



Microbiomes of permafrost affected soils (Fildes peninsula, King George Island)

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The bacterial communities of Antarctic soils have been studied by many researchers mainly by the use of both culture-based and culture-independent methods. According to the previous studies, microbial communities of soils of Maritime Antarctica are dominated by following bacterial phyla: Acidobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, Proteobacteria and Verrucomicrobia. Various islands of Maritime Antarctic demonstrate substantial differences in the phylotypes composition of the soil microbial communities caused by the fluctuations in climate and soil physico-chemical conditions of soils. The microbiome composition of pristine and antropogenically affected soils samples from Fildes peninsula was investigated by use of 16S rRNA pyrosequencing. DNA was extracted from 0.2 g of soil using PowerSoil DNA Isolation Kit. Pyrosequencing was carried out using GS Junior system (Roche). The raw sequences were processed using QIIME ver. 1.8.0. The taxonomic analysis of the soil microbiomes revealed 20 bacterial and archaeal phyla, more that 96 % of sequences in the amplicon libraries were presented by Proteobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, Acidobacteria and Verrucomicrobia. Archaea presented the minor portion of the microbial diversity (0,1% in average). Microbiomes of the antropic soils sampled, close to Bellingshausen station were enriched with Cyanobacteria, Shingomonadaceae, and Intrasporangiaceae while pristine soils, located close to glacier was enriched was inhabited mostly by the bacteria from the families Verrucomicrobiaceae, and Chitinophagaceae. The initial soils in paraglacial area are characterized by the dominance of bacteria belonging to Xanthomonadaceae, Shingomonadaceae and Nocardiodaceae families, while the more developed Cryosols were dominated by Chtoniobacteriaceae and Chitiniphagaceae bacteria. These could be explained by development succession, where the early stages are dominated by the copiotrophic bacteria and the latest are enriched by oligotrophic ones

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