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Bacterial Community Structure in Glacier Ice and Subglacial Streams, Antarctica

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Antarctic glacier retreat is expected to have an important impact on the microbial communities embedded in perennial ice. In this context, our study focused on investigating the bacterial diversity from glacier ice and subglacial streams of King George Island, NW Antarctica, in relation with the spatial distribution and substrate geochemistry.

Samples were collected from Barton, Weaver and Potter Cove areas. Physicochemical measurements indicated a low mineral content and slightly alkaline pH in glacier ice relative to subglacier water. All ice samples showed a reduced organic carbon content and a homogenous Na-HCO₃ type chemistry, while stream water was more heterogeneous, belonging to Na-Ca-HCO₃ and Na-Cl types, with a high Al, Fe and Sr content.

Illumina MiSeq sequencing of 16S rRNA gene highlighted variations of bacterial diversity with the type of habitat, locations and geochemical characteristics. Phyla distribution in the two types of habitats showed the dominance of *Proteobacteria* followed by *Bacteroidetes*, with spatial variations of other phyla representation between the peninsulas. High content of *Proteobacteria* characterized both the ice and stream microbial communities, with a major presence of *Acinetobacter* mainly in glaciers.

Analysis of the distribution pattern of bacterial communities in ice and subglacial streams, in relation with the habitat geochemistry, contributes to unravel the impact of melting glaciers on the resilience of the embedded microbiome.