Title: Scaling of ^{18}O-informed Microbial Growth Rates Links Microbial Activity to Soil Carbon Flux

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Project Goals: The work proposed here will integrate genomics- and isotope-enabled measurements of **G**rowth **R**ate, growth **E**fficiency, and the stoichiometry of **E**ssential **N**utrients during growth, an integration we call GREEN 'omics. Our **overarching objective** is to develop and apply 'omics approaches to investigate microbial community processes involved in nutrient cycling. The specific objectives of our proposed work are 1) to evaluate the microbial ecology of nutrient uptake, testing hypotheses about nutrient assimilation in response to temperature variation; 2) to evaluate the ecology of nutrient-use efficiency for soil microorganisms within a framework of ecological theory, and 3) to develop new isotope-enabled genomics and transcriptomics techniques that probe the microbial ecology of nutrient dissimilation. Green'omics sentence here. This work will push the frontier of isotope-enabled genomics by connecting quantitative stable-isotope probing to ecological theory about nutrient assimilation, nutrient-use efficiency, metabolic efficiency, and by applying these tools to understand the basic biology and ecology of soil microorganisms and how they transform nutrients in the environment.

Abstract text: Global climate projections depend on estimates of soil carbon accumulation and decomposition[1-3], processes driven by microorganisms[3-6]. Given the vast diversity of soil microorganisms, different microbial taxa may have individualistic effects on carbon (C) fluxes in soil, yet testing this idea has been challenging. We identify the growth of individual soil microorganisms using ^{18}O-H_2O quantitative stable isotope probing (qSIP)[7,8] from soils collected along an elevation gradient in Northern Arizona. To understand the microbial ecology of nutrient uptake and nutrient use, we supplied soils with ^{18}O-H_2O either alone (control), or in combination with glucose (C amended) or glucose with $[NH_4]_2SO_4$ (C + N amended). We then converted relative measures of growth to quantitative rates of carbon flux for individual bacteria. Taxon-specific productivity (μg C g soil^{-1} week^{-1}) was then modeled as a function of per-capita growth

rate, taking into account relative abundance, 16S content per unit soil, as well as 16S copy number and genome size (calculated using a bioinformatic approach[9]) to estimate taxon-specific cell size and carbon content. We then modeled bacterial respiration rate (μg C g soil^{-1} week^{-1}) as a function of taxon-specific growth rate and taxon-specific carbon use efficiency (CUE).

Here, we show strong differences in the bacterial taxa responsible for respiration from four ecosystems, indicating the potential for taxon-specific control over soil carbon cycling. Trends in functional diversity, defined as the richness of bacteria contributing to carbon flux and their equitability of carbon use, paralleled trends in taxonomic diversity although functional diversity was lower overall. Nutrient amendment diminished functional diversity, consolidating carbon flow through fewer bacterial taxa. Among genera common to all ecosystems, *Bradyrhizobium*, the Acidobacteria genus *RB41*, and *Streptomyces* together composed 45-57% of carbon flow through bacterial productivity and respiration. We conclude that the bacterial taxa that used the most carbon amendment (glucose) were also those that used the most native soil carbon, suggesting that the behavior of key soil taxa may influence carbon balance. Mapping carbon flow through different microbial taxa as demonstrated here is a crucial step in developing taxon-sensitive soil carbon models that may reduce the uncertainty in climate change projections.

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