

MAPPING THE MICROBIOME OF ICTALURID CATFISH: TISSUE AND SPECIES-SPECIFIC COMMUNITY COMPOSITION

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Host mucosal immunity is regulated by the complex interplay between environmental factors, host genetics, and commensal and pathogen dynamics. Microbial imbalances due to physiological stressors, changes in nutrition, and/or antibiotic application can potentiate over-exuberant host immune responses and lead to declining fish health in aquaculture settings. To better understand the catfish (*Ictalurus spp.*) microbiome under homeostatic conditions, we carried out high-throughput 16S v4 amplicon sequencing of replicated individual gill and intestine samples from channel catfish (*I. punctatus*), blue catfish (*I. furcatus*), and hybrid catfish (*I. punctatus x I. furcatus*). Sequencing was carried out on an Illumina MiSeq instrument using 150 bp paired-end (PE) chemistry. A total of 10,612,766 raw reads were captured. Paired ends were assembled with PANDAseq, resulting in 2,853,669 filtered PE contigs with an average of 356,708 contigs per species. Reads were processed by QIIME to identify 1,158,301 operational taxonomic units (OTUs). These were then assigned taxonomic identities and used to generate phylogenetic and summary statistic comparisons of diversity and community composition among samples. The distribution and abundance of bacterial sequences were different among each species and tissue analyzed. Our foundational results should establish a baseline against which we can monitor the impact of changes in nutrition, culture system, or therapeutant on the catfish microbiome.