

5 Major Factors Shaping Microbial Health in Marine Aquaculture

5.1 Water quality and environmental conditions

Microbial communities respond quickly to the physical and chemical environment. Temperature influences growth rates and seasonal succession; salinity filters taxa according to osmotic tolerance; dissolved oxygen affects aerobic and anaerobic processes; and pH, ammonia, nitrite, and organic matter alter both microbial metabolism and host stress. In Sanggou Bay, temperature, dissolved oxygen, and transparency were significantly associated with bacterioplankton dynamics and seasonal pathogen patterns (Lu et al., 2025).

These relationships are rarely linear or universal. Experimental shrimp work showed that salinity interacted with *V. harveyi* exposure to reshape gut-community structure and network properties (Deris et al., 2022). Monitoring schemes should consequently interpret microbial signals together with environmental trajectories rather than treating water chemistry and microbiology as separate data streams.

5.2 Stocking density and culture intensity

Higher culture intensity increases feed demand, waste production, host-to-host contact, and microbial exchange. These processes can stimulate heterotrophic growth and create niches for opportunistic organisms, particularly when oxygen supply or waste removal becomes limiting. The effect is not simply “high density causes disease”; management technology determines how biological loading is handled.

For this reason, microbial monitoring may be most useful when interpreted relative to biomass and production stage. The same bacterial density can have different meanings early and late in a production cycle. Longitudinal biofloc observations demonstrate that microbial succession accompanies increasing culture age and organic loading, suggesting that stage-specific reference ranges are preferable to one farm-wide threshold (Kim et al., 2022).

5.3 Feed and feeding management

Feed influences microbial health through two pathways. Consumed feed changes the intestinal chemical environment and substrate availability, while uneaten feed and fecal material enter the surrounding system and stimulate environmental microorganisms. The resulting changes can alter oxygen demand, nutrient transformations, biofilm growth, and microbial exchange between water and host.

Feed management should therefore be included in microbial interpretation even when it is not the primary research variable. Studies comparing aquaculture management systems show that environmental and intestinal microbiomes respond to production practices, including probiotic and biofloc approaches (Waiho et al., 2023). Future farm baselines should record major diet transitions and feeding-rate changes so that ordinary nutritional responses are not misclassified as disease warnings.

5.4 Water exchange, aeration, and system management

Water exchange and aeration alter microbial dispersal, oxygenation, particle suspension, and resource availability. Recirculating systems add biological filtration, creating engineered microbial niches that perform essential nitrification and other transformations. These microorganisms can also disperse between system water and animal surfaces, making the boundary between “environmental” and “host-associated” microbiota particularly porous.

Atlantic salmon raised in RAS showed temporal changes in skin, gill, and water microbiomes, including a period interpreted as possible dysbiosis that later recovered (Lorgen-Ritchie et al., 2022). In biofloc shrimp systems, microbial communities also changed markedly as the system matured (Kim et al., 2022). These observations favor adaptive baselines tailored to system design rather than comparisons with a supposedly universal marine microbiome.

5.5 Antibiotics, disinfectants, and other chemical interventions

Chemical disease control can alter non-target microorganisms as well as pathogens. This matters because treatment may temporarily suppress one pathogen while changing ecological niches, selecting resistant populations, or disrupting host-associated communities. In gilthead seabream, bacterial infection and subsequent oxytetracycline