frontiers | Frontiers in Marine Science

EDITORIAL
published: 25 May 2022
doi: 10.3389/fmars.2022.912884

Editorial: Omics and Fish Nutrition

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Keywords: aquafeed, metabolomics, transcriptomics, nutrients, proteomics

Editorial on the Research Topic

Omics and Fish Nutrition

According to a new report published by Food and Agriculture Organization (FAO, 2020), global fish production reached around 179 million tons and aquaculture production accounted for 63.7% of the total production. The rapid expansion of aquaculture industry has been associated with numerous challenges such as shortage of resources for sustainable production of aquafeeds (Zhou et al., 2019; Bruni et al., 2021). For a long time, the focus of traditional fish nutrition studies has been primarily on nutrients requirement and fish metabolism, but nowadays the interaction of nutrients and physiological responses has drawn attention of fish nutritionists. Omics technologies including transcriptomics, proteomics, and metabolomics have made a large contribution to better understanding of fish response to nutrients and dietary manipulations. The omics approaches have been successfully implemented for exploring the molecular basis of complex traits such as feed efficiency, muscle myopathies, immunity, and disease tolerance (Vallejos-Vidal et al., Vallejos-Vidal et al., 2022).

TRANSCRIPTOMICS IN UNDERSTANDING FISH PERFORMANCE

Transcriptomics is often used in identifying the expression of genes in mRNA transcripts in response to different factors. Nutrients can modify gene transcription and translation thereby regulating the animals' growth and reproduction performances. For example, the liver transcriptomic analysis revealed that n-3 LC-PUFA can promote the ovary development through upregulating the expression of vitellogenesis and zonagenesis related genes (Wang et al., 2021). It was earlier assumed that protein requirement of fish cultured under optimal and high temperatures differs, and interestingly the transcriptomic analysis in a recent study indicated that such variations in dietary protein requirement are associated with the metabolic alterations of three major nutrients in the liver (Cai et al., 2020).

PROTEOMICS IN EVALUATING PROTEIN METABOLISM

Proteomic analysis has been employed as an efficient and useful tool in assessment of the metabolism of proteins. For example, it suggested that different forms of lysine and leucine affect

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Specialty section:
This article was submitted to Marine Fisheries, Aquaculture and Living Resources, a section of the journal Frontiers in Marine Science

Received: *05 April 2022*
Accepted: *11 May 2022*
Published: *25 May 2022*

Citation:
Lu K-l, Rahimnejad S and Li S-l (2022) Editorial: Omics and Fish Nutrition. Front. Mar. Sci. 9:912884. doi: 10.3389/fmars.2022.912884

the absorption, synthesis and degradation of protein and ultimately the fish growth (Wei et al.). Moreover, the proteomics suggested that the impairment of growth performance in fish fed terrestrial proteins corresponds with the inhibition of cellular protein biosynthesis (Cao et al.). In the future, proteomics could be implemented as a key tool for understanding the role of specific amino acids in satisfying the physiological needs of fish.

METABOLOMICS PROMOTES NEW INSIGHTS IN FISH NUTRITION

Metabolomics can provide new insight into the alterations of nutrients metabolism by identifying small molecule metabolites. The results obtained from metabolomics can indicate the holistic vision of fish metabolism and health monitoring (Roques et al., 2019). Fish fed plant-based diets showed metabolic disturbances illustrated by lower muscle PUFA concentration. Moreover, the metabolomics data revealed the increased muscle malate, fumarate and glycine concentrations which are associated with energy metabolism (Wei et al., 2017). Also, metabolomic analysis suggested that taurine modulates carbohydrate, amino acids, and lipids metabolic pathways in Nile tilapia (Shen et al., 2018). Furthermore, metabolomics results in a rainbow trout study indicated that fish fed the diets in which fish meal and fish oil were replaced with alternative sources exhibited higher energy requirements (Cao et al.).

Overall, omics provides a global insight into molecular response and metabolism of fish in response to nutritional factors. In the future, it could provide novel methods and specific markers for evaluating the nutritional and health status of fish. It will also contribute to elucidating the hidden effects of specific nutrients or feedstuffs in fish.

AUTHOR CONTRIBUTIONS

K-LL and SR were responsible for the idea of this Research Topic and wrote and reviewed this editorial. S-LL contributed to the review of the editorial. All authors contributed to the article and approved the submitted version.

FUNDING

This work was funded by National Natural Science Foundation of China (32072984), Natural Science Foundation of Fujian Province (2020J01664) and Shanghai Talent Development Fund (2019097).

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.