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Research Paper

Molecular Nutrition of Aquatic Animals: Mechanistic Insights, Technological Advances, and Aquaculture Applications

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Abstract
Population expansion and changing dietary habits are driving an increase in global demand for aquatic protein. A critical area for developing a sustainable aquaculture is molecular nutrition, which analyzes the relationships between nutrients and gene expression at the molecular level. This article summarizes the key molecular pathways of nutrient consumption in aquatic animals, including the metabolism of proteins, lipids, carbohydrates, and micronutrients. It also looks at the technological advancements, like gene editing tools and omics methods, that have transformed this field of study. The complex relationships between nutrition and environmental stressors are highlighted, as species-specific advancements in finfish, crustaceans, and mollusks. The review also covers the real-world uses of molecular nutrition in sustainable aquaculture methods, genetic enhancement, and precision feed formulation. Lastly, it highlights the necessity of interdisciplinary research to address global aquaculture concerns and ensure food security by identifying key obstacles and opportunities.

Keywords: *Molecular nutrition, aquaculture, nutrient metabolism, gene editing (or Omics), sustainable aquaculture.*

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I. Introduction

Aquaculture has emerged as one of the fastest-growing food production industries in the world and a vital component of global food security [1]. Aquaculture currently produces more than 52% of the world's fish for human consumption [2]. This percentage is expected to climb further when capture fisheries decline [2]. By 2050, there will be approximately 9.7 billion people on the planet, necessitating a 25–70% increase in aquatic food supply to meet nutritional demand [3]. Aquaculture systems are under massive pressure to grow sustainably in the face of limited natural resources, climate change, disease outbreaks, and environmental deterioration [4]. Efficiency advancements have been halted by traditional nutrition research, which has concentrated on feed conversion ratios and growth performance [5].

Molecular nutrition has emerged as a result of this change in the frontier to the molecular level [6]. Molecular nutrition offers a mechanistic understanding that goes beyond empirical observation by explaining how nutrients function as signaling molecules to control physiological processes [7]. It makes it possible to precisely formulate feeds that match an animal's genetic and metabolic pathways, improving disease resistance, maximizing nutrient use, and minimizing environmental waste [8]. For example, studies using transcriptomics have found important genes in salmon that are involved in the metabolism of omega-3 fatty acids, enabling the creation of plant-based diets that maintain high fillet nutritional quality [9]. The complex relationships between dietary nutrients and an organism's gene expression, protein function, and metabolic pathways are studied in this review.

Examining the fundamental molecular processes controlling nutrient utilization in finfish, crustaceans, and mollusks, this review summarizes the swift advancements in this revolutionary concept. It explains the complex relationship between nutrition and environmental stressors, highlights species-specific advancements, and analyzes the technological revolution driven by omics and gene-editing techniques. Lastly, it critically evaluates how this knowledge is translated into useful applications for genetic selection, precision feeding, and sustainable aquaculture. It also outlines the ongoing difficulties and future research directions that are crucial for ensuring a robust and fruitful future for the blue economy.

II. Core Molecular Mechanisms of Nutrient Utilization

2.1 Carbohydrate Metabolism

Aquatic animals utilize carbohydrates as a major source of energy, although different species use them in different ways [10]. Compared to carnivorous species like salmon and trout, herbivorous and omnivorous species like tilapia and carp have a greater potential to use carbohydrates [11]. This discrepancy is explained by changes in the expression and activity of important enzymes involved in the metabolism of carbohydrates, including glucose-6-phosphatase, hexokinase, and glucokinase [12].

The uptake of glucose by cells is mostly dependent on glucose transporters (GLUTs) [13]. GLUT1, GLUT2, GLUT4, and GLUT5 are among the GLUT isoforms that have been found in fish [14]. GLUT2 is mostly expressed in the liver and pancreas and is involved in glucose sensing and regulation, whereas GLUT1 is widely expressed and is in charge of basal glucose uptake [15]. GLUT4 induces glucose absorption in response to insulin and is expressed in muscle and adipose tissue. It is insulin-dependent [16]. The gut expresses the fructose transporter GLUT5 [17].

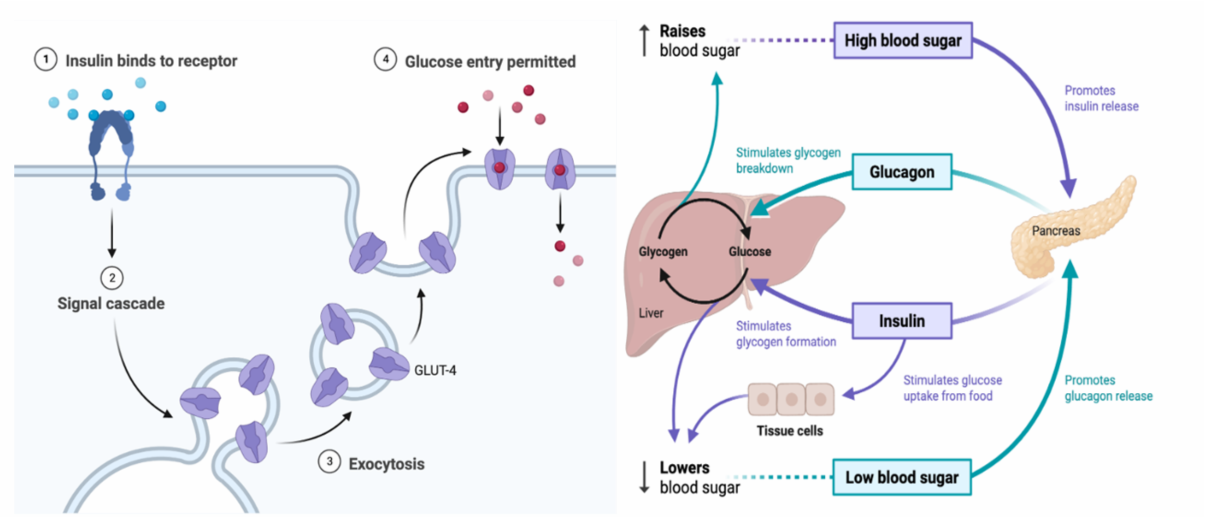


Figure 1: illustrates the key mechanistic steps in insulin signaling pathways, insulin binding signal cascade, exocytosis, glucose entry into the hepatocyte, and general blood glucose regulation by the insulin

Carbohydrate metabolism largely depends on insulin signaling pathways [18]. Increased glucose uptake and the translocation of GLUT4 to the cell membrane result from the binding of insulin to its receptor on the cell surface, which sets off a series of intracellular signaling cascades [19]. Furthermore, insulin maintains glucose homeostasis by inducing the synthesis of glycogen and preventing the production of gluconeogenesis [20].

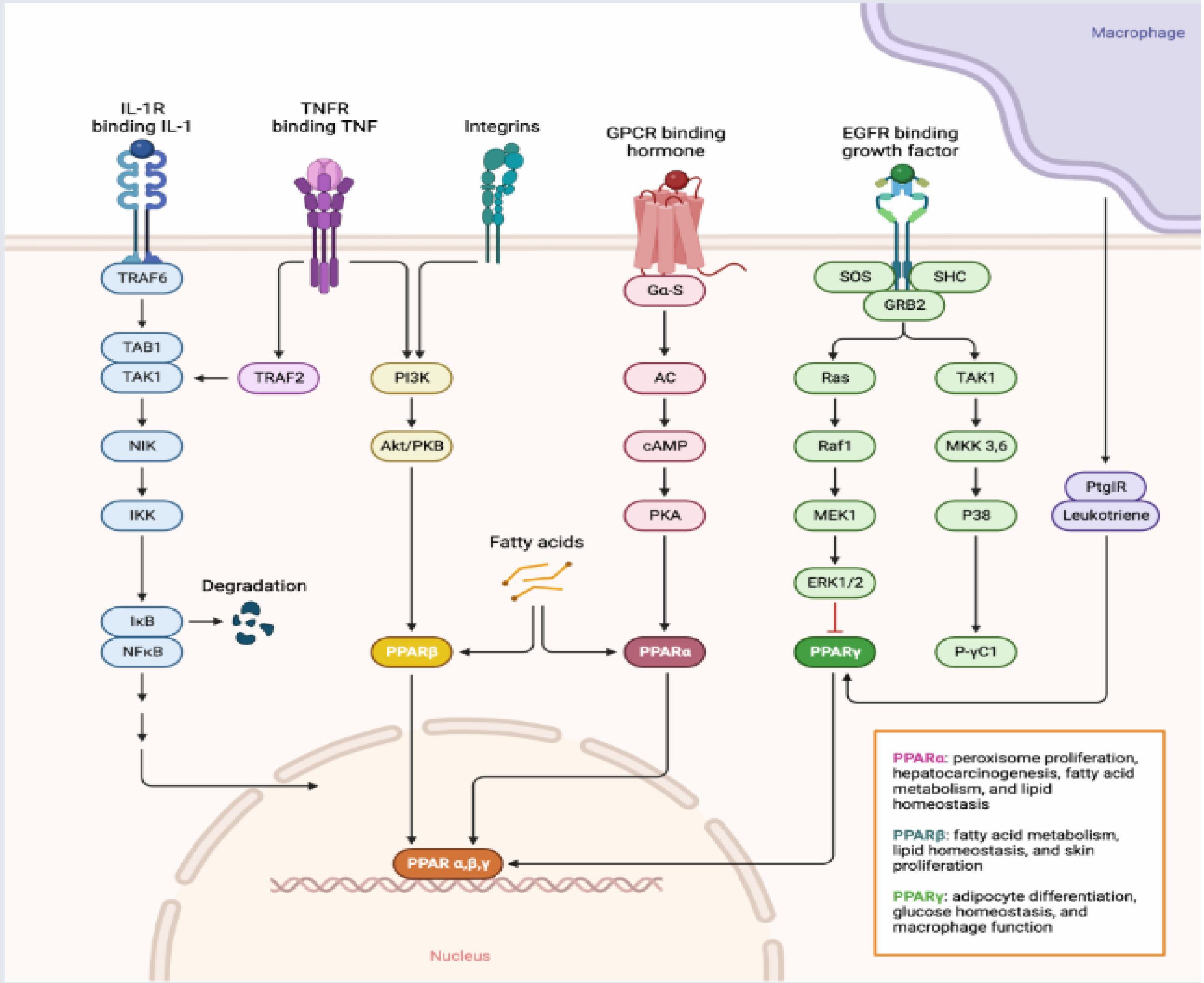
2.2 Lipid and Fatty Acid Regulation

Lipids are vital for aquatic organisms because they provide energy, form a structural component of cell membranes, and act as building blocks for hormones and signaling chemicals [21]. A complicated web of genes and signaling pathways governs the absorption, synthesis, storage, and oxidation of lipids [22].

The key enzymes in the production of polyunsaturated fatty acids (PUFAs) are fatty acid desaturases (FADS) [23]. PUFAs, such as eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), are necessary for development, reproduction, and immunological function in aquatic species [24]. FADS genes encode enzymes that catalyze the desaturation of fatty acids, turning saturated and monounsaturated fatty acids into PUFAs [25].

Nuclear receptors known as peroxisome proliferator-activated receptors (PPARs) control energy homeostasis and lipid metabolism [26]. PPARs bind to particular DNA sequences and trigger the transcription of genes related to the intake, oxidation, and storage of fatty acids [27]. Three PPAR isoforms have been found in fish: PPARα, PPARβ/δ, and PPARγ [28]. PPARα is predominantly expressed in the liver and plays a role in fatty acid oxidation, whereas PPARβ/δ is expressed in several organs and regulates energy metabolism [29]. Adipose tissue expresses PPARγ, which is important in lipid storage and adipocyte development [30].

Figure 2: Illustrating PPAR Signaling Pathway



2.3 Protein and Amino Acid Metabolism

Proteins are particularly important for the growth, development, and upkeep of bodily tissues in aquatic animals [31]. Amino acids, the building blocks of proteins, are also involved in many metabolic activities, such as neurotransmitter synthesis, energy production, and immunological function [32].

The uptake of amino acids into cells is accomplished by amino acid transporters (SLCs) [33]. Numerous SLC families, including SLC1, SLC6, SLC7, and SLC38, have been found in aquatic animals [34]. These transporters are expressed in a variety of organs, including the colon, liver, and muscle, and they have distinct substrate specificities [35].

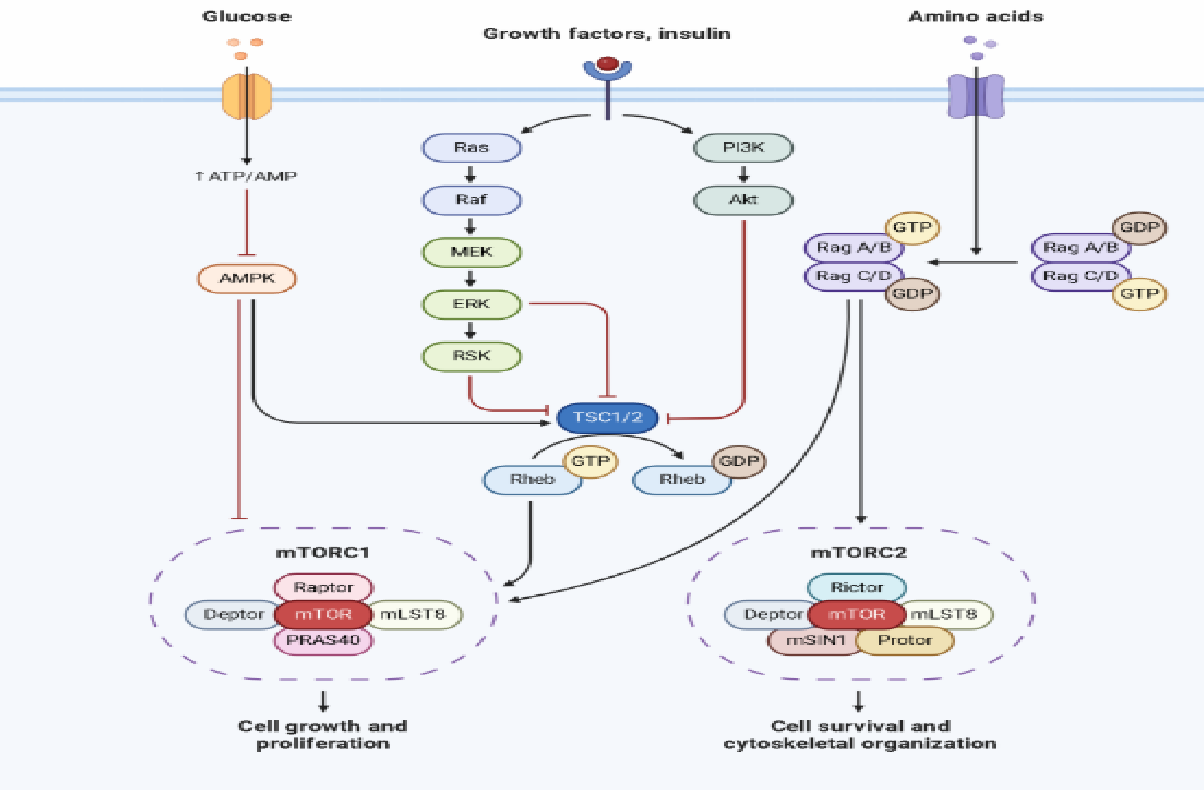


Figure 3: Illustrating mTOR Signaling Pathways

Protein synthesis and cell proliferation are crucially regulated by the mammalian target of rapamycin (mTOR) signaling pathway [36]. mTOR is a serine/threonine kinase that regulates cell division and metabolism by combining signals from growth factors, nutrients, and energy levels [37]. Amino acids, especially leucine, trigger mTOR signaling in aquatic animals, which phosphorylates downstream targets such as ribosomal protein S6 kinase (S6K) and eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1) to stimulate protein synthesis [38].

2.4 Micronutrient Homeostasis

Aquatic animals' regular physiological processes depend on micronutrients, such as vitamins and minerals [39]. They are essential for immunological response, antioxidant protection, and enzyme catalysis [40].

Growth, reproduction, and immune system function all depend on vitamins like vitamin C and vitamin D [41]. While vitamin D controls the metabolism of calcium and phosphorus and is involved in immunological function, vitamin C is a potent antioxidant that shields cells from oxidative damage [42]. Different types of aquatic animals use and synthesize vitamins differently [43]. For instance, whereas certain fish species need vitamin C in their diet, others can manufacture it [44].

Minerals, including iron, zinc, and selenium, are also essential for aquatic creatures [39]. While selenium is a part of antioxidant enzymes like glutathione peroxidase, zinc is involved in DNA synthesis, immunological function, and enzyme catalysis [45]. Energy metabolism and oxygen transport depend on iron [46]. Many transporters and proteins, including metallothioneins, which bind to heavy metals and prevent their toxicity, control the intake and homeostasis of minerals [47].

III. Technological Drivers of Molecular Nutrition Research

3.1 Omics Approaches

Transcriptomics, proteomics, and metabolomics are examples of omics technologies that have transformed molecular nutrition research by offering a thorough understanding of gene expression, protein abundance, and metabolite profiles in response to dietary nutrients [48].

The study of RNA expression levels, or transcriptomics, has been harnessed extensively to find genes related to physiological reactions and nutritional metabolism [6]. Researchers have been able to analyze the transcriptomes of aquatic species under various feeding situations. The likes of RNA-seq are a high-throughput sequencing technique [49]. For instance, RNA-seq research has found genes related to immunological function in shrimp, lipid metabolism in salmon, and carbohydrate metabolism in tilapia [50].

Proteomics offers insights into the functional roles of proteins in food metabolism by analyzing protein abundance and post-translational modifications [51]. Proteins involved in nutrition absorption, metabolism, and signaling in aquatic animals have been identified by proteomics based on mass spectrometry [52]. For instance, proteomics research has found proteins involved in crab protein synthesis and fish lipid transfer [53].

The study of metabolite profiles, or metabolomics, gives an overview of an organism's metabolic condition [54]. Metabolomics based on mass spectrometry and nuclear magnetic resonance (NMR) has been utilized to identify compounds involved in aquatic animal physiological responses and nutritional metabolism [55]. Metabolomics research, for instance, has revealed metabolites related to fish energy metabolism and mollusk amino acid metabolism [56].

A systems-level understanding of nutrition, metabolism, and physiological responses is provided by multi-omics integration, which integrates data from transcriptomics, proteomics, and metabolomics [57]. Researchers can find important regulatory networks and pathways related to nutrient use by combining this data. For instance, multi-omics research has revealed pathways related to immunological function in shrimp and lipid metabolism in salmon [58].

3.2 Functional Validation

Gene editing tools, such as CRISPR-Cas9 and RNA interference (RNAi), have enabled researchers to validate the functional roles of genes involved in nutrient metabolism (Salum et al., 2026). CRISPR-Cas9 is a powerful gene editing tool that allows for precise modification of the gene (S.-W. Wang et al., 2022). In aquatic animals, CRISPR-Cas9 has been used to knock out genes involved in carbohydrate metabolism, lipid metabolism, and immune function (J. Wen et al., n.d.). For example, knockout of the glucokinase gene in zebrafish resulted in impaired glucose metabolism, while knockout of the FADS gene in salmon reduced the synthesis of PUFAs (Xi et al., 2023)

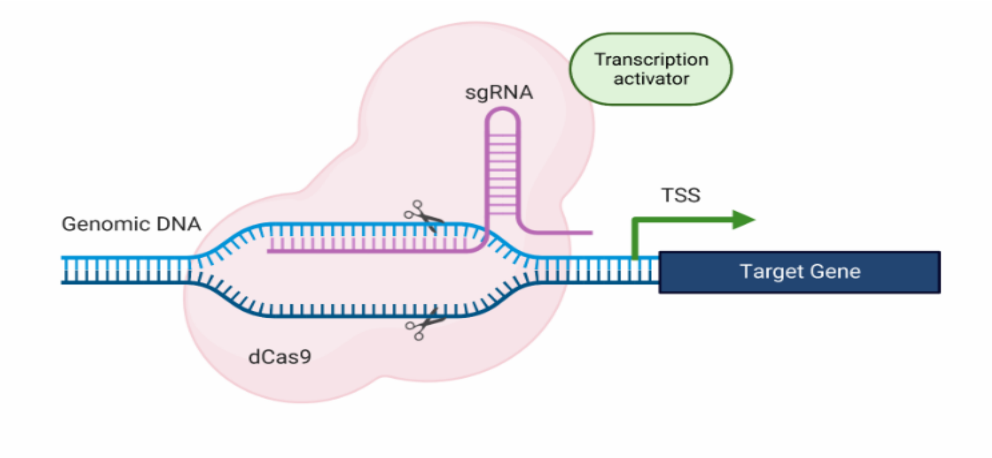


Figure 4: Showing CRISPR-mediated Transcriptional activation

RNAi is a tool that uses small interfering RNAs (siRNAs) to silence gene expression [59]. In aquatic animals, RNAi has been used to knock down genes involved in nutrient metabolism and physiological responses [60]. For example, knockdown of the mTOR gene in shrimp reduced protein synthesis and growth, while knockdown of the PPARγ gene in fish reduced lipid storage [61].

Evaluation Metric	CRISPR/Cas9 Mediated Knockout	RNA Interference (RNAi) Knockdown
Primary Level of Action	**Genomic DNA:** Permanently disrupts or deletes the target gene sequence.	**Post-Transcriptional RNA:** Degrades or blocks target mRNA before translation.
Phenotypic Stability	Permanent, irreversible, and completely heritable across generations.	Transient, temporary, and reversible as the injected RNAi molecules degrade.
Success in Essential Genes	Can result in lethal phenotypes if the nutrient pathway is critical for early larval survival.	Ideal for essential genes, allowing researchers to partially suppress a pathway without killing the animal.
Nutritional Research Utility	Best for creating permanent knockout lines to study absolute metabolic requirements or developing elite aquaculture strains.	Highly efficient for short-term feeding trials, nutrient-switch challenges, and rapid screen protocols.

Table 1: Targeted Gene Editing and Knockdown Applications in Aquatic Nutrition

3.3 Bioinformatics Tools

The vast volumes of data produced by omics technology are analyzed and interpreted using bioinformatics techniques [62]. Aquatic animal genomic, transcriptomic, and proteomic data are accessible through databases like the Aquaculture Genome Database (AGD) and Fish Base [49]. Researchers can compare gene sequences, find orthologs, and examine patterns of gene expression using these databases [63].

Nutrient-gene interactions have been predicted, and important regulatory genes have been identified using machine learning algorithms like random forests and support vector machines [64]. For instance, machine learning models have been created to predict how dietary ingredients affect fish gene expression and to pinpoint genes related to shrimp feed efficiency [6].

The process of identifying genetic areas linked to quantitative features, like growth, feed conversion ratio, and nutrient utilization, is known as quantitative trait locus (QTL) mapping [65]. QTL mapping has been applied in aquatic animals to find genetic areas linked to lipid metabolism in shrimp, growth in salmon, and feed conversion ratio in tilapia [66].

IV. Species-Specific Advances

4.1 Finfish

Finfish account for more than 80% of the world's aquaculture production, making them the most commonly farmed aquatic creatures [67]. Understanding the mechanisms of nutrient use and creating plans to increase feed efficiency and growth have been the main goals of finfish molecular nutrition research [68].

Zebrafish (*Danio rerio*) are a model species for molecular nutrition research because of their tiny size, quick generation period, and well-characterized genome [69]. Zebrafish research has uncovered the molecular processes underlying the metabolism of proteins, lipids, and carbohydrates [70]. For instance, zebrafish research has revealed genes related to the absorption and metabolism of glucose and demonstrated that insulin signaling is essential for maintaining glucose homeostasis [71].

Molecular nutrition research has also focused on commercial finfish species such as grass carps (*Ctenopharyngodon idella*), catfish (*Ictalurus punctatus*), tilapia (*Oreochromis niloticus*), and Atlantic salmon (*Salmo salar*) [72]. Grass carp is a key component of freshwater aquaculture, and the most widely farmed finfish species worldwide by volume [73]. The focus of molecular nutrition research in grass carp has been on clarifying the processes behind its herbivorous dietary adaptation, which include the control of pathways for the consumption of fiber and carbohydrates [74]. While research on the transcription factor that mediates the stimulatory effect of glucose on glycolytic and lipogenic gene expression (ChREBP) and a transcription factor of the basic helix-loop-helix leucine zipper family that primarily mediates insulin action on hepatic lipogenic gene expression (SREBP1c) signaling axes, has shed light on how dietary starch levels affect hepatic fat deposition, transcriptome and proteome investigations have discovered important enzymes involved in cellulose digestion and glucose tolerance [75]. It has been revealed that treatments using functional amino acids, particularly methionine and lysine, reduce excessive lipogenesis and promote intestinal health [76]. The creation of inexpensive, high-fiber feeds that maximize growth performance while maintaining metabolic balance in this globally relevant species is supported by these molecular discoveries. Research has concentrated on PUFA production and lipid metabolism in Atlantic salmon [77]. To increase the PUFA content of salmon fillets, researchers have identified genes related to fatty acid desaturation [77]. Research on tilapia has concentrated on feed efficiency and the metabolism of carbohydrates [78]. Researchers have created low-carb diets that increase feed efficiency and growth by identifying genes related to glucose uptake and metabolism [79]. Recent studies have centered on the immune system and protein metabolism in catfish [80]. Scientists have discovered genes related to protein production and created diets that improve immunity and resilience to illness [81].

4.2 Crustaceans

Crustaceans like crabs and shrimp are particularly significant aquaculture species in Asia [82]. Understanding the mechanisms of nutrient utilization during molting and creating plans to enhance growth and disease resistance have been the main goals of molecular nutrition research in crustaceans [83].

The most widely farmed crustaceans are shrimp, including the Pacific white shrimp (*Litopenaeus vannamei*) [84]. Nutrient allocation during molting is crucial for growth and survival, according to studies on shrimp [85]. Shrimp need a lot of energy and protein to create new exoskeletons during molting [48]. Scientists have discovered genes related to energy metabolism and protein synthesis during molting, and they have created diets that enhance growth and nutrient usage [48].

Important aquaculture species include crabs, such as the mud crab (*Scylla paramamosain*). Research on crabs has concentrated on immunological response and lipid metabolism [86]. Studies have also demonstrated that dietary lipids are crucial for regulating immune function and have identified genes involved in lipid transport and storage [87]. For instance, it has been demonstrated that when PUFA supplements are administered to the crabs, improves their immunity and resistance to illness [88].

4.3 Mollusks

Mollusks, including mussels and oysters, are significant aquaculture species, especially in North America and Europe [89]. Understanding how nutrients are used in response to environmental stressors and creating plans to enhance development and survival have been the main goals of molecular nutrition research in mollusks [90].

Filter feeders, like the Pacific oyster (*Crassostrea gigas*), get their nourishment from phytoplankton [91]. Recent studies on oysters have demonstrated a close relationship between food metabolism and environmental variables such as temperature, salinity, and dissolved oxygen [92]. Researchers have discovered genes related to the intake and metabolism of nutrients, and they have demonstrated that oysters may adjust their gene expression in response to environmental changes [90].

Mussels that are filter feeders and depend on phytoplankton for sustenance include the blue mussel (*Mytilus edulis*) [93]. The mechanics of biomineralization, the process by which mussels create their shells, have been the subject of several studies [94]. Researchers have discovered genes related to biomineralization and demonstrated the critical function that dietary minerals like phosphorus and calcium play in shell development [95].

V. Nutrient-Environment Interactions

5.1 Climate Stress

Aquaculture is seriously threatened by climate change since it can alter the temperature, salinity, and dissolved oxygen of the water [96]. These alterations may have an impact on aquatic species' physiological reactions and nutritional metabolism [97].

Temperature is one of the most important environmental factors affecting nutrient metabolism in aquatic animals [98]. Temperature changes can alter the expression and activity of enzymes involved in nutrient metabolism, thereby affecting nutrient utilization [80]. For example, high temperatures can increase the metabolic rate of fish, leading to increased energy demand and reduced feed efficiency [22]. Low temperatures can reduce the activity of digestive enzymes, leading to reduced nutrient uptake and growth [80].

Another crucial environmental stressor that has an impact on aquaculture is hypoxia, or low dissolved oxygen levels [99]. Because hypoxia inhibits the action of enzymes involved in energy synthesis, it can decrease nutritional absorption and metabolism [100]. Hypoxia can activate hypoxia-inducible factors (HIFs) in fish, which control the expression of genes related to energy metabolism and oxygen transport [101].

5.2 Pollutant Exposure

Pollutants in aquatic species, including pesticides, heavy metals, and microplastics, can build up and impair physiological reactions and nutrient metabolism [102].

Heavy metals such as lead, cadmium, and mercury have the potential to attach to and hinder the action of proteins and enzymes involved in the metabolism of nutrients [103]. Exposure to heavy metals can impair fish metabolism and nutrient intake, which can slow growth and lower survival [104].

Microplastics are tiny plastic particles that are found in large quantities in aquatic environments [105]. Aquatic creatures may consume them and allow them to build up in their tissues [106]. By decreasing food absorption and changing the gut microbiota, microplastics can have an impact on nutritional metabolism [107]. Fish exposed to microplastics may have immunological suppression, inflammation, and decreased growth [108].

Pesticides like carbamates and organophosphates can inhibit the neurotransmission-related enzyme acetylcholinesterase [109]. By decreasing feed intake and changing the activity of digestive enzymes, pesticide exposure in aquatic animals can impact nutrient metabolism [102].

5.3 Immune-Nutrient Crosstalk

Nutrition plays a vital role in regulating immunological function within aquatic species [110]. Deficits in specific nutrients, like vitamins, minerals, and amino acids, can weaken the immune system and make a person more vulnerable to illness [111].

Dietary supplements called probiotics and prebiotics can improve immune function by changing the gut microbiome [112]. Prebiotics are indigestible food components that encourage the growth of good bacteria in the stomach, whereas probiotics are living microorganisms that boost the host's health [113]. Probiotics and prebiotics have been demonstrated to boost immunity, improve nutrient utilization, and lower disease incidence in aquatic species[114].

Signaling mechanisms, including nuclear factor-kappa B (NF-κB) and mitogen-activated protein kinase (MAPK), also control nutrient-mediated immune activity [115]. These pathways control the expression of immune response-related genes and are triggered by immunological stimuli [116]. Dietary elements, including vitamins and polyunsaturated fats (PUFAs), can improve immunological function and alter these signaling pathways in aquatic animals [117].

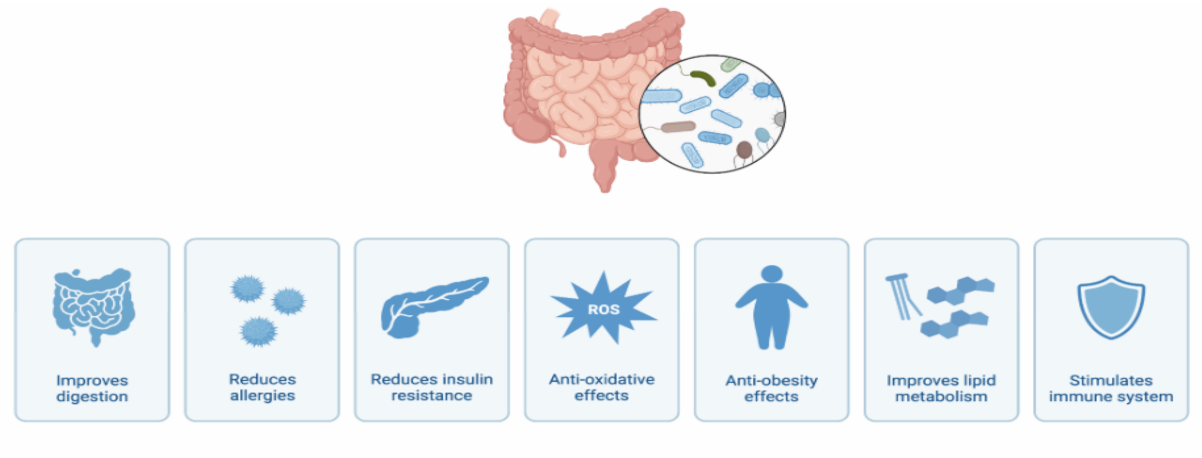


Figure 5: Illustrate the health benefits of Probiotics in fish

VI. Aquaculture Applications

6.1 Precision Feed Formulation

The process of developing a diet specifically designed to meet the nutritional needs of aquatic animals is known as precision feed formulation [118]. Researchers can enhance feed efficiency, growth, and health by upgrading dietary nutrient composition using molecular data [8].

For instance, scientists have identified genes related to lipid metabolism in Atlantic salmon using transcriptome data [119]. They have improved the PUFA content of salmon fillets and lowered the risk of fatty liver disease by creating diets that are high in PUFAs and low in saturated fats, based on recent research [9]. Researchers have identified proteins involved in the metabolism of carbohydrates in tilapia by using proteomic data [120]. They have created low-carb diets that increase feed efficiency and growth based on this research.

6.2 Genetic Improvement

Selecting individuals with desired characteristics, such as a fast growth rate, feed conversion ratio, and disease resistance, is known as genetic improvement in aquaculture [121]. Single-nucleotide polymorphisms (SNPs) are one type of molecular marker that can be used to identify individuals with these qualities and speed up the breeding process [122].

Molecular markers are used in the marker-assisted selection (MAS) method to choose aquatic species that possess desired characteristics [123]. MAS has been applied to aquatic species to select for disease resistance in shrimp, growth in salmon, and feed conversion ratio in tilapia [124]. A more sophisticated method called genomic selection predicts an individual's breeding value using genome-wide markers [125].

6.3 Sustainability

Sustainable aquaculture is the production of aquatic animals in a method that reduces their negative effects on the environment and guarantees the industry's long-term survival [126]. Molecular feeding can support sustainable aquaculture by decreasing the need for fishmeal and fish oil, increasing nutrient uptake, and lowering waste generation [127].

The production of fishmeal and fish oil, which are important parts of aquaculture feeds, is not sustainable because of overfishing [128]. Alternative protein and lipid sources that can take the place of fishmeal and fish oil in aquaculture diets include plant proteins, insect meals, and algal oils, according to research on molecular nutrition [129]. For instance, scientists have created diets for salmon that are low in fishmeal and high in plant proteins, which lessen aquaculture's negative environmental effects while increasing feed efficiency [130].

Another crucial component of sustainable aquaculture is the recycling of nutrients [131]. Researchers can create methods for recycling nutrients from waste materials like excrement and uneaten feed by comprehending the metabolic pathways of aquatic organisms [132]. For instance, waste products from fish farms are utilized in integrated multi-trophic aquaculture (IMTA) to fertilize seaweed and shellfish farms, which supply the fish with food [133].

Metabolic Category	Target Gene(s)	Key Species Mentioned	Molecular Tool Used	Functional Role / Phenotypic Outcome
Carbohydrate Metabolism	Glucokinase (*gck*)	Zebrafish (*Danio rerio*)	CRISPR/Cas9	Regulates glucose phosphorylation; knockout leads to severe glucose intolerance and impaired postprandial glucose clearance.
	Glucose-6-phosphatase (*g6pc*)	Rainbow Trout / Common Carp	RNAi (Knockdown)	Controls gluconeogenesis; silencing reduces endogenous glucose production, highlighting its role in the "glucose-intolerant" nature of carnivorous fish.
Lipid Metabolism	Fatty Acid Desaturase (*fads2*)	Atlantic Salmon (*Salmo salar*)	CRISPR/Cas9	Catalyzes the synthesis of long-chain polyunsaturated fatty acids (LC-PUFAs); knockout drastically reduces tissue EPA and DHA levels.
	Carnitine Palmitoyltransferase 1 (*cpt1*)	Nile Tilapia / Channel Catfish	CRISPR/Cas9 & RNAi	Controls mitochondrial β-oxidation of fatty acids; disruption alters lipid accumulation patterns in the liver and muscle tissues.
Protein & Amino Acid Metabolism	Target of Rapamycin (*tor*)	Grass Carp / Rainbow Trout	RNAi (Knockdown)	Master regulator of protein synthesis; silencing suppresses intracellular signaling responses to dietary essential amino acids (e.g., Leucine).
Micronutrient Regulation	Vitamin D Receptor (*vdr*) / SLC Transporters	Zebrafish / Marine Medaka	CRISPR/Cas9	Mediates calcium/phosphorus absorption and trace element transport; knockouts display skeletal deformities and altered mineral homeostasis.

Table 2: Comparative Evaluation of Functional Validation Tools in Aquatic Nutrition Research

VII. Challenges and Future Directions

7.1 Current Challenges

Molecular nutrition research has come a long way, but there are still some issues that need to be resolved [134]. The scarcity of genetic resources for non-model aquatic species is one of the main obstacles [135]. The lack of sequencing and inadequate annotation of the genomes of many aquatic species restricts the use of gene editing and omics technologies [136].

The conversion of laboratory results to commercial scales presents another difficulty [137]. Many studies on molecular nutrition are carried out in well-regulated laboratory environments, and it is frequently challenging to duplicate these findings in commercial aquaculture settings [138]. This is because commercial aquaculture involves intricate relationships between the environment, nutrition, and management techniques [139].

Another significant obstacle in molecular nutrition research is ethical issues [140]. Concerns regarding the possible advantages and disadvantages of genetically altered aquatic creatures are brought up by gene editing technologies like CRISPR-Cas9 [141]. To guarantee the ethical and safe use of these technologies, precise rules and regulations are required [142].

7.2 Emerging Research Areas

A new field of study that could transform molecular nutrition is the epigenetic regulation of nutrient metabolism [143]. Heritable variations in gene expression that do not entail modifications to the DNA sequence are referred to as epigenetics [144]. Dietary nutrition and environmental factors can impact epigenetic changes, including DNA methylation and histone acetylation [145]. Epigenetic changes have been demonstrated to impact immunological response, growth, and development in aquatic species [146].

Another new field of study is the relationship between gut bacteria and host nutrients [147]. The immune system, disease resistance, and nutritional metabolism are all significantly impacted by the gut bacteria [148]. The gut microbiota of aquatic animals can be affected by host genetics, ambient conditions, and dietary nutrients [149]. Gaining knowledge about how the host and gut bacteria interact can help us better understand how the immune system and nutrient utilization work [150].

The long-term impacts of early dietary experiences on adult metabolic characteristics are referred to as nutritional programming [151]. Growth, development, and disease resistance in aquatic animals can be impacted by early nutritional experiences [110]. Gaining an understanding of nutritional programming can assist in establishing ways to enhance the health and performance of aquatic animals as well as offer insights into the mechanisms of nutrient utilization [151].

7.3 Future Research Priorities

A future research focus that can offer a systems-level understanding of nutrition, metabolism, and environmental interactions is the integration of multi-omics with ecological modeling [152]. Researchers can forecast how dietary nutrients and environmental conditions will affect aquatic animals' growth, survival, and reproduction by merging data from omics technologies with ecological models [136].

Another objective for future research is the development of affordable molecular techniques for on-farm nutritional monitoring [153]. There is a need for portable and reasonably priced molecular tools that can be utilized on farms to evaluate the nutritional status of aquatic animals because the majority of molecular nutrition investigations are currently carried out in laboratory settings [154].

International cooperation is crucial to solving the world's aquaculture problems [155]. By collaborating, researchers can exchange information, resources, and knowledge and create creative ways to enhance aquaculture's sustainability [156].

VIII. Conclusion

Molecular nutrition has evolved as a critical field for advancing sustainable aquaculture. The main molecular pathways of nutrition use in aquatic animals, including the metabolism of proteins, lipids, carbohydrates, and micronutrients, have been summarized in this article. It has also examined the technological drivers, such as omics approaches and gene editing tools, that have revolutionized research in this area. The common relationships between nutrition and environmental stressors have been emphasized, as in species-specific advancements in finfish, crustaceans, and mollusks. The practical uses of molecular nutrition in genetic engineering, sustainable aquaculture methods, and precision feed formulation have also been covered in this review. Lastly, it has highlighted the necessity for interdisciplinary research to address global aquaculture concerns and assure food security by identifying important challenges and future directions.

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