

parahaemolyticus was specifically tested with shrimp aquaculture water and designed around field deployment (Rahman et al., 2022; Pu et al., 2026).

Flow cytometry offers a different advantage: it rapidly measures phenotypic distributions of microbial cells without first knowing their taxonomy. Machine-learning analysis has shown that flow-cytometric fingerprints can contain information associated with bacterial community composition, although taxonomic abundance prediction remains imperfect (Heyse et al., 2021). In barramundi hatcheries, FCM and 16S sequencing showed complementary trends, suggesting a feasible future division of labor in which rapid fingerprints flag unusual community states and sequencing is reserved for diagnostic clarification (Figure 1) (Bui et al., 2026).

	Taxonomic breadth	Functional resolution	Quantification capability	Analytical speed	Field deployability	Operational complexity / cost
Culture-dependent methods	Low	Low	Medium	Medium	Low	Medium
qPCR / dPCR	Low	Low	High	High	Medium	Medium
16S rRNA sequencing	High	Medium	Medium	Medium	Low	High
Shotgun metagenomics	High	High	Medium	Low	Low	High
Multi-omics	High	High	Low	Low	Low	High
Flow cytometry (FCM)	Low	Low	Medium	High	High	Medium
LAMP / biosensors	Low	Low	Medium	High	High	Low

Low
 Medium
 High

Methods are complementary; no single platform is optimal for all monitoring purposes.

Figure 1 Comparison of major microbial monitoring technologies for marine aquaculture health management

4 Microbial Indicators for Health Assessment in Marine Aquaculture

4.1 Potential pathogenic microorganisms as risk indicators

Potential pathogens remain necessary indicators because an increasing pathogen burden can mark rising infection pressure. In marine aquaculture, *Vibrio*, *Photobacterium*, and *Tenacibaculum* are particularly relevant in many fish, shrimp, and shellfish contexts, while *Aeromonas* and other opportunistic genera are important in particular host and environmental settings. Long-term Sanggou Bay monitoring found seasonal enrichment of potentially pathogenic *Vibrio*, and experimental shrimp studies show that *Vibrio harveyi* exposure can restructure the gut community (Deris et al., 2022; Lu et al., 2025).

Nevertheless, genus-level detection alone is a weak diagnostic criterion. Different *Vibrio* lineages have sharply different ecological roles and virulence potential. Oyster hatchery monitoring provides a useful warning: *Vibrio* groups observed during some larval crashes appeared more likely to respond to deterioration than to initiate it (Cram et al., 2024). Pathogen surveillance should therefore combine abundance, species or strain identity where possible, virulence markers, host signs, and environmental context.