Genome-Wide Insights into Whole Gut Microbiota of Rainbow Trout, Oncorhynchus Mykiss Associated with Changes in Dietary Composition and Temperature Regimens

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Abstract : Gut microbiomes play a significant role in the growth, metabolism, and health of fish. However, we know very little about the interactive effects of variations in dietary composition and temperature on rainbow trout gut microbiota. Exactly 288 rainbow trout weighing $45.6g \pm 0.05$ (average \pm SD) were fed four isocaloric, isolipidic, and isonitrogenous diets comprising 40% crude protein and 20% crude lipid and formulated as 100 % animal-based protein (AP) and a blend of 50 fish oil (FO)/50 camelina oil (CO), 100 % AP and 100 % CO, 100 % plant-based protein (PP) and a blend of 50FO/50CO or 100 % PP and 100 % CO in 14 or 18°C for 150 days. Gut content was analyzed using 16S rRNA gene and shotgun sequencing. The most abundant phyla identified regardless of diet were Tenericutes, Firmicutes, Proteobacteria, Spirochaetes, Bacteroidetes, and Actinobacteria, while Aeromonadaceae and Enterobacteriaceae were dominant families in 18°C. Moreover, gut microbes were dominated by genes relating to an amino acid, carbohydrate, fat, and energy metabolisms and influenced by temperature. The shared functional profiles for all the diets suggest that plant protein sources in combination with CO could be as good as the fish meal with 50/50 FO & CO in rainbow trout farming.

Keywords: aquafeed, aquaculture, microbiome, rainbow trout

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