

Greenhouse gas producing microbial communities in thawing permafrost



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Introduction

High northern latitudes are at the leading edge of global climate change. Effects of warming are already evident in the disappearance and degradation of permafrost. Thawing permafrost enables the microbial degradation of previously sequestered carbon releasing greenhouse gas (GHG) providing positive feedback to global warming.

Aim

To characterise microbial communities along a degradation - GHG production gradient using 16S rRNA gene amplicon pyrosequencing, metagenomics and metatranscriptomics.

Field site



Palsa hollow

Palsa hummock



Stordalen Palsa Mire, Sweden

- Degradation gradient of Palsa hummock → hollow → fen
- Palsa hummock decreased by at least 11%, fen increased by 50% last 30 years²
- GHG (100 year CO₂ equivalents) produced by peat microbes *in situ*:
 - hummock was 1.7 μM
 - hollow was 21 mM
 - fen was 163 mM

Methods

Three extraction methods for total nucleic acids were tested:

- MoBio PowerSoil Total RNA (PSoil)
- MoBio PowerMax RNA/DNA (PMax)
- modified acid-phenol¹

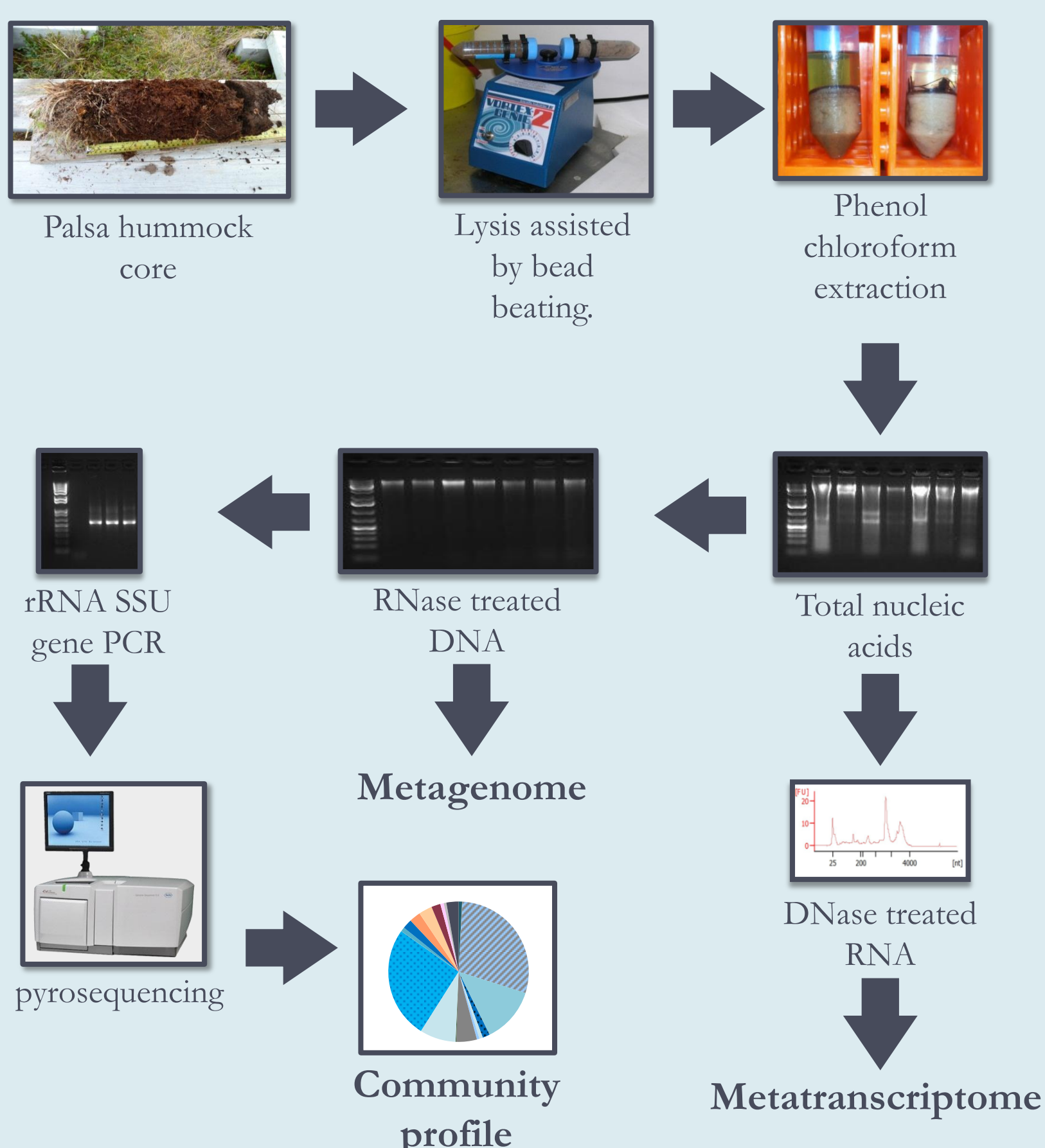


Figure 1. Flow diagram of methods

Results

Community composition

- Acidobacteria dominated Palsa peats
- Proteobacteria major component of aerobic peats
- Methanogenic Euryarchaeota dominate anoxic peat
- No significant changes in detected OTUs between extraction methods

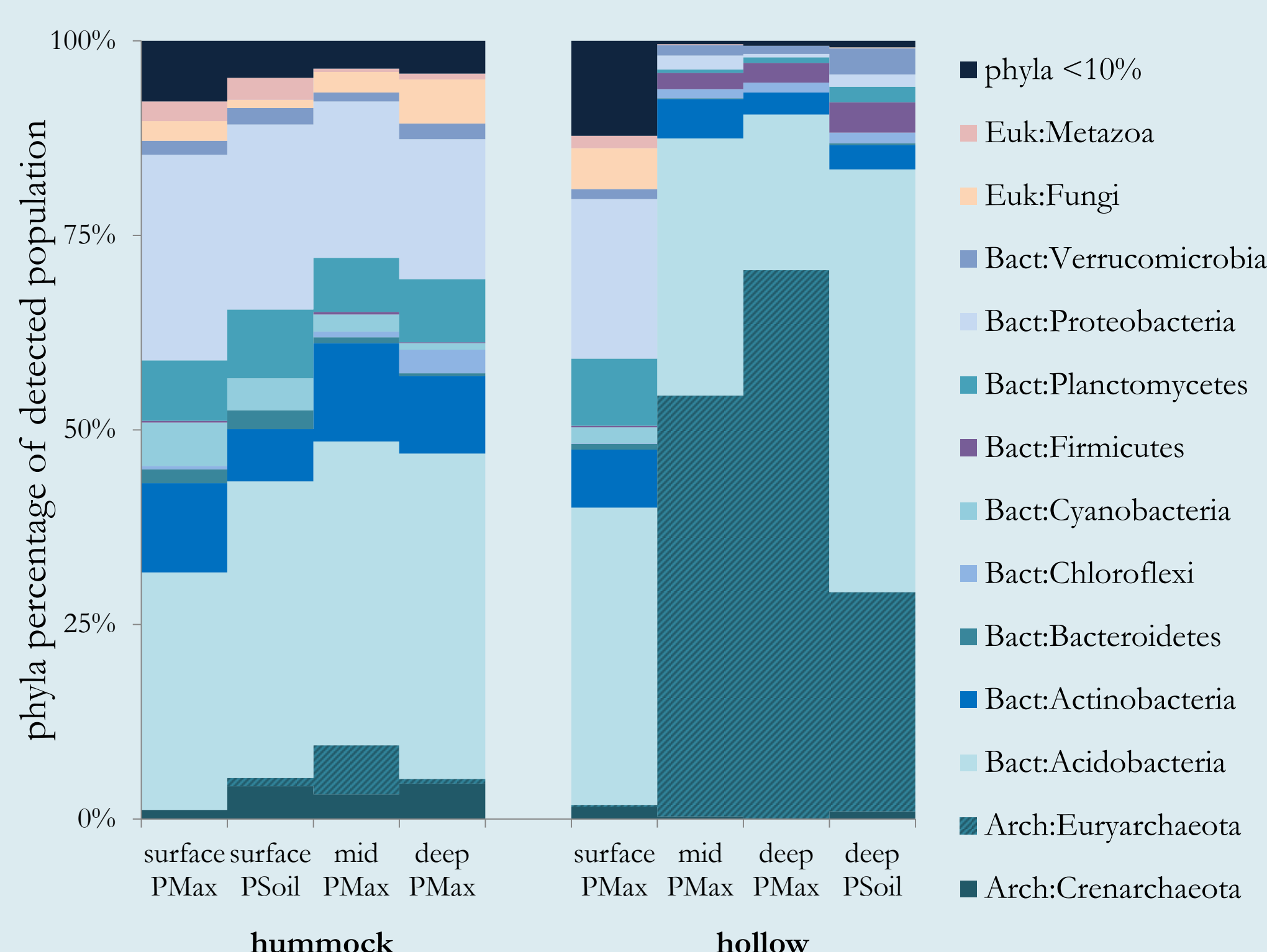


Figure 2. Microbial community composition of active layer peat in (low GHG) hummock and (high GHG) hollow.

Community Diversity

- Lower than non-permafrost soil
- Decreased with depth and at water table
- Sampling and sequencing effort captured majority populations in permafrost affected soils
- Highest with preferred extraction method

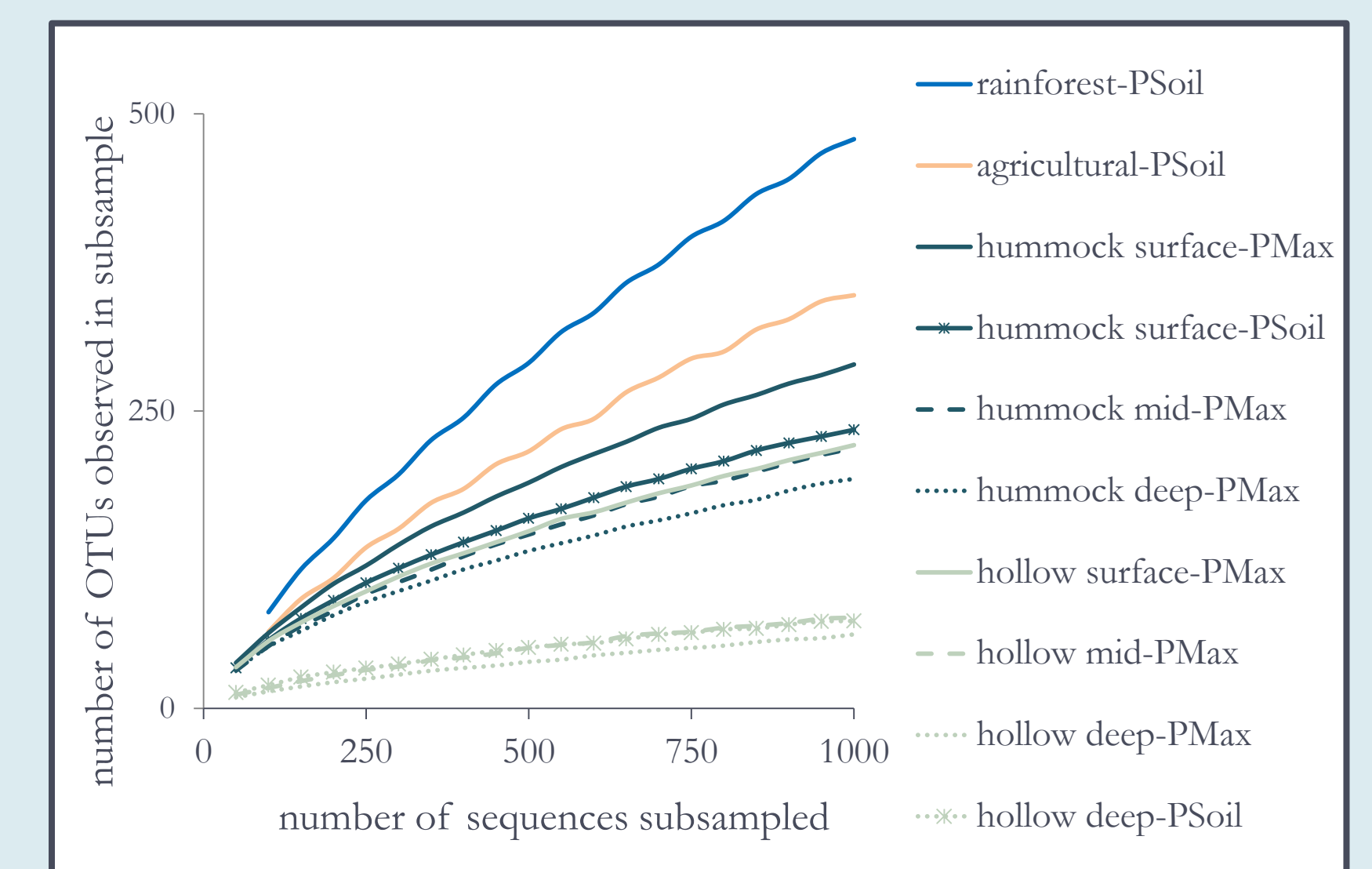


Figure 3. Observed diversity estimates from 16S rRNA gene pyrosequencing of DNA extracted from ~100 mg soil. OTUs clustered at 97% similarity.

Conclusion

Significant increase in GHG production was correlated with shifts in microbial community. Microbial community was highly diverse at hummock surface sites but shifted to a low diversity community dominated by a single species (OTU) of methanogenic Archaea at the water table.

Future work

- Samples from start, middle and end of thaw season
- Samples from fen, the end point of degradation at three depths
- Metagenome and metatranscriptome production and analysis

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