

## 78. The Thaw: Investigating Microbial Contribution to Permafrost Carbon Liberation through Functional Meta-omics

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**Project Goals:** Microbial communities are key drivers of the carbon cycle, and through climate change induced thaw, permafrost associated carbon is increasingly exposed to microbial degradation. The consequent release of carbon dioxide and methane may exacerbate further thaw through a positive feedback mechanism. This project endeavors to determine the fate of cryosequestered and newly deposited carbon, by investigating a succession of microbial communities along a chronosequence of gradating permafrost thaw in Stordalen mire, subarctic Sweden. This study utilizes a range of meta-omic techniques including metagenome enabled community profiling and population genome recovery as well as metatranscriptomics to gauge in situ functional activity. Visual linkage of function to microorganisms using quantum dot labelling and confocal microscopy is also being explored. Importantly, this microbial ecology component is part of a much broader collaborative project featuring interdisciplinary expertise in metaproteomics, biogeochemistry and systems modelling.

Permafrost regions lock away around 50% of global soil carbon (1). However, the permafrost carbon sink is becoming a source for diverse microbial life that may fix carbon as biomass, or release it into the atmosphere as carbon dioxide or methane. Methane producing archaea (methanogens) reduce acetate (acetoclasts), or carbon dioxide and hydrogen (hydrogenotrophs), to produce energy for growth. The byproduct of this process is methane, which has 25 times the radiative forcing of carbon dioxide per molecule, making it a potent greenhouse gas (2). High methanogen abundances in thawing and thawed sites at Stordalen mire (3) contribute to increased methane generation (1), however aerobic methane-oxidizers (methanotrophs) also play an important role in controlling the flux of this methane. Observations of fluctuations in methanotroph diversity and metabolic efficiency following a thaw progression are currently lacking, yet they are central to understanding this rapidly changing environment. Thorough characterization of the microbial constituents of the thaw affected carbon cycle is facilitated by a comprehensive meta-omics approach.

An expansive data set (over 200 metagenomes and 24 metatranscriptomes spanning four depths, four months and five years) is revealing interactions between community members despite the enormous complexity of each environment in the thaw progression. GraftM (4), a new metagenome analysis tool, was developed specifically for such datasets, and efficiently and rapidly searches data for marker genes that can be taxonomically classified. GraftM identified and phylogenetically placed the methanogenesis gene *mcrA*, and methanotrophy genes *pmoA* and *mmoX*, in the metagenomes and transcriptomes. Initial analysis has determined distinct successional changes within communities as thaw progresses. Within the methanotrophs, there is a definite shift from Alphaproteobacteria to Gammaproteobacteria populations at both the genome and transcriptome level. Populations have also been identified outside of expected niches with aerobic methanotrophs appearing in deeper anoxic peat levels, alluding to the heterogeneity of the permafrost microenvironments. The recovery of over 100 population genomes is expanding insight into metabolic pathways, and when linked with metatranscriptomic information, can show up-regulation of some genes over others and may shed light on the propensity or tolerance of clades to particular environments.

Future efforts will be directed towards visualizing key players driving important metabolic processes such as methanogenesis, methane oxidation and cellulose degradation. Microbial data will be integrated with an extensive chronicle of geochemical data that encompasses carbon isotope,  $\alpha C$ , dissolved organic matter, and methane concentration measurements. Ultimately, amalgamation of biotic and abiotic data will allow for the training of models and enable predictions on the impact of thaw to the global carbon system.

References:

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