Gene expression dynamics in thawing permafrost soils

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Approximately 1700 Pg of soil organic carbon (SOC) are stored in Arctic permafrost, more than twice the amount of carbon in the atmosphere [1-3]. Microbial decomposition of thawing permafrost SOC and release of greenhouse gasses carbon dioxide and methane are considered to be positive feedbacks to global warming. Microbial communities in permafrost are taxonomically diverse and capable of mineralizing even recalcitrant and old carbon sources [1]. However, a detailed understanding of microbial activities associated with permafrost thaw [4] is lacking. Here, we describe and analyze the first metatranscriptomes from upper and deeper permafrost soils underlying moist acidic tundra before and after 11 days of thaw, represented by ~0.5 billion complementary DNA (cDNA) Illumina sequence reads. Bacteroidetes, Firmicutes, ascomycete fungi, and methanogens showed the most drastic increase in gene expression in the top permafrost, and all major classes of hydrolases involved in the cleavage of complex biopolymers into C1 and C2 substrates were expressed in both frozen and thawed soils. Methyl Coenzyme Reductase A (*mcr*A) was the most abundant expressed gene in the upper thawed permafrost and could be annotated to the versatile methanogenic archaeon *Methanosarcina barkerii*. Evidence of methanogenesis from the C1 and C2 substrates methanol and acetate was higher in frozen and thawed permafrost respectively. Data mining is ongoing and we hope to present additional interesting changes in gene expression upon permafrost thaw such as the response of defense mechanisms against bacteriophages and fungal antibiotics.

[1] Dutta, K., *et al* (2006). *Global Change Biology* **12**, 2336-2351 [2] Schuur, E.A.G. *et al* (2008). *Biosciences* **58**, 701-714 [3] Zimov, S.A. (2006). *Geophys. Res. Lett.* **33**, L20502, doi:10.1029/2006GL027484 [4] Coolen, M.J.L. *et al* (2011). *Environm. Microbiol.* **13**, 2299-2314