

Genomics of Serrasalminae teleosts through the lens of microbiome fingerprinting

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Abstract

Associations between host genotype and the microbiome of holobionts have been shown in a variety of animal clades, but studies on teleosts mostly show weak associations. Our study aimed to explore these relationships in four sympatric Serrasalminae (i.e. piranha) teleosts from an Amazonian lake, using datasets from the hosts genomes (SNPs from GBS), skin and gut microbiomes (16S rRNA metataxonomics), and diets (COI metabarcoding) from the same fish individuals. Firstly, we investigated whether there were significant covariations of microbiome and fish genotypes at the inter and intraspecific scales. We also assessed the extent of co-variation between Serrasalminae diet and microbiome, to isolate genotypic differences from dietary effects on community structure. We observed a significant covariation of skin microbiomes and host genotypes at interspecific ($R^2=24.4\%$) and intraspecific ($R^2=6.2\%$) scales, whereas gut microbiomes correlated poorly with host genotypes. Serrasalminae diet composition was significantly correlated to fish genotype only at the interspecific scale ($R^2=5.4\%$), but did not covary with gut microbiome composition (Mantel $R=-0.04$; only 6 microbiome taxa involved). Secondly, we tested whether microbial taxa represent reliable host traits to complement host genotypic variations in these species. By using an NMDS ordination-based approach, we observed that subsets of the skin and gut microbiomes selected by a machine-learning Random Forest algorithm can complement host genotypic variations by increasing significantly the average interspecific differentiation. The complementarity of genome and microbiome variations suggests that combining both markers could potentially benefit our understanding of the evolution of Serrasalminae in future studies.

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