

# Phenotypic Response of the Soil Microbiome to Environmental Perturbations

Advancing the understanding of how soil microbial communities respond to—and affect—changing environmental conditions

Soil microbes play a major role in supporting plant growth and nutrient cycling. Changing climate and precipitation patterns, however, can affect soil fertility and productivity. An important scientific challenge is understanding how interacting members of microbial communities, across trophic levels, respond to changes such as longer periods of drought or depleted soil nutrients. This knowledge is crucial for better managing plant growth and identifying key processes in soil carbon storage and the land-atmosphere exchange of carbon dioxide.

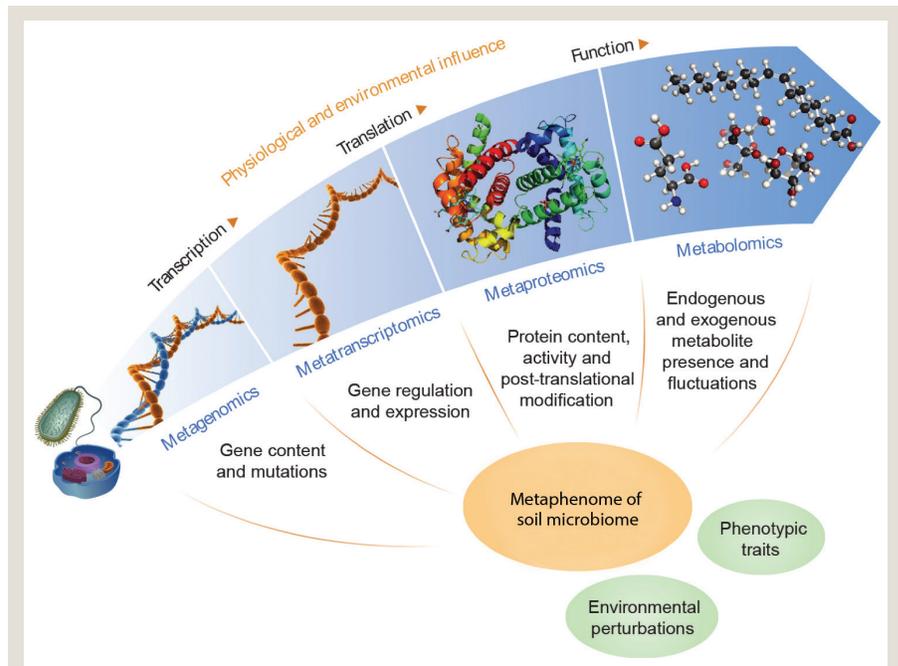
To tackle this challenge, the Genomic Science program within the U.S. Department of Energy's (DOE) Office of Biological and Environmental Research (BER) supports the Phenotypic Response of the Soil Microbiome to Environmental Perturbations Science Focus Area (SFA) led by Pacific Northwest National Laboratory (PNNL).

The PNNL Soil Microbiome SFA is focused on understanding the basic biology underpinning how interactions among various soil microbial community members lead to the emergence of community functions. Moisture, in particular, drives microbial interactions and influences everything from cell function to substrate fate within soils. This results in repeatable, predictable phenotypes. The sum of these phenotypes comprises the “soil metaphenome,” or the collective physiological responses of the soil microbiome. Understanding how the soil metaphenome shifts in response to moisture will provide a basis for modeling and predicting how soil microbial communities react to other changing environmental conditions.

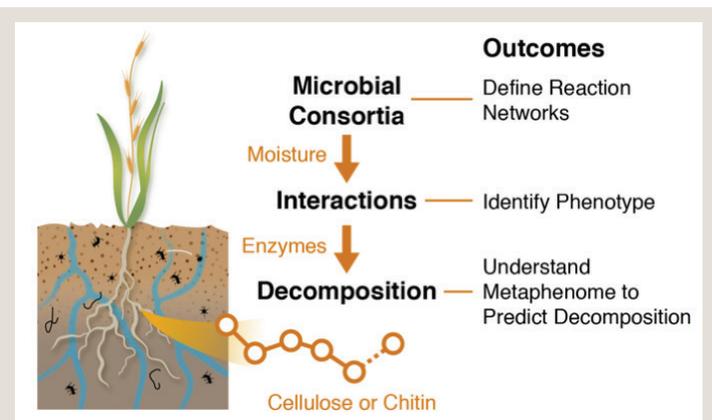
## Multiscale Approach

To decipher the soil metaphenome, SFA researchers are building an experimental and modeling framework across levels of complexity—from the field to reduced-complexity consortia—using a grassland soil model. Grasslands contain about 20% of global carbon stocks, and soil microorganisms are key players in the cycling of these carbon pools. A current knowledge gap is how changes in the environment, such as shifts in precipitation patterns, may influence the cycling of carbon and other nutrients in grassland soils in the future.

The SFA is focusing on decomposition of chitin, an abundant molecule in soil. Chitin decomposition is defined by the soil's moisture content, nutrient availability, temperature, pH, and other biogeochemical factors. Soil moisture content also governs the spatial constraints of interacting soil microbiome members and their access to resources.



**Metaphenome of Soil Microbiome.** *The microbial metaphenome scales beyond the metagenome and metatranscriptome to capture emergent traits of the microbiome under specific environmental conditions (e.g., available resources and spatial, biotic, and abiotic constraints). Information gleaned from the integration of omics technologies is essential for gaining a mechanistic understanding of the microbiome metaphenome. [Adapted by permission from Springer Nature from Jansson, J. K., and E. S. Baker. 2016. “A Multi-Omic Future for Microbiome Studies,” Nature Microbiology 1, 16049. DOI: 10.1038/nmicrobiol.2016.49. Copyright 2016.]*



**Predicting Organic Carbon Decomposition.** *Moisture influences the physiology and connectivity of soil consortia to drive interactions and phenotypes that determine how plant (cellulose) and fungal (chitin) inputs are decomposed.*



SFA researchers focus on studying the functional modules resulting from interactions between soil microbes at the microscopic scale. Model soil consortia were derived that consist of various species that interact during chitin decomposition. The expressed functions encoded in the soil metagenome and in the reduced-complexity model soil consortia are, in turn, governed by the physiological status of member populations.

## Project Goals

Ultimately, the Soil Microbiome SFA aims to achieve a systems-level understanding of the soil microbiome and its phenotypic responses to changing moisture. This goal is accomplished through the:

- Design of integrated experiments to confront both scaling challenges and interkingdom interactions that regulate networks of biochemical reactions.
- Use of high-resolution experimental data to parameterize individual- and population-based microbial community models for predicting interspecies and interkingdom interactions.
- Testing of predictions in soil using advanced chemical imaging and fluorescent probes to reveal spatially explicit microbial interactions.

## Key SFA Hypotheses

Five hypotheses drive the PNNL Soil Microbiome SFA experiments. These hypotheses address the functional relationships of consortia that decompose soil organic matter and the responses of the microbiome to changing moisture.

- **Predictable Reaction Modules Exist.** In soil, reproducible and predictable reaction modules (i.e., subreaction networks that perform defined metabolic functions) exist based on resource availability and species' genetic potential.
- **Desiccation Disconnects Microbial Interactions.** Compared to moist conditions, soil desiccation results in disconnected metabolic processes among consortia, causing distinct consortial units, secondary metabolites, and soil phenotypes.
- **Desiccation Reproportions Active Consortia.** During desiccation, a shift occurs in the fraction of microbial consortia actively contributing to decomposition, which results in a consortial minority contributing disproportionately to carbon and nutrient cycling.
- **Fungi Connect Consortia During Desiccation.** With increasing desiccation, fungi will bridge disconnected resource islands, thereby connecting distal consortial units.
- **Viral Predation Increases with Moisture.** With increasing soil moisture, viruses and phages have a greater influence on community carbon flow through predation and cell lysis.



**Cross-Scale Experimental Approach.** SFA researchers work across scales of complexity—from enrichment cultures in the lab to natural systems in the field—to identify meaningful biological interactions and consistent biochemical functions in soil microbial communities.

- Testing and validation of discoveries and outcomes from controlled field experiments.
- Establishment of a soil microbiome database to capture and share data, models, and methods with the broader science community.

Knowledge gained from this project is providing fundamental understanding of how enzymes, metabolites, and microbial consortia interact to decompose organic carbon and enable prediction of how biochemical reaction networks and related functions shift in response to critical perturbations including drought.

## Contacts and Websites

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[pnnl.gov/projects/soil-microbiome-science-focus-area](http://pnnl.gov/projects/soil-microbiome-science-focus-area)

### Genomic Science Program

[genomicscience.energy.gov](http://genomicscience.energy.gov)

### Biological Systems Science Division

[science.osti.gov/ber/research/bssd](http://science.osti.gov/ber/research/bssd)

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