

Illumination of Impact of Climate Change on Permafrost Microbial Communities

Frontiers in Biological Sciences

Seminar Series

Presented by...

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Abstract Climate change has unknown consequences for the vast reserves of terrestrial carbon currently sequestered in soil. For example, warming causing thaw of permafrost soil in the arctic, increasing accessibility of previously frozen carbon pools to microbial degradation and greenhouse gas emission. However, study of soil microorganisms is challenging because of the soil microbial diversity and soil matrix complexity. In addition, >90% of soil microorganisms have never been cultivated, and their properties are unknown.

To address this challenge we developed molecular 'omics approaches that bypass the need for cultivation to gain understanding of the soil microbial community structure and function. We used a combination of deep sequencing of 16S rRNA genes (microbiomics), total DNA sequencing (metagenomics), total RNA sequencing (metatranscriptomics), and shotgun community proteomics (metaproteomics) to determine the impact of permafrost thaw on soil microbial communities and functions in Alaska and to study native prairie soils. In Alaska, we looked at a site undergoing a natural thaw transition and thaw caused by fire, as well as a transect across a site with permafrost deformations, known as polygons. In all cases there were dramatic changes in microbial community composition and function with thaw.

In the prairie we developed a new set of tools to tackle the high microbial complexity and simultaneously determine gene abundance and expression. Results indicate that soil microbial communities are responsive to climate change, and some key processes, including carbon cycling and greenhouse gas emissions, are altered as a result. These data should eventually be used to better inform climate models.

More info?

See

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