## **Carbon Metabolism in Pleistocene Permafrost Microbial Communities**

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Permafrost is gaining interest as a model for astrobiology. Since six of the other eight planets in our solar system, as well as their moons, asteroids, and comets are permanently frozen, life on these celestial bodies is most likely to be found in a subzero environment. On Earth, life can exist in permafrost for millennia and may act as an analogue reflecting potential inhabitants on extraterrestrial cryogenic bodies. Active microbial life exists in even the most ancient permafrost, but we know little about the metabolic strategies utilized by permafrost microbes that enable survival through millennia entrained in ice. Even in nutrient rich permafrost, most resources are sequestered away from the microorganisms by freezing conditions. To investigate community activity and metabolic strategies through geologic time with no influx energy or new material we sampled from a chronosequence of Pleistocene permafrost ranging in age from 19,000 - 33,000 years before present. We measured extracellular enzyme activity specific to carbon metabolic processes using a fluorometric enzyme assay. Across all age categories, enzyme activities indicated the communities were capable of metabolizing a variety of carbohydrate and amino acid substrates. Highly active enzymes included those involved in the degradation of cellulose indicating the presence of carbon-associated metabolic strategies in permafrost microbial consortia. As permafrost age increased, enzyme diversity, taxonomic diversity, enzyme activity, and ATPase activity decreased, which is consistent with previously collected metagenomic data. These data likely reflect lower biomass in older samples but shows maintenance of cellular activity over time. Taken together these data demonstrate that active, carbon-utilizing microbial communities exist in Pleistocene permafrost despite limited nutrients and increasingly stressful conditions.