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Linking microbial genes to emergent outcomes in soil systems

Microbes encode for vast genetic potential, yet predicting functional outcomes of microbial communities is challenging, especially in soils where highly diverse (thousands to millions of taxa) and abundant (10^9 cells per gram of soil) microbial populations reside.

While significant advances have been made in profiling microbial communities via their genomic signatures using multi-omics techniques, gaps in gene-to-function links and their representation in models exist. For example, although microbes catalyze trace gas production and consumption of greenhouse gases (e.g., CO_2 , CH_4 , N_2O), atmospheric tracers (e.g., OCS , $^{18}\text{O}-\text{CO}_2$), and microbial signalling compounds (e.g., hundreds of volatile organic compounds), the key enzymes (if known) often have poorly resolved functional diversity and phylogenetic distribution. Furthermore, even when gene-to-function links are resolved in reductionist experiments, soil gas fluxes are poorly predicted from soil genomic data, which is often presumed to be related to soil heterogeneity and mismatches in spatial and temporal scales (e.g., static -omics vs real time gas fluxes).

To address these challenges, we use experimentation across scales to constrain genetic traits for trace gas metabolisms, develop soil gas sensors to better match microbial and gas flux data, and leverage constrained and controlled model ecosystems to advance our ability to scale from genes to ecosystems. In this talk, I will present recent research illustrating these approaches to build predictive understanding of biosphere-atmosphere trace gas exchange and soil microbial function.

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