Genomics of Serrasalmidae teleosts through the lens of microbiome fingerprinting

François-Étienne Sylvain¹, Eric Normandeau¹, Aleicia Holland², Adalberto Luis Val³, and Nicolas Derome¹

¹Université Laval 'Institut de Biologie Intégrative et des Systèmes ²La Trobe University College of Science Health and Engineering ³Instituto Nacional de Pesquisas da Amazonia

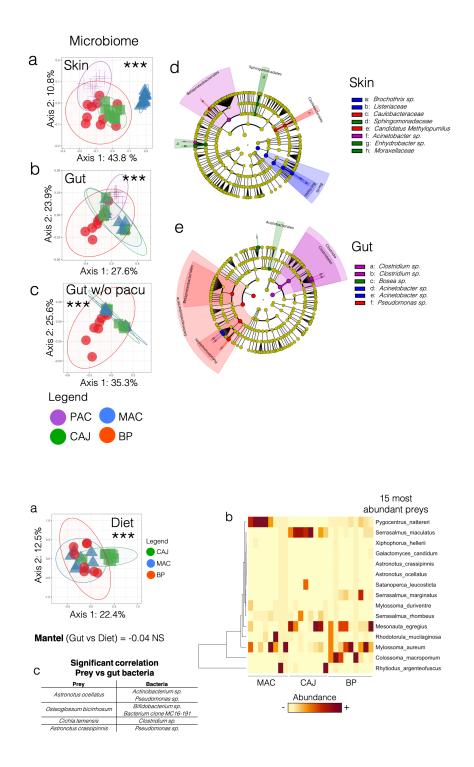
September 25, 2021

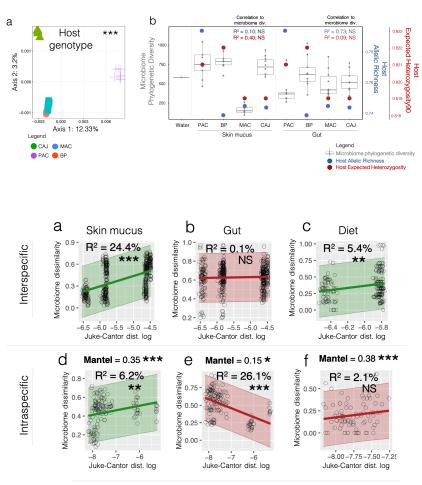
Abstract

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 Serrasalmidae (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 Serrasalmidae 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 (R2=24.4%) and intraspecific (R2=6.2%) scales, whereas gut microbiomes correlated poorly with host genotypes. Serrasalmidae diet composition was significantly correlated to fish genotype only at the interspecific scale (R2=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 Serrasalmidae in future studies.

Hosted file

FES2_Manuscript_Piranhas_AUGUST2021.docx available at https://authorea.com/users/437216/ articles/539002-genomics-of-serrasalmidae-teleosts-through-the-lens-of-microbiomefingerprinting





Genetic distance between individual fish (pairwise comparisons)

