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Abstract

The profound interplay between intestinal microbiota and animal biology has received ample scientific attention. Yet the alternations of microbiota populating the fish intestine with respect to starvation remain incompletely understood. The present study used 16S rRNA sequencing to investigate changes of intestinal microbiota in grass carp (*Ctenopharyngodon idellus*) during starvation. The microbial community structure of starved fish differed from that of the fed fish (day 0 of the experiment) ($F=25.8$, PERMANOVA $P=0.0001$). Compared with the fed fish, starved fish had a higher abundance of *Vibrio* and a lower abundance of *Bacteroides*, *Fusobacterium*, *Coprococcus* and *Citrobacter* genera. Predicted functions indicated that microbiota changed the specific metabolic pathways and functions to adapt to the food deprivation. The expression of *TLR3*, *TLR5b*, *TLR7*, *IL-1 β* , and *TNF α* genes was generally

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