



Diversity of the Microbiome in Fish: Composition, Function and Implications for Aquatic Health & Aquaculture: A Review

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Abstract: The fish microbiome represents a highly diverse and dynamic assemblage of microorganisms inhabiting key anatomical sites such as the gut, skin, and gills, where they play essential roles in host nutrition, immune regulation, physiological homeostasis, and protection against pathogens. Increasing evidence highlights that microbiome diversity and stability are critical determinants of fish health, disease resistance, and productivity, with significant implications for sustainable aquaculture and aquatic ecosystem management. The composition and function of fish-associated microbial communities are shaped by intrinsic host factors including species, developmental stage, genetics, and diet, as well as extrinsic environmental variables such as water quality, temperature, salinity, and aquaculture system design. Disruptions in these microbial communities can lead to dysbiosis, increasing susceptibility to infectious diseases and compromising mucosal barrier function. Advances in microbiome research have enabled the development of targeted strategies such as probiotic and prebiotic supplementation, environmental microbiome management, and microbiome-based disease control to enhance fish health and reduce reliance on antibiotics. This review synthesizes global literature on the anatomical and functional diversity of the fish microbiome, elucidates its role in host–microbe–environment interactions and disease processes, and highlights emerging microbiome-centered applications as key tools for improving aquatic health and sustainability in modern aquaculture.

Keywords: Microbiome, Fish, Probiotics, Aquatic Health, Aquaculture.

1. INTRODUCTION

A microbiome includes all the microorganisms in a particular ecosystem. Occasionally it comprises the total of the genetic material of the microbes, symbiotic and pathogenic, living in and on all vertebrate animals. Microbiomes play important roles in maintaining aquatic animal health, nutrient cycling and climate change regulation (Lennon et al., 2023). The composition and function of gut, skin, and gill microbiomes in fish and shellfish, as well as aquatic ecological drivers behind tissue microbiome assembly. Microbes perform a number of important ecosystem services in water. Microbes also support ecosystems through their involvement in nutrient cycling, especially the nitrogen cycle (McKenney et al., 2018). Interestingly, a study of 140 sample of ocean water from around the world wide revealed that 73% of the prokaryotic gene abundance in all of the ocean samples can be attributed to the same functional core of the human gastrointestinal microbiome.

Aquatic animals are surrounded by a milieu of microbes and evidence suggests that the composition of

environmental microbiomes influences the microbiomes of aquatic animals. For example, in zooplankton, alterations of the environmental microbiome by anthropogenically introduced antibiotics to aquaculture industry causes a shift in the host-associated microbiome, which in turn influences growth of plankton populations (Callens et al., 2018). A meta-analysis of the gut microbiomes of freshwater and saltwater fish and surrounding environmental samples indicated that the gut microbiome is not a reflection of the local habitat but rather the specific gut environment of the fish (Wong and Rawls, 2012). This review explains the role of the fish microbiota in regards to the host physiology, feeding habitat, digestion and metabolism, and also its control over stress responses, reproduction, development, and immune responses. In addition to future implications of fish microbiota handling and possible research guidelines for this growing aquaculture field.

2. Microbial Diversity across Anatomical Sites

The microbiome of fish is a complex and group of microorganisms inhabiting various anatomical sites including the gastrointestinal tract, skin and gills. These

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communities vary in structure, abundance and function depending on the specific micro environment they occupy and play crucial roles in host immunity, metabolism and disease resistance against pathogens. The niche-specific microbiota not only reflect the physiological role of each tissue but also respond distinctly to environmental, dietary and host genetic factors.

2.1. Gut Microbiome

The fish gut microbiome presents an invaluable window into host microbiota-environment interactions, offering insights with direct implications for aquaculture sector. The composition of fish gut microbiota is shaped by a combination of environmental, biological and behavioural parameters, which collectively influence microbial communities across diverse fish species (Nayfach et al., 2021; Bertoncin et al., 2022). The gut microbiota includes Proteobacteria, Firmicutes, Fusobacteria, Actinobacteria and Bacteroidetes. Their relative abundance varies not only between species but also within individuals depending on environmental exposure and rearing practices. For instance, Fusobacteria, such as *Cetobacterium*, are often abundant in freshwater fishes and are known for producing vitamin B12 and fatty acids that contribute to host metabolism (Ghanbari et al., 2015).

The gut environment is predominantly anaerobic or microaerophilic, favouring the proliferation of fermentative bacteria capable of producing the acetate, propionate and butyrate. These microbial metabolites play essential roles in maintaining intestinal epithelial health, regulating immune responses and inhibiting pathogen colonization (Ghanbari et al., 2015; Nayak, 2010). The gut microbiome is not only a reflection of the host's internal structure but also of external management factors. Microbiomes are leveraged to enhance fatty acid production in muscle tissue and improve fish health development. The gut microbiome helps protect the intestinal barrier, prevent the overgrowth of opportunistic pathogens and modulate the host immune system, all of which are crucial for maintaining fish health (Nohesara et al., 2023). Therefore, understanding and manipulating the fish gut microbiome has become an important strategy for developing sustainable and disease-resistant aquaculture practices. The gut microbiome is increasingly recognized as an important indicator of environmental health and the adaptability of fish populations, offering valuable insights for conservation efforts (Soh et al., 2024).

In addition, the gut microbiome also has implications for disease prevention and therapeutic intervention. A gut microbiome-characterized by reduced microbial diversity

and increased abundance of opportunistic pathogens of aquatic animals such as *Aeromonas*, *Vibrio*, or *Pseudomonas* has been linked to disease susceptibility and inflammation (Ghanbari et al., 2015). Therefore, maintaining a stable and diverse gut microbiota is essential for sustainable fish farming and health management. Advancing sustainable aquaculture and implementing effective conservation strategies for vulnerable fish populations hinges on a comprehensive understanding of gut microbiome dynamics. Research has shown that gut microbiota plays a fundamental role in host resilience, immune function, and adaptation to environmental changes, all of which are critical for both farmed and wild fish (Fonseca and Fuentes, 2023; Zhu and Wang, 2023).

2.2. Skin Microbiome

Teleost are associated with diversified microbial communities in the mucosa of the skin, gill and gut. Healthy fish skin harbours an indigenous microbial community that facilitates the homeostasis of host immunity, removes waste products and outcompetes the colonization of pathogens (Hu et al., 2021). The epidermal mucus exerts an innate immune response secreted from goblet cells, which act as a primary barrier for pathogenic microbes. In mucus contains antimicrobial peptides, proteases, lysozymes and lectins that are known to support innate immunity (Dash et al., 2018). The mucus in fish skin is known to entrap and slough off microbes constantly; therefore, skin prevents the colonization of pathogenic microbes. Although fish skin constantly renews mucus, a healthy resident microbial community is maintained in the mucus layer. However, the community structure of the skin microbiome is shaped by multiple factors, such as environmental conditions, health status and host genetics (Van Cise et al., 2020; Xavier et al., 2020). As microbiome of fish plays significant role in their health and development through symbiotic relationship (Collin et al., 2021) though less abundance of community exists in skin mucus compared to gut (Hu et al., 2021).

The bacterial phyla of fish skin such as Proteobacteria, Firmicutes, Actinobacteria and Cyanobacteria. At the genus level, bacterial organisms include *Aeromonas*, *Pseudomonas*, *Vibrio*, and *Shewanella* are commonly reported. These microbes can exist as commensals under normal conditions but may act as opportunistic pathogens when the host is stressed or immunocompromised (Lowrey et al., 2015). A component of the fish skin is the mucus layer, which contains various innate immune molecules such as lysozymes, lectins, antimicrobial peptides (AMPs) and immunoglobulin-like proteins. This mucus not only acts as a

physical barrier but also serves as a selective substrate for beneficial microbes, thus helping to shape and stabilize the skin microbiota (Salinas et al., 2011).

Environmental condition or husbandry-related factors such as stocking density, handling, and poor water quality and temperature shocks can destabilize the skin microbial community, a condition known as dysbiosis. It is often results in reduced microbial diversity and a shift toward potentially pathogenic taxa. Such imbalances have been associated with increased incidence of parasitic and bacterial infections, including diseases caused by *Ichthyophthirius multifiliis* (white spot disease) and *Flavobacterium columnare* (columnaris disease) (Boutin et al., 2014). Skin ulceration and muscular necrosis are dominated by *A. hydrophila*; the freshwater pathogen would cause infection-related mortality in catfish farming system (Siao et al., 2021). Infections caused the loss of 3 million pounds of farm-raised catfish in Alabama, United States, in 2017, making *A. hydrophila* the most prevalent pathogen in catfish (Siao et al., 2021). However, within the same species of fish, they found different mucosal microbiomes (Butt and Volkoff, 2019). Gaining a better understanding of the skin-mucus microbiota of farmed fish could help to manage the health and disease of high densities aquaculture species.

In aquaculture, maintaining beneficial skin microbiota is importance for disease prevention and improved aquatic animal health. Strategies such as probiotic bathing, water microbiome management, and stress minimization are increasingly being explored to support the natural skin microbiome and reduce dependency on antibiotics.

2.3. Gill Microbiome

Gill surfaces are the primary site of gas exchange in fish and are colonized by microbial communities. Like the skin and gut, the gills are coated in a layer of mucus that is constantly replaced, providing both a defence against and habitat for pathogenic or commensal prokaryotes. Antimicrobial peptides found in the skin and intestines of fish are also present in the gill mucus, highlighting the importance of the gills as a first line of defence against pathogenic infection. Gill microbiota can reflect internal and external diseases (Legrand et al., 2018).

The mucosal surface of the gills constitutes the most extensive biological interface between the fish and external environment. This surface is colonized by a complex highly diverse microbial community that promotes gill mucosal homeostasis and thereby contributes to overall fish health (Elshehtawy et al., 2021). Recently, an increased prevalence of the gill pathogen *Candidatus Branchiomonas cysticola* and changes in mRNA abundance of cellular stress, inflammation, and repair and proliferation genes in gill tissue were reported after thermal delousing (Ostevik et al., 2022).

Gill microbiomes respond to changes in the environment. Following exposure to suspended sediments, clownfish (*Amphiprion percula*) larvae gill microbes had higher abundances of pathogenic taxa (*Flavobacterium*, *Pasteurella*, *Edwardsiella*, *Chryseobacterium*, *Pseudomonas*, *Corynebacterium*) (Hess et al., 2015). Though the microbiome was not characterized, a study with Atlantic salmon found that gill mucus cell count increases

Table 1. Major microbial groups associated with fish microbiome, their functional roles, and implications for aquatic health and aquaculture

Microbial group	Dominant Taxa (Examples)	Primary functions	Implications for fish health	Relevance to aquaculture
Proteobacteria	<i>Vibrio</i> , <i>Pseudomonas</i> , <i>Aeromonas</i>	Nutrient metabolism, immune modulation	Includes both beneficial and opportunistic pathogens	Dysbiosis linked to disease outbreaks
Firmicutes	<i>Lactobacillus</i> , <i>Bacillus</i>	Enzyme production, pathogen inhibition	Enhances gut health and digestion	Widely used as probiotics
Bacteroidetes	<i>Flavobacterium</i> , <i>Bacteroides</i>	Carbohydrate degradation	Supports nutrient absorption	Influenced by diet formulation
Actinobacteria	<i>Microbacterium</i> , <i>Corynebacterium</i>	Vitamin synthesis, antimicrobial activity	Maintains microbial balance	Sensitive to water quality
Fusobacteria	<i>Cetobacterium</i>	Vitamin B ₁₂ production	Improves growth and feed efficiency	Common in freshwater species
Archaea (minor)	Methanogens	Fermentation processes	Limited but emerging roles	Potential biomarker for gut health

with salinity and fluctuations in ion regulation-additional research is needed to determine whether gill microbiomes play an active role in ion regulation (Hess et al., 2015).

The function of gill-associated bacteria may contribute to mucus degradation, ammonia detoxification and modulation of innate and non-specific immune responses, helping to maintain the integrity of gill tissues. Some commensal organisms may also produce antimicrobial compounds that inhibit colonization by pathogenic bacteria. However, due to the thin epithelium and rich vascularization of the gills, this site is particularly vulnerable to environmental insults and microbial dysbiosis (Dhanasiri et al., 2011). Stressful conditions, such as poor water quality (e.g., high ammonia or nitrite levels), elevated organic loads, hypoxia, or abrupt temperature changes, can destabilize the gill microbiota. This can lead to increased susceptibility to opportunistic pathogens, including *Flavobacterium*, *Vibrio*, and *Tenacibaculum* species. Such infections are commonly associated with bacterial gill disease (BGD), a condition characterized by hyperplasia, necrosis, and impaired gas exchange (Dhanasiri et al., 2011; Rosado et al., 2019). From an aquaculture perspective, the health of the gill microbiome is critical for fish performance, survival, and health. Strategies such as maintaining high water quality, reducing stocking stress and administering water probiotics or immunostimulants are being explored to preserve gill microbial homeostasis and prevent gill-associated diseases.

3. Microbial Transmission and Colonization

The initial development of microbiome colonization may occur vertically (from parent to offspring) or horizontally from the surrounding environment, with the relative contribution of these routes varying across species and rearing conditions (Funkhouser & Bordenstein, 2013). In hatchery systems, egg disinfection and water sterilization practices can disrupt natural microbial transmission, potentially reducing microbial diversity during early developmental stages (Llewellyn et al., 2014; De Schryver & Vadstein, 2014). Such alterations in early microbial exposure may influence host health and immune development, thereby prompting growing interest in microbial inoculation strategies and probiotic interventions to support healthy microbiome establishment in the aquaculture industry (Ringo et al., 2018; Vadstein et al., 2018).

4. Microbiome and Disease in Fish

The composition and stability of the fish microbiome are closely related to disease susceptibility and overall health status. A microbiome helps protect fish from pathogens,

whereas any disruption of this balances-known as dysbiosis. It is increasing their susceptibility to opportunistic infections and inflammatory disease. This relationship is essential for disease prevention and health management strategies in aquaculture systems.

4.1. Dysbiosis and Disease Susceptibility

4.1.1. Dysbiosis: Refers to an imbalance normal microbial community, often characterized by reduced microbial diversity and overgrowth of pathogens. It can be triggered by a variety of stressors including poor water quality, overcrowding, temperature fluctuations, dietary changes, and antibiotic use (Xiong et al., 2019).

For example, high levels of *Aeromonas hydrophila* and *Vibrio* spp. have been reported in diseased fish suffering from dysbiosis, such as catla and tilapia with hemorrhagic septicemia and fin rot (Huang et al., 2020; Bujan et al., 2022). These pathogens exploit weakened mucosal barriers and immune suppression, often resulting in systemic infections.

4.2. Mucosal Microbiomes as Barriers

The skin, gill and gut microbiomes serve as critical first-line defenses by occupying niche spaces on mucosal surfaces and secreting antimicrobial substances. In healthy fish, these microbial barriers competitively exclude invading pathogens by outcompeting them for nutrients level and adhesion sites. When these microbial communities are destabilized due to environmental stressors or antibiotic exposure of pathogen colonization increases, leading to epithelial cell damage and inflammation of acute or chronic level (Llewellyn et al., 2014). Recent studies have shown that fish with stable and diverse microbiota exhibit stronger resistance to infections such as *Edwardsiella tarda* and *Streptococcus iniae*, compared to those with low microbial richness (Lowrey et al., 2015). This suggests that microbial diversity itself may be a biomarker of fish health and resilience.

4.3. Role in Chronic Inflammation and Gut Pathology

Chronic dysbiosis has been related to gut pathologies such as enteritis and epithelial erosion in salmon and common carp. In Atlantic salmon, prolonged feeding of soybean meal-based diets induces an inflammatory gut response and microbial shifts that favor pro-inflammatory taxa, including *Mycoplasma* and *Desulfo vibrio* (Ulloa et al., 2021). Gut microbiota imbalances have also been associated with altered intestinal barrier integrity, leading to leaky gut syndrome and translocation of bacteria into the bloodstream-further worsening systemic infections.

4.4. Antibiotic Use and Microbiome Disruption

The use of antibiotics in aquaculture sector, especially in

developing countries, has led to serious consequences for microbial health. Antibiotics not only eliminate pathogenic bacteria but also disrupt beneficial microbial communities in aquatic animals (Dehler et al., 2017). Post-antibiotic dysbiosis is frequently associated with secondary infections of parasites, reduced immunity and poor feed conversion efficiency. Moreover, the emergence of antimicrobial resistance (AMR) within fish microbiota has raised concerns about zoonotic transmission and environmental contamination. Multi-drug-resistant *Vibrio* and *Aeromonas* strains have been detected in both wild and farmed fish microbiomes, posing a threat to both aquaculture sustainability and public health concern by Santos and Ramos (2018).

5. Applications in Aquaculture

The fish microbiome has emerged as a promising way for improving aquaculture productivity, sustainability and fish health. The microbiome is increasingly being viewed as a targetable aquaculture industry that can be engineered or enhanced to promote disease resistance, feed efficiency, water quality, and stress tolerance. With the advent of omics technologies, microbiome-based interventions are becoming more precise and impactful.

5.1. Probiotics and Prebiotics

The use of probiotics-live microbial supplements that give health benefits to the host. In aquaculture, probiotics such as *Lactobacillus spp.*, *Bacillus spp.*, *Shewanella putrefaciens* and *Pediococcus acidilactici* are administered through feed or water to enhance gut microbial balance, inhibit pathogens and boost immunity (Nayak, 2010; Ringo et al., 2018). These beneficial microbes produce antimicrobial compounds (e.g., bacteriocins, organic acids), compete for adhesion sites and stimulate mucosal immunity.

Prebiotics are non-digestible feed ingredients (e.g., inulin and β -glucans) that selectively stimulate the growth of beneficial microbes. Their inclusion in diets enhances microbial richness and metabolic activity, improving nutrient utilization and gut integrity (Hoseinifar et al., 2016). When combined, synbiotics (probiotic + prebiotic) have result on synergistic effects, improving feed conversion ratio and survival in several fish species including tilapia, carp, and salmonids.

5.2. Microbiome-Targeted Disease Management

Microbiome modulation is a non-antibiotic strategy for disease prevention. It is promoting microbial communities that resist pathogen colonization; fish are better protected from infections like *Vibriosis*, *Aeromoniasis*, and Enteritis. Probiotic administration has been shown to reduce mortality

in *Litopenaeus vannamei* challenged with *Vibrio harveyi* and to enhance resistance to *Aeromonas hydrophila* in common carp (Kim and Austin., 2006; Xiong et al., 2019). Furthermore, viable exclusion strategies are being developed, where selected beneficial strains are introduced early in larval stages to occupy ecological niches and prevent pathogenic colonization. Such approaches reduce the need for antibiotics and lower the risk of antimicrobial resistance (Dehler et al., 2017).

5.3. Environmental Microbiome Management

In Recirculating Aquaculture Systems (RAS) and biofloc systems, managing the environmental microbiome is as important as animal health. Biofilters and microbial additives are used to maintain nitrifying bacterial load that convert ammonia to nitrate, improving water quality and reducing stress-induced dysbiosis (Giatsis et al., 2015). In aquaculture systems incorporate bioremediation microbes such as *Nitrosomonas* and *Nitrobacter* to stabilize water chemistry and suppress pathogen loads. The practice of “green water” (algal-bacterial mixtures) in larviculture is a microbiome-centered strategy that improves larval survival and promotes the development of beneficial gut flora (Caruffo et al., 2021).

5.4. Next-Generation Technologies

Modern multi-omics tools (metagenomics, meta transcriptomics, and metabolomics) have enabled in-depth profiling of microbiomes in different aquaculture species and production systems. These tools facilitate real-time health monitoring by identifying shifts in microbial signatures that precede disease outbreaks or stress responses (Li et al., 2021). These approaches aim to directly manipulate microbial community structure for enhanced performance traits such as growth rate, immunity and feed conversion efficiency. Additionally, microbiome transplantation is being explored as a way to restore healthy microbiota in fish post-antibiotic treatment or after environmental disruptions by Gomez and Balcazar (2008).

6. CONCLUSION

The diversity of the microbiome in fish is major role for maintaining physiological balance, enhancing immunity and providing resistance against pathogens (Llewellyn et al., 2014). This microbial community is influenced by several factors such as species, developmental stage, diet and environment conditions (Ghanbari et al., 2015). Therefore, a diversity of microbiome is development of probiotic and immunostimulant strategies to promote fish health and sustainable aquaculture practices (Ringo et al., 2020). The future research integrating advanced molecular technique

will continue to uncover the functional roles of fish microbiomes and support the optimization of microbiome-targeted interventions.

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