

Host habitat is the major determinant of fish gut microbiome structure

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Abstract

Most current knowledge about gut microbiomes has been obtained from studies on mammals, while the microbiomes of fish, the most diverse group of vertebrates (~33,000 species), are less well understood. Specifically, the major influencing factors and unique features of fish gut microbiomes remain unclear. To bridge this knowledge gap, a recent study analyzed the gut contents of 227 fish representing 85 different freshwater fish (FWF) and saltwater fish (SWF) species. rRNA sequencing revealed that Proteobacteria and Firmicutes were the two most abundant phyla, indicating a different composition from the typical vertebrate microbiome, which is composed mainly of Firmicutes and Bacteroidetes. Habitat (freshwater versus saltwater) more strongly influenced the host microbiome than host taxonomy or trophic level and the microbiome taxonomic and functional profiles were better indicators of a fish's habitat than of its taxonomy. Interestingly, the microbiomes of freshwater and saltwater fish showed distinct functions. The gut microbiome communities of fish also differed significantly from those of other vertebrate classes. Although studies in other regions and studies that consider other factors, such as environmental microbes, are necessary. The results provide insights into the factors shaping the fish gut microbiome and the microbial community differences between fish and other vertebrates.