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TITLE: Gut Microbial Divergence between Two Populations of the Hadal Amphipod *Hirondellea gigas*

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ABSTRACT:

Hadal environments sustain diverse microorganisms. A few studies have investigated hadal microbial communities consisting of free-living or particle-associated bacteria and archaea. However, animal-associated microbial communities in hadal environments remain largely unexplored, and comparative analyses of animal gut microbiota between two isolated hadal environments have never been done so far. In the present study, 228 Gb of gut metagenomes of the giant amphipod *Hirondellea gigas* from two hadal trenches, the Mariana Trench and Japan Trench, were sequenced and analyzed. Taxonomic analysis identified 49 microbial genera commonly shared by the gut microbiota of the two *H. gigas* populations. However, the results of statistical analysis, in congruency with the alpha and beta diversity analyses, revealed significant differences in gut microbial composition across the two trenches. Abundance variation of *Psychromonas*, *Propionibacterium*, and *Pseudoalteromonas* species was observed. Microbial cooccurrence was demonstrated for microbes that were overrepresented in the Mariana trench. Comparison of functional potential showed that the percentage of carbohydrate metabolic genes among the total microbial genes was significantly higher in the guts of *H. gigas* specimens from the Mariana Trench. Integrating carbon input information and geological characters of the two hadal trenches, we propose that the differences in the community structure might be due to several selective factors, such as environmental variations and microbial interactions. **IMPORTANCE** The taxonomic composition and functional potential of animal gut microbiota in deep-sea environments remain largely unknown. Here, by performing comparative metagenomics, we suggest that the gut microbial compositions of two *Hirondellea gigas* populations from the Mariana Trench and the Japan Trench have undergone significant divergence. Through analyses of functional potentials and microbe-microbe correlations, our findings shed light on the contributions of animal gut microbiota to host adaptation to hadal environments.

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