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# Editorial: Environment-microbe-host interactions in aquaculture ecosystems

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Editorial on the Research Topic
Environment-microbe-host interactions in aquaculture ecosystems

## Introduction

Aquaculture production has been continuously expanding in the last seven decades, being the fastest growing food production section in the word (Edwards et al., 2019). Aquatic animals contain a wide range of bioavailable nutrients including animal protein, essential fatty acids, minerals and vitamins (Thilsted et al., 2016), which is crucial for global food security, reduction of poverty and diet-related diseases of humans (Béné et al., 2016). To embrace the sustainable development of aquaculture, intensive studies have been done to improve feed efficiency and fish nutrition as well as to reduce waste discharge and dependency on marine ingredients (Boyd et al., 2020). Even though, aquatic animals are facing new challenges from shifting feed ingredients, upgrading rearing systems and rapid climate change, which impose uncertainty on pathogens management and host health status (Naylor et al., 2021). Under such circumstances, a better understanding of the interactions between environment, microbe and host would benefit the development of management strategies to increase the tolerance and adaptation of aquaculture species to changing rearing conditions.

In order to strength the understanding of sophisticated aquaculture production ecosystem, we launched this Research Topic to call for aquaculture researchers worldwide to present their latest studies. This Research Topic presents four high-quality original research articles from four countries and thirty authors that provide insights into the microbial ecology of aquaculture systems. Here, we present and summarize the highlights of the four contributions in the following three sections.

## Host and microbiome interactions

Fish microbiome develops fast during the early life stage, and has great impact on survival, nutrients digestion and fish growth performance (Deng et al., 2021). Both Almeida et al. and Bradshaw et al. suggest that age is a main driver of the variations in host microbiome during early life stages, using Sole (*Solea senegalensis*) and Florida pompano (*Trachinotus carolinus*) as model species, respectively. Specifically, Almeida et al. characterized the microbiome development of Sole (*Solea senegalensis*) from egg through fish life cycle by collecting samples from gill, intestine, fin and mucus tissues. The variation of potential probiotic and pathogen species were identified, and negative correlations were detected between them, suggesting that probiotic supplementation could serve as a preventative strategy to suppress the potential proliferation of pathogens. More importantly, the persistent presence of two probiotic species starting from the egg stage and the big change in microbial diversity on the weaning stage were detected by Almeida et al., suggesting that larval and weaning stages are two sensitive time windows for fish microbiome modulation, which may have long-lasting effect on the later life stages. There results implied the co-progression between host and microbiome, and more studies on determining the potential factors and on quantifying to which extend these factors could shape the fish microbiome assembly are needed.

## Host and environment interactions

Changing rearing systems or conditions cause stress to aquatic animals, however, resistant and adaptation to the changing environment would advantage the expansion and harvest of these animal species. In our Research Topic, two contributions investigated the responses of host to different environmental factors, such as oxygen (Zhou et al.) and salinity (Bradshaw et al.). Zhou et al. found that hypoxia increased the gill lamellae length and spacing and the gene expression related to lipid decomposition in liver of yellowtail kingfish (*Seriola lalandi*). After reoxygenation treatment, genes related to lipid metabolism and protein repairment and synthesis were upregulated, which may relate to the clearance and repairment of misfolded proteins. Salinity, on the other hand, changed the gill histopathology with 10 ppt having a higher percentage of epithelial lifting than the fish larvae reared in 20 and 30 ppt (Bradshaw et al.). In addition, lowering the salinity caused no statistical significance on the abundance of antioxidant genes and immune-related genes, suggesting the tolerance of Florida pompano (*Trachinotus carolinus*) larvae to low salinity at 10 ppt with minimal impact on the immune response. Both Zhou et al. and Bradshaw et al. observed the gill structure alteration to adapt different rearing oxygen and salinity levels, suggesting environmental factors play an important role in nutrient metabolism and host homeostasis.

## Environment and microbiome interactions

Rearing water microbiome is shaped by many environmental factors, such as oxygen and salinity (Deng et al., 2019), however, how these environmental factors impact the host microbiome remains largely unexplored. In our Research Topic, how water microbiome (Bruno et al.), oxygen (Zhou et al.) and salinity (Bradshaw et al.) influence the assembly of host microbiome were investigated. Specifically, Bruno et al. showed that several key microorganisms and red mark syndrome (RMS) pathogens were higher present or expressed in water and sediment samples from RMS-affected tanks as evidence by 16S rRNA sequencing and quantitative real-time PCR results. This result highlights the important of water microbiome management in aquaculture production and expand thihe understanding of aetiology of this emerging disease, which have the implication on the modulation of RMS disease outbreak. Results from Zhou et al. showed that several intestinal genera, including *Prevotella*, *Bacteroides*, *Roseburia*, and *Blautia*, were associated with the hypoxia condition. Furthermore, function annotation of the host microbiome revealed changes in metabolism, cellular processes and signaling, and organizational system during the physiological adaptation to hypoxia or reoxygenation conditions. Another study from Bradshaw et al. showed that water microbiome derived from salinity10 ppt were clearly distinct from salinity 30 ppt in terms of beta diversity. Besides, lower salinity changed the host microbiome and increased the abundance of potentially pathogenic genera (PPGs), such as *Flavobacterium* and *Pseudomonas.*

Besides aforementioned environmental factors, different water treatment approaches, such as flow-through system (FTS) vs recirculating aquaculture system (RAS) (Attramadal et al., 2012) or supply of dissolved organic carbon substrates to mature the rearing water microbiome (Attramadal et al., 2016; Deng et al., 2022a), were found to have substantial impact on the microbial population in the water environment. Furthermore, compared to FTS, RAS showed more balanced gut microbiota colonization process and higher survival of cultured fish species during early life stages (Deng et al., 2022b).

In conclusion, contributions to this Research Topic use 16S rRNA sequencing or transcriptomics to investigate the impact of age, oxygen, salinity, and water microbiome on not only development of host microbiome (including both potential probiotics and pathogens) but also on the morphology, histology and histopathology of host tissues. These outcomes highlight the synergetic adaptation of host microbiome and host physiology to changing rearing conditions, and strength our understanding of the interactions between environment, microbes and host in aquaculture ecosystems, which has the implication on the modulation of host performance and maintenance of host homeostasis.

## Author contributions

YD: Conceptualization, Writing – original draft, Writing – review & editing. LF: Writing – review & editing. YR: Writing – review & editing.

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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.

## Publisher's note

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