

Ten *Pseudomonas* spp. from Svalbard Active Layer are using amino acids for energy

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The goal of this project is to study the microbial decomposition within active layer permafrost in Ny Alesund, Svalbard.

The *in situ* population of microbes in the Ny Ålesund, Svalbard permafrost active layer are mostly uncharacterized. It is unknown how microbes survive in this nutrient limited seasonally thawed and frozen soil. Our goal was to isolate representatives of the microbial community to infer their environmental interactions. Complementary techniques were performed by culturing, sequencing, and testing isolates for temperature sensitivity of enzyme activities for carbon and nitrogen hydrolytic enzymes. Active layer soil was rendered on R2A agar and isolates were whole genome sequenced with Illumina MiSeq. The annotated genomes contain metabolic pathways for carbon and sulfur assimilation and CO<sub>2</sub> emission. Soil enzyme activities suggest that these organisms are accustomed to carbon and nitrogen starvation. Leucine aminopeptidase activities up to 200 nmol/hour signify that these isolates gather carbon and nitrogen compounds from amino acid degradation. The low temperature enzymatic activities for N-acetyl-β-D-glucosaminidase and xylosidase showed cold adaptation of *Pseudomonas* spp. These metabolic pathways combined with the low temperature enzymatic activities indicate that these organisms acclimate to harsh conditions in the active layer and show their potential for quick adaptation to increasing temperatures in the Arctic. These findings suggest that increasing temperatures associated with climate change could fundamentally shift microbial activity and substrate availability in these systems in short term. However, the microbial population may be able to adapt to these environmental changes long term.

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