Does microclimate variation in tundra ecosystem drive microbial community assembly?

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Introduction

- Arctic ecosystems are warming nearly three times faster than the global average
- These regions store an enormous amount of carbon in permafrost and organic matter, which is at risk of being released as the climate warms.
- Soil microbes use organic carbon for energy and, in the process, release greenhouse gases like CO_2 and CH_4.
- The type of microbes present and their metabolic activities directly influence how much and what kind of greenhouse gases are emitted.
- Local environmental conditions such as moisture, temperature, and oxygen availability shape microbial communities and their activity.
- As Arctic soils warm, variation in site specific conditions may lead to significant differences in greenhouse gas release across the landscape.
- Studying these microbial environment interactions helps us better predict future climate feedbacks.

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References:

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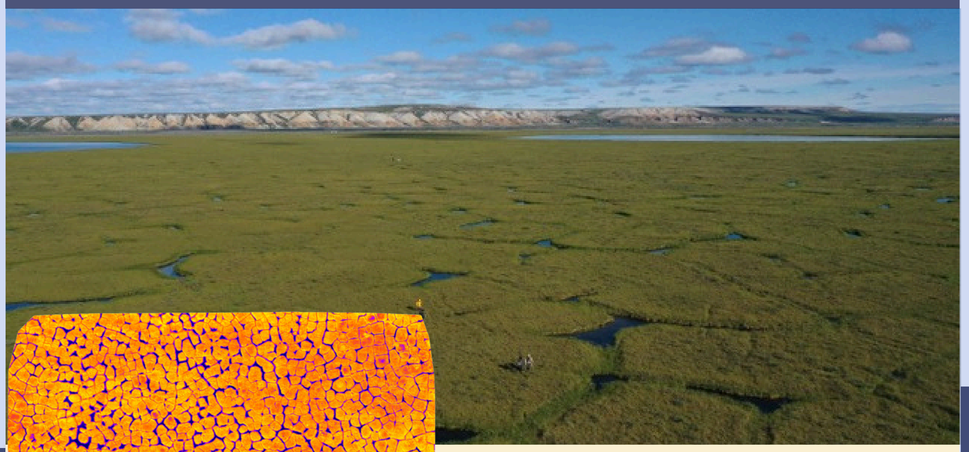
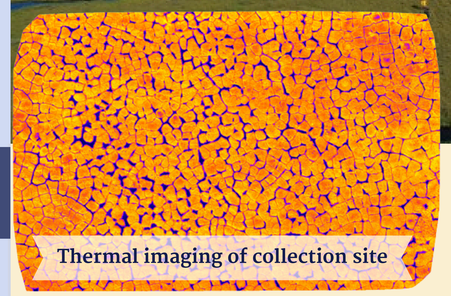
Hypothesis

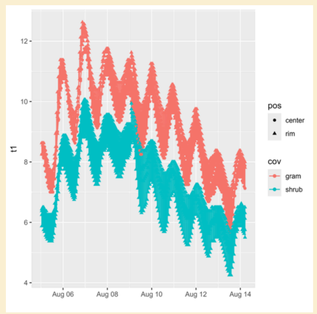
Variations in topography, soil moisture, and temperature will significantly influence the composition of soil microbial communities and the abundance of functional groups involved in greenhouse gas (GHG) emissions in Arctic tundra ecosystems.

Site Information





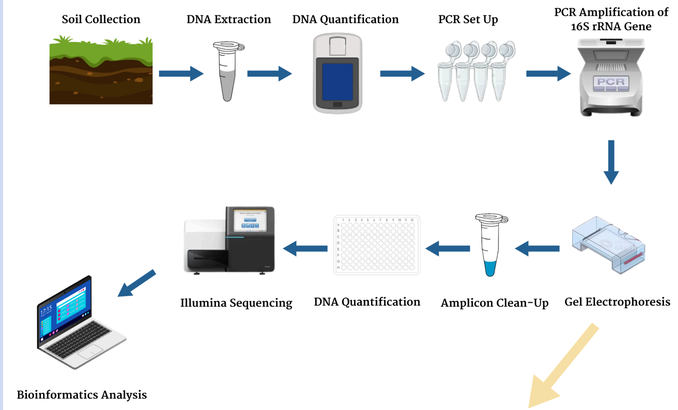
Thermal imaging of collection site

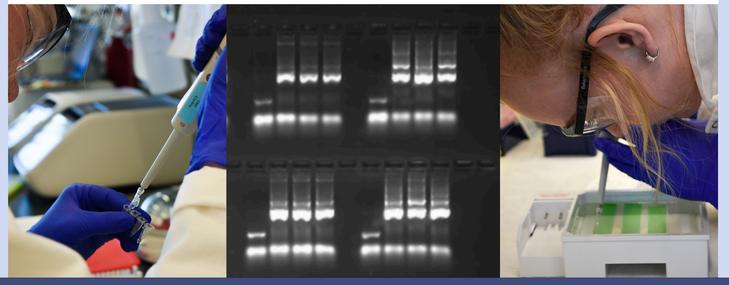


- ~45 km south of Deadhorse, Alaska, in polygonal tundra with actively degrading ice wedges
- 62 soil samples collected from the top 10 cm of soil
- Sampling locations selected to represent a range of microclimatic conditions
- Topographic variation (high vs. low positions)
- Areas under diverse plant communities

Soil temperature and moisture sensors installed at each site to track microclimate variability over time

Methods





Future Steps

- Submit the pooled library for Illumina MiSeq sequencing
- Perform bioinformatic processing
- Correlate microbial community data with soil moisture, temperature, and GHG flux data
- Interpret how local environmental variation influences microbial drivers of greenhouse gas emissions

Predicted Outcomes

- Distinct microbial communities will be associated with different microtopographic positions

Future Research Directions

- Conduct metagenomic or metatranscriptomic analyses to investigate the functional genes and active metabolic pathways involved in carbon cycling.
- Expand sampling across seasons to understand how microbial community composition and activity shift with changing Arctic conditions.
- Integrate microbial and environmental data into predictive models to better forecast greenhouse gas emissions under future climate scenarios.