

Adaptation and Composition of Methanotrophic Communities in Permafrost Soils of the Lena Delta, Siberia

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Wet tundra environments of the Siberian Arctic are considerable natural sources of methane, a climate relevant trace gas. Current climate models predict a significant change in temperature and precipitation in the northern hemisphere. The potential impact on the Arctic carbon reservoirs is highly influenced by changes in microbial processes like methanogenesis and methane oxidation. Methanogenesis describes the terminal step in the anaerobic degradation of organic matter by methanogenic archaea. The emission rates of the biologically produced methane from arctic Permafrost soils are highly divergent. Seasonal methane emission from a low-centred polygon, which are characteristic for the microrelief of the Lena Delta, ranged between $53,2 \pm 8,7 \text{ mg d}^{-1} \text{ m}^{-2}$ from the polygon depression and $4,7 \pm 2,5 \text{ mg d}^{-1} \text{ m}^{-2}$ from the polygon rim. The amount of methane released is mainly controlled by obligately aerobic or microaerophilic α - and γ -Proteobacteria, the methane oxidizing bacteria (MOB).

First research on the activity of the methanotrophic community in floodplain soils of Samoylov Island (Lena Delta, Siberia) at different temperatures indicate a change in the temperature optimum with depth. While MOB in the upper soil layers of the *Typic Aquorthel* appeared to have their highest activity at temperatures $> 21 \text{ }^\circ\text{C}$ the maximum methane oxidation rates in deeper and colder horizons were determined at $4 \text{ }^\circ\text{C}$. The activity of MOB also seems to depend on the methane concentration whereat the substrate affinity of the methane oxidizing community appeared to decrease with depth. Fluorescence *in situ* hybridization of MOB also indicates a shift in the community structure with depth from the appearance of Type I MOB (γ -Proteobacteria) only to coexisting Type I and Type II (α -Proteobacteria) MOB.

Further research on the adaptation to temperature changes in combination with biomarker analysis, cell counts and community changes using CARD-FISH will be done. For detailed diversity analysis a clone library of the methane oxidizing community in low-centred-polygons from the Lena Delta will be constructed.