

Spatial variance of methane oxidation rates in Siberian permafrost soils in dependence of the temperature: An indicator for microbial changes of structure and diversity?

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Wet tundra environments of the Siberian Arctic are considerable natural sources of methane, a climate relevant trace gas. The Arctic appears to warm more rapidly and to a greater extent than the rest of the earth surface and it is suggested, that the tundra in Alaska and Russia has changed from a net sink to a net source of atmospheric carbon [1]. The potential impact on the carbon reservoirs of Arctic soils is highly influenced by changes in microbial processes like methanogenesis and methane oxidation.

The latter process is due to the activity of methane oxidising (methanotrophic) bacteria that consequently determine the amount of methane that is released from Siberian permafrost soils. In Arctic environments, biological processes are controlled by an extreme temperature regime in the upper active layer of the permafrost accompanied by seasonal freezing and thawing. Therefore, methane oxidation rates within two soil profiles from Samoylov Island (N 72°22', E 126°28', Lena Delta, Siberia) were determined in dependence of the temperature through conversion of $^{14}\text{CH}_4$ to $^{14}\text{CO}_2$. Moreover, total, methanotrophic and cells of the domain *Bacteria* were counted using fluorescence *in situ* hybridisation (FISH) and DAPI staining. The rates obtained indicate a shift in the temperature optimum of methanotrophic activity with increasing soil depth. The methanotrophic bacteria of the upper soil layers showed their highest activity at 21 °C. However, in deeper horizons close to the permafrost table the maximum methane oxidation rates were determined at 4 °C. These results may indicate the existence of specialised and cold adapted methanotrophic communities in horizons close to the permanently frozen ground of Siberian permafrost soils. It will further be investigated if these results will also be reflected in the diversity and structure of the methanotrophic communities. For these purposes clone libraries will be designed and complemented by a molecular fingerprinting of the dynamic within the methanotrophic community.

Reference:

[1] IPCC (2001) Climate Change 2001: The Scientific Basis: http://www.grida.no/climate/ipcc_tar/wg1/index.htm