Microbial Communities Generating Greenhouse Gases in Thawing Permafrost

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Project Goals: The IsoGenie project ("Genes, isotopes, and ecosystem biogeochemistry: dissecting methane flux at the leading edge of global climate change") focuses on integrating microbial and geochemical studies to improve our understanding of carbon cycling in a subarctic wetland where climate change induced permafrost thawing is transforming carbon sinks into sources. Our research goals are: (1) to discover relationships between microbial community composition and metabolism to ecosystem carbon cycling; (2) to learn how these relationships are affected by shifting environmental variables, and (3) apply this knowledge to better understand and predict changing carbon budgets in subarctic ecosystems experiencing substantial climate change. One of the aims of this research was to characterize microbial communities along a degradation gradient using 16S rRNA gene amplicons, meta-genomics, -transcriptomics and -proteomics.

High northern latitudes are at the leading edge of global climate change with the effects of warming already evident in degrading permafrost. Increased thawing of permafrost, a significant global carbon sink, releases previously sequestered labile carbon. Thawing initiates a transition from intact permafrost (Palsa hummock) through an intermediate thaw state (collapsed Palsa; hollow) to fully degraded inundated end state (fen). The transition to a fen state has been associated with dramatic increases in biogenic methane production and other greenhouse gases (GHGs). GHGs produced by peat microorganisms are 10-fold and 100-fold higher in the hollow and fen samples respectively, as compared to hummock samples (100 year CO_2 equivalents). The exact combination of *in situ* ecological conditions triggering GHG efflux is unknown, however the rising water table associated with thawing permafrost is believed to lead to anoxic conditions favourable to microbial methane production.

Here, microbial communities along a degradation gradient in Stordalen Mire (Abisko National Park, Sweden) were characterized using 16S rRNA gene amplicon pyrosequencing. Sampling sites and depths were selected based on geochemical data, including GHG flux. Changes in microbial community structure along the degradation gradient were substantial and occurred at the high water mark (middle sampling depth) in the hollow sites (Figure 1). Microbial communities below the waterline in hollow peats (positive methane flux) were relatively low complexity and were dominated by a single archaeal species within the order *Methanomicrobiales* and two bacterial species of the order *Acidobacteriales*. Microbial community richness and composition in the hummock samples (low to negative GHG flux) approached that of non-permafrost soils. *Acidobacteria* were dominant across all sample sites and depths, comprising between 20% and 42% of the OTUs observed. The ubiquity of *Acidobacteria* across all samples is consistent with

members of this phylum being adapted to low energy, low nutrient, highly acidic and water stressed environments.

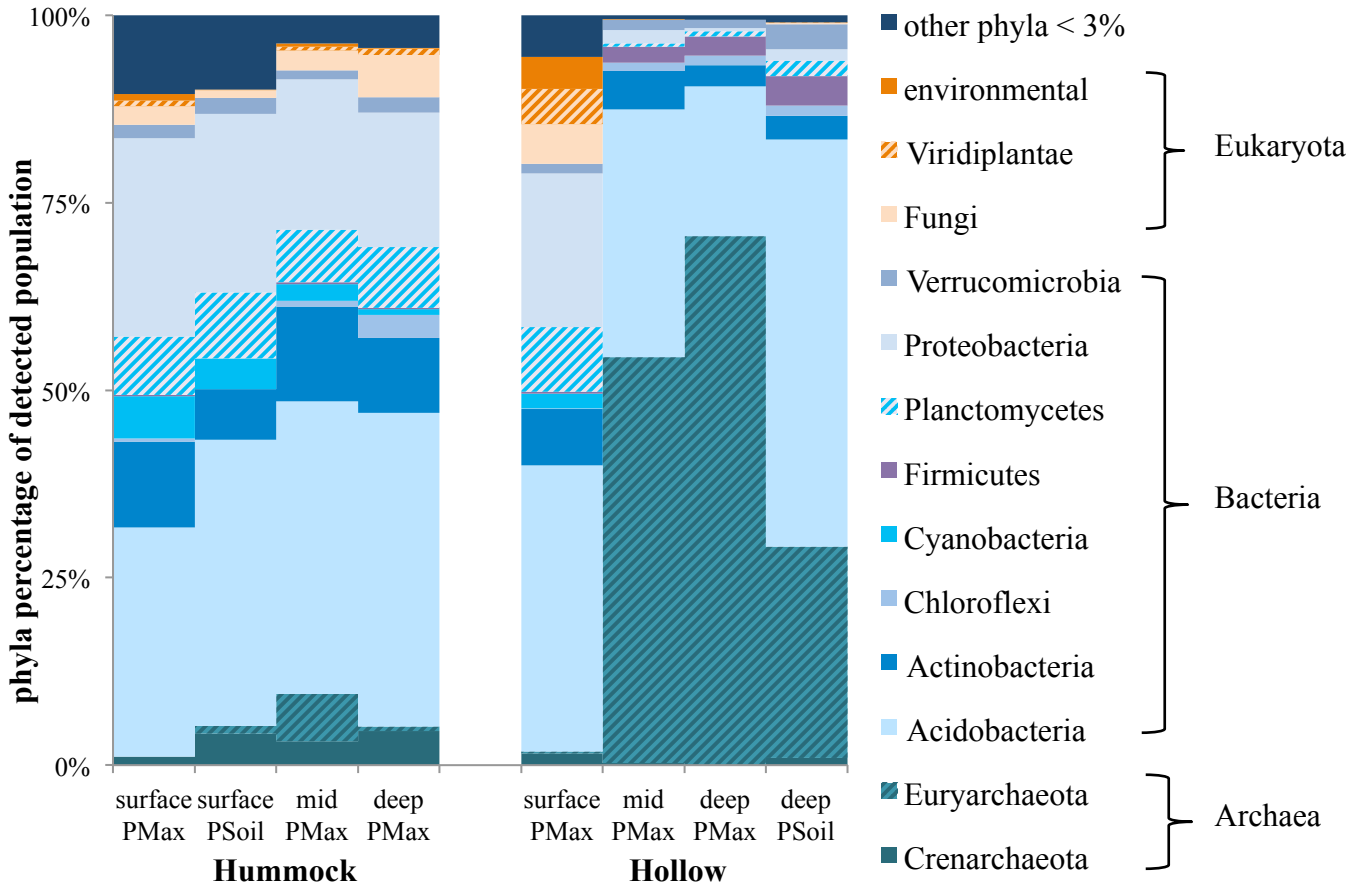

Figure 1. Microbial community composition of active layer peat in (low GHG) Hummock and (mid GHG) Hollow. Two extraction methods, PMax (PowerMax kit, MoBio) and PSoil (PowerSoil Total RNA/DNA co-elution kit, MoBio), were tested in this study.

To further elucidate these emerging patterns in microbial community structure and diversity, samples collected during 2010 and 2011 (June, July, August, and October) are currently being sequenced. The third year of sample collection is scheduled for the 2012. Metagenomic sequencing of select samples are being undertaken to facilitate the recovery of the dominant *Methanomicrobiales* and *Acidobacteriales* genomes. In addition, microbial community profiles generated from all samples, together with GHG data will be used to select samples for combined metagenome, metatransciptome and metaproteome analysis. Integration of meta'omic data with the isotopic geochemistry will clarify ecosystem variables related to GHG production. Insights gained regarding the ecological triggers of GHG emission over the degradation gradient will inform emission projections, filling a gap in current climate modelling scenarios.

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