# The Impact of Global Warming on the Carbon Cycle of Arctic Permafrost: An Experimental and Field Based Study

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https://www.princeton.edu/southafrica/permafrost-project/

**Project Goals:**

1. **Perform ~2 year long, thawing experiments under water saturated and water under saturated conditions on well-characterized, intact cores of Arctic active-layer and permafrost from a proposed reference ecosystem site where $CO_2$ and $CH_4$ fluxes, temperatures, humidity, soil moisture, nutrients, microbial diversity and activities, as well as C isotopic analyses, are currently being measured in the field.**
2. **Perform phylogenetic, metagenomic, transcriptomic and proteomic analyses of these cores prior to and during the experiments.**
3. **Characterize the composition of the solid and dissolved organic matter, the inorganic geochemistry, the vertical flux of volatile organic acids, $O_2$, $H_2$, $CO_2$ and $CH_4$ and the isotopic systematics of $CO_2$ and $CH_4$ during the experiments.**
4. **Compare the results of these experiments with field measurements, and based upon both data sets construct a 1D biogeochemical reaction/transport model that predicts the $CO_2$ and $CH_4$ release into the atmosphere as permafrost thaws.**
5. **Development of a high sensitivity $^{14}C$ RNA isotope microarray and a CRDS for C and H isotopic analyses of atmospheric $CH_4$.**

Forty 1 meter long cores were collected from a 7 meter diameter polygon located near the McGill Arctic Research Station during April 2011 where the depth to permafrost is 70 cm. Total community genomic DNA (cgDNA) was isolated from the 2011 samples using four different commercially available kits to determine the best DNA extraction protocol for metagenomics. The v1 region of the 16S rRNA gene was amplified directly from cgDNA or re-amplified from 16S rRNA amplicons. Taxonomic analysis revealed similarity in bacterial communities derived from different extraction kits. The significant variation in the bacterial community structure as a function of depth in the active layer previously reported in the 2010 core samples does not appear to be an artifact of extraction protocols. Gemmatimonadetes is the dominant bacterial phylum in the uppermost active layer, whereas Firmicutes and Actinobacteria are the dominant phyla near the permafrost table and within the permafrost consistent with geochemical evidence of increasing anaerobicity with depth. The organic matter from these cores ranged from 6% total organic C at the surface to 1% at 10 cm depth with C/N = 13-16. NMR and FT-ICR-MS reveal the composition of this organic matter is significantly different from that reported in boreal soils and peat deposits (1). $^{14}C$ analyses are underway.

Microcosms of subsamples from the cores amended with select nutritional amendments revealed significant $CO_2$ production and $CH_4$ consumption and the presence of stress responsive proteins (e.g. DnaK, GroEL) and proteins essential for energy production and survival under carbon starvation (e.g. F0F1 ATP synthase, acyl-CoA dehydrogenase). Proteins from the genera *Bradyrhizobium, Sphingomonas, Lysinibacillus* and *Methylophilaceae* were detected, and these bacteria were also identified by 454 pyrosequencing on the same samples. Metaproteomics of the pristine core samples,

however, yielded relatively few protein identifications suggesting a relative lack of microbial activity and limited microbial biomass. Metaproteome efforts have been focused on evaluation and optimization of experimental protocols to efficiently extract proteins from these low biomass cores. Lipidomic analyses of the core samples are underway.

Continuous *in situ* gas flux analyses of $CO_2$ and $CH_4$ fluxes from permafrost and ice-wedge active layer (AL) soils were conducted using CRDS's during July 2011. Polygon AL soil flux showed a net outward $CO_2$ flux (175 to 3,155 mg/m$^2$-day) and consumption of atmospheric $CH_4$ (-1.2 mg/m$^2$/day). Gas flux from the ice-wedge AL surface was in a similar range as the polygon, having slightly higher maximal $CO_2$ flux (3670 mg/m$^2$/day) and net $CH_4$ consumption (-2.0 mg/m$^2$/day). The $\delta^{13}C$ of the $CO_2$ efflux from the surface were consistent with microbial activity, ranging from -10.6 ‰ to -15.5 ‰ for the polygon and ice-wedge soils, respectively. In both AL soils, gas flux fluctuates diurnally. The $CO_2$ out flux was found to be anti-correlated to surface temperature (R = -0.67), whereas the $CH_4$ in flux was found to be correlated to surface temperature (R = 0.76). Using a vertical gas probe, the $CO_2$ concentrations increased with depth and corresponded to a $CO_2$ flux 19 to 41 mg/h in the polygon AL soils *vs*. 18 to 54 mg/h in the ice-wedge soils. Through the same profile, the $CH_4$ concentration decreased from 0.59 ppmv to < 0.1 ppmv within 30 cm of the surface in the ice wedge and from 0.62 to 0.18 ppmv at the base of the polygon AL. Below the surface, the $\delta^{13}C$ of $CO_2$ was more $^{13}C$ depleted than at the AL surface, reaching -18.9 ‰ and -21.3‰ at the base of the AL in the polygon and ice wedge soils, respectively. These data suggest that both polygonal and ice-wedge AL soils contribute net efflux of $CO_2$ and consumption of $CH_4$ during the summer season and that the more saturated ice-wedge soils may have a more favorable environment for methanogenic bacterial activity with depth with greater stratification in fluxes of gases through the profile. Defining these relationships is critical for accurately modeling the extent and rate of + or - feedback in global climate models.

Thawing experiments on the 2011 cores have begun with an initial active layer thaw over a one-month period to simulate Arctic spring thaw. Previous reports of dramatic shifts in the phylogenetic and functional gene structure of active layer and permafrost after only 2 weeks of warming (2, 3) motivated us to relate this sudden change to initial C and N fluxes in our thawing experiments. Once the community and fluxes have stabilized we will initiate permafrost thawing.

All components for the Scintillator Layered Imaging Microscope for Ecological Research (SLIMER) have been assembled and the spatial accuracy and resolution validated with an $\alpha$ source. The next step will be to increase S/N for low energy $\beta$ sources. The sensitivity and reproducibility of the PU-CRDS has been significantly increased to that it is now capable of measuring the $\delta^{13}C$ of 2 ppmv $CH_4$ with a precision of ±2‰. Modifications are underway to make the PU-CRDS robust under field conditions for transport to the Arctic.

Two posters given at the Fall Meeting of AGU and data shared with the RCN on Permafrost Carbon stimulated much discussion and new collaborations.

**References**


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