

Taxonomic and functional characterization of a microbial community from a volcanic **englacial ecosystem** in Deception Island, Antarctica



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Glaciers are populated by a large number of microorganisms. Solar radiation, nutrient availability and water content greatly determine the diversity and abundance of these microbial populations, the type of metabolism and the biogeochemical cycles. In order to study their metabolic potentials, samples of englacial ice were taken from an Antarctic glacier. Microorganisms were analyzed by a polyphasic approach that combines a set of -omic techniques: 16S rRNA sequencing, culturomics and metaproteomics. This combination provides key information about diversity and functions of microbial populations, especially in rare habitats. Several essential proteins and enzymes related to metabolism and energy production, recombination and translation were found that demonstrate the existence of **cellular activity at subzero temperatures**. In this way it is shown that the englacial microorganisms are not quiescent, but that they maintain an active metabolism and play an important role in the glacial microbial community.

