

Fish-Microbe-Environment Interactions: The Role of the Fish Microbiome in Aquatic Ecosystem Health

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ABSTRACT

Fish are intimately associated with diverse microbial communities that inhabit their gastrointestinal tract, skin, gills and other mucosal surfaces, collectively forming an integral component of the fish holobiont. Increasing evidence indicates that these microbial communities are not only essential for digestion, metabolism and immune regulation but also respond dynamically to environmental conditions. The fish-microbe-environment interaction therefore represents a complex biological interface through which changes in aquatic ecosystems can influence fish health, while fish-associated microorganisms can, in turn, contribute to ecosystem functioning. This review synthesizes current knowledge on the composition, diversity and functional roles of fish-associated microbiomes and examines the major biotic and abiotic factors shaping these communities. Particular emphasis is placed on the influence of temperature, dissolved oxygen, pH, salinity, eutrophication and anthropogenic contaminants, including heavy metals, pesticides, pharmaceuticals, antibiotics and microplastics. The review further explores microbiome dysbiosis, host immunity, nutrition, metabolism and disease susceptibility, along with the role of beneficial microorganisms in maintaining fish health. Recent advances in 16S rRNA sequencing, metagenomics, meta transcriptomics, metabolomics and other multi-omics approaches have greatly improved our understanding of microbial community structure and function. Importantly, alterations in fish-associated microbiomes may serve as sensitive biological indicators of environmental stress and may complement conventional physicochemical and biological approaches to aquatic ecosystem assessment. The potential applications of microbiome-based biomarkers, probiotics, environmental monitoring and conservation are discussed, together with current methodological limitations and future research priorities. Understanding fish-microbe-environment interactions may provide a promising framework for linking microscopic microbial changes with fish health, biodiversity and broader aquatic ecosystem functioning.

Keywords: Fish microbiome, fish-microbe interactions, aquatic ecosystem health, environmental stress, dysbiosis, aquatic pollution, microbial biomarkers, fish health, metagenomics; microbiome-based monitoring.

1. Introduction

Aquatic ecosystems are complex and dynamic biological systems in which fish interact continuously with their physical, chemical and biological surroundings. Microorganisms occupy a central position in these systems because they participate in nutrient transformation, organic-matter decomposition, energy flow, host-microbe interactions and maintenance of ecosystem functioning. Fish maintain intimate associations with diverse microbial communities inhabiting their gastrointestinal tract, skin, gills, oral cavity and other mucosal surfaces. These microorganisms are increasingly recognized as an integral component of fish biology rather than transient or opportunistic organisms, and the concept of the fish as a holobiont, comprising the host and its associated microbial communities, has gained considerable attention in aquatic biology and environmental science (Llewellyn *et al.*, 2014; Legrand *et al.*, 2020).

The gastrointestinal tract is one of the most important interfaces between the host, microorganisms and the external environment. Unlike terrestrial vertebrates, fish live in direct and continuous contact with water, allowing environmental microorganisms to enter through the gills, skin and gut. Associated microorganisms may originate from water, sediments, food and other sources and subsequently colonize different host niches (Nayak, 2010). The gut microbiota is composed predominantly of bacteria, although archaea, fungi, protozoa and viruses also contribute. Its composition differs among fish species and is influenced by host physiology, feeding habits, developmental stage, habitat and environmental conditions (Nayak, 2010; Egerton *et al.*, 2018).

The fish microbiome performs several important physiological functions. Gut microorganisms contribute to digestion, nutrient utilization, metabolic regulation, intestinal development and immune function; certain taxa produce digestive enzymes, vitamins and bioactive metabolites, while others break down poorly digestible dietary components, thereby influencing growth, nutritional status and energy metabolism (Nayak, 2010; Talwar *et al.*, 2018). The microbial community also helps maintain intestinal barrier integrity and interacts with the immune system. A balanced community may provide colonization resistance against pathogens, whereas disturbances can increase susceptibility to disease and physiological stress (Llewellyn *et al.*, 2014; Legrand *et al.*, 2020).

The microbiome extends beyond the intestine. Skin and gills are directly exposed to the aquatic environment and are protected by mucus containing diverse microbial communities that interact with host immune components and environmental microorganisms. Skin and gill microbiomes may be especially responsive to environmental change, although the magnitude and direction of responses depend on fish species, body site, type of stressor and host condition (Schar *et al.*, 2025). Microbiome composition is not static: it is shaped by host species, age, sex, genetics, trophic position, feeding behaviour and physiological condition, together with temperature, pH, dissolved oxygen, salinity, nutrient availability, water chemistry and seasonal variation (Egerton *et al.*, 2018; Singh *et al.*, 2025). Environmental fluctuations can simultaneously affect free-living microbial communities and those associated with fish.

Environmental change can therefore influence fish health partly through alterations in the microbiome. Temperature affects microbial growth, host metabolism and immune function, and variations in dissolved oxygen, salinity, pH and food availability can alter community structure and host physiology. A recent synthesis showed that environmental conditions and external stressors can induce microbial dysbiosis, impair intestinal barrier integrity and promote oxidative stress in aquatic animals (Yoon *et al.*, 2026).

A major application of fish microbiome research is understanding the biological effects of aquatic pollution. Fish are exposed to heavy metals, pesticides, pharmaceuticals, antibiotics, petroleum-derived compounds, endocrine-disrupting chemicals and plastic-associated contaminants. Unlike conventional physicochemical measurements, which quantify contaminant concentrations in water or sediment, microbiome-based approaches provide information about biological responses within exposed organisms (van der Oost *et al.*, 2003). Heavy metals such as cadmium, lead, mercury, chromium and copper can affect microbial composition and host physiology through oxidative stress, cellular damage and disruption of metabolic pathways, and beneficial microorganisms and probiotics are being explored to reduce metal-induced toxicity and microbiome disruption (Wang *et al.*, 2024). Fish–microbe interactions thus operate in both directions: contaminants can alter the microbiome, while selected microorganisms may influence contaminant toxicity and host resilience.

Emerging contaminants, including pharmaceuticals, antibiotics, personal-care products, nanoparticles and endocrine-disrupting chemicals, occur in aquatic environments at biologically relevant concentrations and can induce intestinal dysbiosis, influencing intestinal metabolism, immune regulation and disease susceptibility (Migiani *et al.*, 2023). Microplastics and nanoplastics are another rapidly developing area: plastic particles act as surfaces for microbial colonization, carrying assemblages sometimes called the “plastisphere,” and following ingestion may modify microbial diversity, intestinal barrier function, inflammation and oxidative stress. The magnitude and ecological relevance of these changes depend on particle characteristics, exposure conditions, fish species and environmental context, and much of the evidence still derives from controlled laboratory experiments, highlighting the need for field-based studies under realistic exposure conditions (Zhang *et al.*, 2024). Antibiotics represent a further connection between the fish microbiome and environmental health: their use in aquaculture can influence intestinal microbial communities and may select for antibiotic-resistant bacteria.

2. The Fish Microbiome

Fish are closely associated with diverse microbial communities colonizing the gastrointestinal tract, skin, gills, oral cavity and other mucosal or internal surfaces. These microorganisms participate in nutrition, metabolism, immune regulation, epithelial protection and resistance against pathogens (Llewellyn *et al.*, 2014; Legrand *et al.*, 2020). Their composition and function are influenced by host characteristics, diet, habitat, developmental stage, season and environmental conditions (Egerton *et al.*, 2018; Talwar *et al.*, 2018; Singh *et al.*, 2025), making the fish microbiome an important biological interface between the fish and its aquatic environment.

The term *microbiota* refers to the microorganisms inhabiting a particular environment or host niche, whereas *microbiome* is broader, encompassing the community and its collective genetic and functional potential. Fish microbiome research has traditionally focused on gut bacteria, but archaea, fungi, protozoa, viruses and bacteriophages also contribute to the broader microbial ecosystem (Llewellyn *et al.*, 2014; Talwar *et al.*, 2018; Singh *et al.*, 2025). High-throughput sequencing and

metagenomics have expanded our ability to characterize communities beyond organisms culturable in the laboratory (Legrand *et al.*, 2020).

An important characteristic is spatial organization. Gut, skin, gill and other sites differ in physicochemical conditions, nutrient availability and host-derived factors. The gut generally supports a relatively specialized community, whereas skin and gill communities are more directly exposed to environmental microorganisms in the water (Legrand *et al.*, 2020). Comparative studies show that fish species, habitat and environmental conditions are major determinants of gut microbial composition, with differences between freshwater and marine fishes and between wild and cultured populations (Singh *et al.*, 2025; Kanika *et al.*, 2025).

2.1 Major microbial communities associated with fish

2.1.1 Gut microbiome

The gastrointestinal tract (GIT) is the most extensively investigated and one of the most functionally important fish microbial habitats. The intestine provides nutrients and host-derived substrates supporting diverse populations, while the microorganisms contribute to digestion, nutrient metabolism, immune regulation and intestinal homeostasis (Nayak, 2010; Talwar *et al.*, 2018); the gut microbiota is thus an important component of the host's physiological system. It is influenced by fish species, age, developmental stage, genetics, trophic position, feeding behaviour, diet, physiological condition, habitat, water quality and season (Sullam *et al.*, 2012; Egerton *et al.*, 2018; Talwar *et al.*, 2018). Habitat and host taxonomy are important determinants of gut microbiome structure (Singh *et al.*, 2025), and farmed fish may differ from wild populations because of differences in feed composition, stocking density, water quality and environmental exposure (Kanika *et al.*, 2025). Diet is particularly important: carnivorous, herbivorous and omnivorous fishes differ in the carbohydrates, proteins, lipids and other substrates entering the gut, creating different ecological niches for microorganisms (Sullam *et al.*, 2012; Egerton *et al.*, 2018).

4. Gut Microbiome and Fish Nutrition

Microorganisms inhabiting the digestive tract contribute to the breakdown, transformation and utilization of dietary nutrients. Gut bacteria can degrade complex carbohydrates, proteins and lipids, synthesize vitamins and other bioactive metabolites, and influence intestinal epithelial function and nutrient transport (Nayak, 2010; Talwar *et al.*, 2018; Egerton *et al.*, 2018). Nutrition in fish should therefore be seen not solely as an interaction between diet and host enzymes but as a host–microbe metabolic system. The contribution varies among species with feeding strategy, trophic position, digestive anatomy, intestinal transit time, water temperature and habitat (Sullam *et al.*, 2012; Egerton *et al.*, 2018). Herbivorous and omnivorous fishes encounter substantial plant polysaccharides and complex carbohydrates, whereas carnivorous fishes consume diets richer in protein and lipid, selecting for microorganisms with different metabolic capabilities (Merrifield and Rodiles, 2015; Singh *et al.*, 2025).

4.1 Microbial contribution to digestion

Fish possess endogenous digestive enzymes produced by the stomach, pancreas and intestinal tissues, but gut microorganisms supplement host digestion by producing additional enzymes and transforming dietary compounds that may otherwise be incompletely digested (Nayak, 2010; Ray *et al.*, 2012). They participate in the degradation of carbohydrates and complex polysaccharides, proteins and peptides, lipids, cellulose and hemicellulose, and chitin and other structural carbohydrates. Intestinal bacteria produce amylases, cellulases, xylanases, chitinases, proteases and lipases, converting complex molecules into smaller compounds more readily absorbed; fermentation of complex carbohydrates, for example, generates organic molecules and short-chain fatty acids that host tissues may use (Ray *et al.*, 2012; Talwar *et al.*, 2018). This is particularly important for fishes eating plant material, while carnivores may derive greater microbial contributions from protein and lipid transformation. Feeding habit therefore acts as an ecological filter shaping the gut microbiome (Sullam *et al.*, 2012; Egerton *et al.*, 2018).

4.2 Microbial enzyme production

A major nutritional function of gut microorganisms is production of extracellular digestive enzymes that complement endogenous fish enzymes. Important microbial enzymes include carbohydrases (amylase, cellulase, xylanase, β -glucosidase), proteolytic enzymes (protease, peptidase), lipolytic enzymes (lipase, phospholipase) and other enzymes (chitinase, phytase). Cellulolytic bacteria break down cellulose and related plant polymers, while proteolytic bacteria hydrolyse proteins into peptides and amino acids (Ray *et al.*, 2012; Ringo *et al.*, 2016). This is relevant to aquaculture because plant-based feed ingredients introduce complex carbohydrates and antinutritional components that some fish digest inefficiently; microbial activity may improve utilization of alternative ingredients and feed efficiency (Ringo *et al.*, 2016; Dawood *et al.*, 2019). Phytase-producing microorganisms can also degrade phytate, which binds minerals in plant-derived ingredients, potentially increasing availability of phosphorus and other minerals. Microbial enzyme production is thus an important mechanism through which the gut microbiome influences feed digestibility and nutrient availability.

4.3 Short-chain fatty acid production

Microbial fermentation of carbohydrates and other substrates escaping digestion in the upper GIT produces short-chain fatty acids (SCFAs): principally acetate, propionate and butyrate, with valerate and branched-chain fatty acids also occurring depending on substrates and community. SCFAs serve as energy substrates and signalling molecules and may influence intestinal physiology, epithelial integrity and immune regulation (Legrand *et al.*, 2020). Acetate is an important fermentation product that can enter systemic metabolic pathways; propionate participates in intermediary metabolism; butyrate is particularly associated with epithelial metabolism and barrier maintenance in vertebrates. Although the importance of individual SCFAs varies among species, microbial metabolites appear to be important mediators of host–microbiome communication (Llewellyn *et al.*, 2014; Legrand *et al.*, 2020), and SCFAs may also influence immunity through host signalling pathways.

Dietary substrate → *microbial fermentation* → *SCFA production* → *intestinal metabolism and signalling* → *fish health*

4.4 Microbial contribution to vitamin synthesis

Gut bacteria may synthesize or transform B-group vitamins, including vitamin B12 and folate. A notable freshwater example is *Cetobacterium somerae* (Fusobacteria), frequently detected in freshwater fish intestines and associated with vitamin B12 production (Tsuchiya *et al.*, 2008; Sugita *et al.*, 2011). B12 is essential for nucleotide synthesis and one-carbon metabolism, so microbial production may contribute to host nutritional status. However, the quantitative contribution of microbial vitamin synthesis to the requirements of different species remains incompletely understood and is an important area for future research, since conventional nutrition studies focus on dietary vitamin content.

4.5 Microbiome and nutrient absorption

Microorganisms influence nutrient absorption directly, by degrading complex dietary compounds, and indirectly, through metabolites that modify epithelial structure and function. The intestinal microbiome can influence amino acid, fatty acid, carbohydrate, mineral and vitamin availability, epithelial integrity and expression of nutrient transport systems (Nayak, 2010; Talwar *et al.*, 2018). A healthy community supports efficient assimilation, whereas dysbiosis may impair intestinal function and reduce nutritional efficiency, so environmental stressors that disrupt the gut microbiota could affect fish nutrition even when diet is unchanged. This matters in aquaculture, where growth and feed conversion depend on nutrient utilization; manipulation of gut microbiota through probiotics, prebiotics and dietary strategies may improve utilization and performance (Tay *et al.*, 2025).

4.6 Role of the gut microbiome in protein metabolism

Proteins supply amino acids for growth, tissue repair, enzymes and hormones. Besides endogenous proteases, proteolytic intestinal microorganisms hydrolyse proteins and peptides into smaller molecules that are further metabolized by microbes or absorbed by the host (Ray *et al.*, 2012; Talwar *et al.*, 2018). Microbial amino acid metabolism can generate biologically active metabolites, some involved in host signalling, whereas excessive protein fermentation under particular diets may generate undesirable metabolites; microbial protein metabolism thus has both nutritional and physiological consequences.

The interaction is important in aquaculture because plant proteins, which differ from animal proteins in amino acid composition, digestibility and antinutritional factors, are increasingly used in feeds and can alter the intestinal community (Ringø *et al.*, 2016; Dawood *et al.*, 2019).

Dietary protein → microbial protein metabolism → amino acids/metabolites → intestinal absorption → growth and physiological performance

4.7 Role of the gut microbiome in lipid metabolism

Lipids are a concentrated energy source and essential components of membranes, hormones and signalling molecules; many fish species require specific polyunsaturated fatty acids (PUFAs) for normal growth and development. Gut microorganisms influence lipid digestion and metabolism through interactions with dietary lipids and bile-associated processes; some possess lipolytic enzymes, and microbial metabolites can influence host lipid pathways. The microbiome may thus affect lipid digestion, fatty acid availability, absorption and transformation, lipid storage and host energy metabolism. Dietary lipid composition can itself modify the gut microbiome, creating a bidirectional relationship (Ringo *et al.*, 2016; Egerton *et al.*, 2018) that is particularly relevant when aquaculture feed formulations change.

4.8 Energy harvesting by the gut microbiome

A key contribution of the microbiome to nutrition is energy harvesting: microorganisms utilize dietary compounds poorly digested by host enzymes and convert them into metabolites the host can use. Dietary polysaccharides escaping digestion are fermented to SCFAs and other organic metabolites that enter host metabolic pathways, increasing usable dietary energy (Nayak, 2010; Legrand *et al.*, 2020). This may be particularly relevant for fish consuming plant-rich diets, and represents a form of metabolic cooperation between fish and microbiome rather than simply a digestive process.

Complex dietary substrate → microbial degradation and fermentation → SCFAs + amino acids + other microbial metabolites → absorption by intestinal epithelium → host energy metabolism → growth, maintenance and reproduction

4.9 Interaction between diet and fish gut microbiome

The relationship between nutrition and the gut microbiome is bidirectional: diet shapes microbial communities, while microorganisms influence how nutrients are processed and used (Egerton *et al.*, 2018; Talwar *et al.*, 2018). Protein level, lipid composition, carbohydrate content, fibre, plant-derived ingredients, probiotics and prebiotics modify community structure, and the resulting community influences digestion, nutrient metabolism, immune function and growth. It is a dynamic feedback system rather than a one-way interaction:

Diet → gut microbial composition → microbial metabolites → nutrient availability → fish physiology; and fish physiology + digestive environment → microbial selection → microbial community structure

4.10 Environmental implications of microbiome-mediated nutrition

The nutritional functions of the microbiome have implications beyond individual physiology. Changes in temperature, dissolved oxygen, pH, salinity and contaminants affect both fish physiology and gut microbial composition, and may modify microbial enzyme production, fermentation pathways and metabolite production, with potential consequences for nutrient utilization and fish performance (Yoon *et al.*, 2026).

5. Fish Microbiome and the Immune System

Fish-associated microorganisms are not passive inhabitants of the gut and mucosal surfaces; they participate actively in the development, regulation and functioning of host immunity, interacting with epithelial cells, mucus, innate immune receptors and immune cells to influence both local mucosal and systemic responses (Llewellyn *et al.*, 2014; Legrand *et al.*, 2020). The interaction is bidirectional: the host immune system regulates colonization and community structure, while microorganisms influence immune development and responsiveness. Germ-free and microbiota-manipulated models demonstrate this: in zebrafish, microbial colonization is associated with development and maturation of innate immune responses (Rawls *et al.*,

2004; Roeselers *et al.*, 2011). The microbiome can thus be regarded as an important component of the fish immune system and mucosal defence network.

5.1 Gut microbiome and mucosal immunity

The gut is one of the largest interfaces between fish and the external environment, with dietary and environmental microorganisms and potential pathogens entering continuously, making intestinal immune protection essential. Commensal microorganisms occupy ecological niches and consume nutrients required by pathogens, and some produce antimicrobial substances, bacteriocins and other inhibitory metabolites (Nayak, 2010; Llewellyn *et al.*, 2014). Microbial-associated molecular patterns are recognized by pattern-recognition receptors, including Toll-like receptors, and controlled microbial stimulation contributes to immune maturation and intestinal immune homeostasis (Rauta *et al.*, 2012; Legrand *et al.*, 2020). Excessive or inappropriate stimulation, however, may produce inflammation, so homeostasis depends on an appropriate relationship between microbes and host immunity.

Gut microorganisms → microbial signals → immune-cell activation/regulation → mucosal defence → pathogen resistance

5.2 Microbiome and innate immunity

Unlike mammals, fish rely heavily on innate immunity, although they also possess an adaptive system. Innate mechanisms include physical barriers, mucus, antimicrobial compounds, complement, phagocytic cells, cytokines and pattern-recognition receptors. Beneficial microorganisms can stimulate immune surveillance and appropriate activation of immune pathways without excessive inflammation (Llewellyn *et al.*, 2014; El-Son *et al.*, 2025), and the gut microbiome is an important determinant of immune homeostasis and disease resistance in cultured fish. Intestinal microorganisms influence macrophages, neutrophils and other leukocytes, and germ-free models show that colonization affects innate immune development, including neutrophil responses (Rawls *et al.*, 2004; Roeselers *et al.*, 2011). During environmental stress, if pollution, temperature stress or poor nutrition disrupts the microbiome, the resulting dysbiosis may alter immune signalling and increase disease susceptibility.

5.3 Microbiome and intestinal barrier integrity

The intestinal epithelium is a physical barrier separating the internal environment from the external environment and its microbes, preventing uncontrolled movement of microorganisms and harmful molecules across the intestinal wall. Beneficial communities support epithelial homeostasis, whereas dysbiosis may be associated with impaired barrier function and inflammation (Legrand *et al.*, 2020; Yoon *et al.*, 2026); compromised gut-barrier integrity and oxidative stress are recurring consequences of environmental stressors affecting gut microbial communities. Contaminants such as heavy metals, pesticides, pharmaceuticals and microplastics may alter community structure while damaging intestinal tissues, so microbiome disruption and intestinal injury may reinforce one another.

Environmental stressor → microbiome alteration → epithelial damage → increased permeability → inflammation → impaired fish health

5.4 Microbial metabolites and immune regulation

Microbial metabolites act as signalling molecules communicating with host tissues. Important examples are short-chain fatty acids, organic acids, amino-acid-derived metabolites, bacterial cell-wall components and other secondary metabolites, which influence epithelial function, inflammatory pathways and immune-cell activity (Legrand *et al.*, 2020). SCFAs, particularly acetate, propionate and butyrate, have received considerable attention because they influence epithelial metabolism and immune signalling; although roles and concentrations differ among species, microbial fermentation is an important route through which dietary substrates influence host immune physiology. Microbial effects on fish immunity should therefore increasingly be understood through a functional rather than purely taxonomic framework.

5.5 Microbiome and pathogen resistance

A stable microbiome provides colonization resistance: resident microorganisms prevent pathogens from establishing by competing for nutrients, occupying epithelial attachment sites, producing antimicrobial compounds, modifying the local

chemical environment and stimulating host immune responses. This is particularly important because fish are continuously exposed to microorganisms in water, sediment and food. Important pathogens, including species of *Aeromonas*, *Vibrio*, *Edwardsiella*, *Flavobacterium* and *Streptococcus*, can exploit weakened host defence or disturbed microbial communities, and disruption of fish microbiomes is associated with increased abundance of potential pathogens, making dysbiosis an important component of disease ecology (Xavier *et al.*, 2024).

Stable microbiome → colonization resistance → immune homeostasis → disease resistance; whereas environmental stress → dysbiosis → reduced colonization resistance → pathogen proliferation → disease

6. Fish Microbiome and Dysbiosis

Dysbiosis is a disturbance in the normal structure, composition or function of a microbial community. In fish it may involve changes in diversity, shifts in dominant taxa, proliferation of opportunistic microorganisms, loss of beneficial microorganisms or altered metabolic activity. It should not be defined simply as an increase or decrease in diversity, because a community can change substantially without adverse effects on the host; microbial function and host physiological responses must also be considered (Xavier *et al.*, 2024).

6.1 Causes of dysbiosis

Dysbiosis may result from temperature fluctuations, salinity changes, hypoxia, poor water quality, eutrophication, heavy metals, pesticides, pharmaceuticals, antibiotics, microplastics, pathogens, dietary changes, poor nutritional conditions, aquaculture stress and high stocking density. Environmental factors and pollutants can disrupt fish gut microbiota, with recurring effects including altered diversity, impaired intestinal barrier function and oxidative stress (Yoon *et al.*, 2026).

6.2 Dysbiosis and fish health

Dysbiosis may affect fish health through several interconnected pathways, and may also influence digestion and nutrient utilization, since altered microbial enzyme production or fermentation can change nutrient availability. Heavy metals, antibiotics, petroleum-derived compounds and microplastics can alter the composition and metabolic activity of fish gut microbiota (Feng *et al.*, 2025).

Dysbiosis → altered microbial metabolites → intestinal dysfunction → inflammation → impaired immunity → increased disease susceptibility

6.3 Dysbiosis as a consequence of environmental stress

The microbiome acts as a biological intermediary between environmental stress and fish health. A temperature change, for example, directly affects fish metabolism while simultaneously altering microbial growth and community composition; likewise, pollutant exposure → altered microbiome → altered metabolism and immunity → physiological stress, which makes dysbiosis particularly relevant to environmental toxicology. Responses are not uniform: they depend on body site, host species, stressor type, intensity and environmental context. External skin and gill communities may be particularly responsive to environmental temperature and disease, whereas gut microbiomes can be strongly influenced by salinity and chemical treatments (Xavier *et al.*, 2024; McMurtrie *et al.*, 2025).

7. Fish Microbiome as a Biomarker of Environmental Pollution

Traditional monitoring relies on physicochemical measurements such as temperature, pH, dissolved oxygen, conductivity, nutrient concentrations and contaminant levels, which describe environmental conditions rather than the biological response of organisms. Microbiome analysis offers a complementary approach because microbial changes can reflect the biological consequences of exposure, and intestinal microbiota have been proposed as biomarkers for evaluating pollutant toxicity in fish (Feng *et al.*, 2025).

7.1 Heavy metals

Cadmium, lead, mercury, chromium, copper and zinc can alter microbial communities through direct toxicity and indirect effects on host physiology. Metal exposure may produce oxidative stress and inflammation while changing the abundance of particular bacterial groups, so microbiome profiling could complement conventional measurements of metal concentrations in water, sediment and fish tissues.

7.2 Pesticides

Pesticides may alter bacterial community composition, microbial metabolism and intestinal integrity; gut microbial dysbiosis is an important component of pesticide-associated intestinal toxicity in fish (2025).

Pesticide → gut microbiome disruption → intestinal injury → inflammation/oxidative stress → fish health effects

7.3 Pharmaceuticals and antibiotics

Pharmaceutical residues expose fish to chronic low concentrations of biologically active chemicals. Antibiotics can directly alter microbial communities and select for resistant microorganisms, so fish microbiomes may provide information about both chemical exposure and biological consequences.

7.4 Microplastics

Microplastics interact with fish microbiomes through ingestion and contact with the gastrointestinal tract; their surfaces support microbial biofilms and may transport microorganisms and contaminants. Microplastic-induced dysbiosis is considered an important pathway linking plastic exposure to intestinal injury and altered host physiology (Yoon *et al.*, 2026).

8. Microplastics–Fish Microbiome Interactions

Microplastics are a major environmental concern because of their persistence and widespread distribution. Fish may ingest them directly from water or sediment or indirectly through contaminated prey. Once ingested, they may interact with the intestinal epithelium and resident microorganisms, while their surfaces become colonized by the plastisphere, creating a three-way interaction: microplastic ↔ microorganisms ↔ fish intestine. Exposure may alter microbial diversity and abundance and can be associated with intestinal inflammation, oxidative stress and barrier dysfunction, but effects depend strongly on particle size, polymer type, concentration, exposure duration and fish species. Microplastics may also carry other contaminants, so combined exposure may produce effects that differ from those of either stressor alone.

9. Environmental Change and Fish Microbiome

Fish microbiomes are continuously exposed to variation in temperature, dissolved oxygen, pH, salinity, nutrients, photoperiod, food availability and hydrological conditions; temperature and other water-quality variables produce measurable changes in fish-associated microbiomes (Xavier *et al.*, 2024; McMurtrie *et al.*, 2025). Temperature affects both microbial growth and fish metabolic rate; warming may favour some taxa while suppressing others. Dissolved oxygen: hypoxia can modify fish metabolism and stress physiology and may indirectly affect the gut microbial environment. Salinity is particularly important for osmoregulating fishes and can alter microbial composition and host responses. Seasonal variation simultaneously alters water temperature, food availability, hydrology and environmental microbial communities, so fish microbiomes may exhibit seasonal turnover.

10. Fish Microbiome and Aquatic Pathogens

A healthy microbial community may prevent pathogen establishment, whereas environmental stress and dysbiosis create opportunities for opportunistic pathogens, including *Aeromonas*, *Vibrio*, *Edwardsiella*, *Flavobacterium* and *Streptococcus*. Microbial competition, antimicrobial compounds, nutrient availability and host immunity all contribute to resistance (Llewellyn *et al.*, 2014; Xavier *et al.*, 2024). Microbiome manipulation, including probiotics, prebiotics, synbiotics and microbiome engineering, is increasingly investigated as an alternative to conventional disease control (El-Son *et al.*, 2025).

11. Fish Microbiome and Antibiotic Resistance

Antimicrobial resistance is an important connection between fish microbiomes and environmental health. Fish and aquaculture environments can become reservoirs of antibiotic-resistant microorganisms and resistance genes, particularly under intensive aquaculture where repeated antibiotic exposure strongly influences community structure.

Antibiotic exposure → susceptible bacteria eliminated → resistant bacteria selected → resistance genes enriched → environmental dissemination

Microbiome-based approaches that reduce dependence on antibiotics, including probiotics, prebiotics and targeted microbial interventions, are increasingly investigated (El-Son *et al.*, 2025). The topic also connects the fish microbiome with the One Health framework, because antimicrobial resistance crosses environmental, animal and human health boundaries.

12. Fish Microbiome and Aquaculture

Fish growth, feed efficiency, disease resistance and survival in aquaculture can all be influenced by microbial communities. Manipulation strategies include probiotics (live beneficial microorganisms given to fish or incorporated into feed), prebiotics (substrates that selectively stimulate beneficial microorganisms), synbiotics (combined probiotics and prebiotics), postbiotics (beneficial microbial products or metabolites) and phytogenic additives (plant-derived compounds that may influence microbial communities and host immunity). Systematic reviews emphasize growing interest in these approaches for improving fish health and reducing dependence on antibiotics (Tay *et al.*, 2025; El-Son *et al.*, 2025).

13. Fish Microbiome and Ecosystem Function

Fish-associated microorganisms may influence broader ecological processes through their roles in metabolism and nutrient transformation. Fish contribute to nutrient cycling through feeding, digestion and excretion, and their microbial communities can modify the transformation of dietary nutrients and therefore the forms in which nutrients are returned to the environment. This supports the concept of fish as holobionts, in which host and microorganisms jointly contribute to ecological processes.

Fish microbiome → host metabolism → nutrient uptake/excretion → food-web interactions → ecosystem processes

14. Fish Microbiome and Biodiversity

Fish species differ in their microbiomes because of differences in evolutionary history, diet, habitat, physiology, behaviour and environmental exposure, so microbiome diversity may provide additional information about ecological niches. Microbiome studies may assist in characterizing fish populations, detecting environmental changes, understanding host adaptation, identifying conservation priorities, monitoring endangered species and understanding species–environment interactions. However, microbiome composition should not yet be treated as a definitive taxonomic marker because communities vary considerably with environmental conditions and season.

15. Modern Techniques for Studying Fish Microbiomes

Research has progressed from culture-based approaches toward high-throughput molecular methods. Culture-dependent methods isolate and cultivate microorganisms on selective or general media; they yield live isolates for functional testing but detect only organisms that grow under the chosen conditions. 16S rRNA sequencing is widely used to characterize bacterial communities, giving taxonomic composition, relative abundance, alpha diversity and beta diversity. Its sequencing investigates fungal communities. Metagenomics (shotgun) reveals the genetic composition of entire communities and potential functional genes. Meta transcriptomics examines microbial RNA and therefore actively expressed genes. Metabolomics measures small molecules and microbial/host metabolites, connecting composition with physiological function. Multi-omics, combining metagenomics + meta transcriptomics + metabolomics + host transcriptomics, gives a more comprehensive understanding of fish-microbe interactions.

16. Fish Microbiome as a Tool for Environmental Monitoring

The use of fish microbiomes as early-warning indicators is one of the most promising environmental applications. Conventional monitoring measures water → contaminant concentration; microbiome monitoring can add contaminant → biological response → microbial alteration. Fish intestinal communities may serve as biomarkers for assessing the biological effects of pollutants (Feng *et al.*, 2025). A future framework could integrate physicochemical parameters + contaminant analysis + fish biomarkers + microbiome analysis rather than relying on a single indicator. Standardized sampling procedures, reference microbiomes, seasonal baselines and functional validation are still required before microbiome-based assessment becomes routine.

17. Restoration and Conservation Applications

Microbiome research could contribute to captive breeding, fish reintroduction, stock enhancement, disease prevention, habitat restoration, probiotic supplementation and conservation of threatened populations. Captive-raised fish experience diets and microbial environments substantially different from the wild, and microbiome manipulation could help prepare them for conditions encountered after release. The field is still developing, and interventions must be evaluated carefully to avoid introducing inappropriate microorganisms into natural ecosystems.

18. Conclusion

The fish microbiome is a fundamental component of aquatic organisms and links fish physiology with the surrounding environment. Fish should be considered not as isolated organisms but as complex host–microbe systems in which communities of the gut, skin, gills, oral cavity and other tissues contribute to nutrition, metabolism, immune regulation, pathogen resistance and homeostasis. Their composition and function are influenced by intrinsic host characteristics and extrinsic factors, including temperature, pH, dissolved oxygen, salinity, food availability, habitat and season (Egerton *et al.*, 2018; Legrand *et al.*, 2020; Llewellyn *et al.*, 2014; Sullam *et al.*, 2012). Gut microorganisms contribute to digestion, production of metabolites such as SCFAs, nutrient utilization, energy metabolism and intestinal integrity, while skin and gill microbiomes form a microbial interface with the environment that inhibits opportunistic pathogens, produces antimicrobial compounds and interacts with the immune system. Environmental stressors can cause dysbiosis, impair gut barrier function and alter immune and metabolic processes, demonstrating the close relationship between environmental quality and microbiome stability (McMurtrie *et al.*, 2025; Yoon *et al.*, 2026).

Environmental degradation can be reflected at the microbial level before severe effects become apparent at population or ecosystem level. Heavy metals, pesticides, petroleum-derived compounds, antibiotics, pharmaceuticals and microplastics can modify the composition, diversity and metabolic activity of fish-associated communities through reduction of beneficial microorganisms, proliferation of opportunistic taxa, altered metabolic pathways and disrupted host–microbe interactions; fish intestinal microbiota are potential indicators of the toxic effects of heavy metals, antibiotics, petroleum hydrocarbons and microplastics (Feng *et al.*, 2025). This makes the fish microbiome a promising component of aquatic environmental assessment. Conventional monitoring remains essential but may not fully describe biological consequences, particularly under mixtures or chronic low concentrations; changes in microbial diversity, community structure, functional genes and

metabolites could be incorporated into a broader biomarker framework for ecosystem health (Feng *et al.*, 2025; Yoon *et al.*, 2026).

However, reliable use as a biomarker requires considerable methodological development. Communities vary naturally with species, age, sex, developmental stage, diet, habitat, season, geography and sampling site, so distinguishing natural variation from stressor-induced dysbiosis is a major challenge, as is deciding whether a change reflects direct exposure, host response, dietary alteration, infection or several interacting factors (Sullam *et al.*, 2012; Legrand *et al.*, 2020); skin and gill responses are also highly context-dependent. High-throughput sequencing and omics (16S rRNA amplicon sequencing, shotgun metagenomics, metatranscriptomics, metabolomics, proteomics), integrated with physicochemical measurements, contaminant analysis, histopathology, biochemical biomarkers and ecological indices, could give a more comprehensive assessment.

Dysbiosis may reduce colonization resistance and weaken mucosal barriers, increasing susceptibility to opportunistic pathogens, while infections and antimicrobial treatments can themselves alter communities, creating feedback between microbiome, stress and disease. This is important in aquaculture, where high stocking density, intensive feeding, handling, poor water quality and outbreaks pressure fish–microbe interactions; probiotics, prebiotics, synbiotics and dietary interventions are promising ways to improve fish health and reduce reliance on chemical therapeutics (Tay *et al.*, 2025; Yoon *et al.*, 2026). The concept also has ecological implications for nutrient cycling, organic matter transformation, host productivity and trophic interactions, helping connect molecular-level responses with population health, biodiversity and ecosystem functioning in systems simultaneously exposed to pollution, habitat modification, climate change, eutrophication, emerging contaminants and biological invasions. Climate change (rising temperature, altered precipitation, changes in dissolved oxygen, ocean warming and acidification) will further complicate these interactions, and stressors may act synergistically, so future work should move beyond single-factor experiments to multiple stressors under realistic field conditions (Yoon *et al.*, 2026).

Several priorities remain: standardized protocols for sampling, DNA extraction, sequencing, bioinformatics and interpretation; reference microbiome profiles for ecologically important species across habitats and seasons; long-term field studies to determine whether changes are persistent, reversible or linked to population and ecosystem change; and validated biomarkers that respond consistently to specific stressors while remaining robust to natural variation. The absence of standardized signatures currently limits regulatory application, and conventional biomonitoring itself lacks globally standardized approaches. Combining microbiome data with environmental DNA, metabolomics, transcriptomics, contaminant measurements, physiological biomarkers and ecological observations, aided by machine learning and AI, could enable predictive monitoring systems that detect environmental deterioration early.

Overall, the fish microbiome is a biological interface connecting environmental conditions with fish health and ecosystem functioning. Its sensitivity to environmental variation, together with its involvement in immunity, nutrition, metabolism and pathogen resistance, makes it a promising target for aquatic environmental research, but it should not be considered a stand-alone indicator; its greatest value will emerge when integrated with physicochemical parameters, contaminant concentrations, conventional biological indicators and ecosystem-level assessments, moving from detecting contamination to understanding its biological consequences. Research on fish–microbe–environment interactions connect microbiology, fish biology, ecology, environmental toxicology and aquaculture, and continued development of standardized methodologies, long-term ecological datasets and multi-omics approaches will be essential for translating it into practical applications. In future, fish microbiome profiles may become an important component of early-warning systems for aquatic pollution, fish disease surveillance, ecosystem health assessment and conservation planning, contributing to more sensitive, mechanistic and biologically meaningful approaches for protecting aquatic biodiversity and sustaining healthy aquatic ecosystems.

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