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WSL Institute for Snow and Avalanche Research SLF
Flüelastrasse 11 | CH – 7260 Davos Dorf
polar2018@slf.ch | www.polar2018.org

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Ice Microbiome: From Antarctic Glaciers to Alpine Ice Caves

Cristina Purcarea¹ (cristina.purcarea@ibiol.ro), Corina Itcus², Constantin Marin³, Soon Gyu Hong⁴, Victoria I. Paun¹, Aurel Persoiu¹, Paris Lavin⁵, Traian Brad⁶, Alexandra Hillebrand-Voiculescu³, Denisa Pascu¹, Cristian Coman⁷, Iris Tusa², Manuela Sidoroff²

¹*Institute of Biology, Romanian Academy, Bucharest, Romania*, ²*National Institute of Research and Development for Biological Sciences, Bucharest, Romania*, ³*Emil Racovita Institute of Speleology, Bucharest, Romania*, ⁴*Korea Polar Research Institute (KOPRI), Incheon, Korea, Republic of*, ⁵*University of Antofagasta, Antofagasta, Chile*, ⁶*Emil Racovita Institute of Speleology, Cluj Napoca, Romania*, ⁷*Institute of Biological Research, Cluj Napoca, Romania*

Environmental changes due to recent glacier retreat phenomenon are expected to challenge the structural and functional variability of ice microbiomes, with different impact on specific glacial habitats.

Our comparative study of Antarctic glaciers and Alpine ice cave investigated the bacterial and fungal diversity from glacier transects and subglacial water flows of Barton and Weaver peninsulas from King George Island, and a 13,000-years old ice chronosequence of Scarisoara ice cave. Illumina sequencing of 16S rRNA and ITS2 genes indicated major differences in microbial composition correlated with the habitat type, spatial distribution, geochemistry and age of ice.

Glacier ice showed lower diversity relative to subglacial water and cave ice. *Proteobacteria* clearly dominated all Antarctic samples, while the major phylum of cave ice block alternated between *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, *Firmicutes* and *Cyanobacteria* based on the age, organic content and light exposure of ice layers. Different Beta/ Gamma-*Proteobacteria* ratios were specific for Antarctic ice/water and cave ice of different age. *Acinetobacter* and *Polaromonas* prevailed in all Antarctic samples with a relative abundance depending on sample type and location. Fungal community analyses based on ITS2 sequencing, currently under way, will complete the comparative microbiomes overview of these icy habitats, and their response to environmental variables.

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