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**Title:** *Bacterial Succession in Glacial Forefield Soils Characterized by Community Structure, and Opportunistic Growth Dynamic*

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The succession of bacterial communities inhabiting the forefield of the Werenskiöld glacier (West Spitsbergen) was investigated. Distribution of bacteria in the soil by culture-independent and culture-dependent approaches were done. During two summer seasons (2010, 2011) we sampled the glacier forefield along a temporal gradient of soils deglaciated between 1930 and 2010. The samples were collected at four stations. The sampling site closest to the glacier was uncovered from underneath the glacier within last 10 years while the furthestmost - over 70 years ago. The oldest soil was uncovered more than 100 years ago.

Number of bacteria in each soil sample was estimated by total direct count (TDC) method following DAPI (4,6-diamidino-2-phenylindole) staining and microscopic enumeration. Soil extract with agar (2%, w/v) and Antarctic Bacterial Medium (ABM) plates and incubation at 10 °C for 14 days for growing culturable bacteria were used. An index of 'opportunism' was determined from the ratio of culturable to total cells (C:T ratio). Soil DNA extraction, PCR of the highly variable V3 region of the 16S rRNA gene and then denaturing gradient gel electrophoresis (DGGE) for estimation bacterial community composition were performed. Results indicated that diverse of number and structure of bacteria between four stations were depended on the distance to head of glacier. On average, the C:T ratio showed a biphasic trend, which exhibited minima in the 0- and 100-year-old soils while a maximum activity per cell was reached in the 80-y soil. Molecular assessment of bacterial diversity of soil DNA revealed that the composition and succession of bacterial populations on the studied stations were different. Relatively high abundance but the lowest heterogeneity of bacteria was observed at the station situated near to the front of glacier. The studied soils substantially differ in both the total number of bacteria, the abundance of heterotrophic bacteria and the composition of bacterial populations. Our results suggest that the subglacial microbial populations can be divided into two groups: autochthonous (chemoheterotrophic bacteria) and allochthonous that retain the ability to proliferate and give rise to active population when conditions become favorable. We also sequenced 27 DGGE OTU-s, and the most common were *Actinobacteria* from genus *Arthrobacter*, class *Gammaproteobacteria* from genus *Pseudomonas* and uncultured bacteria which be also isolated from Arctic permafrost, Tibet and



Antarctica as well.

We conclude that bacterial succession in the glacier forefield is a dynamic process with adaptation to the differing stages of succession occurring on both the individual and community levels. Soil age and soil water content could be singled out as having significant effects on the structure and composition of the bacterial community.