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Frozen in Time? Microbial Strategies for Survival and Carbon Metabolism Over Geologic Time in a Pleistocene Permafrost Chronosequence

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Permafrost is gaining interest as a model for exobiology. 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 exits in even the most ancient permafrost, but we know little about the strategies utilized by permafrost microbes that enable survival over geologic time. Here we describe a 16S rRNA gene and shotgun metagenomic study targeting a chronosequence (12kyr – 35kyr) of Pleistocene aged permafrost. 16S rRNA sequencing and analysis showed decreasing microbial diversity and higher abundance of endospore-forming Firmicutes in increasingly older samples. 16S rRNA gene and metagenomic data showed significant age-based clustering. The youngest samples were enriched in genes involved in the degradation of complex polysaccharides whereas older samples had significantly greater abundance of genes involved in amino acid degradation. These data suggest increasing reliance on scavenging of detrital biomass in older permafrost. An abundance of conjugation genes in the oldest samples indicate the importance of rapidly acquiring new adaptive traits. The oldest samples were also enriched in chemotaxis, cell envelope synthesis, surface attachment, and stress resistance genes. We binned 30 draft genomes from metagenomic assemblies including several members of Thaumarchaeota. Together, these data increase understanding of how permafrost microbes transform organic matter over geologic time and identify adaptations enabling long-term survival with no influx of new energy or materials.