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A cave ice microbiome

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Microbial diversity across the perennial ice block of Scarisoara Ice Cave, Romania, was assessed by Illumina sequencing of both 16S rRNA and ITS2 genes and by shotgun metagenomics. Ice core chronosequences up to 13 000 years BP containing clear and organic-rich layers were collected and analyzed. Total and viable cell content determined by flow cytometry varied in the 10^3 – 10^6 cells mL⁻¹ interval, showing a decrease with the age of ice deposits. Chemical composition of the ice substrate, showing large variations over the last 5000 years was analyzed in relation to the microbial density and diversity of corresponding ice layers. The cave microbiome is dominated by Proteobacteria with taxa variations based on the age and geochemistry of the ice layers. Archaeal OTUs, mainly present in older ice and dominated by Euryarchaeota, also showed a distinct metabolism depending on organic content and independent of the age of the ice. The fungal community belonged to Ascomycota, Basidiomycota, Cryptomycota, Zygomycota and Cercozoa, with different content of genera from cold habitats. Shotgun sequencing of seven ice samples gDNA and the metagenome reconstitution of their microbiome revealed both structural and functional variability in the microbial communities across the cave ice block.