

Increasing Biological Fidelity of Arctic Greenhouse Gas Emissions from Permafrost to Improve Climate Modeling

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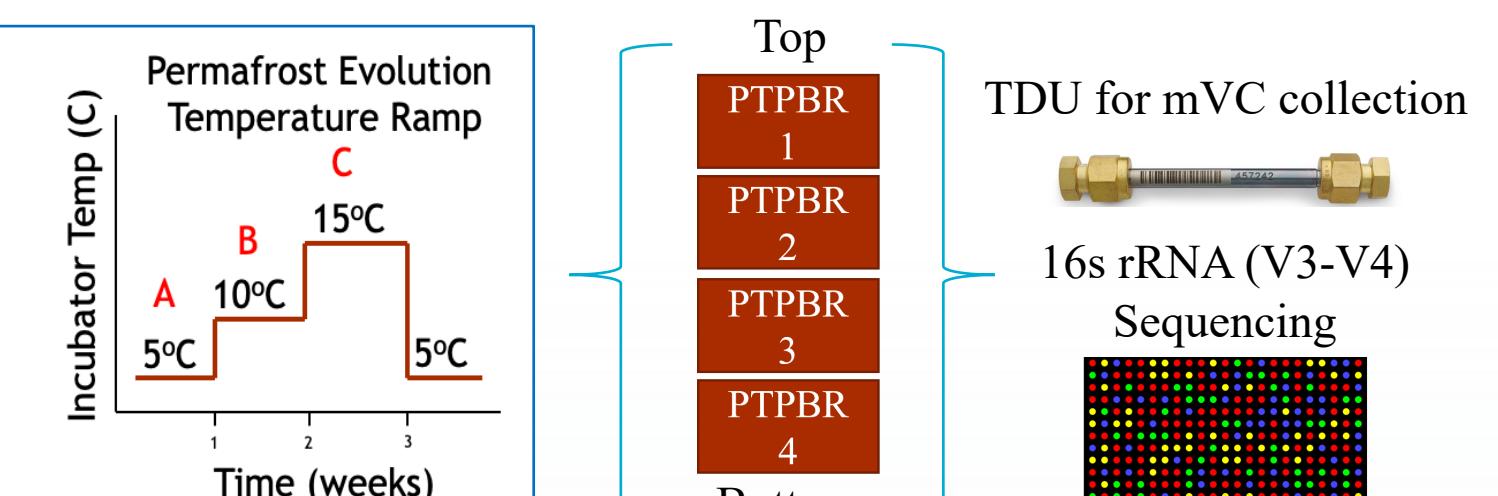
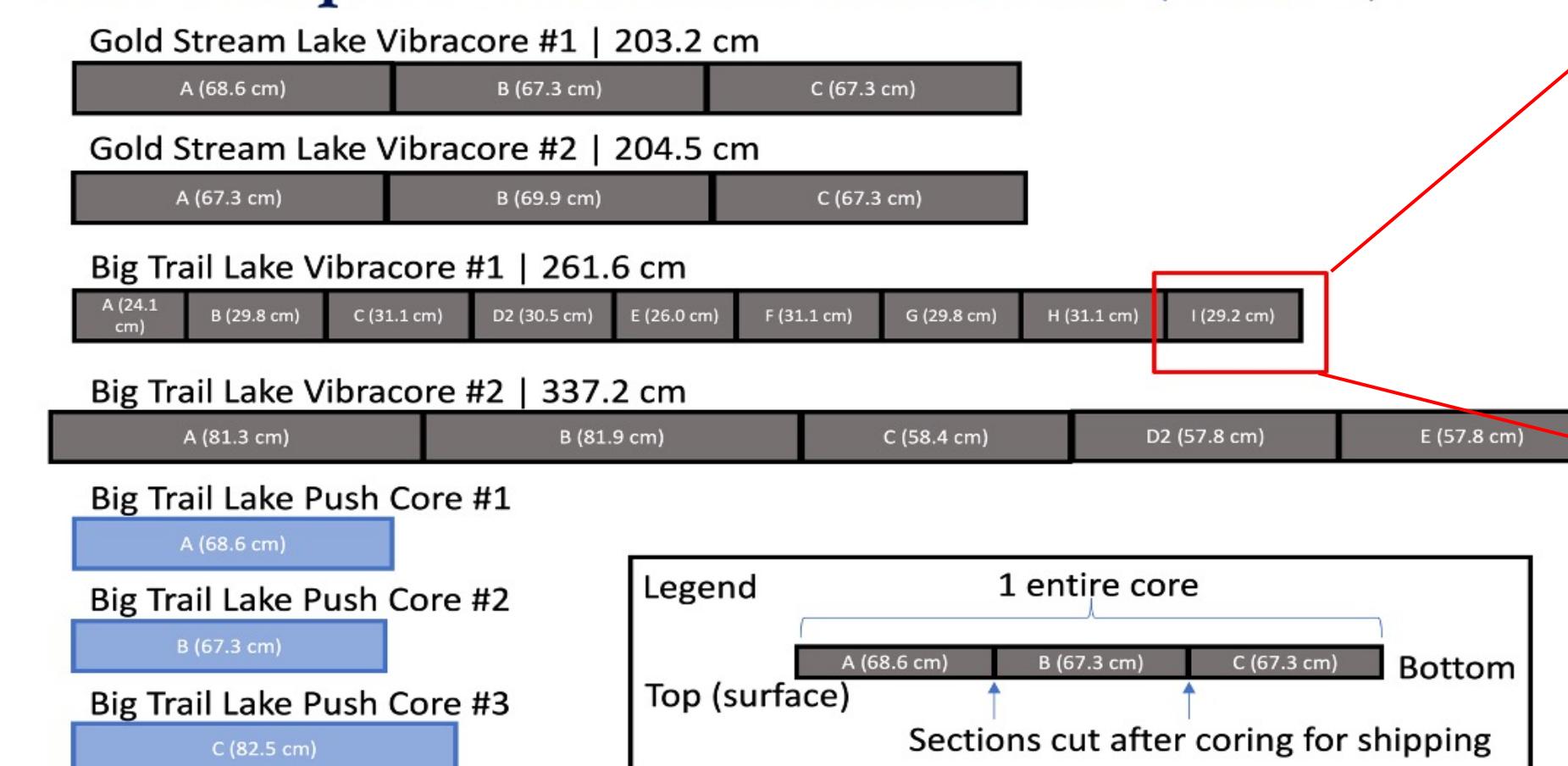
Abstract

The enhanced rate of Arctic warming will accelerate permafrost degradation contributing to a large magnitude of uncertainty for greenhouse gas emissions. Accurate measurements of biogeochemical changes are needed to address climate feedbacks through high resolution modeling and develop potential mitigation strategies. Our work seeks to increase biological fidelity of greenhouse gas emissions to improve understanding of the role of biology on permafrost degradation, resilience, and subsequent greenhouse gas release. This work will ultimately allow us to define the climate feedbacks and improve existing earth systems models in permafrost ecosystems.

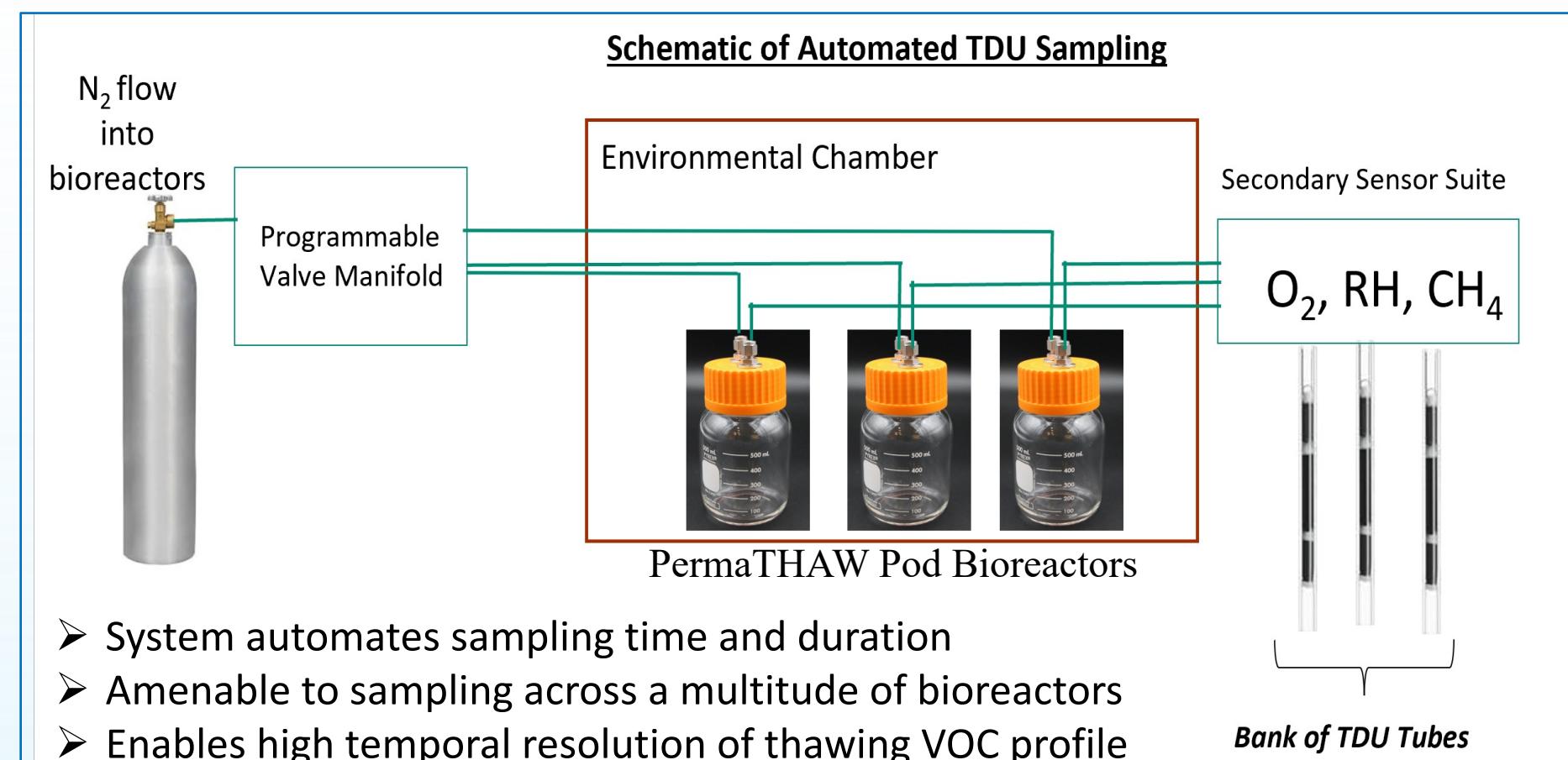
Here, we utilized PermaTHAW Pod bioreactors to evolve thermokarst soil samples and measure high-resolution chemical profiles to identify mVCs microbial fingerprints. Our goals are to explore and understand ecological patterns arising from long dormant permafrost-bound organisms and their impact on the biogeochemical climate feedback cycles occurring in ecological hotspots such as thermokarst lakes. Our proposed approach will develop innovative real-time measurement of mVCs over time to monitor microbial metabolic dynamics in a simulated thermokarst permafrost microcosms.

mVCs & Metagenomics Pilot Evolution Experiments

Core Samples Collected Before Thaw (March 2022)

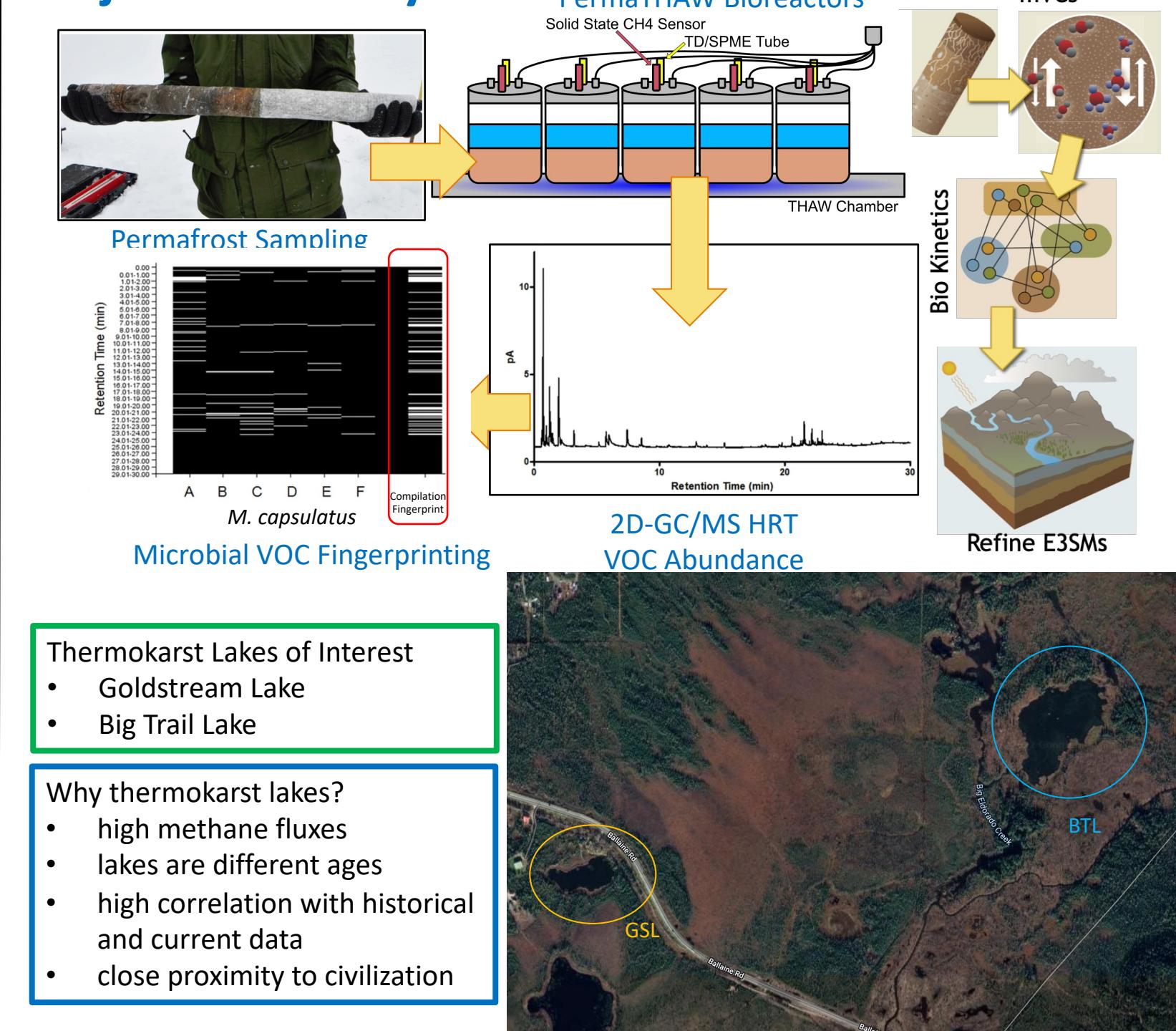


VOC Pilot Evolution Experiment:



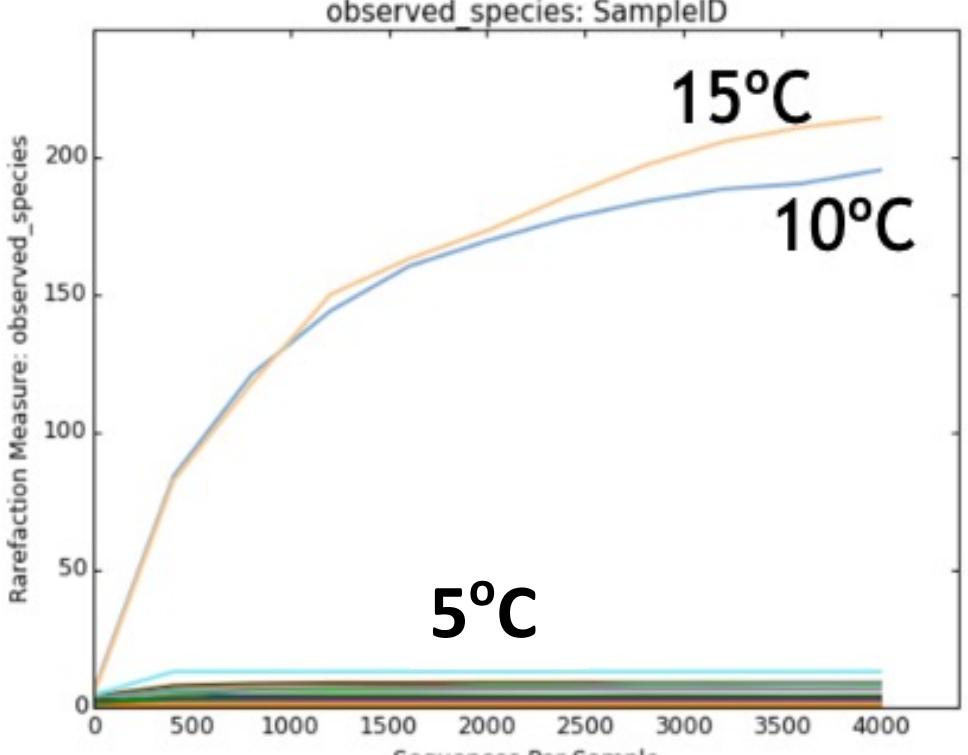
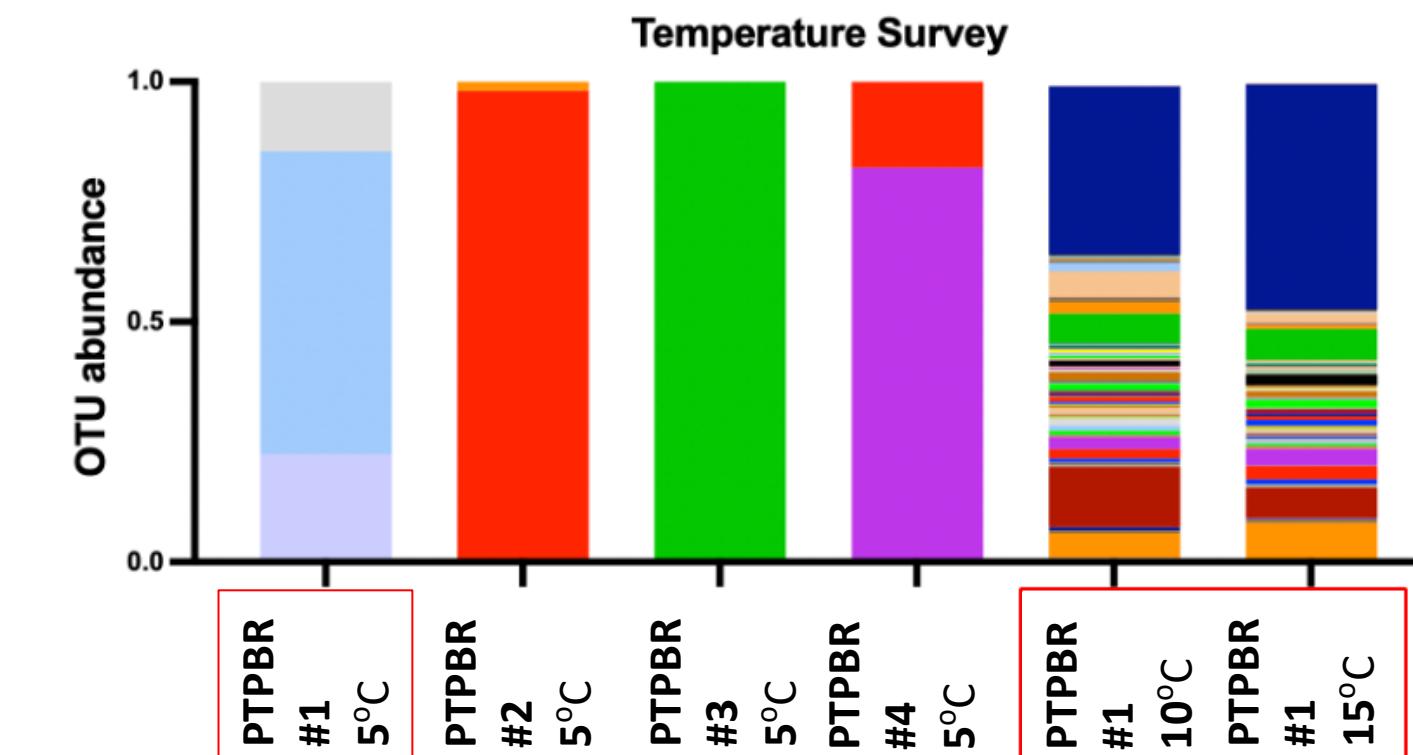
Please contact Haley Bennett for literature references
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Project Summary



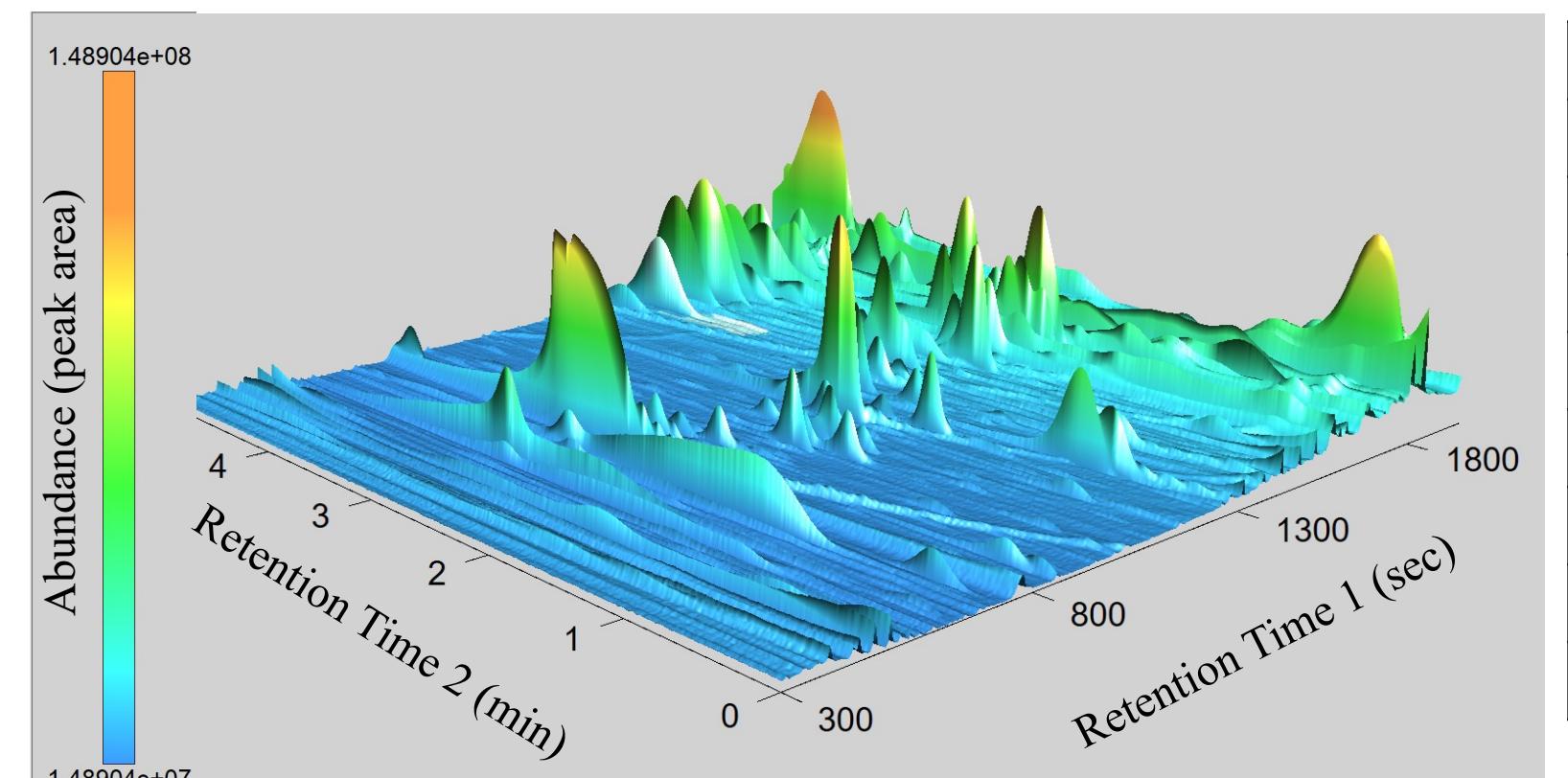
16S rRNA Sequencing & mVCs Analysis

Permafrost 16S rRNA Gene Sequence Evolution Results



- Diversity of microbes grows logarithmically as temperature rises from 5°C
- Thousands of mVCs detected were not identified by HRMS libraries
- Over 50% of identified mVCs were biologically relevant
- Majority of biologically relevant compounds have not been linked to specific bacterial strains in literature

Evolution Experiment Gas Sampling at 15°C



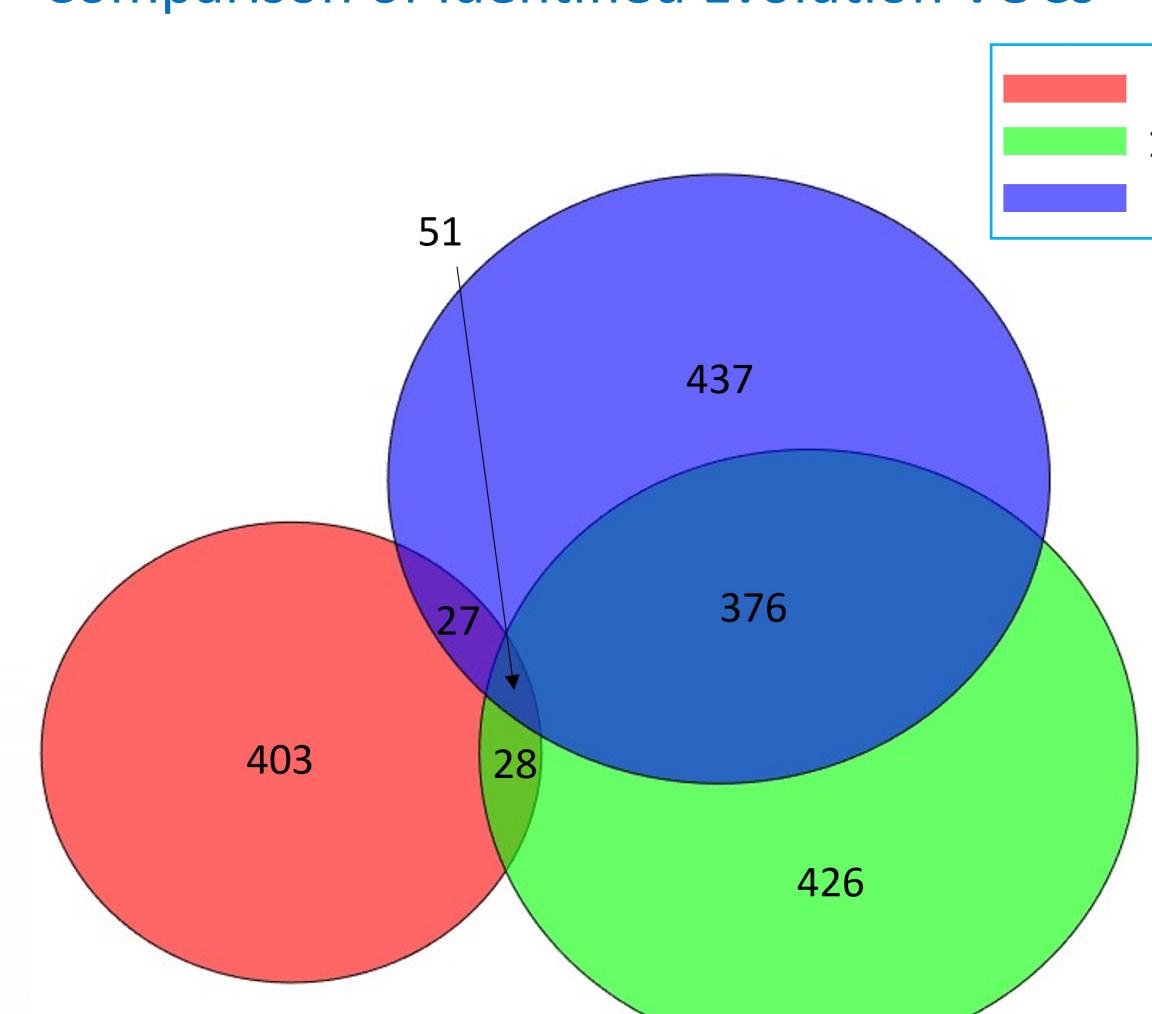
Detected Microbial Evolution mVCs

Compound	Potential Role	Temp	Microbial Source
Etoxeridine	Metabolite	5°C	E.coli
2,4,6-trimethyldecane	Metabolite	10°C	Bacillus
L-Glutamic Acid	Metabolite	10°C	E.coli
Indole	Secondary metabolite	10°C/15°C	Shikimate pathway
2,3-indolinedione	Antifungal Metabolite	10°C/15°C	Pseudomonas
L-Pyroglutamic acid	Metabolite	15°C	Cyano/proteobacteria
Hexadecanenitrile	Lipid, VOC	All	Pseudomonas
Benzoic acid	Secondary metabolite	All	E.coli

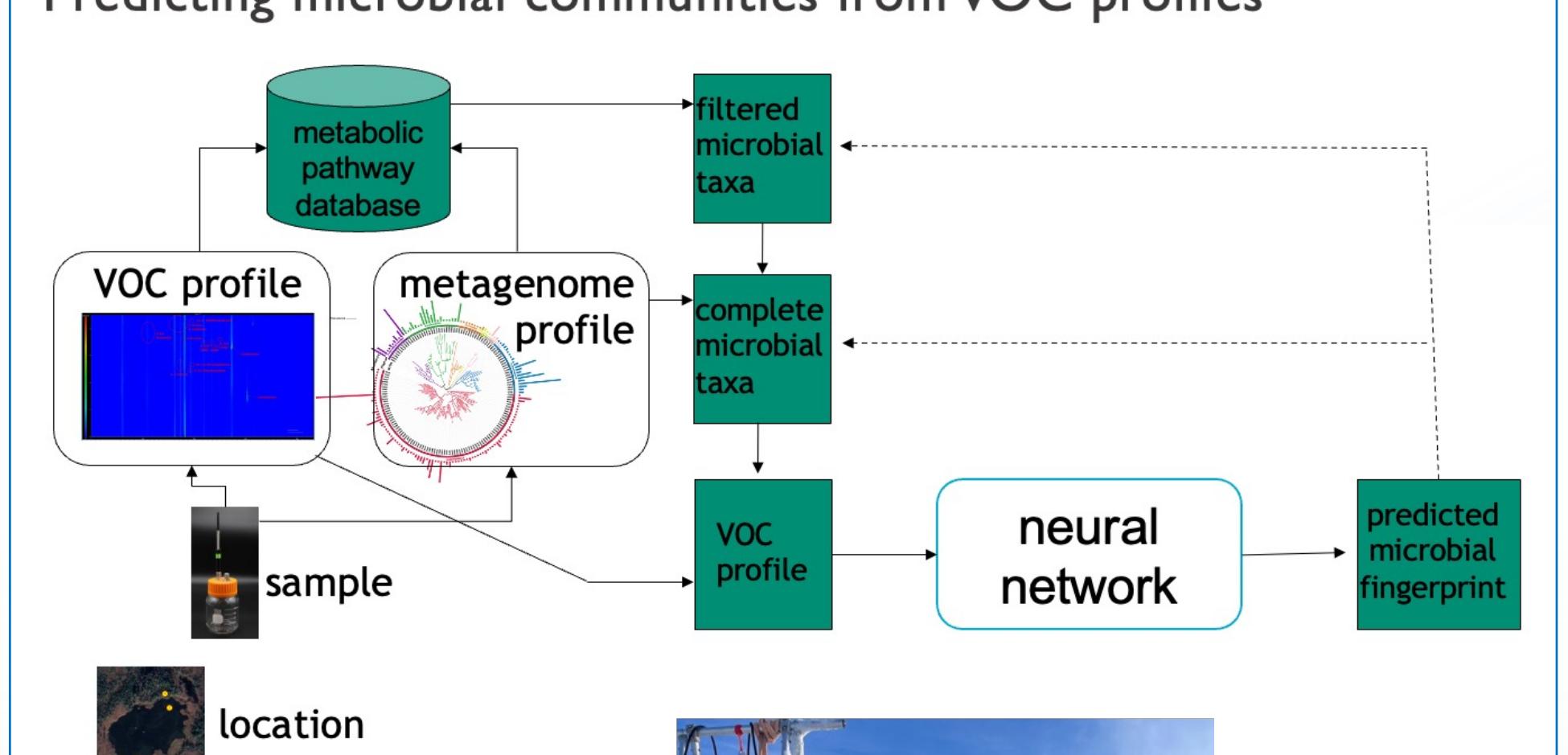
Highlighted cells correspond to bacteria identified in 16s rRNA sequencing results

Permafrost Volatolomics Library

Comparison of Identified Evolution VOCs



Predicting microbial communities from VOC profiles



- Successful elicitation of microbial activity at higher temperatures compared to the lower base temperature. Complete 16s rRNA sequencing (V1-V9) on Oxford Nanopore PromethION should reveal species specific microbes in permafrost
- HRMS libraries used for identification can be biased against biochemicals. Investigation could reveal previously unknown mVCs
- Employing machine learning tactics on the megavariate data collection to automate the linking of the mVCs to microbial sources. Builds volatolomic library
- Culturing/isolation of higher temperature microbes from PTPBR and study individual mVCs fingerprint to deconvolute the megavariate data and identify species-unique mVCs



A collaborative project with:

Please contact Chuck Smallwood with any programmatic questions
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