

## Poster #1-29

### **Awakening the Sleeping Giant: Multi-omics Enabled Quantification of Microbial Controls on Biogeochemical Cycles in Permafrost Ecosystems**

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Arctic soils store large amounts of biomass and water from warmer periods in the history of the Earth that became preserved in permafrost during cooling and glaciation events. Permafrost soils contain a broad diversity of cold-adapted microbes, whose metabolic activity depends on environmental factors such as temperature changes that cause cycles of freezing and thawing in the soil. Permafrost defines just the thermal state of soil, meaning the soil's hydrology, physics and chemistry can differ vastly among locations. Microbial metabolism leads to decomposition of soil organic matter, substantially impacting the cycling of nutrients and significantly affecting the arctic landscape. However, the relationship between permafrost microbial properties and biogeochemical cycles is poorly understood. Ribosomal gene surveys have demonstrated dramatic differences in permafrost microbiome structure across the entire Arctic region, although the causes or the consequences of these differences are unknown. Emerging metagenomic studies are uncovering the extent and depth of the permafrost genetic reservoir. Using cutting-edge multi-omic approaches, this project studies the functional and phylogenetic evolution of permafrost microbial communities during thaw across multiple arctic locations. This project uses field experiments, laboratory manipulations, and multi-omics approaches to examine how microbial processes, biogeochemical transformations, and hydrology interact during permafrost thaw in different sites in Alaska in order to determine how these factors drive biogeochemical cycles in different Arctic soils.

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