Exploring the potential regulation mechanisms of host-microbiome comprehensive interactions on growth traits in *Cyprinus carpio*

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Abstract

This study investigates how host genetics and gut microbiota interact to regulate growth in common carp. Key findings include: significant gut microbiota differences between high- and low-growth groups, with ten bacterial taxa differing between them. A GWAS identified three growth-associated loci (on chromosomes 18, 23, and 32), located within genes *PARD3B*, *RCC2*, and *ITGA10*. Notably, mutations in *RCC2* may disrupt cell regulation, increase immune-related bacteria, trigger immune responses, and reduce growth rate. The study highlights how host genetic variation can shape gut microbiota, thereby influencing growth, offering insights for microbiome engineering in aquaculture.

Introduction

☆ Global aquaculture is growing, but common carp show large unexplained growth variation under identical farming conditions.

☆ Gut microbiota critically affects host nutrition and immunity, yet its direct link to growth variation in aquaculture-and how host genetics drives this link-remains poorly understood.

☆ The authors performed re-sequencing (96 samples) and 16S rRNA sequencing (20 samples) on high and low-growth carp to uncover host-microbiota interactions that regulate growth, aiming to inform breeding strategies.

METHODS

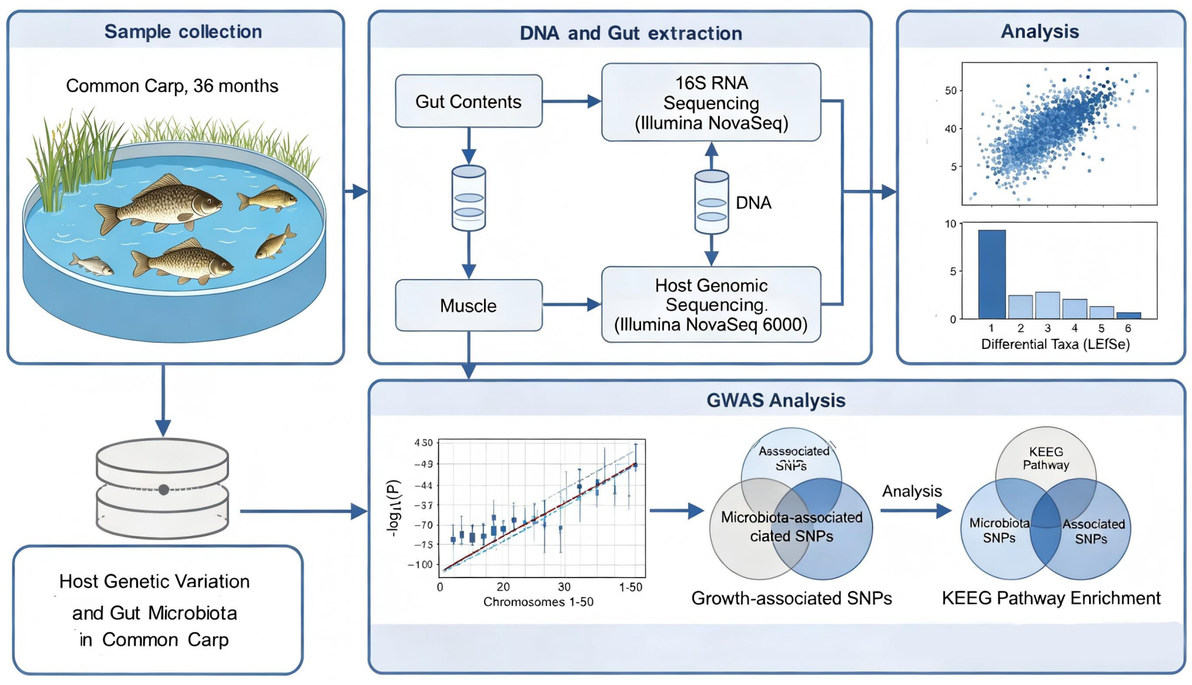


Figure. 1 Schematic workflow of the study on host genetics and gut microbiota in common carp.

Samples were collected from 36-month-old common carp, followed by host whole-genome sequencing and gut 16S rRNA sequencing. Microbiota composition was analyzed via LEfSe, and GWAS was performed to identify SNPs associated with growth traits and microbiota. Multi-omics integration included overlapping SNP identification and KEGG pathway enrichment analysis to explore host-microbiota interactions.

Result

The LDA effect size (LEFSe) analysis was performed with a threshold of LDA score > 2.5 and $p < 0.05$, revealing that 22 bacterial biomarkers showed differences between the two groups at four different classification levels (Figure 2A). At the genus level, the Wilcoxon rank-sum test revealed that 13 bacterial genera were significantly enriched in the gut microbiota of HG and LG groups, respectively ($p < 0.05$)(Fig. 2B).

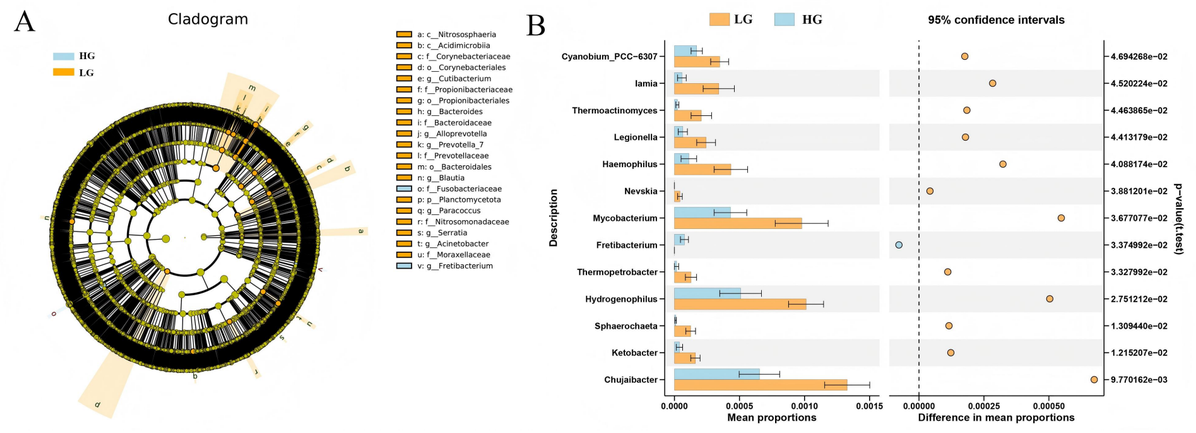


Figure. 2 Analysis of key components and correlation of intestinal bacterial communities of HG and LG.

The association between the host genome and body weight traits was investigated by GWAS. The Manhattan map (outermost circle in Fig. 3A)illustrate the association between body weight traits and significant SNPs found in the host genome. In addition, the relationship between 2 different microbial and host genomes is shown in Figure 3A. The number of different SNPs common and unique in different permutation groups was counted (Fig. 3B), and analysis found that only Iamia and growth traits shared similar genetic regions on chromosome 23 (10,968,715: A > C) and 32 (16,293,406: T > G), while Thermoactinomyces and growth traits shared similar genetic regions on chromosome 18 (6,901,682: A > C). Iamia and Thermoactinomyces can be identified as biomarkers associated with host genomes, gut microbes, and growthtraits.

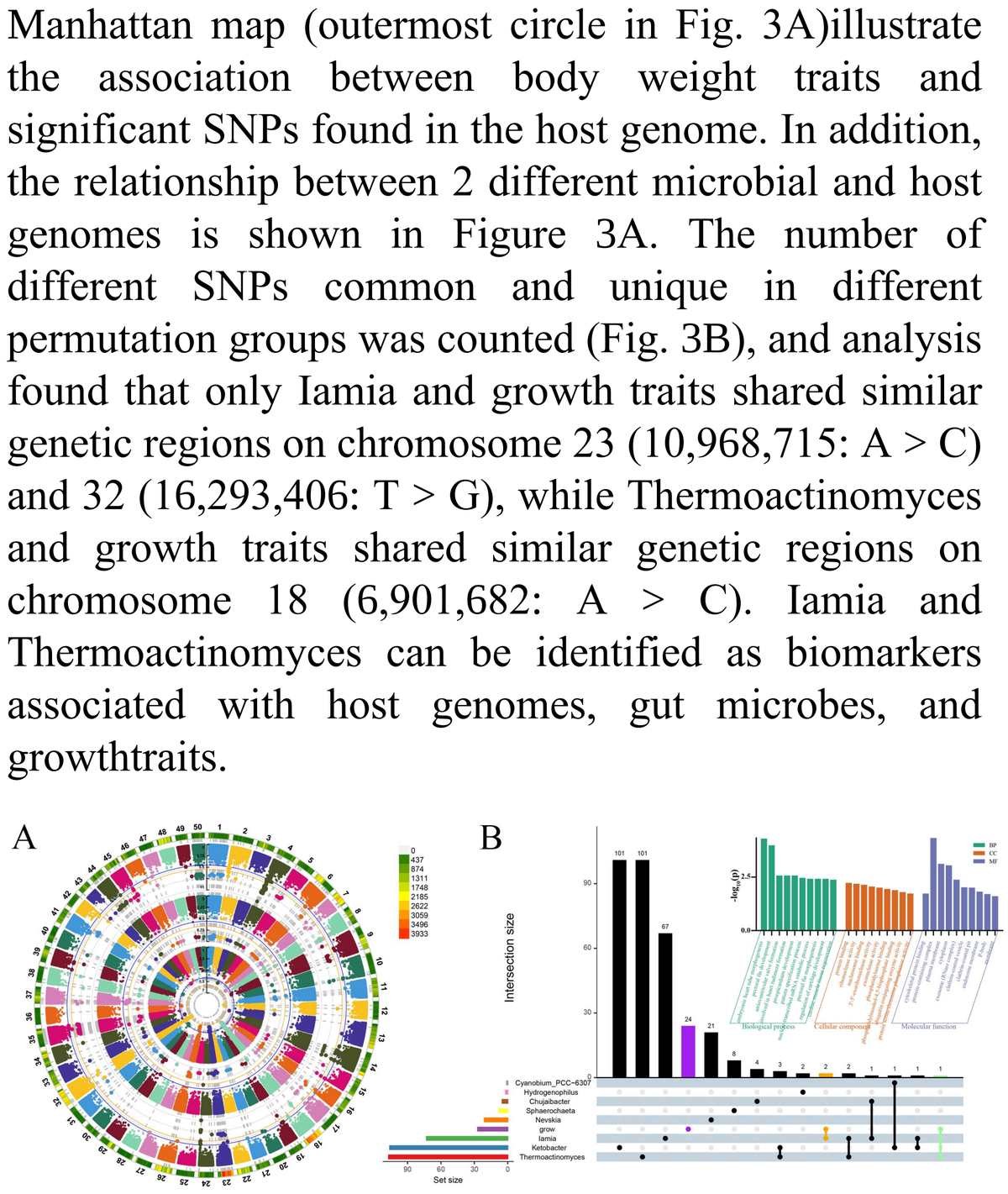


Figure. 3 GWAS and Upset analysis of the effects of genetic factors on growth and microbiota.

Conclusion

This study reveals that growth variation in common carp is driven by host genetic polymorphisms and specific gut microbiota . However, the small sample size and lack of metabolomics limit mechanistic depth, and future work should integrate multi-omics and functional validation to enable precision microbiome engineering in aquaculture.