

FISH GUT MICROBIOME IN AQUACULTURE: ROLE IN NUTRITION, IMMUNITY, AND DISEASE RESISTANCE: A REVIEW

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Abstract

Aquaculture is one of the fastest growing food sectors, providing a major source of animal protein throughout the world. However, its productivity is often challenged by feed inefficiency, disease outbreaks and environmental stress. The fish gut microbiome has emerged as a vital factor linking diet, immunity and disease resistance. It consists of diverse beneficial microorganisms that aid in nutrient digestion, vitamin synthesis and the development of a strong immune system while also preventing the growth of harmful pathogens. A balanced microbiota improves feed conversion, growth performance and overall fish health. In contrast, an imbalance or dysbiosis in gut microbes may lead to poor digestion and higher disease susceptibility. Recent research highlights use of probiotics, prebiotics and functional feeds to modulate the gut microbiome, that improve disease resistance naturally. Understanding these microbial interactions provides new opportunities for sustainable aquaculture and eco-friendly fish health management.

Introduction

Aquaculture is one of the fastest-growing food producing sectors worldwide and plays a vital role in meeting global protein demands. It has a major impact on the economy and food security, particularly in developing nations. More than half of all fish consumed worldwide are already sourced from aquaculture, according to recent estimates but the industry's explosive growth also brings with it problems including disease outbreaks, environmental stress and inefficient feed (Fisheries, 2018). Therefore, sustainable aquaculture relies on both better farm management and enhancing fish health through microbiological and nutritional approaches

(Rimoldi et al., 2023). The word microbiome refers to the collective genomes of all the microorganisms that lives in a specific environment. These microbes and their host develop a symbiotic connection in fish which helps in metabolic efficiency and defense against harmful germs. Diet, species type, salinity of water and ecological circumstances are some of the variables that affect the gut microbiomes stability and diversity. Research indicates that microbial composition and functions are greatly influenced by hosts environment and nutrition which in turn affects fish physiology as a whole (Kim et al., 2021).

The immune system, microbial interactions and nutritional digestion all take place in the fish gut which is a complex and dynamic system. Like animals on land, fish have a varied collection of bacteria called the gut microbiome that live in their gastro-intestinal system. Beneficial bacteria that help with digestion, vitamin production and immunological regulation include *Lactobacillus*, *Bacillus*, *Pseudomonas*, *Aeromonas* and *Shewanella* species (Menanteau-Ledouble et al., 2022).

The gastrointestinal tract of fish is a complex ecosystem where host tissues and microbial communities interact closely. This intestinal environment is in charge of breaking down nutrients, absorbing them and preserving a barrier that keeps infections out. Together, bacteria, fungus, viruses and archaea make up the gut microbiota, sometimes mentioned to as the microbiome which is the microbial community that lives in the intestine and affects host growth, metabolism and immune function (Spilsbury et al., 2022). The gut microbiome of fish is extremely dynamic and sensitive to environmental changes because in contrast, to terrestrial animals they live in aquatic habitats where water, food and sediment are continuous sources of microbial interaction (Dhanasiri et al., 2024).

The gut microbiota of fish is becoming more widely acknowledged in aquaculture systems as a dynamic 'metabolic organ' that interacts with environmental stresses, host metabolism and feed inputs. According to metagenomic studies, teleosts share a core of dominating phyla like as Firmicutes, Fusobacteria and Proteobacteria; however, the functional repertoires of these communities differ significantly depending on the culture environment and food composition (Kanika et al., 2025). Because of its functional flexibility, microbiome engineering may play a key role in aquafeed design and system management, enabling the transition from growth measurements to microbiome-mediated health (Kanika et al., 2025). The interaction between the gut microbiota and the immune system is as significant in high-density aquaculture settings, where fish are constantly

exposed to stresses and infections. According to research, commensal bacterial taxa help fish avoid colonization and defend against pathogens by promoting mucosal immunity, improving the synthesis of mucus layers and modifying phagocyte function (Perry et al., 2020). The conclusion is obvious: in intense aquaculture settings, regulating the gut microbiota involves strengthening immunological resistance in addition to food absorption (Perry et al., 2020). The impact of the microbiome on feed usage and nutritional efficiency presents a strong argument for adopting more sustainable aquaculture methods. Research on diets high in chitin and insect meal shows how the gut microbial population may change in reaction to new substances, influencing the creation of short-chain fatty acids, the breakdown of nutrients, and the harvesting of energy (Hasan et al., 2023). This shows that feed formulations that take into consideration microbiome reactions have the potential to improve environmental sustainability and production while lowering dependency on conventional fishmeal (Hasan et al., 2023).

A crucial mediator between host physiology, ecological factors and diet conformation is the fish gut microbiota. According to recent research, good bacteria help in digestion by generating vitamins, short-chain fatty acids and enzymes that enhance nutrient absorption. At the same time, they produce antimicrobial chemicals or compete with pathogens to boost the immune system and prevent infections (Xavier et al., 2024). Dysbiosis, an imbalance that raises the risk of disease and impairs growth performance may result from changes in the microbiome composition brought on by stress, poor water quality or antibiotic abuse (Tolas et al., 2025). Due to the increasing growth of aquaculture, disease control and feed efficiency have become top economic and sustainability goals. The gut microbiota of fish has become a changeable element that connects food to immunological maturation, pathogen resistance and nutrient extraction (Luan et al., 2023). According to recent research, the composition of microbial communities varies significantly from that of terrestrial vertebrates

and is greatly impacted by aspects such as host environment, life stage and feed formulation all of which may be changed in production systems (Kim et al., 2021).

According to modern studies, altering the intestinal microbiota of fish may have a beneficial impact on the feed conversion ratio, growth rate and illness resistance of aquaculture species. For example, diets supplemented with probiotics and insect meal increased gut microbial diversity and decreased the number of dangerous infections which helped both freshwater and marine animals thrive more effectively (MDPI, 2023). Likewise, the use of functional diets and sustainable raising conditions has been associated with increased microbial diversity which improves resilience and lowers mortality in farmed fish (Ashrafi et al., 2024). Additionally, multi-omics research has shown that beneficial bacteria are essential for boosting mucosal barrier function and immune gene expression, two important defenses against pathogenic invasion. The grass carp gut microbiomes critical function in preserving host health and fostering resilience to environmental stresses was validated by a metagenomic investigation (Li et al., 2024). Thus, knowledge of the gut microbiota of fish grasps great promise for the advancement of sustainable aquaculture. Farmers may lessen their reliance on antibiotics, increase production and support ecologically friendly aquaculture systems by controlling and optimizing microbial populations through ecological practices and functional diets. In addition to enhancing fish welfare, this all encompassing strategy promotes the long term feasibility of the worldwide aqua-culture sectors (Kanika et al., 2025).

Composition and drivers of fish gut microbiomes

The dominant microbial phyla in many teleosts includes *Proteobacteria* and *Firmicutes*, with additional groups e.g., *Fusobacteria* and *Actinobacteria*, varying by species and atmosphere (Kim et al., 2021). Host habitat marine and freshwater, rearing environment like pond, tank, recirculating aquaculture systems, and diet are among the strongest determinants of

community structure, often outweighing taxonomic relatedness at higher levels (Kim et al., 2021) (Table 1). Life stage is also critical, larval and juvenile microbiomes are more dynamic and sensitive to colonization events which has implications for larviculture practices (Borges et al., 2021). One of the main elements influencing the composition of gut microbes is diet. When insect meals such as *Tenebrio molitor*, were used to replace a portion of the fishmeal of two teleost species, the intestinal microbiota responded by changing the dominant bacterial taxa. Although overall diversity did not significantly decrease, the relative abundance of taxa linked to advantageous processes rose when specific insect meal inclusions were made (Panteli et al., 2021).

One important internal element is life stage ie; larval, adolescent and adult. Early in their development, the gut microbiota of common carp (*Cyprinus carpio*) closely correlates with the type of feed and the microbiota of the pond water. As fish age, the gut microbiome becomes more stable, less impacted by ephemeral environmental microbes, and more dominated by taxa that support immunological and digestive processes (J. Zhang et al., 2024). Gut communities are also shaped by environmental bacteria, such as water and sediment, especially during early life or during open system rearing. Microbes from the biofloc and water, for instance, contribute to the gut microbial pool in largemouth bass raised in biofloc systems; this effect is more noticeable in specific environmental conditions like temperature, organic matter, dissolved oxygen, that promote the survival of aquatic microbes which may colonize the fish gut (Jin et al., 2024).

Host habitat (freshwater, marine or brackish) has strong influence over which microbial taxa are present. Fish from marine settings have gut microbiomes that are enriched for certain *Proteobacteria* and *Firmicutes* families that are less prevalent in freshwater species, according to a worldwide analysis of farmed and wild fish from numerous countries. On the other hand, freshwater species can exhibit higher abundances of *Bacteroidota* or *Fusobacteria*. Salinity, the

ionic makeup of the water and the microbiological source pools in those ecosystems are thought to be the main causes of these changes (Kanika et al., 2025). The make-up of the gut microbiome may be quickly altered by stressors including virus challenge, toxic algal blooms or abrupt changes in temperature or dissolved oxygen. For instance, exposure to a *Microcystis aeruginosa* bloom changed the metabolome and microbiome structure of fish, increasing opportunistic species and decreasing beneficial ones. These alterations frequently

occur before observable health loss (Gallet et al., 2023). Seasonality and geographic location are other significant factors. Fish from certain climatic zones had more diverse gut microbiomes, according to a study of fish from subtropical rivers and samples taken at the same location over various seasons showed changes in core taxa. In catchment regions, temperature, precipitation and nutrient runoff alter the water microbiota which in turn affects how fish assemble their guts, particularly when they are larval or juvenile (Kanika et al., 2025).

Table 1: Major Drivers Influencing the composition of fish gut microbiome in Aquaculture

Driver or Factor	Effect on Gut Microbiome Composition	Example Species	Key Observations	Reference
Diet and Feed Type	Diet composition (protein, carbohydrate and lipid) reshapes bacterial dominance; inclusion of insect meal promotes beneficial taxa like <i>Lactobacillus</i> and <i>Clostridium</i> .	<i>Dicentrarchus labrax</i> , <i>Sparus aurata</i>	Fish meal substitution with <i>Tenebrio molitor</i> maintained diversity and improved gut function	(Panteli et al., 2021)
Life Stage	Larval and juvenile stages have unstable, environment-linked microbiota; adults develop more specialized, host adapted consortia	<i>Cyprinus carpio</i>	Early stages influenced by pond microbes; adult microbiota more stable and function specific	(J. Zhang et al., 2024)
Habitat (Marine or Freshwater)	Salinity and ion composition select different microbial groups; marine fish richer in certain Proteobacteria and Firmicutes, freshwater in Fusobacteria	Global aquaculture review	Environmental salinity and microbial source pools drive taxa variation	(Kanika et al., 2025)
Rearing System / Environment	Water and sediment microbiota colonize gut, especially in open or biofloc systems; environmental microbes influence community structure	Largemouth bass	Biofloc water contributed functional bacteria improving digestion and immunity	(Jin et al., 2024)

Host Species / Genetics	Closely related species share some core taxa but vary in abundance; host genotype affects microbial selection	Grass carp, Nile tilapia	Gut community reflects both phylogeny and habitat adaptation	(Li et al., 2024)
Environmental Stress (Toxins, Pathogens, DO, Temperature)	Stress disturbs microbiome balance; opportunistic bacteria increase while beneficial taxa decline	Multiple species	Exposure to <i>Microcystis aeruginosa</i> blooms caused dysbiosis and reduced immune capacity	(Gallet et al., 2023)
Geographical / Seasonal Variation	Temperature, rainfall and nutrient runoff alter water microbiota and indirectly the gut composition	Subtropical riverine fishes	Seasonal shifts change diversity and relative abundance of core microbes	(Kanika et al., 2025)

Microbiome roles in nutrition and feed efficiency

The creation of short-chain fatty acids, vitamin synthesis and nutrient breakdown are all facilitated by gut bacteria and may increase the growth and efficacy of host feed conversion (Luan et al., 2023) (Figure 1). Numerous experimental investigations demonstrate that dietary modifications (such as adding insect meal, plant proteins or prebiotic fibers) alter the composition of gut microbes in ways that are associated with enhanced nutrient absorption and digestive enzyme activity (Hasan et al., 2023). These results lend credibility to the use of functional feeds that are intended to foster advantageous taxa that improve the hosts ability to digest food and absorb nutrients (Rimoldi et al., 2023). For instance, a multi-omics study on grass carp *Ctenopharyngodon idella* revealed that fish fed herbivorous, omnivorous or carnivorous diets differ not only in taxonomic composition but also in genes linked to carbohydrate metabolism, short-chain fatty acid production and polysaccharide degradation. These fishes gut microbiomes frequently reflect the macronutrient composition of their diets (Li et al., 2024). Measurable changes in growth rate and feed conversion ratio are correlated with these functional modifications, suggesting a robust

relationship between microbial gene potential and nutrient absorption (Li et al., 2024). Substituting insect proteins like *Tenebrio molitor* for fishmeal, for instance, causes minor but noticeable changes in the microbial taxa linked to lipid digestion and proteolytic activity. A study on rainbow trout revealed that eating insect based diets changed the abundance of gut communities in taxa linked to lipid metabolism without significantly altering environmental microbiomes (Bruno et al., 2023). This implies that, when combined with the right gut flora, alternative proteins may preserve or enhance digestive function (Bruno et al., 2023).

Fish exposed to poor quality diet or unbalanced feed components have decreased microbial richness which is frequently linked to worse development and digestive enzyme performance, suggesting that gut microbiome diversity also acts as a buffer against nutritional stress. Improved feed conversion is typically associated with the restoration or maintenance of richness through diet composition like adding fibers, balanced protein sources or digestibility enhancers. Grass carp diet experiments highlight these ideas even if direct trials are still rare (Li et al., 2024). The idea that dietary manipulations can enhance feed efficiency by influencing the functional capacity of gut microbes is supported by a number of

other recent research. Using metagenomic sequencing of gut contents, a multi-omics study in grass carp (*Ctenopharyngodon idella*) compiled a large non-redundant gene catalogue (approximately 575,000 genes). The study found that fish fed diets with higher plant polysaccharides have more microbial taxa linked to polysaccharide degradation, carbohydrate metabolism and short chain fatty acid pathways. The presence of important enzyme encoding genes like glycoside hydrolases, cellulases, was positively connected with growth performance and nutrient digestibility, indicating that the gene pool of the microbiome is a powerful predictor of feed conversion under various macronutrient regimes (Li et al., 2024).

Prebiotics such as FOS and GOS, the probiotic supplementation improved gut health, altered transcriptome profiles and changed metabolism in Atlantic salmon after saltwater transfer. Improved feed utilization under stress conditions was correlated with these treatments alteration of the microbiota composition which increased taxa associated with mucosal integrity and SCFA production (Dhanasiri et al., 2023). When compared to controls, European seabass juveniles fed microalgae together with a high dosage of phytase demonstrated noticeably better feed efficiency and weight gain. The gut bacterial community changed: depending on the phytase dose there was a modulation in Bacilli, Actinobacteria, Beta-proteobacteria, Gamma-proteobacteria and Alpha-proteobacteria. This

suggests that enzymatic addition can affect the composition of the microbiome and indirectly improve utilization of feeds that may otherwise contain less digestible carbohydrates or anti nutritional elements (Peralta-Sánchez et al., 2024) (Table 2).

In European sea bass, comparative experiments with various insect meals showed that diets containing the exuviae of black fighter fly larvae or pupae increase the relative abundance of the chitinolytic bacteria e.g. *Paenibacillus*, Firmicutes families like Bacillaceae, Lachnospiraceae and Actinobacteria. Additionally, the number of copies of chitinase genes increased. These functional alterations were linked to greater chitinous material digestion and better use of components derived from insects which produced feed efficiency metrics that were on par with or marginally superior to those of conventional fishmeal diets (Rangel et al., 2022).

In accumulation to the expected functional raise of the glycolysis, xylose or glucose degradation, and amino acid synthesis pathways, another research in Nile tilapia *Oreochromis niloticus* given plant polysaccharide based prebiotics exposed a dose dependent intensification in the abundance of *Bacillus* and related taxa. Feed conversion ratios increased at modest dosages, indicating that certain prebiotics may influence the microbiota to adopt metabolic profiles that promote effective nutrient absorption and energy extraction (Bera et al., 2023).

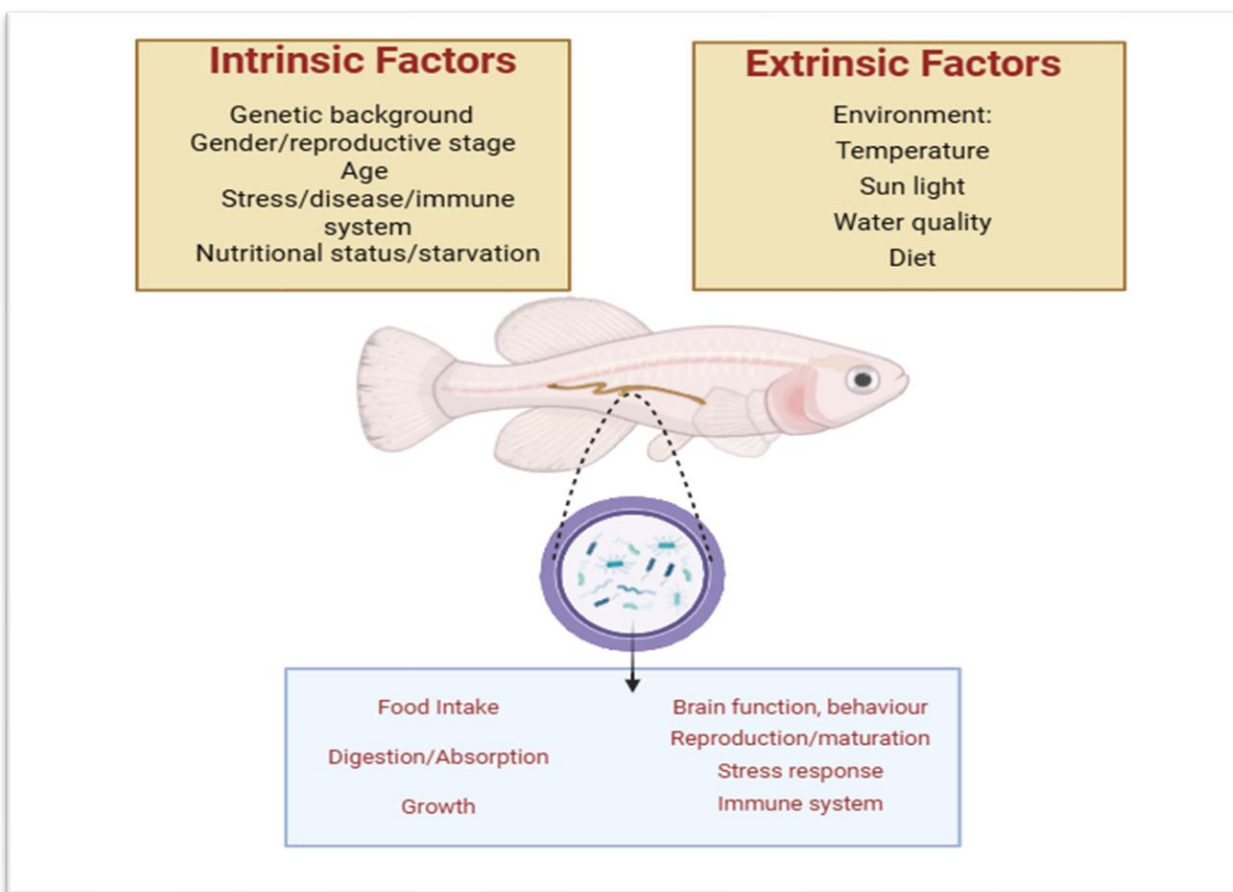


Fig 1. Microbiome roles in nutrition and feed efficiency

Table 2. Recent Studies on Fish Gut Microbiome, Nutrition and Feed Efficiency

Fish species	Dietary change	Microbiome response	Effect on growth/feed use	Reference
Grass carp (<i>C. idella</i>)	Diets with different plant and animal nutrients	More bacteria for carbohydrate breakdown and SCFA formation	Better feed use and faster growth	(Li et al., 2024)
Atlantic salmon (<i>S. salar</i>)	Prebiotics and <i>Pediococcus acidilactici</i>	Increase in useful gut bacteria and better gut health	Improved digestion after seawater transfer	(Dhanasiri et al., 2023)
European seabass (<i>D. labrax</i>)	Microalgae with phytase enzyme	Balanced gut bacteria and better nutrient digestion	Higher weight gain and feed efficiency	(Peralta-Sánchez et al., 2024)
Europeans seabass (<i>D. labrax</i>)	Insect meals (BSF larvae, exuviae)	More chitin-digesting bacteria such as <i>Paenibacillus</i>	Maintained or slightly better feed use than fishmeal diets	(Rangel et al., 2022)

Nile tilapia (<i>O. niloticus</i>)	Plant-based prebiotics	More <i>Bacillus</i> and carbohydrate-digesting microbes	Improved feed conversion at moderate doses	(Bera et al., 2023)
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Microbiome immune system interactions

Two way interactions are shown by mechanistic study and reviews from recent years: microbial metabolites and microbe associated molecular patterns MAMPs affect innate and adaptive immune pathways, while host immunological state and mucosal environment dictate which microorganisms persist (B. Zhang et al., 2024). Following targeted microbiome manipulation, experimental probiotic and immunostimulant trials show improved mucosal and serum immunological indicators such as lysozyme, complement and cytokine expression which frequently translates into increased survival following pathogen exposure (Calcagnile et al., 2024). By interacting with mucosal tissues, microbiota affect the development of fish immune systems. Research indicates that the gut lining of fishes expresses pattern appreciation receptor that recognize microbe associated molecular patterns, which in turn trigger the production of immunoglobulins, cytokines, and antimicrobial peptides. Variations in temperature or salinity can upset this equilibrium and affect the microbiome in ways that weaken mucosal defense (Morshed & Lee, 2023).

According to a long term study, Atlantic salmon that received synbiotic supplementation (probiotic and prebiotic) both during and after antibiotic treatment showed faster immune recovery, less dysbiosis and more stable microbial communities than controls. This stability was linked to reduced inflammatory signatures, enhanced mucosal barrier indicators and immune gene overexpression (Dhanasiri et al., 2024). The genetic background of the host also affects the microbiome and immune responses. For example, variations in gut community diversity and immune gene transcription were observed in diploid and triploid *Carassius auratus*, suggesting that genetic ploidy affects the composition of the microbiome as well as the immune systems sensitivity to microbial stimuli

(Cai & Wei, 2023). Mucosal epithelia actively modify their glycocalyx, mucus production and antimicrobial peptide repertoire in response to microbial signals, in addition to sampling and tolerating commensals. These interactions at mucosal interfaces are dynamic and context dependent. By altering colonization niches and nutrition availability this remodeling generates feed back loops wherein microbial metabolic products, such vitamins or short chain fatty acids, influence the reliability of the epithelial obstructions and the recruitment of immune cells. In fact, it has been demonstrated that nutritional SCFAs enhance distinctive protection, alter gut microbiota and boost disease resistance in aquatic hosts (Li et al., 2022) (Table 3).

Environmental stresses, such as high temperatures, low flowing oxygen or sudden variations in salinity are frequently identified as causes of dysbiosis that occurs prior to disease epidemics. The structure of the microbial population and fish mucosal immunity are closely related and disruption can upset this equilibrium, impairing barrier function and changing cytokine expression patterns (Hopo et al., 2024). In several studies, stress driven dysbiosis demonstrates reduced taxonomic richness and loss of beneficial functional guilds such as fiber degraders or SCFA producers which correspond with damaged mucosal barriers and altered immune gene transcription (Bera et al., 2023). The most promising therapies, as seen from an applied standpoint, include host, microbial and environmental measures; husbandry techniques that maintain microbial diversity, tailored synbiotic regimens scheduled around stressors or treatments, and selective breeding for genotypes that are favorable to the microbiome. According to reviews, probiotics and prebiotics also known as synbiotics, work better together to maintain immune response and microbiome resilience than either one alone

(Srirengaraj et al., 2023). However, rather than universal products, tailored, evidence based approaches will be crucial due to the diversity of species, life phases and production systems, Frontiers fish gut microbiota review (Kanika et al., 2025). There are still significant holes. Few studies confirm whether immune biomarker improvements such as elevated mucosal Ig, AMP, cytokine changes translate into improved growth,

feed conversion or survival under commercial stressors. Additionally, longitudinal multi-omics datasets that link taxonomic shifts to metabolic output (metabolome, metatranscriptome) under real farm settings are uncommon. Emerging engineering techniques include synthetic consortia, CRISPR phage technologies, and aquaculture microbiome engineering (MA et al., 2025).

Table 3: Fish microbiome immune interactions

Aspect	Key Findings	Aquaculture Implication	Recent Reference
Microbial signals	SCFAs and MAMPs boost mucosal defense and cytokine response.	Support disease resistance.	(Li et al., 2022)
Host regulation	Host genes shape microbial balance.	Breed microbiome-friendly strains.	(Kanika et al., 2025)
Environmental stress	Heat or salinity shifts reduce diversity and weaken barriers.	Keep stable water conditions.	(Bera et al., 2023)
Synbiotics	Pre- and probiotics restore balance after antibiotics.	Use during stress or recovery.	(Srirengaraj et al., 2023)
Genetic effect	Diploid vs. triploid fish show immune and microbiome shifts.	Include ploidy in breeding plans.	(Huo et al., 2023)
Microbiome engineering	Synthetic microbes enhance gut health and immunity.	Test in long-term trials.	(MA et al., 2025)

Microbiome influence on disease resistance and dysbiosis

While dysbiosis such as loss of variety or expansion of opportunists, frequently occurs prior to illness outbreaks, a stable, diversified gut microbiome is frequently linked to resilience to opportunistic infections (Medina-Félix et al., 2023) (Figure 2). Although results might vary depending on the strain and environment, probiotic, synbiotic and feed additive trials have shown decreased pathogen burdens and mortality from bacterial and certain viral challenges (Calcagnile et al., 2024). A study on *Cynoglossus semilaevis* found that individuals who were more resistant to vibriosis had different microbial community profiles, including higher abundances

of specific commensals that seem to suppress *Vibrio* proliferation. This suggests that disease resistance in fish is frequently associated with the resilience of their gut microbiome (Zhou et al., 2022). Dysbiosis such as loss of microbial diversity or overgrowth of opportunists, is often seen before overt symptoms in disease outbreaks, indicating that the makeup of the microbiome may be an early indicator (Zhou et al., 2022). This is supported by probiotic intervention experiments which showed that supplementing juvenile olive flounder (*Paralichthys olivaceus*) with fish-derived *B. subtilis* or *E. faecium* improved gut histology such as villus length, integrity, decreased pathogen load and increased survival after pathogen challenge when fish meal was

reduced in the diet (Choi et al., 2025). A new study on feed additives provides more support for the idea that supplementing largemouth bass with *Bacillus velezensis* decreased mortality following largemouth bass virus infection. Changes in lipid metabolism such as diglyceride formation and the microbiomes regulatory impact on mucosal antiviral immunity were two ways the protection was achieved (Cheng et al., 2025). Additionally, it has been demonstrated that dietary prebiotics such as beta-glucans can change the gut microbiota by altering the relative abundances of beneficial versus hypothetically pathogenic taxa. Although immune challenge results can occasionally differ, fish that consume enriched prebiotic diets frequently exhibit improved disease resistance or at the very least decreased pathology (Menanteau-Ledouble et al., 2022).

Fish gut communities frequently serve as a frontline barrier: early changes in diversity or dominance might occur before clinical outbreaks, whereas stable, varied microbiota prevent opportunistic blooms and inhibit pathogen colonization. Individuals resistant to vibriosis carried unique intestinal communities, according to recent research utilizing *Cynoglossus semilaevis*. This suggests that alterations in community structure might be early indicators of disease risk (Zhou et al., 2022). Specific probiotic strains made from fish can lessen the burden of infections and repair gut tissue. According to

studies conducted on olive flounder and kindred species, supplementing with specific strains of *Bacillus* and *Enterococcus* enhanced gut histology such as villus integrity, altered immunological markers and reduced pathogen burdens under challenge circumstances. These benefits were frequently strain dependent (Lee et al., 2025). Multi-omics research demonstrates that certain *Bacillus* species defend against viral risks by altering host metabolism and mucosal immunity, going beyond single probiotics. *Bacillus velezensis* supplementation reduced mortality in large mouth bass following LMBV acquaintance; multi omics studies connected protection to modifications in lipid metabolism such as diglyceride pathways and to the microbiome mediated augmentation of mucosal antiviral responses (Cheng et al., 2025). Prebiotics like beta-glucans also change the microbial makeup and host metabolism. In certain immune challenge trials, feeding beta-glucan may result in less pathology or milder symptoms because it changes the metabolome which includes lipid profiles, and bacterial abundance patterns. Although outcomes differ depending on the species, dosage and pathogen, combining prebiotics with carefully selected probiotics (synbiotics) seems like a viable way to increase the resistance of farmed fish (Menanteau-Ledouble et al., 2022) (Table 4).

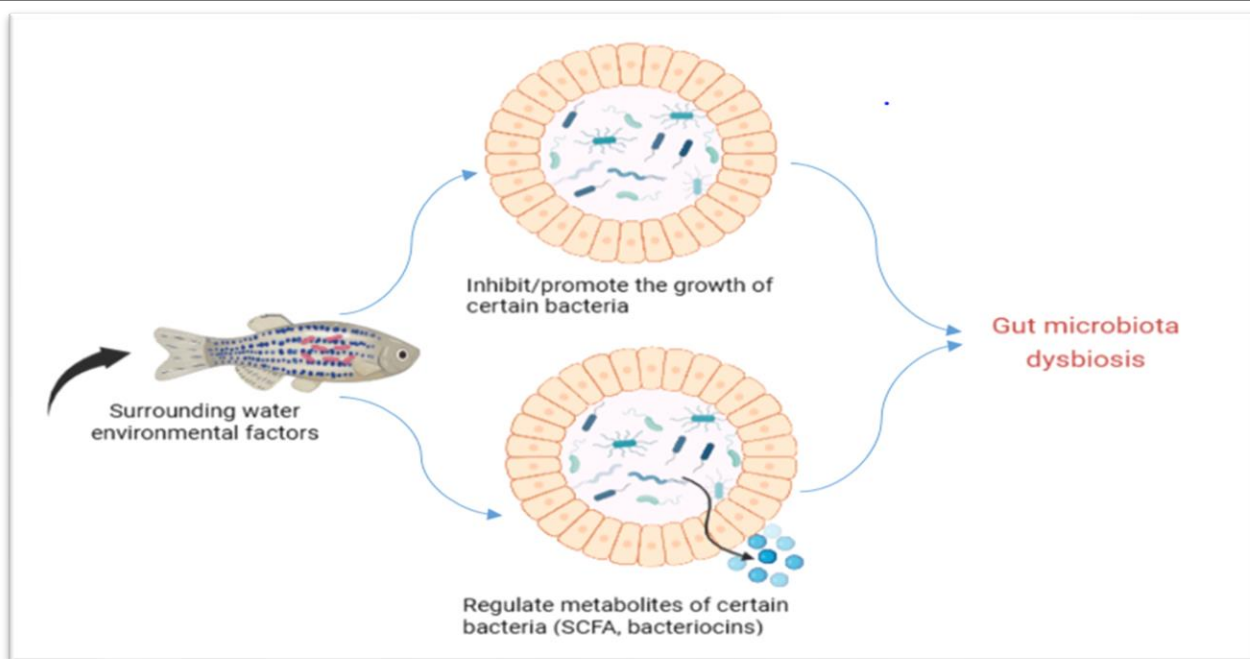


Fig 2. Microbiome influence on disease resistance and dysbiosis

Table 4: Microbiome influence on disease resistance and dysbiosis

Intervention	Microbiome change	Typical observed outcome	References
Natural commensal profiles (resistant hosts)	Higher relative abundance of protective taxa	Lower vibriosis incidence; predictive community signatures	(Zhou et al., 2022)
Fish-derived <i>Bacillus</i> / <i>Enterococcus</i> probiotics	Increased beneficial taxa, improved gut histology	Reduced pathogen load; better survival in challenge tests	(Choi et al., 2025)
<i>Bacillus velezensis</i> supplementation	Microbiome regulation and metabolic shift (lipid pathways)	Decreased LMBV mortality; enhanced mucosal antiviral immunity	(Cheng et al., 2025)
Beta-glucan (prebiotic) diets	Altered bacterial richness/diversity and metabolome	Improved metabolic markers; sometimes reduced pathology	(Menanteau-Ledouble et al., 2022)

Strategies to modulate the gut microbiome in aquaculture

Probiotics, prebiotics and synbiotics

When given by feed or water, several probiotic strains like as *Bacillus spp.*, *Pediococcus* and certain autochthonous isolates have been shown in numerous controlled experiments from recent years to enhance nutritional utilization, immunological markers and disease resistance (Calcagnile et al., 2024). Systematic reviews

emphasize the necessity for standardized effectiveness studies by pointing out encouraging results but also pointing out heterogeneity caused by probiotic strain, dosage, host species and study design (Melo-Bolivar et al., 2021). Prebiotics are indigestible food ingredients such as fibers and oligosaccharides that specifically promote good gut flora. According to a recent study on Atlantic salmon, *Pediococcus acidilactici* plus prebiotics such as fructooligosaccharides FOS, supplemented the

diet during the post smolt stage helped preserve the compositions of the gut microbiota during seawater transfer, enhanced the metabolome and transcriptome profiles and promoted improved health metrics (Dhanasiri et al., 2023) (Figure 3). Probiotics & prebiotics are combined in synbiotics in an attempt to achieve synergistic effects, stimulating the introduction and feeding of advantageous bacteria. When compared to antibiotic treatment without synbiotics, a synbiotic diet as FOS and *Pediococcus acidilactici* helped maintain the composition of the gut microbiota, enhanced growth performances and moderated resistant gene manifestation in a longitudinal study of Atlantic salmon receiving antibiotic treatment (Dhanasiri et al., 2024)

(Table 5). According to recent meta analyses, feeding technique, environmental factors and strain specificity all have a significant impact on how successful probiotics are in aquaculture. While *Bacillus subtilis* and lactic acid bacteria consistently increase gut integrity and feed conversion, controlled experiments in several species demonstrate that responses vary with temperature and salinity changes. The lack of uniformity in trial designs and the reporting of immunological markers and microbiota was also highlighted in a thorough assessment conducted in recent years, underscoring the necessity of standardized procedures to increase repeatability (Calcagnile et al., 2024).

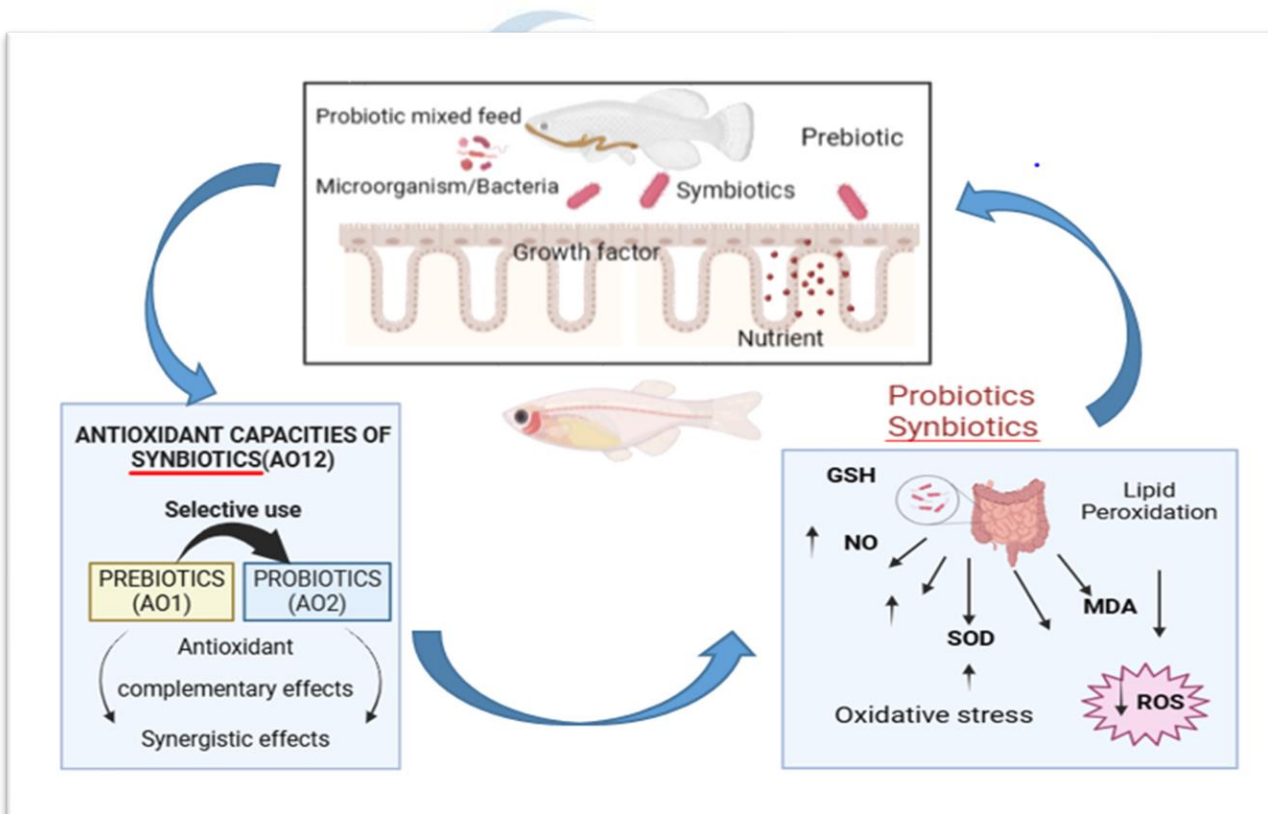


Fig 3. Action of probiotics, prebiotics and synbiotics in fish gut health

Furthermore, mechanistic studies employing multi-omics techniques have demonstrated that prebiotics such fructooligosaccharides FOS and galactooligosaccharides GOS not only support

good bacteria but also alter host gene expression related to immunological modulation and intestinal health. The synergistic potential of synbiotics in aquaculture settings was confirmed

when *Pediococcus acidilactici* and FOS were combined in Atlantic salmon, altering metabolic

and immunological pathways beyond probiotic-only effects (Dhanasiri et al., 2023).

Table 5: Probiotics, Prebiotics and Synbiotics in Aquaculture

Host / System	Treatment	Key Findings	Reference
Various fish species	Probiotic supplementation via feed/water	Improved feed efficiency, immunity and disease resistance; highlights need for standardization	(Calcagnile et al., 2024)
Atlantic salmon (post-smolt)	FOS and <i>P. acidilactici</i>	Preserved microbiota during seawater transfer; improved metabolome and health markers	(Dhanasiri et al., 2023)
Atlantic salmon (antibiotic stress)	Synbiotic (FOS and <i>P. acidilactici</i>)	Maintained microbiota, improved growth and immune expression	(Dhanasiri et al., 2024)
Freshwater fish	Mixed probiotics (<i>Bacillus</i> , LAB)	Enhanced growth, feed conversion and water quality	(Nathanailides et al., 2021)

Functional feeds and feed ingredients

Attention must be paid to the impacts on the microbiome when using sustainable components (plant proteins, insect meals and algae products). Several studies have demonstrated that these changes in ingredients affect the ecology of gut microbes, although they may be countered by formulating products with microbial modulators or digestibility enhancers (Hasan et al., 2023). Prebiotics, immunostimulants and enzyme supplements are examples of functional additives that can enhance host responses and specifically encourage good bacteria (Rimoldi et al., 2023). Because of their antibacterial and antioxidant qualities, plant based additives including flavonoids, tannins, saponins and essential oils are becoming more and more well liked. According to recent study, adding *Moringa oleifera* leaf extract to carp diets changed the intestinal microbiota, boosting the ratio of Firmicutes to Bacteroidetes and enhancing the movement of anti-oxidant enzymes (Lu et al., 2022).

As aquafeed formulations increasingly incorporate alternative proteins (such as insect meals, algae derived biomass and single cell proteins) attention has shifted not only to nutrient replacement but also to the downstream effects on gut microbial ecology. For example, a recent study demonstrated that insect meal inclusion in freshwater and marine feeds influenced the richness and composition of gut bacterial communities, with impending implications for host digestion and resistant status (Hasan et al., 2023). The functional additives themselves are now well described in terms of their mechanistic impact on gut health and microbiome host interaction, going beyond chemical replacement. In order to increase resistance to infections and oxidative stress, a new study describes how immunostimulants such as beta-glucans, nucleotides, phytochemicals, and enzyme supplements work through gut barrier integrity, immune gene expression and metabolites connected to the microbiome (Onomu & Okuthe, 2024) (Table 6).

Table 6: Recent findings on functional feed ingredients and additives

Focus (Ingredient / Additive)	Key outcomes	References
Insect meals and alternative proteins	Altered gut microbiota richness in freshwater/marine species	(Hasan et al., 2023)
Functional additives (immuno-stimulants, phytogenics, enzymes)	Mechanistic pathways via microbiome and immune metabolism	(Onomu & Okuthe, 2024)
Plant, insect, algae, single-cell proteins	Potential negative microbiome/immune shifts when replacing fish-meal	(Aragão et al., 2022)

Microbiome engineering and next-generation approaches

Recent developments in aquaculture microbiome research are shifting toward precision microbiome engineering where beneficial microbial communities are intentionally shaped to improve host health and feed efficiency. Targeted bacteriophage therapy, selective colonization and rational design of probiotic consortia are among the leading innovations. Phage therapy has shown potential to selectively eliminate pathogenic bacteria while maintaining beneficial microbes. However, experts emphasize the need for biosafety testing, regulatory frameworks and monitoring tools to prevent unintended microbial resistance and ecological imbalance (Amillano-Cisneros et al., 2025) (Table 7). Microbial transplantation and the creation of synthetic microbiomes are also becoming more widely acknowledged as sustainable aquaculture techniques. Scientists are now able to forecast how microbial communities interact and affect host metabolism because of developments in metagenomics, metabolomics, and

transcriptomics. In order to improve the stability and resilience of gut ecosystems, a new study emphasizes the development of microbial consortia that are specific to species and conditions through the use of omics and AI based prediction (MA et al., 2025). As a significant step toward sustainable aquaculture, these next generation techniques seek to create 'designed microbiomes' that promote immunity, disease resistance and nutrient utilization (MA et al., 2025).

Moreover, microbial metabolites control human immunity and energy metabolism, as demonstrated by omics guided functional study of engineered microbiomes. Targeting microbial activities can be just as successful as altering the makeup of bacteria, according to a research on largemouth bass (*Micropterus salmoides*) which showed that microbial modification changed metabolite pathways linked to enhanced disease resistance and intestinal homeostasis (J. Zhang et al., 2025).

Table 7: Recent findings on microbiome engineering and next generation approaches

Focus	Main findings	Reference
Phage therapy in aquaculture	Demonstrated targeted bacterial control and need for biosafety standards	(Amillano-Cisneros et al., 2025)
Synthetic microbial consortia	Reviewed omics-based microbiome design for fish gut stability	(MA et al., 2025)

Omics-guided microbial modulation in fish	Identified metabolite shifts linked to disease resistance in largemouth bass	(J. Zhang et al., 2025)
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Methods and technical considerations

To go from taxonomic description to functional inference, robust microbiome studies need to integrate multi omics such as metagenomics, metatranscriptomics & metabolomics, carefully collect samples as mucosa and luminal contents, have sufficient sequencing depth and use suitable negative controls (Liu et al., 2023). Inconsistent methodologies frequently restrict cross study comparisons; data sharing and meta-analytic frameworks will speed up reproducibility and translation (Luan et al., 2023). Reliable scientific and technical techniques are necessary for accurate evaluation and modification of the fish gut microbiota. High-throughput sequencing and multi-omics profiling have replaced culture-dependent methods in the sector due to advancements in molecular biology. While metagenomics, metatranscriptomics and metabolomics provide information on community activities and metabolic pathways, the majority of current research use 16S rRNA gene sequencing to ascertain the makeup of microorganisms (Wang et al., 2025).

In fish gut microbiome research, a smooth transition from taxonomic surveys to mechanistic inference depends on careful experimental design and sampling. For instance, its important to distinguish between luminal and mucosa associated microbial communities. While luminal content may capture transitory diet driven taxa, mucosal samples often represent host-microbe interactions more directly. The significance of high sequencing depth and functional annotation for inference was highlighted by a recent work in grass carp that used deep metagenomic sequencing (approx. 575 k non-redundant genes) and discovered that community functions in the gut separated into two ecological groups (Li et al., 2024). Furthermore, consistent information acquisition e.g., eating history, age, environment and the meticulous inclusion of negative controls e.g., sample blank water, reagent controls, are essential for guaranteeing repeatability and comparability between investigations (Li et al., 2024) (Table 8).

Table 8: Technical and Multi-Omics Considerations in Fish Gut Microbiome Research

Aspect	Key Insight	Reference Link
Sampling strategy	Mucosal vs. luminal sampling affects microbial diversity and host linkages.	(Li et al., 2024)
Sequencing depth	Deep metagenomic coverage improves detection of low-abundance taxa.	(T. Zhang et al., 2025)
Data reproducibility	Standardized controls and metadata enhance cross-study comparisons.	(Cai et al., 2023)
Multi-omics integration	Combining metagenomics with metabolomics reveals functional pathways.	(Gupta et al., 2024)
Bioinformatics workflows	Unified pipelines minimize compositional bias and improve accuracy.	(Z. Zhang et al., 2025)
Functional inference	Linking gene functions to host	(Z. Zhang et al., 2025)

	immunity enhances biomarker discovery.	
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Knowledge gaps and future directions

Key research gaps remain in sympathetic the efficient role of the fish gut microbiome. First, the direct causal links between specific microbial taxa or metabolites and host growth, immunity or stress tolerance are still unclear. Second, the ecological stability and persistence of introduced probiotics or engineered microbial consortia require long term monitoring to assess their sustainability. Third, the interaction between host genetics and microbiome composition is an underexplored area influencing trait expression and adaptability. Finally, clear regulatory frameworks are needed to guide the safe application of microbiome based products in aquaculture. Progress will depend on standardized methodologies, integrative multidisciplinary research and active collaboration among microbiologists, nutritionists, geneticists and industry professionals (Zhang et al., 2022).

Practical recommendations for aquaculture practitioners

Use probiotic strains that have been thoroughly studied and supported by peer review for the intended species and in reports, include information on dosages and methods of administration (Calcagnile et al., 2024). To identify early dysbiosis while changing feed components, keep an eye on growth, gut histology and microbiome composition (Hasan et al., 2023). Invest in regular microbiome surveillance for high value species to identify adverse trends prior to the onset of clinical illness (Spilsbury et al., 2022). Practitioners should select strains that have undergone thorough peer reviewed testing for the particular species and production system in order to provide the most possible benefit from probiotics in aquaculture. For instance, when the dose and feeding technique are precisely specified, the recorded use of specific strains of *Bacillus* and *Lactobacillus* in marine fish has demonstrated effectiveness in enhancing growth and disease resistance.

Reporting strain designation, colony forming units per kilogram or liter, supplementation time and distribution method such as feed, water immersion, etc., is therefore crucial. This level of openness facilitates replication and informed decision making by other farms (Calcagnile et al., 2024).

Early monitoring of gut health indicators and microbial alterations is crucial when switching feed ingredients e.g., substituting algal or insect meal for fishmeal, so that any developing dysbiosis may be treated before clinical issues occur. An integrated picture of how the animals are adapting to the new diet may be obtained by tracking growth rate, feed conversion ratio, gut histology such as villus height, mucous cell profile and the conformation of the gut-microbiota on a regular basis. Timely remedial actions, including rebalancing beneficial additions or reversing substances, are made possible by early detection of negative tendencies (Hoseinifar et al., 2024). Investing in routine microbiome surveillance can be a proactive health management technique for high value species or intensive culture systems. An early warning system, such as detecting shifting diversity before illness becomes apparent, the appearance of opportunistic pathogens or falling proportions of beneficial taxa, can be provided by scheduled sampling e.g., monthly or quarterly, to evaluate important gut microbial markers. It is easier to identify the underlying reasons and carry out specialized therapies when these data are combined with feed, water quality and husbandry records (Tay et al., 2025).

Finally, integrating microbiome related actions into farm management systems and standardizing documentation should be part of operational protocols. This entails documenting the probiotic type, dosage, and timing of the intervention as well as the feed history, environmental aspects such as water temperature, salinity and stocking density and health results. When working with researchers, comparing batches or testing performance, such metadata becomes quite

useful. Additionally, as microbiome based goods and procedures frequently need for proof of performance and safety, openness is beneficial when collaborating with regulatory bodies or quality assurance programs (Fachri et al., 2024).

Conclusion

Evidence for the gut microbiota as a key integrator of immune function, disease resistance and nutrition in farmed fish has grown between 2020 and 2025. Standardized effectiveness testing, mechanistic clarity and regulatory direction are necessary for the widespread adoption of many applied therapies, such as probiotics, synbiotics and functional meals, despite their demonstrated benefits. It will take commensurate advancements in experimental design, multi omics incorporation and industry-research collaborations to translate microbiome knowledge into steady production benefits.

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