

# Phenotypic Response of the Soil Microbiome to Environmental Perturbations

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

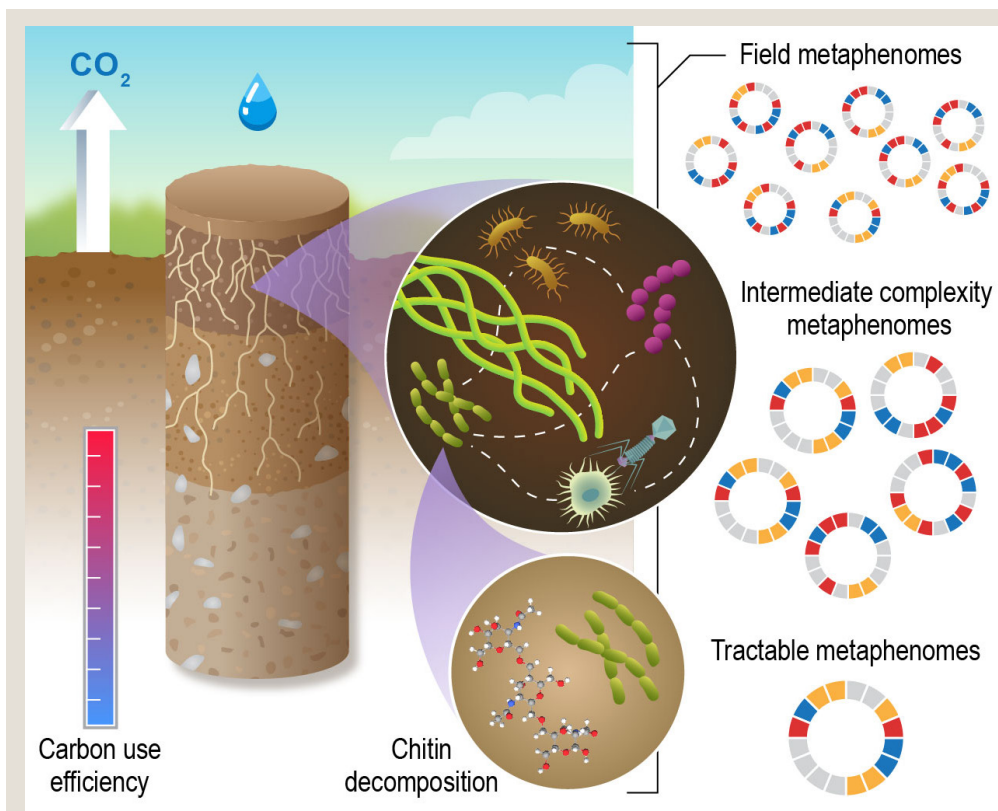
Soil microbes play a major role in supporting plant growth and nutrient cycling. Changing climate and precipitation patterns can affect soil fertility and productivity. An important scientific challenge is understanding how interacting members of microbial communities, across trophic levels, respond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

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 (Soil Microbiome SFA) led by Pacific Northwest National Laboratory (PNNL).

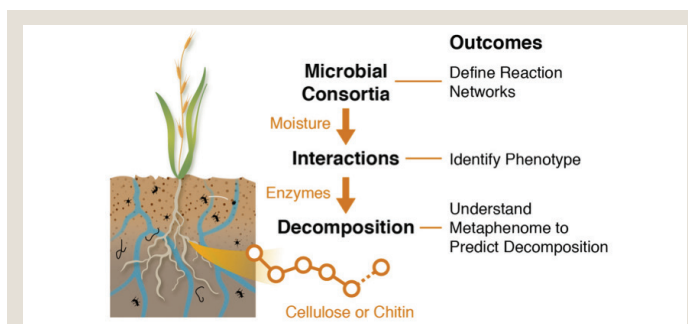
The PNNL Soil Microbiome SFA focuses on understanding the basic biology underpinning how interactions among various soil microbial community members lead to the emergence of community functions. Moisture, in particular, drives microbial interactions and influences everything from cell function to substrate fate within soils, resulting 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



**Metaphenome of the Soil Microbiome.** The Soil Microbiome Science Focus Area, led by Pacific Northwest National Laboratory (PNNL), identifies molecular-level metabolic interactions governing decomposition, moisture effects on microbial phenotypes during decomposition, and their implications for carbon use efficiency. By working across scales of biological and ecological complexity and using complementary network modeling approaches, researchers identify how the genetic potential of individual microorganisms is expressed through interactions with other organisms and the environment, collectively composing a metaphenome.



**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.



pools. A current knowledge gap is how changes in the environment, such as shifts in precipitation patterns, may influence future cycling of carbon and other nutrients in grassland soils.

To understand carbon cycling in soil, this SFA focuses on chitin decomposition as a model molecule because it is abundant in soil. Chitin decomposition is determined by soil 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.

To understand microbial interactions during decomposition, model soil consortia were derived from PNNL's Irrigated Tall Wheatgrass Field Experiment. 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

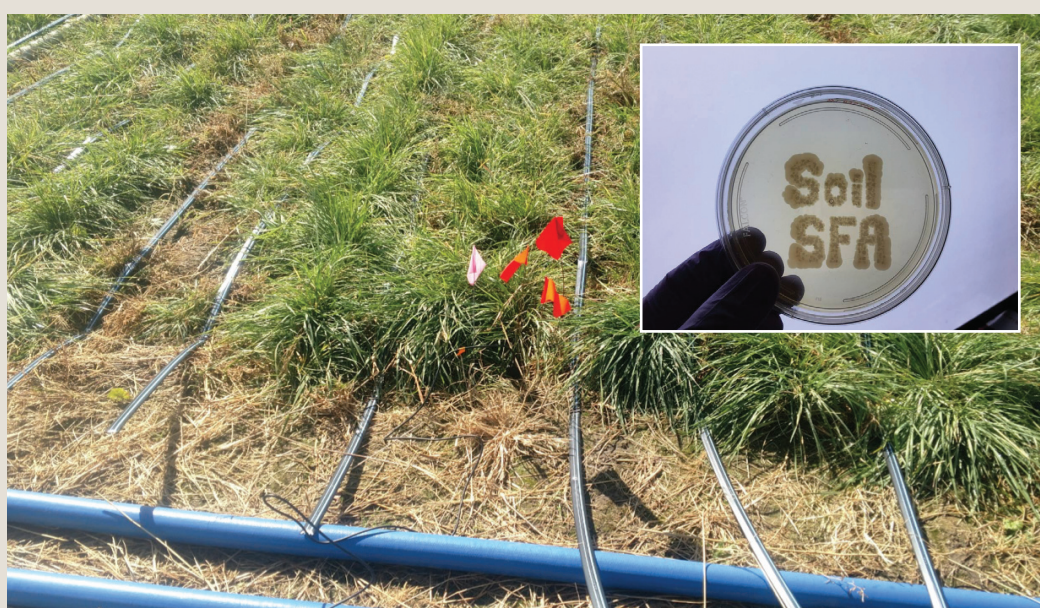
PNNL's Soil Microbiome SFA aims to achieve a systems-level understanding of the soil microbiome and its phenotypic responses to changing soil moisture. This goal is accomplished through:

- 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 population- and community-microbial models for predicting interspecies and interkingdom interactions.

## Key SFA Hypotheses

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

- **Metabolic Complementarity.** Soil microorganisms with complementary genomic capabilities coordinate their metabolism and express phenotypes that promote positive interactions and growth during chitin decomposition.
- **Moisture Phenotypes.** By regulating microbial connectivity, wet and dry conditions select for different organisms and phenotypes that optimize metabolic interactions and resource allocation during decomposition.
- **Substrate Chemistry.** Substrate chemistry selects for phenotypes that optimize metabolic interactions.
- **Viral Shunt.** Depending on soil moisture, lytic cycles of viral production can alter soil carbon cycling by directly affecting host population dynamics through lysis and turnover and by exerting auxiliary metabolic functions.
- **Carbon Use Efficiency.** Microbial phenotypes that contribute to carbon use efficiency scale in a predictable manner across levels of biological complexity.



**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 of predictions in soil using advanced chemical imaging and fluorescent probes to reveal spatially explicit microbial interactions.
- 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 provides fundamental understanding of how enzymes, metabolites, and microbial consortia interact to decompose organic carbon and enables prediction of how biochemical reaction networks and related functions shift in response to critical perturbations including drought.

## Contacts and Websites

### Principal Investigator

Kirsten Hofmockel, kirsten.hofmockel@pnnl.gov, 509.371.6444

### BER Program Manager

Dawn Adin, dawn.adin@science.doe.gov, 301.903.0570

### Phenotypic Response of the Soil Microbiome to Environmental Perturbations SFA

[www.pnnl.gov/projects/soil-microbiome](http://www.pnnl.gov/projects/soil-microbiome)

### 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)

### DOE Office of Biological and Environmental Research

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

### DOE Office of Science

[science.osti.gov](http://science.osti.gov)

### U.S. Department of Energy

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