Microbes Persist: Towards Quantitative Theory-Based Predictions of Soil Microbial Fitness, Interaction and Function in KBase

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Project Goals: Microorganisms play key roles in soil carbon turnover and stabilization of persistent organic matter via their metabolic activities, cellular biochemistry, and extracellular products. Microbial residues are the primary ingredients in soil organic matter (SOM), a pool critical to Earth's soil health and climate. We hypothesize that microbial cellular chemistry, functional potential, and ecophysiology fundamentally shape soil carbon persistence, and we are characterizing this via stable isotope probing (SIP) of genome-resolved metagenomes and viromes. We focus on soil moisture as a 'master controller' of microbial activity and mortality, since altered precipitation regimes are predicted across the temperate U.S. *Our SFA's ultimate goal is to determine how microbial soil ecophysiology, population dynamics, and microbe-mineral-organic matter interactions regulate the persistence of microbial residues under changing moisture regimes.*

Abstract: Our SFA has pioneered new methods to quantify element fluxes with genome-resolved taxonomic resolution —especially quantitative stable isotope probing (**qSIP**), which allows us to evaluate *in situ* activity of individual taxa in complex communities by adding isotope tracers such as ^{18}O-enriched 'heavy water' or ^{13}C-enriched compounds. We have recently developed a computational workflow that accepts both amplicon or metagenomic sequence SIP input and calculates atom fraction excess (enrichment) as well as ***growth*** and ***mortality*** rates for individual amplicon sequence variants (ASVs) or metagenome assembled genomes (MAGs)**.** Experiments using ^{18}O-H_2O labeling and qSIP provide critical information on organism growth rates and mortality *in situ*. The analytical pipelines we are developing within KBase establish a standard qSIP analytical workflow, and a qSIP database suitable for robust cross-site comparisons and for model benchmarking. The workflow will enable uniform bioinformatics and calculations of qSIP data (e.g., a uniform approach to density shift calculations), and the database will facilitate robust comparisons across experiments. Integration within KBase will support analyses that compare traits of organisms with their performance in nature, across environments.

The qSIP pipeline is fully integrated with a genomes-to-trait workflow (**microTrait**) and compatible with a dynamic energy budget-based trait-based model (**DEBmicroTrait**). With microTrait and DEBmicroTrait, we have developed and tested a computational workflow to (1) infer ecologically relevant traits from microbial genomes, (2) systematically reduce the high-dimensionality of genome-level microbial trait data by inferring functional guilds (sets of organisms performing the same ecological function irrespective of their phylogenetic origin), (3) quantify within-guild trait variance and capture trait linkages in trait-based models, (4) explore trait-based simulations under different scenarios with varying levels of microbial community and

environmental complexity, and (5) benchmark emergent model substrate utilization (digested as chemical abundance data) and qSIP-derived growth and mortality rates (from qSIP database).

Combining both the qSIP and DEB-microTrait tools within KBase will provide a strong foundation for researchers who wish to use quantitative *in situ* measurements of microbial ecophysiology and population dynamics to benchmark models and build a predictive understanding of biological processes controlling material fluxes in complex environments.