

## GUT BACTERIAL DIVERSITY OF FRESHWATER FISH—A REVIEW

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### ABSTRACT

Gut bacteria that are part of the gut microbiota evolve together with their hosts, share the same niche among the gut microbiota and play important roles in metabolism, nutrition, and immunity. Several types of microbiota found in the digestive tract have an important role in increasing feed utilization, fish health, and improving the quality of the environment and microorganisms. Gut bacterial diversity studies were carried out as a step to obtain information on how diverse the intestinal bacterial community of freshwater fish is and from any class. The approach taken in this diversity study can be done through a metagenome approach and a bacterial culture approach. Metagenome studies on the diversity of fish gut bacteria can be done using the DGGE (Denaturing Gradient Gel Electrophoresis) method and can also be done through NGS (Next Generation Sequencing), both based on the 16s rRNA gene. Different locations can affect the diversity of gut bacteria even if the host type is the same. Fish species can also affect gut bacterial communities, particularly the feeding habits of the host fish. This review demonstrates the differences in the gut microbiota of freshwater fish collected from different habitats. This shows the effect of habitat or location on the diversity of fish gut microbes. This study provides the first insight into the diversity of bacterial communities in the gut of freshwater fish and provides a reference for future studies.

**KeyWords:** *Diversity, Gut Bacteria, Freshwater fish, Metagenomic*

### 1. INTRODUCTION

Intestinal (Gut) bacteria that are part of the gut microbiota evolve together with their hosts, share the same niche among the gut microbiota and play important roles in metabolism, nutrition, and immunity [1]. Several types of microbiota found in the digestive tract have an important role in increasing feed utilization, fish

health, and improving the quality of the environment and microorganisms [2]. The gut microbiota performs functions including fermenting unused energy substrates, boosting the immune system, preventing the growth of harmful pathogens, regulating intestinal development, and producing enzymes and vitamins for the host [3,4]. However, under certain conditions, some species of bacteria can cause disease by causing infection in the host [3]. The gut microbiota of carp living in Lake Balaton under oligo-mesotrophic conditions is dominated by anaerobic fusobacteria, but some obligate anaerobes and other facultative anaerobes are found in the digestive tract [5]. Proteobacteria, Fusobacteria, and Tenericutes are the dominant microbiota in the hindgut of goldfish [6]. Although in other studies this is not the case [7]. Catfish are dominated by Proteobacteria and Firmicutes [8]. Therefore, it is very interesting to review the diversity of bacterial communities in the guts of fish that live in freshwater.

## 2. APPROACHES TO STUDYING THE DIVERSITY OF INTESTINAL BACTERIA

Intestinal bacterial diversity studies were carried out as a step to obtain information on how diverse the intestinal bacterial community of freshwater fish is and from any class. The approach taken in this diversity study can be done through a metagenome approach and a bacterial culture approach. The influence of the aquatic environment in which they live can also be seen and studied through the description of the diversity of bacteria and compared whether the diversity of bacteria in the water as a fish substrate affects the bacterial community found in the guts of fish that live in that environment and whether there are differences in the bacterial community between the environments where the fish live. with the bacteria present in the intestines of fish and how it correlates. Metagenome studies on the diversity of fish gut bacteria can be done using the DGGE (Denaturing Gradient Gel Electrophoresis) method and can also be done through NGS (Next Generation Sequencing), both based on the 16s rRNA gene. Figures 1 and 2 are schematic diagrams of the DGGE and NGS analysis.

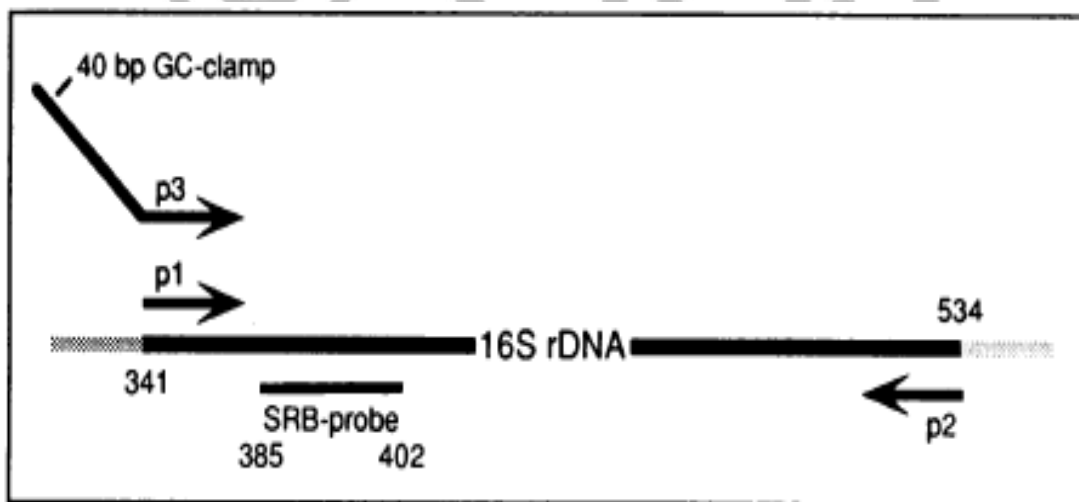
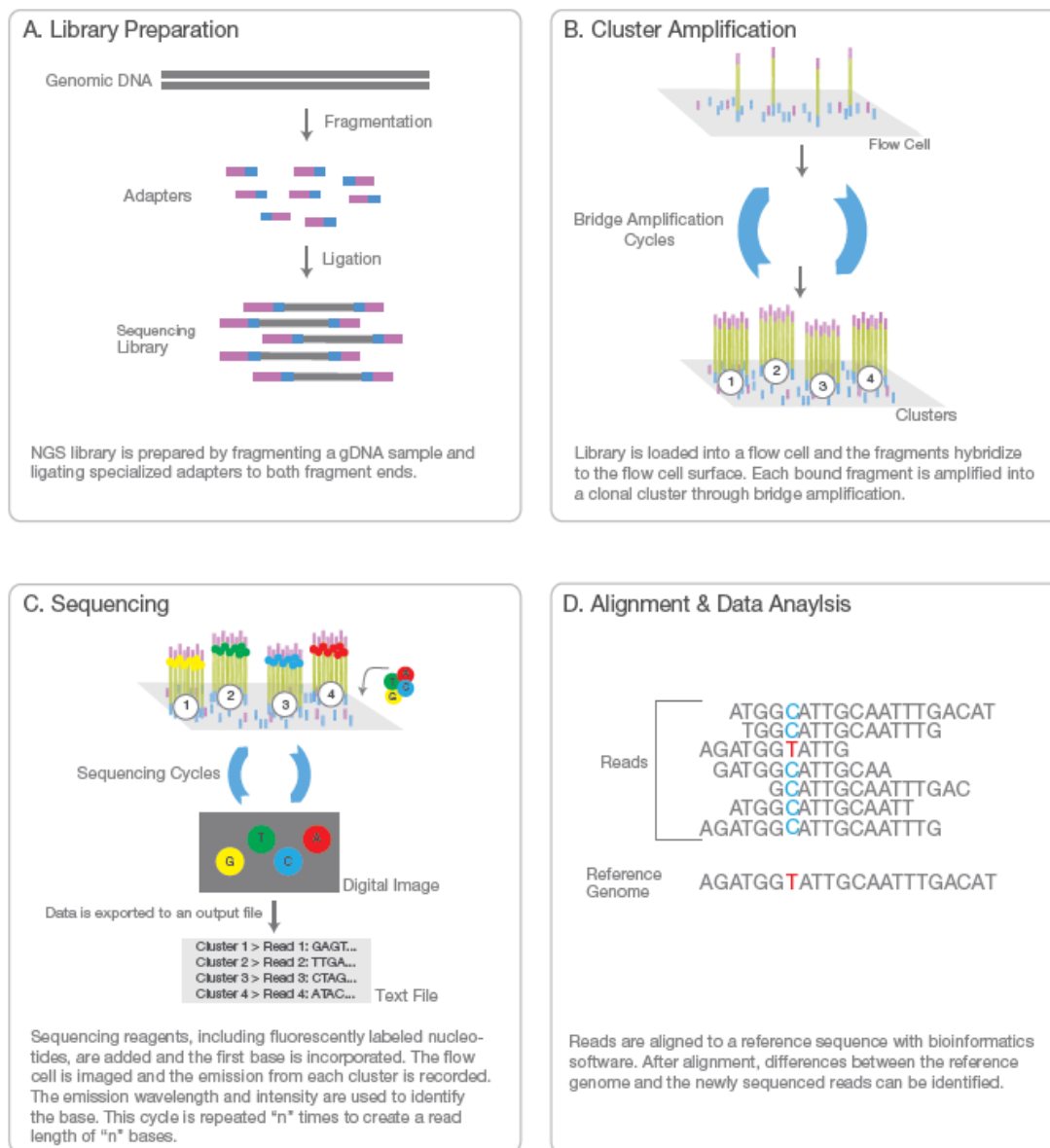


Figure 1. Schematic diagram of the rDNA region amplified by PCR for DGGE analysis.



**Figure 2. Schematic diagram of Next-Generation Sequencing Analysis**

The metagenome approach to analyze intestinal bacterial communities can 'capture' DNA containing information on the types of bacteria, both culturable and unculturable, but this approach cannot produce live bacterial isolates. With this approach, one can obtain bacterial isolates for further bacterial utilization. The collection of intestinal bacterial isolates obtained can also be identified morphologically, biochemically, and molecularly [9].

### 3. Diversity of bacterial communities in the gut of fish that live in freshwater in various locations

Different locations can affect the diversity of gut bacteria even if the host type is the same. Fish species can also affect gut bacterial communities, particularly the feeding habits of the host fish. Table 1 shows previous research on the diversity of bacterial communities in the intestines of carp that live in freshwater at various locations.

**Table 1. Previous research on the diversity of bacterial communities in the gut of Carp fish in various locations**

No	Type of Fish	Habitat	Intestinal Bacteria (Phylum)	Citation
1	<i>Aristichthys nobilis</i> (Bighead carp)	Guanyin dang Fish Cultivation Center in Jingzhou Province, China	Proteobacteria Planctomycetes Fusobacteria Firmicutes Cyanobacteria/Chloroplast Bacteroidetes Verrucomicrobia Tenericutes Synergistetes Spirochaetes Chloroflexi Chlamydiae Armatimonadetes Acidobacteria Actinobacteria	[10]
2	<i>Carassius gibelio</i> (Prussian carp)	Malye Chany Lake, west siberian, Rusia	Actinobacteria Bacteroidetes Cyanobacteria Firmicutes Planctomycetes Gemmatimonadetes Chloroflexi Acidobacteria Chlamydiae Fusobacteria Nitrospira Proteobacteria	[11]
3	<i>Cyprinus carpio</i> (Common carp)	Saudi Arabia	Proteobacteria Firmicutes Actinobacteria Proteobacteria Unidentified	[12]
4	<i>Ctenopharyngodon idellus</i> (Grass carp)	China	Unclassified bacteria Verrucomicrobia Tenericutes Synergistetes Spirochaetes Proteobacteria Planctomycetes Nitrospirae Lentisphaerae Gemmatimonadetes Fusobacteria Firmicutes Fibrobacteres Deinococcus-Thermus Deferribacteres Cyanobacteria Chloroflexi Chlorobi Chlamydiae Caldiserica	[13]

No	Type of Fish	Habitat	Intestinal Bacteria (Phylum)	Citation
			Bacteroidetes Aquificae Actinobacteria Acidobacteria	
5	<i>Cyprinus carpio</i> (Common carp)	Saudi Arabia	Proteobacteria Firmicutes Unidentified	[14]
6	<i>Cyprinus carpio</i> (Common carp)	Saudi Arabia	Proteobacteria Actinobacteria Firmicutes Unidentified	[8]
7	<i>Cyprinus carpio</i> (Common carp)	Cirata Reservoir, West Bandung	Tenericutes Streptophyta Planctomycetes Spirochaetes Verrucomicrobia Actinobacteria Ascomycota Acidobacteria Proteobacteria Bacteroidetes Fusobacteria Firmicutes Cyanobacteria Chlamydiae Chloroflexi	[9]
8	<i>Hypophthalmichthys</i> spp. (Bigheaded carp)	Lake Balaton, Hungary	Actinobacteria Bacteroidetes Chlorobi Chloroflexi Cyanobacteria Elusimicrobia Firmicutes Fusobacteria Lentisphaerae Nitrospirae Planctomycetes Proteobacteria Verrucomicrobia	[5]
9	<i>Cyprinus carpio</i> (Common carp)	Liangzi Lake, China	Others Bacteroidetes Firmicutes Tenericutes Fusobacteria Proteobacteria	[6]

Table 2 shows previous research on the diversity of bacterial communities in the intestines of Cichlid fish that live in freshwater.

**Table 2. Previous research on the diversity of bacterial communities in the gut of Cichlid fish**

No	Type of Fish	Habitat	Intestinal Bacteria (Phylum)	Citation
1	<i>Oreochromis mossambicus</i>	Mula River and Lake Ta-	Unclassified bacteria Others	[15]

No	Type of Fish	Habitat	Intestinal Bacteria (Phylum)	Citation
	(Mossambicus Tilapia)	legaon Dabhade, Maharashtra, India	OD1 Chloroflexi Verrucomicrobia Bacteroidetes Planctomycetes Cyanobacteria Actinobacteria Firmicutes Proteobacteria Fusobacteria	

Table 3 shows previous research on the diversity of bacterial communities in the intestines of Catfish that live in freshwater.

**Table 3. Previous research on the diversity of bacterial communities in the gut of Catfish**

No	Type of Fish	Habitat	Intestinal Bacteria (Phylum)	Citation
1	<i>Clarias Gariepinus</i>	Saudi Arabia	Proteobacteria Firmicutes Unidentified	[12]

#### 4. Conclusion

This review demonstrates the differences in the gut microbiota of freshwater fish collected from different habitats. This shows the effect of habitat or location on the diversity of fish gut microbes. This study provides the first insight into the diversity of bacterial communities in the gut of freshwater fish and provides a reference for future studies.

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