

Trait-based modeling approach to carbon use efficiency

Gianna Marschmann^{1*} (glmarschmann@lbl.gov), **Jinyun Tang**¹, Ulas Karaoz¹, Kate Zhalnina¹, Heejung Cho¹, **Jennifer Pett-Ridge**², **Eoin Brodie**¹

¹Earth and Environmental Sciences Area, Lawrence Livermore National Laboratory, Berkeley, CA; ²Physical 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 organic matter stabilization 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 microbial substrate uptake depends strongly on moisture availability and altered precipitation regimes are predicted across the temperate U.S. *Our SFA's ultimate goal is to determine how soil microbial ecophysiology, population dynamics, and microbe-mineral-organic matter interactions regulate the persistence of microbial residues under changing moisture regimes.*

Abstract: To understand the ecology and biogeochemistry of plant-soil-microbe interactions, it is necessary to quantify and model how substrates control growth and interactions among biological organisms (and abiotic factors, e.g., adsorptive mineral soil surfaces). To address these substrate-consumer relationships, many substrate-kinetics and growth rules have been developed, including the famous Monod kinetics for single-substrate-based growth and Liebig's law of the minimum for multiple-nutrient-colimited growth. However, the mechanistic basis that leads to these various concepts and mathematical formulations and the implications of their parameters are often quite uncertain. Here, we show that an analogy based on Ohm's law in electric circuit theory can unify many of these different concepts and mathematical formulations [1]. We outline how this Ohm's law analogy can be integrated with Dynamic Energy Budget (DEB) models of microbial metabolism that partition biomass into reserve and structural components, and compute structural growth based on reserve dynamics. This biomass partitioning separates extracellular substrate competition from internal microbial physiological tradeoffs (e.g., maintenance vs. growth vs. enzyme production), enabling the tracking of dissipative loss associated with microbial substrate assimilation, somatic maintenance, structural biomass growth, and extracellular enzyme production, and allowing power-yield tradeoffs in metabolism to emerge dynamically.

Evolutionary trade-offs between power and yield can be observed in genomes where higher rRNA operon copy numbers scale positively with power (growth rate) and negatively with yield (carbon-use efficiency - CUE). Recent modeling work [2] predicted that intrinsic physiological differences between microorganisms can account for substantial variance in predicted yield, with

genome size negatively correlating with yield. In a model system representing rhizosphere and bulk soil – derived from an annual grassland soil in California, where we have 39 sequenced genomes representing *Proteobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Acidobacteria*, we find that the power-yield phase space is partitioned into distinct trade-off regions, either dominated by maintenance requirements (positive relationship between power and yield) or relating to carbon and energy allocation (negative relationship). For growth on multiple distinct carbon sources, power-yield strategies of isolates fall on a Pareto optimal curve. Bacteria with larger genomes have less flexible power-yield trade off strategies, suggesting a trade-off between catabolic diversity and metabolic flexibility in isolates occupying distinct ecological niches in rhizosphere vs. bulk soil. Analysis of variance of genomic features and substrate properties furthermore revealed that yield might be a species-specific metabolic property: across substrates, isolate identity explained 38% of the variation in CUE and 88% of the variation within a substrate type. Class (phylum) taxonomic order explained 20% (13%) of the variation in CUE across all substrates and 69% (63%) of the variation within each substrate type. Changes in substrate supply will alter the performance of individual isolates; e.g., in the rhizosphere, we find that low Gibbs energy substrates that are preferentially assimilated select for organisms with metabolic traits that result in higher CUE, but we predict that these changes will not be as strong as changes in CUE that arise owing to differences in community composition. These changes and the potential for manipulating CUE through substrate addition in the rhizosphere can be further explored within our genome-informed, network-based modeling framework for microbial metabolism and plant biogeochemistry.

References

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