

2.2 Host-Microbiome interactions in cultured marine animals

Host-associated microbiota occupy interfaces where nutrition, immunity, and environmental exposure meet. Gut microorganisms can participate in nutrient transformation and production of metabolites, while mucosal communities on the skin and gills interact directly with host defenses and incoming environmental microorganisms. Research across fish increasingly supports the view that host identity, development, environment, and diet jointly structure these communities rather than one factor acting independently (Yajima et al., 2023; Zhao et al., 2023).

A protective microbiome should nevertheless be understood functionally rather than as a fixed list of beneficial taxa. Some resident organisms may occupy niches that would otherwise be available to pathogens, produce antagonistic compounds, or influence mucosal immune responses. Conversely, a normally harmless member may become problematic when environmental conditions or host defenses change. This context dependence is especially important in aquaculture, where the same bacterial genus may contain commensal, probiotic, and pathogenic strains. Consequently, genus-level sequence data should rarely be interpreted as direct evidence of disease or protection (Mougin and Joyce, 2023).

2.3 Microbial homeostasis and dysbiosis

Microbial homeostasis is better described as a resilient range than a constant community composition. A healthy animal or production system can undergo substantial temporal turnover while retaining important ecological functions. Atlantic salmon gill communities, for example, restructure through the marine production cycle, and not every change in richness or diversity corresponds to poorer gill health (Clinton et al., 2024). This finding argues against using a single diversity index as a universal health threshold.

Dysbiosis becomes more informative when several signals converge: abrupt community turnover, enrichment of opportunists, loss of persistent host-associated taxa, altered network structure, functional changes, and measurable deterioration of host or environmental condition. In shrimp white feces syndrome, experimental work provided evidence that altered intestinal microbiota can contribute to disease processes rather than merely reflect them (Huang et al., 2020). Yet causality should not be assumed in every system. Oyster hatchery research has shown that some microorganisms enriched during production crashes appear to proliferate after host deterioration rather than initiate it (Cram et al., 2024).

3 Microbial Monitoring Technologies for Marine Aquaculture

3.1 Conventional microbial monitoring methods

Culture-dependent microbiology remains useful because isolates can be phenotyped, tested for pathogenicity or antimicrobial susceptibility, preserved, and examined experimentally. Selective media and colony enumeration are relatively inexpensive and provide information on culturable populations that molecular surveys alone cannot deliver. Their principal weakness is incomplete coverage: many environmental microorganisms are difficult to culture under routine laboratory conditions, while culture and biochemical identification may take longer than desirable during rapidly developing disease events (Rahman et al., 2022).

The most practical strategy is therefore complementary rather than competitive. Culture is particularly valuable when an isolate is required for challenge testing, antimicrobial susceptibility, genomic characterization, or probiotic development; sequence-based and molecular methods are better suited to broad surveillance and rapid detection. Maintaining this distinction prevents the common error of treating a DNA sequence as equivalent to a viable pathogenic organism.

3.2 Molecular detection of target microorganisms

PCR and qPCR transformed pathogen surveillance by allowing specific microbial targets to be detected without lengthy cultivation. qPCR additionally estimates target abundance, making it more useful for longitudinal monitoring than simple presence/absence testing. Digital PCR partitions reactions and can provide absolute nucleic-acid quantification without a conventional calibration curve. In seawater experiments, a propidium-monoazide-ddPCR approach was able to distinguish viable-target DNA from dead-cell DNA for toxigenic *Vibrio cholerae*,