

The Phylogenetic Organization of Tundra Bacterial Growth in Response to Short-Term and Long-Term Warming

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Project Goals: This work focuses on quantifying the response of soil bacteria to the effects of climate change in the Arctic tundra. Growth rates of individual bacterial taxa are measured using a stable isotope label, and ecological and phylogenetic organization of the warming response is assessed. The experiment is part of a larger project aiming to integrate stable isotope techniques in the field with –omics approaches in order to measure microbial growth and metabolic rates *in situ*, thereby providing an ecological perspective of soil nutrient cycling at the taxon level. We are implementing these new methods to investigate the effects of elevated temperature on soil microbial nutrient transformations across four ecosystems from the Arctic to the tropics. At the Arctic site at Toolik Lake Research Station, specifically, future work will also investigate the effects of climate change on ecological interactions of bacteria and fungi and use stable-isotope-informed metagenomics to identify which soil taxa and metabolic processes are most temperature sensitive.

Increases in Arctic temperatures have thawed permafrost and accelerated soil microbial activity, releasing greenhouse gases that amplify climate warming. Additionally, warming has accelerated shrub encroachment into tundra, altering litter quality and causing further changes in soil microbial processes. We quantified the growth response of individual bacterial taxa to the long-term effects of warming using a 30-year field experiment in tussock tundra. To uncouple the direct effects of warming on bacterial growth rates from effects mediated by other ecosystem responses to warming, we also conducted a parallel short-term experiment (3 months). Intact, active layer soil was assayed in the field for 30 days with ¹⁸O-labeled water. Rates of ¹⁸O incorporation into DNA were estimated for each taxon as a proxy for growth. Warming doubled bacterial growth rates summed across entire assemblages, with long-term and short-term experiments exhibiting similar aggregate responses, but driven by very different taxa in the short- and long-term warming experiments. The increase in short-term warming was most attributable to emergent growing taxa not detected in other treatments, but the increase for long-term warming was attributable to taxa that co-occurred in the control. Phylogenetic organization of growth was detected to the order level in all treatments. Growth was phylogenetically conserved in a deeper level in control plots (variation explained by class: 38%, order: 14%) than the warming treatments (class: < 1%, order: 54% and 51%), but both the short-term and long-term warming responses (i.e. change in warmed growth rate compared to control) were not

explained by phylogeny and occurred among unrelated taxa that varied widely in their metabolic and physiological traits. Most significant responses were positive and occurred in the long-term warming treatment. In conclusion, tundra bacterial activity greatly increased in response to short-term and long-term warming, and taxa growing in each treatment exhibited deep phylogenetic organization with bacterial orders tending to have similar growth rates. The responders to climate change appear unconstrained by taxonomy nor functional role. Identifying how individual taxa and cohesive phylogenetic groups are affected by climate change may help move toward a mechanistic understanding of ecosystem processes that will influence how much Arctic soils are likely to feed back to the changing climate.

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