



QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM: How Soils Work: A Multi-Omic Approach to Soil Microbial Community Ecophysiology

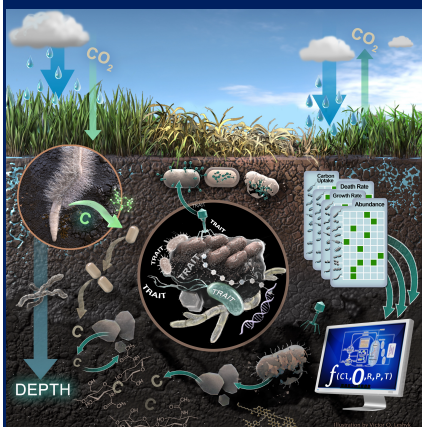
Jennifer Pett-Ridge
Lawrence Livermore Laboratory



Date:
10/22/2026

Time:
10:30 AM – 11:45 AM

Location:
SSB 130



About The Speaker:

Jennifer Pett-Ridge is a Distinguished Member of Technical Staff and lead of the 'Carbon Initiative' at Lawrence Livermore Laboratory. She also works as an adjunct professor at UC Merced and an investigator at the UC Berkeley Innovative Genomics Institute where she studies soil microbiome interactions using isotope tracing, quantitative systems biology and modeling. Jennifer leads several Department of Energy (DOE) team projects, focused on the mechanisms that lead to soil carbon persistence, the capacity and costs of CO₂ removal in the USA (Roads to Removal) and novel bio- and geoengineering approaches for soil carbon drawdown. She has been recognized with the US DOE Ernest Orlando Lawrence Award, is a fellow of the American Geophysical Union and American Association for the Advancement of Science (AAAS) and was recently elected to the Alameda County Women's Hall of Fame.

Abstract:

Soil water and resource availability are major drivers of microbial community assembly, gene expression and system function and exert influence on a variety of temporal scales—ranging from short pulse dynamics to seasonal and annual precipitation patterns. Determining how growing roots or changing water dynamics impact microbial growth and activity is crucial for assessing how changes in climate may impact soil functionality. To understand how altered resource and precipitation regimes affect the microbial ecophysiological traits associated with soil carbon cycling, we have used multi-omics approaches (including metagenomics, metatranscriptomics, lipidomics, and metabolomics) along with quantitative stable isotope probing (qSIP) to interrogate Who is where? and What are they doing? in wild soil communities collected from Mediterranean grassland soil experiments. Our results indicate only a fraction of the total microbial community is actively growing in any season or habitat. Using transcript-based modules, we find coherent patterns in microbial community-wide gene expression as taxa encounter living versus decaying roots, and before and after drought events. While theory predicts that carbohydrate compounds (glycolysis) would be preferred over organic acids (gluconeogenesis), our results indicate that gluconeogenesis is generally dominant, while glycolysis is temporally and spatially variable. Using metagenomics and 16S rRNA gene qSIP, we tracked growth and mortality and found that a history of limited moisture (50% precipitation) causes a legacy effect of reduced growth and mortality, demonstrating the interplay between annual/seasonal dynamics and short-term responses. Additionally, we found that growth after rewetting can be predicted from genomic traits such as genome size, codon bias, and GC content—indicating key features of fast-responding taxa to soil water pulse-dynamics. These results point to genome level traits that are predictive of microbial growth responses, and show how differences in resources and soil moisture can influence microbial activities.

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