

**Bacterial diversity in Siberian permafrost soils based on 16S rDNA clone libraries  
and *in-situ* cell counting**

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Permafrost soils of the Siberian Arctic are exposed to extreme environmental conditions. Except for the short summer period, when thawing of the uppermost 20 to 50 cm of the permafrost sediment allows for the formation of a so-called active layer, the soils are frozen throughout the entire year. Active layers show steep temperature gradients between 10 to 18 °C in the top and 0 to 1 °C in the bottom part. Seasonal freezing and thawing also lead to the formation of symmetrically patterned low-centred ice wedge polygons which determine a pronounced small-scale heterogeneity of permafrost soils with regard to their physical and chemical properties.

Vertical profiles of potential methane oxidation rates in respond to temperatures between 0 and 38 °C indicated shifts between a cold adapted methanotrophic community in the top and a cold loving methanotrophic community in the bottom active layer. Based on these results we used 16S rDNA clone libraries as well as *in-situ* cell counting to compare the bacterial communities of two active layer depths of a polygon rim and a polygon centre. We will show that the composition of the bacterial soil community depends on soil depth and soil properties. We will also show that bacterial diversity, characterized by richness, relative abundance and genetic relatedness of their operational taxonomic units (OTUs), is comparably high in Siberian permafrost soils, in temperate terrestrial and marine environments. According to cell counts in the range of  $10^7$  to  $10^9$  this holds also for the number of bacterial cells detected *in-situ*.