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Active bacterial microbiota in the gut of glacier invertebrates as revealed by 16S rRNA deep sequencing analysis.

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On glaciers, diverse psychrophilic and psychrotolerant organisms form unique ecosystems. Although many studies on the glacier microorganisms have been conducted, information on the glacier invertebrates remains limited. In this study, to evaluate the role of glacier invertebrates in the glacier material cycles, we performed the census of active bacterial microbiota in the gut of glacier invertebrates by deeply sequencing 16S rRNA genes and their transcripts.

We collected the glacier ice worm *Mesenchytraeus solifugus* in Alaska and the glacier stonefly *Andiperla willinki* in Patagonia. DNA and RNA were simultaneously extracted from their homogenates and the habitat ice surface layer, and the V3_V4 region of bacterial 16S rRNA was amplified by PCR and RT-PCR using a Bacteria-universal primer set. Then, paired-end amplicon sequencing was performed on an Illumina MiSeq.

The bacterial taxonomic compositions between the DNA and RNA samples of ice worms differed in several aspects. For example, Clostridia were abundantly found in the RNA samples, while it comprised only a minor portion in the DNA samples. Indeed, the bacterial community structures were clearly separated between the DNA and RNA samples by UniFrac analysis, and these were also distinct from those of the habitat glaciers. We are now conducting the same analysis for the stonefly samples. With these analyses, we are attempting to identify taxonomic groups active as gut symbionts in the glacier invertebrates. Our results will contribute to further understanding of the glacier ecosystems.

keywords:glacier ecosystem,gut bacteria,16S rRNA,MiSeq