



Microbial comparison in guts of *Hypophthalmichthys moritrix*, *Hypophthalmichthys nobilis* and water in different habitats of Taihu Lake

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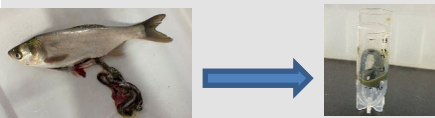
1. Introduction

Gut microbes, a community of microbiota colonized in the intestine, are closely associated with the host's nutritional status, growth and development, feeding differences, immunity function, and disease resistance. Silver carp and bighead carp have been used as an important method of biological manipulation to control cyanobacteria blooms in eutrophic water bodies in Taihu Lake. this study investigated the microbial composition, diversity, community structure, and predictive function in guts of two economical filter-feeding fish species and surrounding water in an unfed aquaculture system.

2. Research Objectives

- (1) The composition, diversity, community structure, and function of the microflora in the fish guts and surrounding water;
- (2) The distinctions of the fish gut microbiota from different habitats;
- (3) The contrasting signatures of the intestinal microflora of different fish species.

3. Materials and Methods



Illumina Nova 6000

5. Conclusion

This study demonstrated significant differences in microbial composition, diversity, community structure, and predictive functions between environment and fish guts, between fish guts from different habitats, and between fish guts of different fish species. Besides, we indicated that habitats seemed to contribute more to the variance of gut microflora than fish species.

4. Results

① composition and diversity of microbial communities

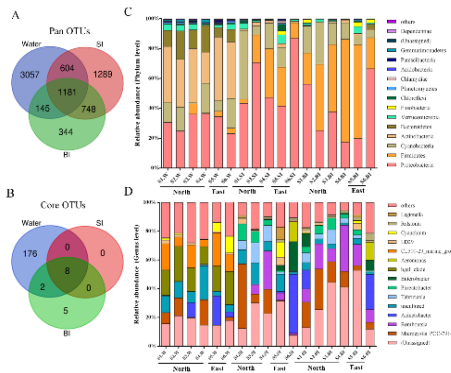


Figure 1. Composition of microbiota in water and fish guts.

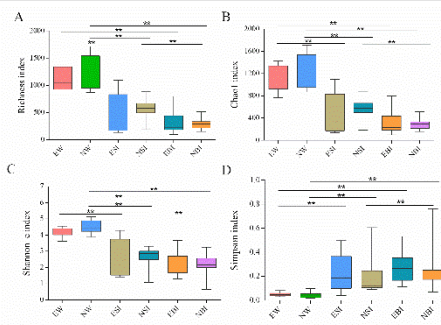


Figure 2. Alpha diversity of microbiota in water and fish guts.

③ Variance analysis of microbial communities

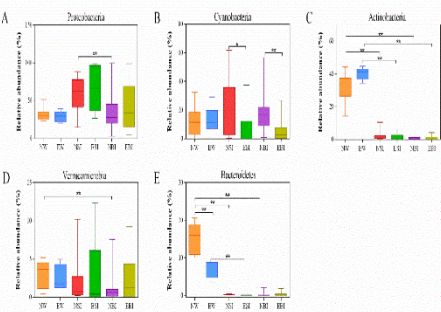


Figure 4. The comparison in microbial abundance (>1%) between groups at the phylum level. (A) Proteobacteria; (B) Cyanobacteria; (C) Actinobacteria; (D) Verrucomicrobia; (E) Bacteroidetes.

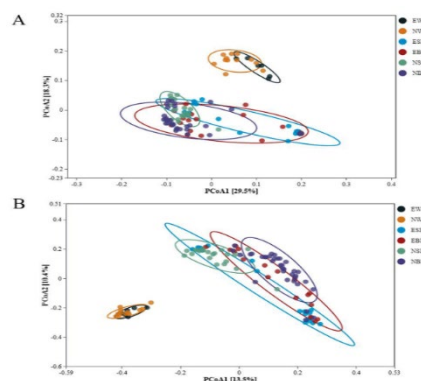


Figure 3. The comparison of microbial community structure. PCoA analysis based on weighted_unifrac (A) and unweighted_unifrac (B) of microbiota community in fish guts and water

④ Relationship between microbial communities and environmental factors

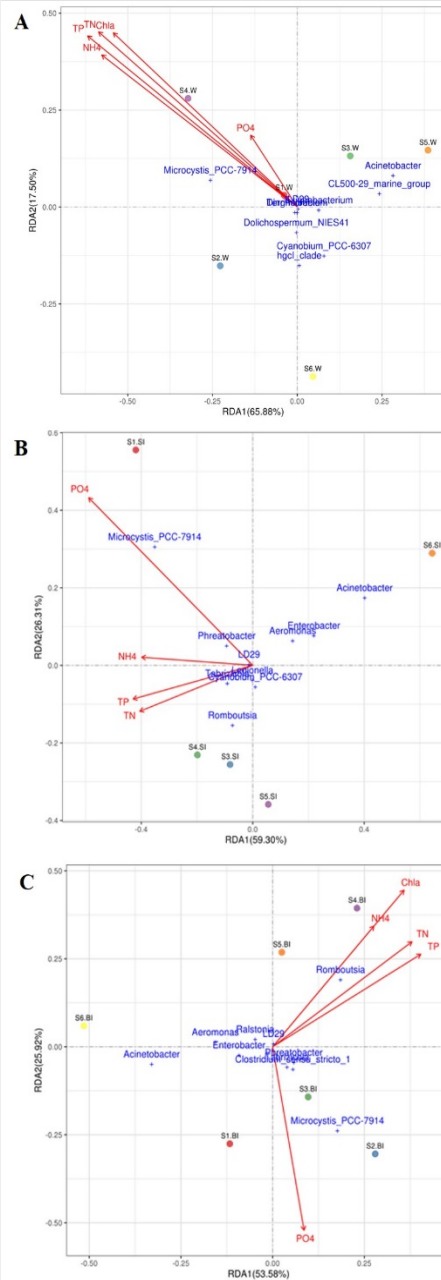


Figure 5. RDA analysis indicating the relationship between environmental factors and the microbial community at the genus level. (A) Water; (B) Silver carp guts; (C) Bighead carp guts.

⑤ Distinct microbiota and function analysis

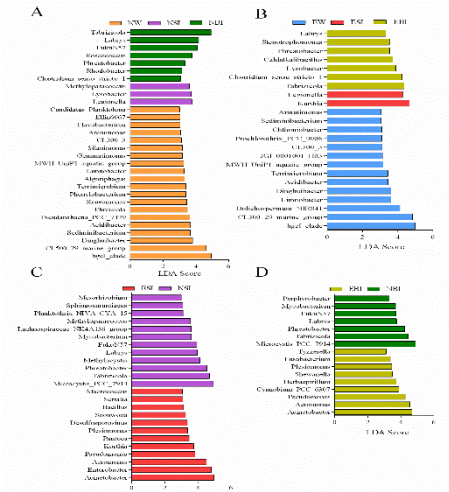


Figure 6. The comparison in microbial abundance (>1%) between groups at the phylum level. (A) Proteobacteria; (B) Cyanobacteria; (C) Actinobacteria; (D) Verrucomicrobia; (E) Bacteroidetes.

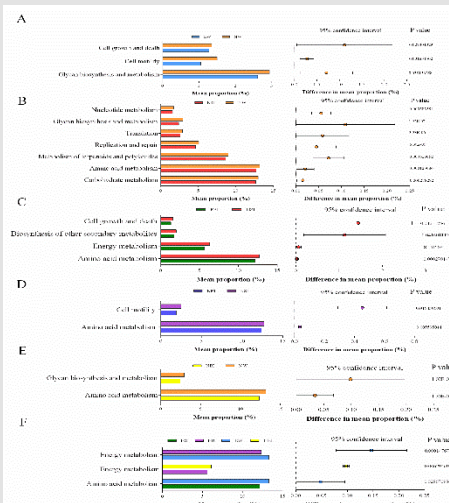


Figure 7. Functional differences (KEGG-Level 2, abundance >1%) in microbial communities among groups.

② Similarity analysis of microbial community structure

Table 1. Adonis analysis between groups.

Groups	R2-value	P-value
EW vs. NW	0.223	0.002
NBI vs. NW	0.319	0.001
NSI vs. NW	0.422	0.001
EBI vs. EW	0.278	0.001
ESI vs. EW	0.242	0.001
EBI vs. ESI	0.0728	0.016
EBI vs. NBI	0.0755	0.003
ESI vs. NSI	0.241	0.001
NBI vs. NSI	0.104	0.001