

KPL-1:

Multi-omics illuminates permafrost soil microbiome response to climate warming



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The Arctic is characterized by vast amounts of carbon stored in permafrost and is an important focal point for the study of climate change as increasing temperature may accelerate microbially-mediated release of carbon stored in permafrost into the atmosphere as CO₂ and CH₄. Yet surprisingly, very little is known about the vulnerability of permafrost and response of microorganisms in the permafrost to their changing environment. To address these knowledge gaps we used omics technologies to explore permafrost microbial communities, to reveal hitherto unknown soil microbial populations and to link them to specific soil biogeochemical processes. For these projects we employed an omics pipeline that includes metagenomics, metatranscriptomics and metaproteomics to determine the phylogenetic and functional gene compositions and their expression in complex, non-sterile soil samples collected from the field at several locations in Alaska. These studies have presented several challenges due to the unprecedented large size of the datasets and the insufficiency of available bioinformatic tools & databases to analyze, correlate and integrate the data. To address these challenges we developed a novel functional gene database and used different assembly and analysis algorithms to determine key features in the datasets. The data reveal the microbial diversity, composition and functional potential in permafrost and how the microbial communities respond to climate change impacts.