

## **Soil microbial community shifts in response to soil thermal insulation in moist acidic tundra of Northern Alaska**

Michael P. Ricketts<sup>1</sup>, Rachel S Poretsky<sup>1</sup>, Jeffrey M. Welker<sup>2</sup>, Miquel Gonzalez-Meler<sup>1</sup>

<sup>1</sup>Biological Sciences Department, Ecology and Evolution, University of Illinois at Chicago

<sup>2</sup>Department of Biological Sciences, University of Alaska, Anchorage, AK, USA

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PI: Gonzalez-Meler, Miquel A.

Email correspondence – ricketts.mikep@gmail.com

In the Arctic tundra, shifts in plant species composition and distribution have been observed in response to increased precipitation, soil warming, and the subsequent increases in active layer depth. Initial abiotic changes provide soil microorganisms access to previously unavailable soil organic matter via thawing soils, increasing soil microbial decomposition and nutrient mineralization rates and resulting in soil organic carbon loss and increased nutrient availability. Here we examine how microbial communities respond to increases in soil thermal insulation due to accumulation of winter precipitation at a snowfence installed in 1994 at Toolik Field Station, Alaska. We hypothesize that soil microorganisms are eliciting vegetation response through the release of nutrients under warmer conditions, providing a competitive advantage to N-rich woody species over herbaceous species. Changes in plant litter and increasing NPP may contribute to SOC re-accumulation and alter microbial community composition. Bacterial phylogeny and relative abundances from soils collected in August of 2012 were determined by 16S rRNA amplicon sequencing of extracted DNA. We found significant shifts in relative abundances of bacteria between snow depth treatments (DEEP, INT, LOW) and the control in both soil horizons (organic and mineral). The most notable shifts include in a decrease in *Verrucomicrobia* of the family Chthionobacteraceae in the mineral horizon of the DEEP zone, an increase in Chloroflexi of the family Anaerolinaceae in both organic and mineral horizons of the DEEP zone, and a highly significant decrease in Actinobacteria in the organic horizon. To investigate potential functional changes within the microbial community, we utilized the software package PICRUSt, able to infer the genetic potential of the community using ancestral state reconstruction based on the phylogenetic data obtained from 16S rRNA sequencing. This analysis revealed a trend of less abundant enzymatic genes responsible for SOM decomposition in all treatment zones relative to the control in the organic horizon, and more abundant genes in the INT and LOW zones relative to the control in the mineral horizon. This suggests soil microbial communities in surface layers are not genetically equipped to degrade organic matter from newly dominant plant species, while communities in deeper soil layers rely on older organic matter released from permafrost thaw, supporting our hypothesis of nutrient release facilitating observed vegetation shifts. These changes in microbial community composition and functionality in response to simulated future climate conditions may substantially alter carbon and nutrient cycling in the ecosystem, initiating a cascade of biotic and abiotic effects.