

Microbial ecology offers a way to address this gap. An aquaculture animal lives within a connected microbial landscape comprising the surrounding water, sediment, tank or cage surfaces, feed, biofilms, and microorganisms associated with the gut, gills, skin, and mucus. These assemblages are not static. They respond to animal development, temperature, salinity, nutrient loading, husbandry, disease, and treatment. In a 13-month survey of Sanggou Bay mariculture, for example, seasonality strongly structured bacterioplankton communities, while potentially pathogenic *Vibrio* became more prominent during late-summer and autumn high-risk periods (Lu et al., 2025). Longitudinal studies in fish, shrimp, and hatchery shellfish similarly show that temporal context is indispensable when microbiomes are interpreted as health indicators (Cram et al., 2024; Bui et al., 2026).

The concept of microbial dysbiosis extends this perspective beyond pathogen abundance. Dysbiosis refers to an unfavorable departure from a host- or system-associated microbial state and may include community restructuring, loss of potentially protective organisms, proliferation of opportunists, altered interactions, or changed microbial functions. Reviews of aquaculture microbiomes have proposed such changes as potential disease biomarkers, while also warning that a universal “healthy microbiome” has not yet been defined (Infante Villamil et al., 2021; Mougin and Joyce, 2023). The distinction matters: a microbial change can precede disease, result from disease, or simply reflect a normal environmental transition.

Technological advances make this ecological information increasingly accessible. Targeted qPCR and digital PCR provide sensitive quantification; 16S rRNA sequencing reveals broad community structure; shotgun metagenomics can recover genes and genomes; metabolomics and transcriptomics add functional information; and rapid approaches such as flow cytometry and isothermal amplification shorten the interval between sampling and interpretation. Field-oriented LAMP assays for marine *Vibrio* illustrate how molecular detection is beginning to move from specialized laboratories toward farm-side surveillance (Rahman et al., 2022; Pu et al., 2026).

The purpose of this review is therefore not to present microbiome sequencing as a replacement for veterinary diagnosis, water-quality monitoring, or conventional biosecurity. Rather, it examines how microbial information can be integrated with those practices to create a more anticipatory health-management system. The discussion moves from microbial ecology and monitoring technologies to candidate health indicators, environmental drivers, early-warning strategies, practical management models, and applications across major marine aquaculture systems. The central argument is that the greatest value of microbial monitoring lies not in identifying a universal “good” or “bad” bacterium, but in detecting meaningful deviations from a well-characterized biological baseline early enough to support proportionate management.

2 Microbial Communities and Health in Marine Aquaculture Systems

2.1 Composition and ecological functions of microbial communities

Marine aquaculture systems contain overlapping but non-identical microbial habitats. Water-column communities respond rapidly to temperature, nutrient availability, phytoplankton, dissolved organic matter, and hydrodynamics, whereas sediment and biofilm communities experience stronger gradients in oxygen and organic loading. Host-associated communities add another level of selection because the gut, gills, skin, and mucus provide distinct physicochemical conditions. Even within a single shrimp, gastrointestinal compartments can contain different community structures, emphasizing that “the microbiome” is not one uniform biological compartment (Garibay-Valdez et al., 2021).

These microorganisms collectively contribute to organic matter degradation and carbon, nitrogen, and sulfur transformations while competing, cooperating, and exchanging metabolites with one another. In biofloc shrimp systems, rearing-water communities show clear succession during the production cycle, with different bacterial groups becoming prominent at different stages (Kim et al., 2022). Metagenomic comparison of grouper cage waters and nearby non-aquaculture waters has likewise linked aquaculture-related nutrient enrichment with shifts in both microbial composition and predicted biogeochemical functions (Liu et al., 2024).