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Bacterial Carbon-Use-Efficiency Predicted from Genome-Specific Metabolic Models Varies Phylogenetically and Correlates with Genome Traits

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Respiration by soil bacteria accounts for one of the largest fluxes of CO_2 from the land surface to the atmosphere, yet bacterial physiology and community composition are poorly represented in C cycle models. A single, constant parameter, carbon use efficiency (CUE), is often used in models to determine the partitioning of C between losses as respiration and incorporation into microbial biomass, which can ultimately enter the soil organic C pool. This parameter has a large impact on estimates and projections of soil C pool sizes and greenhouse gas emissions from soil; however, it is not well-understood how CUE varies between bacterial taxa and whether this variation makes microbial community composition an important factor in predicting C cycle fluxes.

We used a novel approach to estimate CUE for over 200 bacterial species based on genome-specific metabolic models built using the Department of Energy's Knowledgebace (kBase). In the absence of resource limitation, CUE varied widely between individual taxa, suggesting that intrinsic variation in potential CUE between taxa may be as large as that previously attributed to abiotic factors like temperature. Additionally, we observed a significant phylogenetic signal in CUE estimates and variation in these values was significantly related to genome traits, including genome size. For example, CUE declined by 4% per mega base pair (Mbp) increase in genome size. Finally, we explored the degree to which particular metabolites imposed constraint on CUE, and found that CUE responded most strongly to a subset of specific amino acids and carbohydrates, including lysine and arabinose. These findings provide a method for estimating CUE, a critical microbial physiological parameter in C cycle models, from genomic data available on the DOE's kBase. The relationships we observe here between microbial community composition, bacterial physiology, and C cycling provide a means for improving the mechanistic representation of microbial processes in C cycle models.