

Phenotypic Response of the Soil Microbiome to Environmental Perturbations

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Project Goals: PNNL's Soil Microbiome SFA aims to achieve a systems-level understanding of the soil microbiome's phenotypic response to changing moisture through spatially explicit examination of the molecular and ecological interactions occurring within and between members of microbial consortia. Integrated experiments will be designed to confront both the scaling challenges and inter-kingdom interactions that regulate networks of biochemical reactions. Individual- and population-based models for predicting interspecies and inter-kingdom interactions will be parameterized using experimental data, and predictions will be tested in soil to reveal spatially explicit microbial interactions. Discoveries from controlled experiments will be tested and validated in the field, using moisture gradient experiments at a new local field site. Data will be captured and shared through the establishment of a Soil Microbiome Knowledgebase (SMK). Knowledge gained will provide fundamental understanding of how soil microbes interact to decompose organic carbon and enable prediction of how biochemical reaction networks shift in response to changing moisture regimes.

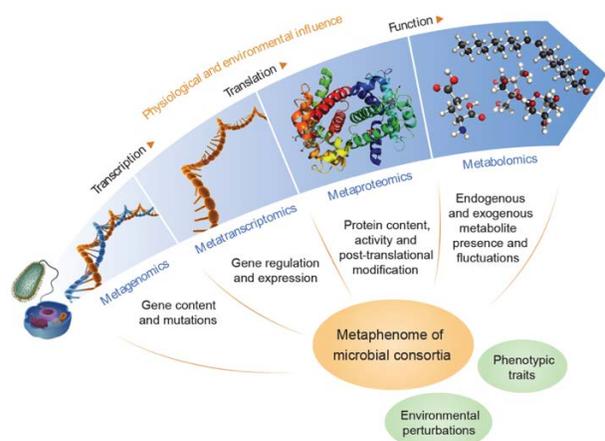


Figure 1. The metaphenome scales beyond the microbial metagenome and metatranscriptome to capture the emergent traits of the microbiome under specific environmental conditions (e.g. available resources; spatial, biotic, and abiotic constraints). Information gained from integration of omics technologies is essential for gaining mechanistic understanding of the soil microbiome metaphenome (*modified from Ref. 1*)

Abstract: Soil is a diverse ecosystem with microbial dark matter that remains to be discovered. Predicting microbial interactions in this complex system represents an exciting frontier and a grand challenge with implications for the productivity and fertility of our nation's soils. The Pacific Northwest National Laboratory (PNNL) Soil Microbiome SFA will result in a molecular understanding of how moisture affects the interactions and phenotypes of microbial consortia, leading to our decadal vision of predicting the soil microbiome metaphenome to manage carbon

(C) and nutrient cycling. By enhancing our understanding of the basic biology of microbial interactions, we will be able to predict ecological outcomes under changing environmental conditions. Moisture in particular drives microbial interactions and influences everything from cell function to substrate fate within soils. If we can understand how the physiology, metabolism, and interactions of soil microbes change in response to moisture, we will have a basis for modeling and predicting the soil microbiome *metaphenome* (Fig.1.).

Here we define the soil *metaphenome* as the product of expressed functions encoded in soil microbial genomes (metagenome) and the environment (resources available; spatial, biotic and abiotic constraints)². The metaphenome is thus comprised of the sum of many phenotypes that are the result of biochemical interactions between members of the soil microbiome. In this SFA we aim to build an experimental and modeling framework across levels of complexity (from field to reduced complexity consortia) to gain fundamental understanding of the soil metaphenome. This knowledge gap is currently a challenge because of the high diversity of soil microbial species and the interdependencies of metabolic exchange between microbes – and across trophic levels. Our approach will thus be to define the soil metaphenome in a model grassland soil by deconstruction of the overall soil *biochemical reaction network* – that is still largely undefined – into smaller *functional modules*. Our obtained results will be transferable to more complex, non-model systems. An example of a functional module is the pathway for chitin degradation under aerobic conditions, with a defined soil moisture content, nutrient availability, temperature, pH, and other biogeochemical factors. The soil moisture content will also govern the spatial constraints of interacting members of the soil microbiome and their access to resources. We aim to focus on functional modules that result from interactions between soil microbes at the microscopic scale. These functional consortia can consist of a variety of interacting species, including bacteria, archaea, fungi and viruses that interact through metabolic exchange and chemical communication signals. The expressed functions encoded in the soil metagenome is in turn governed by the physiological status of the member populations. Only viable, active cells will contribute to the chitin degradation phenotype in the above example. *Our approach thus aims to 1) define the contributions of active cells and active metabolic pathways (expressed genes, proteins) that contribute to the soil metaphenome and 2) to define functional modules that can be plugged in to fill current gaps in the soil biogeochemical reaction network.*

References

1. Jansson, J.K. and E.S. Baker. 2016. A multi-omic future for microbiome studies. *Nature Microbiology*. 1:1-3.
2. Jansson, J.K. and K.S. Hofmockel. 2018. The soil microbiome: From metagenomics to metaphenomics. *Current Opinion in Microbiology* (in press).

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