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## Central Antarctic environments – genomic insights into microbial biogeochemistry

### Content

We combine our expertise to explore community function and diversity in samples collected from Vostok, Antarctica: to establish the dispersal capability and viability of microorganisms in Central Antarctica; to characterize changes in microbial functional diversity across habitat types (snow, ice, lake water accretion ice) and link these to selective pressures; to understand ecosystem stability and resilience over time in a climate change scenario; to evaluate the potential of microorganisms to alter the geochemical signatures of trace gases and molecules in ice. Four samples representing different type of ice- the firn-ice interface, the old ice from the base of the glacier and the lake ice were studied. They are the ice cores from depths of 99, 3404, 3413 and 3617 m. The samples were treated and decontaminated in the IGE cold room, then processed in IGE clean room for further decontamination, melting and concentration. The concentration factor ranged from 800 to 4600 depending on the sample. The final volume of the samples (400 mkl) was shared equally between two parties for further analysis. Two different methods of DNA extraction and the methods of High-Throughput Sequencing which are widely used now for recovering microbiome from different environments were applied. Parallel to that the chemical analysis of these samples was performed. Bacterial DNA signatures were obtained using MiSeq Illumina amplicon sequencing of the bacterial V3-V4 region of the 16S rRNA gene. Out of 2035 OTUs (operational taxonomic units), the most representative 311 OTUs were selected. Statistical data processing was carried out. A significant contribution of contaminants to the sequencing results (up to 80%) was shown. It was also shown that 3 main bacterial species contribute 50% to negative controls. The main groups of contaminants are representatives of Firmicutes, Bacteroidetes, Actinobacteria, Verrucomicrobia, Alpha- and Gammaproteobacteria. The group of sequences obtained only for the studied ice samples includes representatives of Deltaproteobacteria, Alphaproteobacteria, Gammaproteobacteria, Bacteroidetes, Actinobacteria, Firmicutes, Planctomycetales. To accurately determine the membership of OTU, each sequence is additionally checked in databases (NCBI) by the source of isolation.

The analysis of the content of 18 main chemical ions in the samples under study also was carried out. DOC analysis showed extremely low values of dissolved organic carbon for the studied samples (in ppbC): V\_3413 - 3.3; V\_3404 - 4.6; V\_3617 - 7.2, which corresponds to independent measurements for the deep atmospheric ice from the Vostok core (5, 2 ppbC) and evidence of the cleanliness of ice core processing. Shown to be inappropriate for chemical analysis using the automatic sample loading. The final results need a careful and thorough interpretation due to contamination whose contribution effect is great because of low biomass in these samples.

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