Exploring Biome-scale Variation in Microbial Taxon-Specific Growth and Mortality at different temperatures through quantitative Stable Isotope Probing with $H_2{}^{18}O$.

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Project Goals:

- To better understand microbial population dynamics and its relationship to microbial energy metabolism and C cycling
- To link processes of individual microbial species to whole system C and element cycling and their responses to temperature
- To discover global patterns in microbial population dynamics across ecosystems

Abstract text: We are investigating if there is a general phylogenetic signal in the impact of temperature on growth and mortality that is consistent across biomes. We collected soils from a tundra at the Toolik LTER in Alaska, a mixed conifer forest outside Flagstaff AZ, the SPRUCE experiment in northern Minnesota, and the Luquillo Experimental Forest in Puerto Rico. These soils represented the arctic, temperate, boreal, and tropical biomes. Each soil was incubated in the laboratory with 99 atom% $H_2{}^{18}O$ at 5 different temperatures: 5, 15, 25, 35, and 45 °C, for either 5 or 10 days. Subsequently, DNA was extracted from the soils and used in quantitative stable isotope probing (qSIP). The data from the qSIP incubations will be used to calculate both taxon-specific and aggregate or average community rates of growth and mortality. Preliminary findings indicate that, while respiration rates increased with temperature, microbial growth was increasingly delayed and suppressed with higher temperatures. Particularly the tundra soil from Alaska was negatively impacted when incubated at 45 °C, and very little DNA was recovered from these samples suggesting substantial microbial death. We are keen to identify microbial populations that have a consistent response to temperature across the four different biomes. These microbial populations support the notion of microbial functional groups, analogous to plant functional groups that have proven useful for modeling plant processes at the ecosystem and global scales.