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Microbiome profiling of small marine invertebrates

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Metazoans commonly harbor essential microbial communities – microbiomes – in their gut, on their skin, and often within some of their organs. The microbiome associated with many large and commercially important animals, from cattle to bees, have been thoroughly investigated and shown to have highly integrated metabolic networks that complement their hosts' and complex coevolutionary histories. However, the vast majority of metazoan diversity is understudied, and we know next to nothing about the microbiomes of most non-model organisms. One large black box is represented by relatively small marine invertebrates (meiofauna and larger organisms <2-3 mm), which play critical roles in ecosystems across the globe. There is considerable evidence that small invertebrates commonly harbor bacteria, archaea, protists or combinations thereof, but no extensive survey across major lineages has ever been performed. We are attempting to fill this gap in knowledge by investigating the microbiomes of small marine invertebrates in the coastal waters of British Columbia (Canada) and the Caribbean (Curação). We have collected more than 1000 specimens belonging to 21 phyla, recorded their main morphological features with photos and videos, and extracted their DNA; we are currently profiling their associated prokaryotic and eukaryotic microbiomes using the hypervariable V3-V4 region of the SSU rRNA gene. We are concurrently characterizing background microbial communities from the same habitats (sediment, water column, and macroalgae) in order to identify the taxa that are specifically associated with the animals. Our data will allow us to describe the microbiome of specimens covering the entire spectrum of the metazoan tree and address fundamental questions: do these small metazoans harbor microbiomes as complex as those of large animals? Does microbiome composition correlate with host phylogeny? If so, at what level? What level of microbiome variability exists within each species?

Keywords: Meiofauna, microbial communities, ecology, morphology, taxonomy

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