

Microbial genomes and community gene expression in high arctic terrestrial ecosystems

The aim of this project is to increase our understanding of activity and processes of the permafrost microbial community soils, focusing on the *in situ* situation and the response to changing temperature and humidity.



The observed temperature increase in the northern hemisphere is likely to affect the permafrost soils (IPCC 2007). Higher temperature leads to an increase in microbial activity, potentially causing an increased methane emission from the soil.

Applying metatranscriptomics and metagenomics, we approach the microbiology of permafrost soils from the viewpoint of systems biology. The genes and transcripts from *in situ* samples are sequenced applying high throughput methods, and community structure, community interactions and metabolic pathways are deduced from the sequence information. The same approach is

also applied under controlled experimental conditions, yielding high quality information on soil responses to changes in environmental conditions.

The main objectives of this project are to:

Objective 1: Explore the community composition and functional potential of active microbial communities in arctic permafrost soils.

Objective 2: Explore *in situ* processes related to methane production and oxidation simulated in controlled temperature experiments.

Objective 3: Assess the critical temperature window for anaerobic/aerobic processes related to methane transformation.

Objective 4: Identify possible indicator organisms and/or functional genes with high responsiveness to climate changes.



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Community composition and gene expression of methane oxidizing bacteria (methanotrophs) in subarctic palsa ecosystems



Palsas are small peat mounds rising out of mires in the subarctic region. They contain a permafrost core of frozen peat and/or silt, small ice crystals and thin ice layers (Seppälä 1986).

Palsas are common in the discontinuous circumpolar permafrost zone occurring in Fennoscandia, Iceland, Canada, Alaska and Siberia. In addition to seasonal variations in temperature and precipitation, palsa mires are currently exposed to rising annual mean surface temperatures due to their location in the high-northern latitudes (IPCC 2007). Seasonal and long-term environmental changes likely alter carbon cycling processes and methane fluxes of palsa mires which are considerably governed by indigenous microbial communities. Thereby, methanotrophs are the major sink for methane in those carbon rich terrestrial habitats.

The aim of this project is to identify methanotrophic key players of the Bøttemyra palsa peatland in Finnmark, northern Norway, and to understand their response to variations in temperature, hydrology and methane concentrations.

In particular we want to:

- describe the community structure of methanotrophs in subarctic palsa peatlands
- establish a representative collection of palsa peatland methanotrophs
- identify the dominant active methanotrophic community
- test the resistance and resilience of methanotrophic palsa communities
- identify the function of novel pmoA (functional marker gene of methanotrophs) sequences

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Methods applied in running projects

- Metagenomics
- Metatranscriptomics (mRNA isolation from soil)
- High throughput amplicon (*pmoA*) sequencing
- PCR and qPCR targeting key genes in methane oxidation and methanogenesis
- Enrichment and isolation of methane oxidizing bacteria
- Single cell genomics