellites as molecular markers with applications in exploitation and conservation of aquatic animal populations. *Genes*, 14, 808.
- Westerhoff, H. V., Palsson, B. O. (2004). The evolution of molecular biology into systems biology. *Nature Biotechnology*, 22, 1249–1252.
- White, J., Lee, G. (2023). Computational molecular biology: interdisciplinary technological integration and new advances. *Computational Molecular Biology*, 13, 1–15.
- Wishart, D. S. (2008). Metabolomics: applications to food science and nutrition research. *Trends in Food Science & Technology*, 19, 482–493.
- Woltereck, R. (1909). Further experimental investigations on species change, specifically on the nature of quantitative species differences in *Daphnids*. *Proceedings of the German Zoological Society*, 1909, 110–172.
- Wu, L., Yang, Y., Wang, X., Weng, Z., Hua, S., Li, D., et al. (2023). Genome-wide QTL mapping and RNA-seq reveal the genetic variation influencing growth traits in giant grouper (*Epinephelus lanceolatus*). *Aquaculture*, 563, 738944.
- Wu, Y., Wu, T., Yang, L., Su, Y., Zhao, C., Li, L., et al. (2023). Generation of fast growth Nile tilapia (*Oreochromis niloticus*) by myostatin gene mutation. *Aquaculture*, 562, 738762.
- Wu, Y., Xie, L. (2024). AI-driven multi-omics integration for multi-scale predictive modeling of causal genotype–environment–phenotype relationships. *arXiv*, arXiv:2407.06405.
- Xiang, Q. Q., Yan, H., Luo, X. W., Kang, Y. H., Hu, J. M., Chen, L. Q. (2021). Integration of transcriptomics and metabolomics reveals damage and recovery mechanisms of fish gills in response to nanosilver exposure. *Aquatic Toxicology*, 237, 105895.
- Xiao, M., Qian, K., Wang, Y., Bao, F. (2020). GC-MS metabolomics reveals metabolic differences of the farmed Mandarin fish *Siniperca chuatsi* in recirculating ponds aquaculture system and pond. *Scientific Reports*, 10, 6090.
- Xiao, Y., Wu, L., He, L., Tang, Y., Guo, S., Zhai, S. (2022). Transcriptomic analysis using dual RNA sequencing revealed a pathogen–host interaction after *Edwardsiella anguillarum* infection in European eel (*Anguilla anguilla*). *Fish & Shellfish Immunology*, 120, 745–757.
- Xu, Y., Dong, P., Sewo, D. Y., Su, S., Li, J., Feng, W., et al. (2024). Multi-omics analysis unravels the underlying mechanisms of the escape response of the common strain black carp (*Cyprinus carpio* var. *baisensis*). *Aquaculture International*, 32(7), 9547–9563.
- Yadav, N. K., Deepti, M., Patel, A. B., Kumar, P., Angom, J., Debbarma, S., Singh, S. K., Deb, S., Lal, J., Vaishnav, A., Das, R. (2025). Dissecting insects as sustainable protein bioresource in fish feed for aquaculture sustainability. *Discover Food*, 5, 47. <https://doi.org/10.1007/s44187-025-00318-5>
- Yadav, N. K., Patel, A. B., Singh, S. K., Mehta, N. K., Anand, V., Lal, J., Dekari, D., Devi, N. C. (2024). Climate change effects on aquaculture production and its sustainable management through climate-resilient adaptation strategies: a review. *Environmental Science and Pollution Research*, 31, 31731–31751. <https://doi.org/10.1007/s11356-024-33397-5>
- Yáñez, J. M., Barria, A., Lopez, M. E., Moen, T., Garcia, B. F., Yoshida, G. M., et al. (2023). Genome-wide association and genomic selection in aquaculture. *Reviews in Aquaculture*, 15, 645–675.
- Ye, H., Lin, Q., Luo, H. (2018). Applications of transcriptomics and proteomics in understanding fish immunity. *Fish & Shellfish Immunology*, 77, 319–327.
- Yeh, Y. C., Kinoshita, M., Ng, T. H., Chang, Y. H., Maekawa, S., Chiang, Y. A., et al. (2017). Using CRISPR/Cas9-mediated gene editing to further explore growth and trade-off effects in myostatin-mutated F4 medaka (*Oryzias latipes*). *Scientific Reports*, 7, 11435.
- Yin, D., Zhao, C. (2025). Multi-omics analysis reveals the cerebral sex-specific responses to chronic hypoxia in yellow catfish (*Pelteobagrus fulvidraco*). *Comparative Biochemistry and Physiology Part D*, 54, 101401.

- Yin, P., Xie, S., Huo, Y., Guo, T., Fang, H., Zhang, Y., et al. (2019). Effects of dietary oxidized fish oil on growth performance, antioxidant defense system, apoptosis and mitochondrial function of juvenile largemouth bass (*Micropterus salmoides*). *Aquaculture*, 500, 347–358.
- Yoshinaga, H., Yasuike, M., Mekuchi, M., Soma, S., Yamamoto, T., Murashita, K., et al. (2023). Multi-omics analysis of hepatopancreas of red seabream (*Pagrus major*) fed a soybean meal-based diet. *Aquaculture*, 574, 739631.
- Young, T., Alfaro, A. C., Villas-Bôas, S. G. (2016). Metabolic profiling of mussel larvae: effect of handling and culture conditions. *Aquaculture International*, 24, 843–856.
- Young, T., Laroche, O., Walker, S. P., Miller, M. R., Casanovas, P., Steiner, K., et al. (2023). Prediction of feed efficiency and performance-based traits in fish via integration of multiple omics and clinical covariates. *Biology*, 12(8), 1135.
- Youssef, T. N., Christian, S. L., Rideout, R., Adamack, A., Thibault, P., Bonneil, E., et al. (2024). Proteomic blueprint of Atlantic cod (*Gadus morhua*) otoliths revealing environmental stress insights through label-free quantitative shotgun proteomics. *BioChem*, 4, 144–165.
- Yu, E., Fu, B., Wang, G., Li, Z., Ye, D., Jiang, Y., et al. (2020). Proteomic and metabolomic basis for improved textural quality in crisp grass carp (*Ctenopharyngodon idellus*) fed with a natural dietary pro-oxidant. *Food Chemistry*, 325, 126906.
- Yu, T., Chen, Y. K., Chen, X. M., Abdallah, G., Guo, Z. X., Zhao, Y. L., et al. (2020). The effect of oxidized fish oil on lipid metabolism in *Rhynchocypris lagowski* Dybowski. *Aquaculture Reports*, 17, 100388.
- Yuan, S., Sun, M., Ma, D., Guo, X., Wang, Z., Niu, J., et al. (2024). Exploring the underlying mechanisms of enteritis impact on golden pompano (*Trachinotus ovatus*) through multi-omics analysis. *Fish & Shellfish Immunology*, 150, 109616.
- Zampiga, M., Flees, J., Meluzzi, A., Dridi, S., Sirri, F. (2018). Application of omics technologies for a deeper insight into quali-quantitative production traits in broiler chickens: a review. *Journal of Animal Science and Biotechnology*, 9, 61.
- Zhang, D. G., Zhao, T., Hogstrand, C., Ye, H. M., Xu, X. J., Luo, Z. (2021). Oxidized fish oils increased lipid deposition via oxidative stress-mediated mitochondrial dysfunction and the CREB1–Bcl2–Beclin1 pathway in the liver tissues and hepatocytes of yellow catfish. *Food Chemistry*, 360, 129814.
- Zhang, D. M., Guo, Z. X., Zhao, Y. L., Wang, Q. J., Gao, Y. S., Yu, T., et al. (2019). L-carnitine regulated Nrf2/Keap1 activation in vitro and in vivo and protected oxidized fish oil-induced inflammation response by inhibiting the NF-κB signaling pathway in *Rhynchocypris lagowski* Dybowski. *Fish & Shellfish Immunology*, 93, 1100–1110.
- Zhang, G., Zhang, J., Wen, X., Zhao, C., Zhang, H., Li, X., et al. (2017). Comparative iTRAQ-based quantitative proteomic analysis of *Pelteobagrus vachelli* liver under acute hypoxia: implications in metabolic responses. *Proteomics*, 17, 1700140.
- Zhang, H., Zhu, Y., Xu, P., Zhao, Z., Feng, J., Wu, B., et al. (2022). Multi-omics data reveal amino acids related genes in the common carp (*Cyprinus carpio*). *Fishes*, 7(5), 225.
- Zhang, J., Xiong, X., Deng, Y., Zheng, Z., Yang, C., Du, X. (2021). Integrated application of transcriptomics and metabolomics provides insights into the larval metamorphosis of pearl oyster (*Pinctada fucata martensii*). *Aquaculture*, 532, 736067.
- Zhang, R., Chen, T., Wang, Y., Short, M. (2023). Systems approaches for sustainable fisheries: a comprehensive review and future perspectives. *Sustainable Production and Consumption*, 41, 1–15.
- Zhang, R., Zhang, L., Ye, X., Tian, Y., Sun, C., Lu, M., et al. (2013). Transcriptome profiling and digital gene expression analysis of Nile tilapia (*Oreochromis niloticus*) infected by *Streptococcus agalactiae*. *Molecular Biology Reports*, 40, 5657–5668. <https://doi.org/10.1007/s11033-013-2667-3>
- Zhang, W., Tan, B., Deng, J., Haitao, Z. (2021). Multiomics analysis of soybean meal induced marine fish enteritis in juvenile pearl gentian grouper. *Scientific Reports*, 11(1), 23319.
- Zhang, X., Wang, F., Dong, Z., Dong, X., Chi, J., Chen, H., et al. (2020). A new strain of yellow catfish carrying genome edited myostatin alleles exhibits double muscling phenotype with hyperplasia. *Aquaculture*, 523, 735187.
- Zhang, Y., Li, Y., Liang, X., Cao, X., Huang, L., Yan, J., et al. (2017). Hepatic transcriptome analysis and identification of differentially expressed genes response to dietary oxidized fish oil in loach *Misgurnus anguillicaudatus*. *PLoS ONE*, 12, e0172386.
- Zhang, Y., Liu, C., Liu, J., Liu, X., Tu, Z., Zheng, Y., et al. (2022). Multi-omics reveals response mechanism of liver metabolism of hybrid sturgeon under ship noise stress. *Science of the Total Environment*, 851, 158348.
- Zhang, Y., Wang, L., Xu, F., Ye, Z., Chen, S., Li, H. (2024). Integrative omics reveals clues as to why *Cynoglossus semilaevis* pseudomales produce no W sperm. *Aquaculture Reports*, 36, 102171.
- Zhang, Z. X., Wang, Z. Y., Fang, M., Ye, K., Tang, X., Zhang, D. L. (2022). Genome-wide association analysis on host resistance against the rotten body disease in a naturally infected population of large yellow croaker (*Larimichthys crocea*). *Aquaculture*, 548, 737615.
- Zhang, Z., Zhou, C., Fan, K., Zhang, L., Liu, Y., Liu, P. F. (2021). Metabolomics analysis of the effects of temperature on the growth and development of juvenile European seabass (*Dicentrarchus labrax*). *Science of the Total Environment*, 769, 145155.
- Zhao, B., Shi, W., Guo, Y., Chen, Y., Wang, H., He, J., et al. (2024). Effect of temperature on the growth, feeding performance, gonadal development, and nutritive compositions in the muscle of fry stream groupers (*Acrossocheilus fasciatus*). *Journal of the World Aquaculture Society*, 55, e13024.
- Zhao, C., Song, Y., Yan, J., Yang, Z., Wang, S., Liu, Y., et al. (2024). Multi-omics analysis revealed the dysfunction of ovary and testis induced by chronic hypoxia in *Pelteobagrus fulvidraco*. *Aquaculture*, 584, 740668.
- Zhao, C., Song, Y., Zhang, G., Zhang, K., Yin, S., Ji, J. (2024). Multi-omics analysis identifies sex-specific hepatic protein-metabolite networks in yellow catfish (*Pelteobagrus fulvidraco*) exposed to chronic hypoxia. *International Journal of Biological Macromolecules*, 268, 131892.
- Zhao, H., Chong, J., Li, D., Xia, J. (2023). Integrated multiple-omics reveals the regulatory mechanism underlying the effects of artificial feed and grass feeding on growth and muscle quality of grass carp (*Ctenopharyngodon idellus*). *Aquaculture*, 562, 738808.
- Zhao, T., Ma, A., Yang, S., Huang, Z. (2021). Integrated metabolome and transcriptome analyses revealing the effects of thermal stress on lipid metabolism in juvenile turbot (*Scophthalmus maximus*). *Journal of Thermal Biology*, 99, 102937.
- Zhao, X., Liu, P., Xia, Z., Cai, M., Tang, Q., Yang, G., et al.

- (2025). Integrated gut microbiota and multi-omics analysis revealed the growth differences of female giant freshwater prawn (*Macrobrachium rosenbergii*). *Comparative Biochemistry and Physiology Part D*, 101432.
- Zhong, L., Liu, S., Zuo, F., Geng, Y., Ouyang, P., Chen, D., et al. (2023). The IL17 signaling pathway: a potential signaling pathway mediating gill hyperplasia and inflammation under ammonia nitrogen stress was identified by multi-omics analysis. *Science of the Total Environment*, 867, 161581.
- Zhou, G., Wang, Y. S., Wang, H. J., Sun, T. L., Peng, R. Q., Li, S. J., et al. (2025). Exploring the gut microbiota and metabolome of *Lateolabrax japonicus*: a multi-omics approach. *Comparative Biochemistry and Physiology Part D*, 54, 101408.
- Zhou, H., Wang, J., Hu, M., Shen, X., Gao, R., Yan, H., et al. (2025). Physiological responses to different temperature in the liver of *Takifugu rubripes* larvae revealed by integrated transcriptomic and metabolomic analyses. *Comparative Biochemistry and Physiology Part D*, 54, 101371.
- Zhou, L., Zhao, B., Guan, N., Wang, W., Gao, Z. (2017). Plasma metabolomics profiling for fish maturation in blunt snout bream. *Metabolomics*, 13, 40. <https://doi.org/10.1007/s11306-017-1182-2>
- Zhou, Q., Chen, Y., Chen, Z., Wang, L., Ma, X., Wang, J., et al. (2022). Genomics and transcriptomics reveal new molecular mechanism of vibriosis resistance in fish. *Frontiers in Immunology*, 13, 960464.
- Zhu, A., Tan, P., Xu, D., Zhang, X., Yan, X. (2023). Proteomics and phosphoproteomics analysis identifies liver immune protein markers in large yellow croakers (*Larimichthys crocea*) fed a soybean oil-based diet. *International Journal of Biological Macromolecules*, 242, 125097.
- Zhu, M., Sumana, S. L., Abdullateef, M. M., Falayi, O. C., Shui, Y., Zhang, C., et al. (2024). CRISPR/Cas9 technology for enhancing desirable traits of fish species in aquaculture. *International Journal of Molecular Sciences*, 25, 9369.
- Zhu, Z. X., Jiang, D. L., Li, B. J., Qin, H., Meng, Z. N., Lin, H. R., et al. (2019). Differential transcriptomic and metabolomic responses in the liver of Nile tilapia (*Oreochromis niloticus*) exposed to acute ammonia. *Marine Biotechnology*, 21, 488–502.
- Ziarrusta, H., Mijangos, L., Picart-Armada, S., Irazola, M., Perera-Lluna, A., Usobiaga, A., et al. (2018). Non-targeted metabolomics reveals alterations in liver and plasma of gilt-head bream exposed to oxybenzone. *Chemosphere*, 211, 624–631.
- Zou, Y., Zhang, Y., Wu, D., Lu, Z., Xiao, J., Huang, H., et al. (2024). Multi-omics analysis revealed the differences in lipid metabolism of the gut between adult and juvenile yellowfin tuna (*Thunnus albacares*). *Frontiers in Microbiology*, 14, 1326247.