Impact of fire and natural thaw on permafrost microbial ecology

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Arctic soils contain an estimated 12-42% of terrestrial carbon, most of which is sequestered in permafrost. Because of climate warming large regions of permafrost have begun to thaw. Wildfires are also increasing in frequency in the Arctic, thus resulting in additional thaw of permafrost. As a result much of the soil organic matter in permafrost is becoming available for mineralization by soil microorganisms. Understanding the dynamics of carbon release from permafrost requires assessment of microbial functions at different depths. Yet, little is known about the vulnerability of permafrost and the potential response of soil microorganisms with depth to availability of newly accessible carbon sources. Here we aimed to use a combination of molecular “omics” approaches to gain an understanding not only of the microbial composition, but also the functional potential of microbial communities at different depths and the response of permafrost microbes to natural thaw and thaw caused by wildfire. Soil samples were collected from the site of the Boundary Fire at Nome Creek, AK and along a natural thaw gradient at Tanana Valley, AK. At Nome Creek, samples were taken from complete soil profile up to a 1 m depth. At Tanana Valley, triplicate cores were collected across a natural thaw gradient: ranging from permafrost to seasonally thawed active layer to thermokarst bog. DNA, RNA and proteins were extracted from the Tanana Valley samples and DNA from the Nome Creek samples. The DNA was sequenced to provide information about microbial community and functional gene composition (metagenomes). The RNA was sequenced to determine which genes were expressed and which members of the community were more active (metatranscriptomes). Shotgun metaproteomics provided information about proteins produced in the samples and was used to estimate biogeochemical processes. The results from Tanana Valley revealed that some microorganisms were active in permafrost and that Fe reduction could be a survival strategy in frozen mineral soils. After thaw, methanogenesis was the dominant process. At Nome Creek, fire had a pervasive impact on both surface and permafrost microbial community structure and metabolic functions. Especially methanogenesis and denitrification potential was significantly decreased by fire. Together these studies have important implications for the impact of climate change on permafrost and reveal changes in microbial processing of carbon and shifts in biogeochemical cycles that can occur as a result of permafrost thaw.