

Spatial structure of permafrost and active layer from the James Ross Island, Antarctica: Geological and Microbiological Insights

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Permafrost is a unique ecosystem of polar environments which is inhabited with diverse population of bacteria with many different roles (Jansson and Taş 2014, Bottos et al. 2014). Based on our knowledge only low information is known about spatial structure of permafrost and active layer from microbiological and geological view (Bottos et al. 2014). Here we described the data obtained from a drill hole in James Ross Island, which is a part of Antarctic Peninsula, the most warming part of Antarctica (Hrbáček et al. 2017).

Our analysed specimens were sampled from the biggest ice-free region at Antarctica Peninsula near polar station of Johann Gregor Mendel (Hrbáček et al. 2017). Specimens were sampled from different depths of permafrost with drilling set. There were made at individual depths physical, chemical and microbiological properties of the permafrost. Main aim of the project is mapping functions and diversity of prokaryotes here, and correlations between biotic and abiotic factors in permafrost and active layers.

The collected material was subjected to determination of elemental composition with X-ray fluorescence spectrometry and a combination of sieving and laser granulometric analysis was used for determination of grain size composition. Furthermore, the elemental ratios selected to reveal the source of rock material and an indication as to which processes in the material occurred were calculated. The metagenomic variations of samples from different depths of the permafrost was based on 16S rRNA sequencing. 16S rRNA analysis has been also carried out on cultured representatives taken from different permafrost depth and active layers.

Based on metagenomics results, main taxa has been represented by phyla *Proteobacteria*, *Actinobacteria*, *Firmicutes*, *Chloroflexi* and *Acidobacteria* in total of 36 phyla. Species diversity correlated with decreasing sampling depth. Along with depth, the course of elementary proportions and elemental ratios has also changed significantly. The sediments of the investigated profile are predominantly composed of coarse-grained material, especially sand and gravel, but the proportion of silt and clay fractions increased with increasing depth, where was detected anaerobiosis zone for microbes represented by classes *Gammaproteobacteria*, *Bacilli*, *Clostridia* and *Bacteroidia*. In addition, a divide of 1,0 m was defined to indicate the lower boundary of the active layer, where was observed the highest ratios in number of bacterial species. In active layer, based on elemental composition and metagenomics was observed the highest metabolic

diversity. A correlation between chemical erosion and phylum *Acidobacteria* was also observed in the upper layers. Culturable species belongs mainly to genus *Arthrobacter*, *Pseudomonas*, *Sphingomonas*, *Sphingopyxis* and *Leifsonia*.

Our study explain spatial roles of prokaryotes based on geological and metagenomic analyses in Antarctic permafrost.

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