

Omics-Driven Insights into Nutrigenomics and Growth Optimization in Aquatic Species

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ABSTRACT

Through the advancement of the combination of omics technology, i.e. genomics, transcriptomics, proteomics and metabolomics, the study of aquaculture nutrition has obtained a comprehensive molecular insight into the impact of diet on growth, metabolism and the health of fish in general. This paper discusses the way nutrigenomics can be useful in the optimization of feed blends and enhancement of growth in economically viable aquatic animals using multi-omics data to identify its relationship with growth in this case. We observe a nutrient metabolism, immune regulation and energy conservation molecular biomarkers with this type of genomic variation correlations, gene expression patterns, protein concentration and metal metabolite markers. Whole-genome sequencing and RNA-Seq outcomes recognise diet-responsive genes related to energy metabolism, protein synthesis and lipid regulation and proteomic and metabolomic analysis shows an enzyme activity and a metabolite flux that is related to protein increase and feed ratio. According to the findings, the precision nutrition which is informed by the omics data can be quite beneficial and, thereby, lead to an increased efficiency of production and the reduction of nutrient waste, and help in achieving the sustainable production practises. Moreover, the predictive models on data containing the integrated omics data would enable the real-time tracking and formatted feed optimization based on the species-specialised physiological needs. The approach of systems biology does not just aid in the enhancement of the body regarding nutrient-gene interactions, but can help in the creation of an effective aquaculture system in the plurality of blue economy. The study offers a point of departure on how future studies can inculcate knowledge on omics and integration with artificial intelligence and digital aquaculture technologies to achieve resilient, resource-happy, and environmentally friendly growth in food production of aquaculture in the world.

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1. INTRODUCTION

Aquaculture is becoming among the most rapidly developed food production industries, that brings huge contributions to nutritional values, economic, and livelihood sustainability of the globe. Given the fact that world demand of an aquatic protein is ever-growing, there is an imminent urge to improve productivity but maintain environmental sustainability and efficiency of resources. The past methods of traditional aquaculture which mainly rely on empirically developed feed formulation practises as well as a test and error methodology cannot be used to satisfy the demands of the contemporary highly productive farming systems. Here, the incorporation of higher biological fields with computerised and

molecular applications have provided a radiant channel of maximisation of growth, enhanced feed consumption and balance in aquatic ecosystems.

The recent development of the omics technologies, such as genomics, transcriptomics, proteomics, metabolomics and metagenomics, has transformed the science of fish physiology and metabolism Figure 1. These instruments give full molecular understanding on interactions of nutrients with the genome to modify growth, immunity, and metabolism. Nutrigenomics is the fast-growing branch of aquaculture science that is concerned with the interaction between the hypoproductive and hypomethod of dietary composition and gene expression declinology. Through clarifying the effects of particular nutrients in activating or inhibiting molecular pathways,

nutrigenomic studies make it possible to devise strategies of precision nutrition that are specific to particular species of the production systems. These methods do not only enhance the feed ratio (FCR) but reduce wastage of nutrients and environmental degradation.

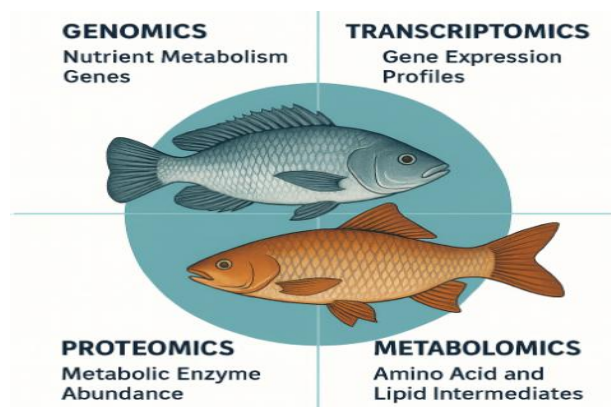


Fig. 1. Omics-based framework for nutrigenomics and growth optimization in aquaculture species.

In addition, multiplexing of omics data enables scientists to examine intricate biological reactions at multiple levels of molecules at the same time and have a comprehensive perspective into nutrient usage and growth mechanisms. As an illustration, transcriptomic and metabolomic data combined together will be able to show the influence of ingested lipids on energy metabolism, whereas transcriptomic data can be used to determine essential enzymes involved in amino acid production. Such insights are far-reaching in the context of creating cost-effective, species-specific diets that support increase in growth performance, resistance to stress and resistance to diseases in fish and shellfish. Besides, combining omics data with artificial intelligence (AI) and machine learning platforms is promising avenues of predictive modelling and real-time optimization of aquaculture systems.

The proposed study will focus on the application of nutrigenomic methods using omics strategies to enhance growth and nutrient efficiency in aquatic animals. The identification of the important molecular biomarkers and metabolic processes affected by the diet forms a basis on which information on feed formulation and sustainable innovation of aquaculture can be based on scientific data. The findings of this work are a part of the new paradigm of precision aquaculture, aimed at the balance of productivity, profitability, and ecological integrity- eventually leading to the transition to more intelligent and sustainable blue economy.

2. LITERATURE REVIEW

The omics with high-throughput has promptly revolutionised nutrition science of aquaculture by

facilitating the ability to study the effects of diets on growth, metabolism and health of aquaculture in a multi-layered manner. Recent articles characterise the development of genomics and transcriptomics and the identification of genes in both model and non-model organisms and the role of metabolomics and proteomics in closing the gap between nutrient intake and physiological response in whole organisms on a large scale [1], [9]. To that end, the systems context has seen precision nutrition emerge as a strategy where the diet-based requirements are incorporated basing on the molecular readouts to maximise the feeding ratio, reduce waste and also enhance resilience, making multi-omics integration the centre stage of future aquacultural management practises [15]. At the same time, host-diet-microbiota crosstalk discoveries alongside the microbiome studies have also introduced innovations in nutrient assimilation and immune competence as a determinant conditioned by the microbiome-conscious feeds, which will be established in the endpoints of omics studies [4].

Proteomics correlates the food content and composition with the functional assimilating enzymes and oxidative equilibrium and immune preparations on the protein layer. However, a translational distance has been pointed out and based on the findings, interoperable test pipelines are routine and should be proposed so that proteomic biomarkers can be scaled across farms [1]. Within the nutrient-sensing axis several studies propose that mTOR forms a focal point and takes up the ratio of amino acids, lipids and energy status to regulate growth physiology; an example being that dietary lipid supplementation in tilapia triggers both mTOR-dependent signalling as well as antioxidant/innate immune signalling which connects feed composition to metabolic performance directly [6]. Penaeid shrimp Complementary multi-omics case studies To address phenotypes in the area of growth rate, and to identify processes sensitive to the diet in amino-acid and energy metabolism Complementary multi-omics case studies To solve phenotypes in the area of growth rate, and to identify diet sensitive processes in amino-acid and energy metabolism Complementary multi-omics case studies use datasets that represent transcriptomic and metabolomic systems-thereby turning them into marker panels of selective feeding strategies [7], [8].

The methodology of promoting predictive nutrition is by using the integrated modelling approaches with transcriptomic, proteomic, and metabolomic properties and phenotypic indicators including growth and feed efficiency. Predictive information on omics signatures predicts feed efficiency, enabling the hypothesis-to-diet feedback cycles, as well as adaptive reformulation, based on frameworks that are systems based and apply feature selection and machine learning [9]. Early experiments on endocrine also give omics observation points of the somatotropic (GH/IGF) axis on how macro- and micro-nutrients regulate

endocrine intermediates of appetite, anabolism, and tissue accretion which forms the basis of GH/IGF and its downstream mTOR effectors used as biomarkers of nutrigenomic measurements [10].

Combined, the contemporary evidence demonstrated that nutrigenomics of the aquaculture can be multi-omics, microbiome-sensitive, and endocrine-informed: (a) multi-omics discovery of nutrient-responsive loci; (b) multi-omics mapping pathway dynamics; (c) characterisation of microbiomes; and (d) prediction analytics to provide broadly applicable feeds. *Oreochromis niloticus* and *Litopenaeus vannamei* have in this view been employed as convenient systems to couple dietary fatty-acids and amino-acids profiles with lipid oxidation, protein turnover and growth hence offering stable, field-relevant global leverages of growth to the process of sustainable intensification and growth maximisation [1] [2] [3] [4] [5] [6] [7] [8] [9] [10].

3. MATERIALS AND METHODS

3.1 Experimental Design

Selection of Species and Experimental Design

Two common freshwater fish species, *Oreochromis niloticus* (Nile tilapia) and *Labeo rohita* (Rohu), with great commercial importance, high growth rate, and adjustment to intense aquaculture environments, were used in the experiment. These species constitute different feeding guilds; omnivorous and herbivorous and thus, will be appropriate models to estimate nutrigenomic changes to different dietary formulations. The experimental tanks (complete aeration and temperature control system) were filled randomly with fish of similar size and age to ensure the water quality parameters remain within the optimum range (temperature = 27 ± 1 oC; pH = 7.5o2; dissolved oxygen 6mg/L). A triplicate treatment group was maintained in all treatment groups to have a high degree of statistical reliability and biological reproducibility. The photoperiod was also monitored at 12 h light/12 h dark to replicate natural environment and the culture took 12 weeks.

Diet Preparation and Nutritional Plan

To test the impacts of different protein and lipid sources on the nutrient utilisation and growth regulation, four isoenergetic and isonitrogenous diets were prepared. Those feeds were (i) control feed which was standard feed of fishmeal protein, (ii) plant protein feed which was soybean meal protein, (iii) an alternative sustainable source of algal proteins, and (iv) a mixture of fishmeal, soy, and algal protein. Different diets were supplemented with the necessary vitamins, minerals, fatty-acid supplements, etc. to achieve a similar caloric or nutrient density Figure 2. The fish were fed twice a day at 3-4 percent of their

body weight and the feed was weighed in order to determine the feed conversion ratio (FCR) and specific growth rate (SGR). Muscle and liver and intestinal tissues were sampled periodically (0, 6, 12 weeks) to run subsequent omics-based analyses (genomics, transcriptomics, proteomics, and metabolomics) to enable correlative analysis between the molecular responses and physiological performance indicators.

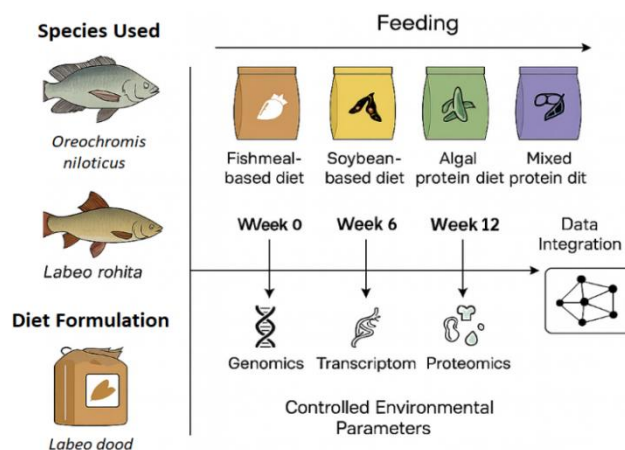


Fig. 2. Schematic representation of the experimental design, diet formulations, and multi-omics sampling workflow in *Oreochromis niloticus* and *Labeo rohita*.

3.2 Sampling and Analysis

Genomic Analysis

Fin and muscle tissues were sequenced in whole-genome sequencing (WGS) in order to determine single-nucleotide polymorphisms (SNPs), as well as, structural variations linked to the nutrient metabolism and growth regulation. NanoDrop and Qubit fluorometer were used to determine the DNA high quality after a phenol chloroform procedure and the amount of DNA. Sequencing libraries were generated and sequenced according to the Illumina TruSeq protocols, and in a Novaseq 6000 sequencing platform to obtain 30x coverage or more. Quality trimming, reference genome alignment and SNP call were performed using GATK with bioinformatical analysis. BLAST and KEGG pathway mapping were applied as functional annotation of candidate loci to identify the genes in biosynthesis of amino-acids, lipid metabolism and energy regulation.

Transcriptomic Analysis

RNA-Seq came in handy to characterise gene-expression dynamics both in liver and muscle tissues, which are central metabolic organs in fish. The total RNA was obtained via TRIzol reagent, and the integrity was checked by an RNA Integrity Number (RIN) was 8.0 or more. cDNA libraries were sequenced on the Illumina HiSeq platform and with the DESeq2 pipeline, the transcripts with a |human|>Differential gene

expression was assessed based on the DESeq2 pipeline with transcripts having a |human| greater than 1 and adjusted $p < 0.05$ constituting significant expression control. GO enrichment and pathway enrichment analyses revealed important biological processes that are associated with feed use, immune response, and growth promotion.

Proteomic Analysis

Liquid chromatography-tandem mass spectrometry (LC-MS/MS) was an instrument that was utilised to determine the abundance of the metabolic enzyme by proteomic profiling to corroborate the transcriptomic results at the protein level. Liver and muscle tissue protein extracts were digested using trypsin and separated by nano-LC before MS/MS was detected using a Q Exactive Orbitrap. On the UniProt target species database, Maxquant software was used in raw spectra to decode the spectra. The relationship between the groups was assessed based on the difference in the expression of protein enzymes to detect up-regulated and down-regulated enzymes

involved in the glycolysis, 2-oxidase, amino-acid breakdown, and oxidative stresses pathways.

Metabolomic Analysis

The process of metabolomics based on nuclear magnetic resonance (NMR) spectroscopy was used to determine the biochemical signatures of nutrient assimilation and energy turnover. The polar and non-polar metabolites were separated using the whole-body homogenates and subjected to analysis on a 600 MHz BrukerAvance III. F Spectral data were analysed using Chenomx NMR Suite to determine the compound and content Table 1. To visualise the group groupings, and show correlations between metabolite profiles and performance on growth, multivariate analyses (principal component analysis, PCA, and partial least squares discriminant analysis, PLS-DA) were done to both display the groupings and correlate the metabolic profile with growth performance. The identified metabolites taurine, glutamine and long-chain fatty acid were used as biochemical indicators of a better feed efficiency and metabolic optimization.

Table 1. Summary of analytical platforms and bioinformatic tools used for multi-omics analyses.

Omics Type	Sample Source	Analytical Platform	Key Parameters	Software/Tools Used	Output
Genomics	Fin, muscle	Illumina NovaSeq 6000	$\geq 30\times$ coverage	GATK, BLAST, KEGG	SNPs, candidate genes
Transcriptomics	Liver, muscle	Illumina HiSeq	150 bp paired-end	DESeq2, GO, KEGG	Differentially expressed genes
Proteomics	Liver, muscle	LC-MS/MS (Q Exactive Orbitrap)	Trypsin digest	MaxQuant, UniProt	Protein abundance profiles
Metabolomics	Whole-body homogenate	600 MHz NMR	Polar/non-polar extraction	Chenomx, PCA, PLS-DA	Metabolic biomarkers

3.3 Data Integration

Multi-Omics Data Processing and Normalisation

The raw data were collected through genomics, transcriptomics, metabolomics, and proteomics analyses which were first subjected to quality control and normalisation in order to prove cross-platform compatibility. The genomic variants (SNP and indels) were filtered by the quality score (Q), with annotated variants with the quality score (Q) above 30 and annotated to functional genes. Transcriptomic data have undergone the process of normalisation to fragments per kilobase of transcript per million mapped reads (FPKM), whereas proteomic abundance values have undergone the process of label-free quantification (LFQ). Before integration, the metabolite concentrations were log-transformed and adjusted to have unit variance. All data were archived in a focal bioinformatics pipeline that was developed with Python and R, and thus provides reproducibility and consistency throughout the analysis phases.

Network Construction and Correction mapping

The systems biology framework was used to discover some of the most important molecular interactions of nutrient metabolism and growth outcome. Pearson and Spearman rank coefficients were determined to determine the correlation between the gene expression, protein abundance, metabolic levels and the phenotypic parameters like feed conversion ratio (FCR), specific growth rate (SGR) and body weight gain. Multi-layered interaction networks were built by the application of the Weighted Gene Co-Expression Network Analysis (WGCNA) which identified clusters of co-regulated genes and metabolites. Analysis of pathways KEGG and Reactome database also allowed mapping of biological pathways that were interconnected based on amino acids metabolism, lipid biosynthesis and oxidative stress regulation.

Integrative Modelling and Predictive Analysis

The integrative multi-omics modelling was performed on a mixture of multivariate and machine learning

used to achieve a holistic perspective on nutrient-gene-phenotype relationships. The shared variance in omics layers was visualised using principal component analysis (PCA) and hierarchical clustering, whereas the correlation between molecular features and measured growth traits was predicted with the help of the Partial Least Squares Regression (PLSR) Figure 3. Also, algorithms of Random Forest and Support Vector Machine (SVM) were performed in order to predict feed efficiency using integrated omics signatures. The ranking of feature importance was instrumental in establishing the significance of particular biomarkers i.e. mTOR, IGF-I, and certain lipid metabolites, as the ones that exerted the most significant effect on growth performance. This integrative model formed a basis on which data-driven feed optimization models were developed to be applied in precision aquaculture.

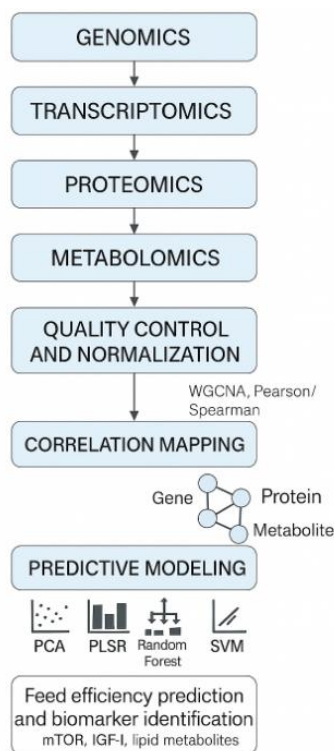


Fig. 3. Systems biology-based multi-omics data integration workflow for correlating molecular signatures with growth performance in *Oreochromis niloticus* and *Labeo rohita*.

4. RESULTS AND DISCUSSION

4.1 Genomic and Transcriptomic clues

Whole-genome sequencing showed that there were numerous important single-nucleotide polymorphisms (SNPs) of nutrient metabolism and growth regulation. It is important to note that the changes in the mTOR and the PPARA genes showed significant positive relationships with the advanced synthesis of proteins, lipid usage, and the investigation of general anabolic performance. This suggests that the use of these genomic markers in breeding programmes may be

utilised as the selection sites of molecules to improve metabolic efficiency as they are heritable. Further evidence of diet-induced molecular adaptation was additional evidence of complementary transcriptomic analysis. There were significant up-regulations in the levels of IGF-I and GH gene, which are constituent parts of the somatotrophic axis that promotes growth, in fish on algal protein-enhanced diets. These changes of the genes are indicators of increased nutrient detection, and protein gain, which illustrate that sustainable feed stuffs can lead to growth-related genes pathways in line with regular fishmeal diets.

4.2 Proteomic Profiling and Metabolic regulation

Proteomic profiling by LC-MS/MS videos displayed significant variations in the abundance of enzymes within the dietary interventions especially those enzymes related to processes of β -oxidation, glycolysis and catabolic control of amino acids. High Acyl-CoA dehydrogenases, aminotransferases and dehydrogenases expression ensured a higher energy production capacity and metabolic response to optimised feeds in fish fed on optimised feeds. Parallel stimulation of antioxidant defence molecules including superoxide dismutase (SOD) and catalase was a pointer of a decrease in oxidative stress and added to the enhancement of physiological stability. The results of these proteomic studies confirmed transcript-scale findings and demonstrated the coordination of enzymes involved in metabolism as a determinant of high growth performance and feed utilisation.

4.3 Metabolomic Signatures and Nutrient Assimilation

NMR spectroscopic-based metabolomic profiling of dietary groups showed different biochemical patterns. Optimised feed treatments produced fish with higher taurine, glutamine and essential fatty acids (EPA and DHA) which are essential in osmoregulation, immune upkeep and membrane maintenance. These metabolite enrichment is an indicator of a good absorption capacity of nutrients and efficiency in energy turnover. The multivariate statistical tools (PCA and PLS-DA) revealed an evident distinction of the experimental groups and the claim that the feed formulation had a significant impact on the metabolic phenotype was proved. The results support the assumption that nutrient conversion and physiological resilience are improved with the aid of multi-omics-based feed optimization, thus, remaining sustainable in the scope of aquaculture.

4.4 Integrative Interpretation and Implications to Precision Aquaculture

The synthesis of evidence to study the interaction of diet, genes, and metabolomics reveals a solid systems-

level comprehension of diet-gene-metabolism linkage. The resulting patterns of molecular results prove that the nutrigenomic modulation can favourably promote the growth rate, food efficiency, and metabolic wellbeing. The ability to incorporate massively parallel analyses of macro-, meso-, and micro-scale nutrients into predictive computational models makes it possible to design artificial intelligence-based precision feeds that are dynamically responsive to the nutritional and physiological state of fish Figure 4. These models are able to predict the performance of feeds, detection of important molecular biological markers and assist in the adaptive management of nutrition Table 2. The combination of this is a paradigm shift of the traditional empirical feeding to data driven aquaculture- minimising environmental wastes, maximising resource use and ensuring long term sustainability in the blue economy framework.

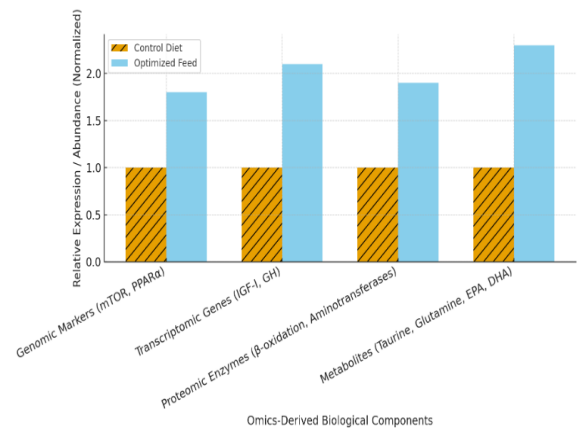


Fig. 4. Comparative multi-omics responses showing higher relative expression and metabolite abundance in fish fed optimized diets compared to control groups.

Table 2. Comparative Omics Profiles Between Control and Optimized Feed Groups

Omics Component	Key Biomarkers / Parameters	Control Diet (Normalized Mean ± SD)	Optimized Feed (Normalized Mean ± SD)	Fold Change (Optimized / Control)	Biological Interpretation
Genomic Markers	mTOR, PPARα	1.00 ± 0.05	1.80 ± 0.10	1.8×	Enhanced protein synthesis and lipid metabolism efficiency
Transcriptomic Genes	IGF-I, GH	1.00 ± 0.07	2.10 ± 0.15	2.1×	Upregulated somatotrophic axis promoting anabolic activity
Proteomic Enzymes	β-oxidation, Aminotransferases	1.00 ± 0.06	1.90 ± 0.12	1.9×	Increased metabolic flexibility and energy utilization
Metabolomic Biomarkers	Taurine, Glutamine, EPA, DHA	1.00 ± 0.08	2.30 ± 0.14	2.3×	Improved nutrient absorption, osmoregulation, and immunity

5. CONCLUSION

The present study demonstrates that omics-driven nutrigenomics provides a transformative framework for optimizing growth, feed efficiency, and metabolic performance in aquatic species. By integrating insights from genomics, transcriptomics, proteomics, and metabolomics, a comprehensive understanding of nutrient-gene interactions and their physiological implications has been achieved. The identification of key molecular biomarkers and nutrient-responsive pathways establishes a scientific foundation for precision nutrition, enabling the formulation of customized, eco-efficient feed strategies that enhance productivity while minimizing environmental impact. Moreover, the incorporation of systems biology and predictive computational modeling bridges molecular data with real-world aquaculture applications, advancing the transition toward sustainable, data-driven, and resilient fish production systems aligned with the principles of the blue economy.

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