

Microbial organic matter degradation in the active layer of Svalbard permafrost

Katie Sipes, Tatiana Vishnivetskaya, Reagan Paul, Karen Lloyd

The active layer of permafrost in Svalbard, Norway (79°N) is deepening at rate of about 1 vertical centimeter per year in most locations around the Bayelva River in the Leirhaugen glacier plain. We used a multifaceted approach to study the organisms that live in these expanding active layers including metagenomes, culturing, and soil geochemistry. *We hypothesized that the organisms that were obtained in culture would be found in the metagenomes and the metagenomes would give insight on the metabolisms of these organisms.* Further, the soil geochemistry would suggest the types of energy sources that the organisms use. Our metagenome data yielded 5 metagenome assembled genomes (MAGs) from two active layer cores. Our culture isolation efforts yielded 10 *Pseudomonas* spp strains. Related isolates have been previously found in soil samples from Peruvian Andean Plateau, Thuringian Basin, Council Alaska, Livingston Island Antarctica and in Western Spitsbergen. We saw evidence for microbial heterotrophy in one of the sites due to the carbon isotope values becoming richer in ¹³C with depth. We also found enzymatic degradation activity of a wide range of small peptides and carbohydrates. This multifaceted approach lays the groundwork to understand how the active layer will become a hot spot for microbial activity as the climate continues to warm.