

Metagenomic Characterization of Intestinal Microbiota in Freshwater Aquaculture Species

Anbu Kani Selvam G.^{1*}, Dhinesh P.² and Chrisolite B.¹

¹Dept. of Fish Pathology and Health Management, Tamil Nadu Dr. J. Jayalalithaa Fisheries University, Fisheries College and Research Institute, Thoothukudi.

²Dept. of Aquatic Animal Health Management, Tamil Nadu Dr. J. Jayalalithaa Fisheries University, Dr. M.G.R. Fisheries College and Research Institute, Ponneri, Tamil Nadu (601 204), India

Corresponding Author

Anbu Kani Selvam G.

Email: imanbuganesan26@gmail.com



OPEN ACCESS

Keywords

Fish gut microbiome, Shotgun metagenomics, Freshwater aquaculture, Functional genomics, Sustainable fisheries

How to cite this article:

Selvam, G. A. K., Dhinesh, P. and Chrisolite, B. 2026. Metagenomic Characterization of Intestinal Microbiota in Freshwater Aquaculture Species. *Vigyan Varta* 7 (03): 143-147.

ABSTRACT

Digestion, food absorption, immunological regulation, and disease resistance are all significantly influenced by the gut microbiota of freshwater aquaculture species. Recent developments in metagenomics, specifically next generation sequencing (NGS) and shotgun sequencing, have allowed scientists to go beyond straightforward microbe identification and do thorough functional assessment of fish gut ecosystems. Proteobacteria, Firmicutes, and Fusobacteriota are regularly found to be dominant in studies including tilapia, carp, and native freshwater species. Additionally, host genetics, nutrition, habitat, and environmental stressors have a significant impact on microbial structure and metabolic capability. Gaining an understanding of these microbial populations presents significant opportunity to enhance conservation, disease control, feed efficiency, and sustainable aquaculture development.

INTRODUCTION

Freshwater aquaculture has become one of the fastest-growing food-producing sectors globally. In underdeveloped countries, species like grass carp, Rohu (*Labeo*

rohita), Nile tilapia (*Oreochromis niloticus*), and other native fishes play a vital role in ensuring protein security. But growing production intensity has also sparked worries

about environmental sustainability, feed costs, and disease outbreaks.

Given this, the gut microbiota of fish has become a crucial factor in determining their productivity and overall health. Due to its wide range of metabolic functions that enhance human physiology, the gut microbiota is frequently referred to as a "extra organ" (Singh *et al.*, 2025). These microbial communities assist in:

- ✓ Digestion of complex carbohydrates
- ✓ Synthesis of essential vitamins (e.g., vitamin B12)
- ✓ Short-chain fatty acid production
- ✓ Immune system maturation
- ✓ Competitive exclusion of pathogens

When the microbial equilibrium is disrupted (dysbiosis), fish may exhibit reduced development and poor feed conversion and may become more susceptible to illness (Kanika *et al.*, 2025). Previously, most of the studies applied 16S rRNA amplicon sequencing which did not facilitate any functional observation, but enabled taxonomic diagnosis. After the emergence of shotgun metagenomics, researchers now have the ability to study entire microbial genomes, build out metabolic pathways, and identify genes associated with virulence or probiotics (Yang *et al.*, 2025). This technical change has seen the development of aquaculture microbiology.

Core Microbial Composition in Freshwater Aquaculture Species

Across multiple freshwater fish species and geographical regions, certain bacterial phyla consistently dominate the gut ecosystem. Proteobacteria, Firmicutes and Fusobacteriota are frequently reported as the primary

components of fish gut microbiomes (Kanika *et al.*, 2025).

Habitat-Based Differences

In Nile tilapia, clear differences have been observed between cultured pond populations and wild lake populations. Lake reared tilapia exhibit higher microbial diversity with Fusobacteriota dominance, whereas pond-reared fish often show Firmicutes enrichment (Ghazali *et al.*, 2025). These differences likely reflect:

- ✓ Dietary diversity
- ✓ Environmental microbial exposure
- ✓ Water quality parameters
- ✓ Farming practices

Similarly, Rohu populations from the Halda River and Kaptai Lake demonstrated distinct bacteriome profiles influenced by ecological and anthropogenic factors (Uddin *et al.*, 2025).

Host Phylogeny and Phylosymbiosis

Strong evidence of phylosymbiosis, in which closely related host species harbor more comparable microbial communities, was found in a comprehensive metagenomic study of 121 freshwater fish species (Tang *et al.*, 2026). A significant amount of microbial variance, especially in skin microbiomes but also in gut communities, was explained by host genetics. This implies that the microbiota and fish have coevolved, with microbial colonization patterns being shaped by host-specific ecological filtration.

Functional Potential Revealed by Shotgun Metagenomics

The greatest advantage of metagenomics lies in its ability to identify not only microbial identity but also microbial function.

i. Vitamin Synthesis and Nutrient Metabolism

One notable example is *Cetobacterium*, a keystone freshwater fish bacterium shown to possess complete vitamin B12 biosynthesis pathways (Tang *et al.*, 2026). Vitamin B12 is crucial for metabolic regulation and nervous system function, highlighting a direct nutritional contribution of gut microbes.

ii. Carbohydrate-Active Enzymes (CAZy)

Shotgun metagenomics of indigenous fish species from the Kizil River revealed enrichment of carbohydrate active enzymes (CAZy families), indicating microbial involvement in complex carbohydrate digestion (Yang *et al.*, 2025). These enzymes enhance feed utilization efficiency, particularly in herbivorous and omnivorous fishes.

iii. Energy Metabolism and Ecological Adaptation

Functional pathway analysis identified:

- ✓ Oxidative phosphorylation enrichment
- ✓ Fructose and mannose metabolism pathways
- ✓ Nitrogen cycling genes
- ✓ Stress response and detoxification pathways

These metabolic features reflect microbial adaptation to host diet and environmental stressors (Yang *et al.*, 2025). Such functional insights help explain why certain fish populations exhibit superior growth or resilience under specific ecological conditions.

Environmental and Management Influences

Environmental variables strongly shape gut microbiome composition. Key factors include:

- ✓ Temperature

- ✓ Dissolved oxygen
- ✓ Salinity
- ✓ pH
- ✓ Nitrogen load
- ✓ Pollution

Studies have demonstrated that crude oil contamination, elevated nitrogen levels and pathogen exposure can alter microbial composition and compromise host immunity (Yang *et al.*, 2025). Farm raised fish generally exhibit reduced microbial diversity compared to wild counterparts due to controlled diets and limited environmental exposure (Kanika *et al.*, 2025). Reduced diversity may increase vulnerability to opportunistic pathogens under stress conditions. Thus, maintaining microbial diversity becomes a critical aspect of sustainable aquaculture.

Implications for Aquaculture Health Management

Metagenomic characterization has several direct applications in aquaculture:

- 1. Development of Precision Probiotics:** Identification of beneficial native strains enables formulation of host-specific probiotics.
- 2. Feed Optimization:** Understanding carbohydrate metabolism pathways allows design of feeds that synergize with gut microbial capabilities.
- 3. Early Disease Detection:** Metagenomic monitoring can detect shifts in microbial communities before clinical disease signs appear.
- 4. Conservation of Indigenous Species:** Microbiome analysis supports ecological restoration and conservation strategies by

understanding host–environment–microbe interactions (Yang *et al.*, 2025).

5. Biosecurity and Sustainability: Integrating microbiome surveillance into hatchery and farm management can improve resilience and reduce antibiotic dependency.

Future Directions

Although significant progress has been made, several gaps remain:

- ✓ Need for longitudinal microbiome monitoring studies
- ✓ Integration of metabolomics with metagenomics
- ✓ Exploration of virome and fungal components
- ✓ Development of microbiome-based biomarkers for health status
- ✓ Expansion of microbial genome catalogs for freshwater species

The construction of comprehensive microbial genome catalogs, such as the Wild Freshwater Fish Microbiome Catalog (Tang *et al.*, 2026), represents a major step forward.

CONCLUSION

Metagenomic characterization of intestinal microbiota has transformed freshwater aquaculture research from descriptive microbial ecology to functional microbial genomics. Dominant bacterial phyla such as Proteobacteria, Firmicutes and Fusobacteriota form the structural backbone of fish gut ecosystems, while host genetics, diet and environmental conditions shape functional potential.

By integrating microbiome science into aquaculture management, the industry can move toward:

- ✓ Improved feed conversion efficiency
- ✓ Reduced disease outbreaks
- ✓ Enhanced environmental sustainability
- ✓ Strengthened conservation strategies

The future of freshwater aquaculture will increasingly depend not only on breeding and nutrition, but also on understanding and harnessing the invisible microbial partners within the fish gut.

REFERENCES

- Ghazali, S. Z., Gani, N. A. S. M., Madiran, N. A., Ismail, N., Hasan, V., Novriadi, R., ... & Kamarudin, A. S. (2025). Metagenomic analysis of gut microbiome in Nile tilapia, *Oreochromis niloticus*: Insights from cultured and lake populations. *Egyptian Journal of Aquatic Research*.
- Kanika, N. H., Liaqat, N., Chen, H., Ke, J., Lu, G., Wang, J., & Wang, C. (2025). Fish gut microbiome and its application in aquaculture and biological conservation. *Frontiers in Microbiology*, *15*, 1521048.
- Singh, B. K., Thakur, K., Kumari, H., Mahajan, D., Sharma, D., Sharma, A. K., ... & Kumar, R. (2025). A review on comparative analysis of marine and freshwater fish gut microbiomes: insights into environmental impact on gut microbiota. *FEMS Microbiology Ecology*, *101*(1), fae169.
- Tang, R., Wang, J., Wang, X., Zeng, M., Gao, W., Yang, K., ... & Song, Z. (2026). Large-scale metagenomic analysis reveals host genetics shapes microbiomes in wild freshwater fish gut and skin. *Cell Reports*, *45*(2).
- Uddin, M. S., Chamonara, K., Nayem, M. R., Siddiqua, A., Chowdhury, S., Hossain,

I., ... & Masum, M. H. U. (2025). First Insight into the Gut Microbiome of Rohu Fish from Halda River and Kaptai Lake Using 16S rRNA Sequencing.

Yang, J., Qiang, Z., Zhang, D., Hao, H., Wei, J., Maira, H. S., ... & Nie, Z. (2025).

Shotgun metagenomics analysis of gut microbiota of three indigenous fish species from the Kizil River, Xinjiang. *Frontiers in Microbiology*, 16, 1617701.