

Cell Size Constraints on Microbial Ecophysiology and Implications for Soil Carbon Cycling

Authors: Gianna Marschmann*¹ (glmarschmann@lbl.gov), Jinyun Tang¹, Ulas Karaoz¹, Jennifer Pett-Ridge³, Eoin Brodie^{1,2}

Institutions: ¹Climate and Ecosystem Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA; ³Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA; ³Physical and Life Sciences Directorate, Lawrence Livermore National Laboratory, Livermore, CA

Website: <https://sc-programs.llnl.gov/soil-microbiome>

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: Size is one of the most important biophysical traits influencing organismal ecology and evolution. Cell volume varies significantly across species and is related to patterns in genome, protein, cellular envelope, and ribosomal content that together can be used to predict key physiological traits of microorganisms that play important roles in soil organic matter turnover and stabilization. Here we coupled an existing allometric scaling model of cellular composition with a genome-informed dynamic energy budget (DEB) representation of microbial metabolism. Allometric predictions for protein synthesis rates that form the core of DEB metabolism were compared to pure culture growth efficiency experiments from the literature. In order to predict the scaling of traits and tradeoffs in rhizosphere and bulk soil communities, the kBASE microTrait software was used to extract fitness traits from isolate genome sequences for model parameterization.

Resource acquisition strategies of soil microorganisms may either be uptake-optimized when precursor compounds (e.g. from root exudation) are available, or depolymerization-optimized when resources are scarce or complex (e.g. from detritus). Due to the size contrast between microbial cells and low molecular weight compounds, uptake is limited mostly by accessible transporter proteins on the cell surface. We find that cellular carbon allocation to the production of transporter proteins, necessary to sustain a cell's maximum specific growth rate, increases with cell size. At the same time, the return on investment into constitutive extracellular enzyme production decreases with increasing cell size.

Microbial growth efficiency is an emergent property of numerous traits in addition to environmental conditions and resource properties. It has also been explicitly linked to the rate and yield of protein synthesis. Recent studies emphasize, that growth rate/yield trade-offs are not universal, but depend strongly on metabolic kinetics and environmental conditions. We find that our allometric scaling approach mirrors protein synthesis phenotypes from the literature. The emergent tradeoff curve of rate and yield as predicted from DEB theory, however, is nonlinear. A metabolic tradeoff between rate and yield is only apparent at high growth rates, while at low growth rates the shape of the tradeoff curve is dictated by storage compound accumulation. The size of the tradeoff region in which a combination of rate and yield is maximized increases with increasing cell size, suggesting higher flexibility in larger organisms consistent with the diffusion-constraint hypothesis in cell size evolution.

This work investigates the consequences of biophysical and physiological constraints in the DEB model by forcing it with different root exudation profiles in batch mode. We are investigating interactions between substrate preference and growth yield and compare emergent guild dynamics to existing metagenomic classifications of rhizosphere and bulk soil adapted communities.

On-going work is focused on coupling our DEB model to a plant-microbial model of soil organic matter turnover. Using a substrate-explicit modeling approach, we will examine biophysical and biochemical properties of low molecular weight compounds that are stabilized on mineral surfaces in distinct soil regimes. We anticipate the fully-coupled model to provide a rank-ordering of biophysical, life-history, and metabolic traits that distinguish microbial strategies. Together, this modeling concept will provide a platform to connect genome-level properties of organisms and phenotypic traits relevant to ecological fitness in the rhizosphere, and ultimately connect microbial ecological processes to soil biogeochemical function.

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