

54. Microbial community structure and activity during thawing of mineral cryosols of the Canadian High Arctic: meta genomics, transcriptomic and proteomics

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Project Goals:

1. Perform ~2 year thawing experiments on well-characterized, intact cores of the Arctic active- layer and permafrost from a proposed reference ecosystem site where CO₂ and CH₄ fluxes, temperatures, humidity, soil moisture, nutrients, microbial diversity and activities and isotopic analyses are currently being measured.
2. Characterize the vertical flux of volatile organic acids, O₂, H₂, CO₂ and CH₄ the isotopic systematics of CO₂ and CH₄ and changes in the transcriptomics, proteomics and C cycle networks in these cores as the permafrost thaws under water saturated and water under saturated conditions.
3. Compare the fluxes measured for the cores with those measured in the field.
4. Based upon these thawing experiments construct a 1D biogeochemical reaction/transport model that predicts the CO₂ and CH₄ release into the atmosphere as permafrost thaws and compare these predictions with observations at the reference ecosystem site.

<http://www.princeton.edu/southafrica/permafrost-project/>

Permafrost thawing and the resulting microbial decomposition of previously frozen organic C, represent a significant potential positive feedback of CO₂ and CH₄ from terrestrial ecosystems to the atmosphere. However, to date, most studies have focused on relatively high carbon soil sites with less available information regarding microbial activity and the potential for CH₄ generation in low carbon/low nitrogen mineral soils such as those found on Axel Heiberg Island, Nunavut, Canada near the McGill Arctic Research Station. As part of a long-term 18-month thawing experiment (Stackhouse *et al.* 2014), soil samples were collected from 1-meter long intact cores consisting of active-layers and permafrost for metagenomic analyses using a 2 x 100 bp paired- end Illumina protocol. Seventy-seven metagenomes, averaging 5 Gbp/ library and representing a matrix of sequence data spanning 5 treatment conditions, 4 depths and 5 time points (unthawed to 18 months thawed) were annotated in MG-RAST. Taxonomic and functional characterization of the metagenomes indicate specific microbial community differences between the upper active layers and the underlying permafrost layer with opposite depth gradients between alpha- Proteobacteria which were more abundant towards the soil surface and Actinobacteria which were more abundant in the lower layers. Over a 12-month thaw period, the microbial community structure in the upper 5 cm active layer remained remarkably constant. In contrast, the microbial community structure shifted towards higher concentrations of Firmicutes and beta-Proteobacteria with time in the lower 65 cm and permafrost layers, i.e. more similar to that in the upper 5 cm soils. Potential CH₄ cycling pathways primarily consisted of methane oxidizers in the upper layers with a paucity of methanogenic archaea in the lower layers. Other differences in carbon- cycling pathways exist with depth, included aromatic ring oxidation and CO₂ fixation potential in the uppermost layer, and carbon reduction pathways in the permafrost layer.

Nitrogen-cycling pathways also differed by depth with N₂ fixation and denitrification pathways present in the upper layers and nitrification pathways in the permafrost layer. The metagenomic sequences generated during the study are being co-assembled to generate high quality databases in order to better identify peptide sequences in metaproteomes and metatranscriptomes. A co-assembly of sequences from ten 5 cm libraries generated 83,205 contigs >200bp. Within these contigs, nearly full-length sequences for the genes encoding particulate methane monooxygenase (*pmoC*, *pmoA* and *pmoB*) with high similarity to high-affinity Type II methanotrophs were identified (Lau *et al.* 2014). Mapping of ~30 million metatranscriptomic sequences generated from total RNA isolated from the upper 5 cm active layer soils, collected during Arctic summer, resulted in the identification of *pmo* transcripts from surface soils underlying the moss from the polygon interior and polygon trough samples but not in a non-vegetated polygon interior sample. The use of co- assembled contigs also formed the database by which the *pmoB* protein was found in two active- layer metaproteomic samples from the core thawing experiment. These combined results support parallel *in situ* field gas flux (CH₄, CO₂) and laboratory column analyses indicating these abundant Arctic mineral cryosols are acting as methane sinks rather than methane sources in the moss and wedge samples. Additional analyses of these combined metagenomic, metatranscriptomic and metaproteomic datasets provide a strategy for linking metabolic potential of the soils with metagenomic sequences and will improve our understanding of the microbial community, phytocommunity and ecosystem gradient.

References

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