

Revealing the Role of Microbial Communities in Carbon Cycling

genomicscience.energy.gov/carboncycle/

As unprecedented levels of atmospheric carbon dioxide (CO₂) continue to increase, the need to understand the response of Earth's ecosystems and climate to a higher-CO₂ world becomes more urgent. Although the global carbon cycle plays a central role in regulating atmospheric CO₂ levels and Earth's climate, our understanding of the interlinked biological processes that drive this cycle remains limited.

The amount of carbon exchanged between the biosphere and atmosphere each year is many times greater than the carbon emitted by human activities. Thus, even minor changes in the rate and magnitude of biological carbon cycling can have immense impacts on whether ecosystems will capture, store, or release carbon. In addition to providing insights for safely increasing carbon sequestration in ecosystems, a quantitative understanding of the biological processing of carbon is needed to more accurately represent the carbon cycle in climate models, thereby improving their projections. Output from these models will be critical in determining the most effective adaptation and mitigation strategies for minimizing the adverse effects of rising atmospheric CO₂ levels.

Through its Genomic Science program, the Department of Energy (DOE) Office of Biological and Environmental Research (BER) supports projects that use the latest developments in genomics and systems biology to link the structural and functional characterization of microbial communities with quantitative measurements of carbon cycle processes.

Microbial Communities and the Carbon Cycle

The global carbon cycle is heavily dependent on microbial communities that fix atmospheric carbon, promote plant growth, and degrade or transform organic material in the environment. Large amounts of organic carbon are currently locked in high-latitude permafrost, grassland soils, tropical forests, and other ecosystems, and microbes play key roles in determining the longevity and stability of this carbon and whether or not it is released into the atmosphere as greenhouse gas (GHG). Yet in many cases, these microbially mediated processes are only minimally represented in carbon cycle models, thus limiting their predictive capability. The following examples describe two of the many different microbial activities for which a greater understanding is needed to improve carbon cycle and climate modeling.

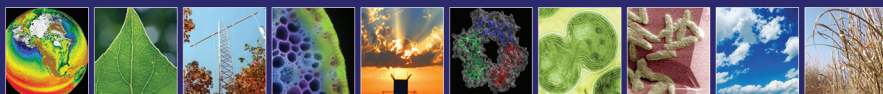


By manipulating different environmental variables, mesocosms of California grassland are used to study the changing composition and activities of soil microbial communities. [Image credit: University of California, Berkeley]

Microbial Carbon Transformations in Soils. Representing the largest and most stable reservoir of carbon in terrestrial ecosystems, soils contain more than twice as much carbon as the atmosphere. Soil microbial communities mediate the multistep conversion of dead plant tissue and organic compounds exuded from plant roots into CO₂ or soil organic matter. The heterogeneous array of carbon compounds in soil can reside in terrestrial ecosystems for decades to thousands of years. Understanding the microbial community reactions and environmental conditions controlling the transformation of organic carbon in soil could lead to opportunities for sequestering vast quantities of carbon in ways that improve soil quality and benefit the environment.

Microbial Carbon Transformations in Permafrost. Permafrost (permanently frozen subsoil) represents about 20% of Earth's surface and holds one-third of global soil organic carbon. With future warming in the Arctic projected to be much higher than the global average, soil microbial activity triggered by permafrost thawing has tremendous potential to rapidly release large quantities of CO₂, methane (CH₄), and other GHGs into the atmosphere. Turnover of plant residues as permafrost thaws is a complex process with numerous biogeochemical routes, and poorly understood microbially mediated processes will be critical in determining the amount and form of carbon released to the atmosphere.

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Thawing permafrost cracks and crumbles, activating microbial metabolism of undegraded organic material once trapped in frozen soil sublayers. [Image credit: Wikipedia]



Understanding the systems biology of important classes of microbes and integrated microbial communities in changing permafrost ecosystems will reveal novel insights into how these processes are controlled.

Focusing the Power of Genomics and Systems Biology on Carbon Cycling

Genome sequencing has ushered in a new generation of “omics” methods (e.g., transcriptomics, proteomics, and metabolomics) enabling systematic investigation of comprehensive networks of genes, proteins, and metabolites within cells. This systems biology approach—which couples modeling and simulation with experiment and theory—aims to define the organizing principles, emergent properties, and resulting detailed organization that control the functions of organisms.

Historically, biology has been confined to the study of individual organisms. Metagenomics, metatranscriptomics, and metaproteomics offer new methods for investigating the metabolisms and lifestyles of microbial communities, including uncultivated organisms from environmental samples. Developing and pursuing metagenomic (or other omic) research techniques not only will help capture the functional potential encoded in genomes, but also will enable new approaches for qualitatively and quantitatively measuring active metabolic processes in the environment. These measurements then can be incorporated into mechanistic and predictive models.

In July 2009, BER solicited its first round of proposals for systems biology research on the contributions of microbes and microbial communities to carbon cycling processes in the following three areas. A full listing of research awards is available at genomicscience.energy.gov/carboncycle/.

- Systems-level studies on regulatory and metabolic networks of microbes and microbial consortia involved in biogeochemical cycling of carbon.
- Development of metatranscriptomic, metaproteomic, and other genome-enabled approaches to understand how shifts in environmental variables impact microbially mediated carbon cycling processes in terrestrial ecosystems.
- Development of methods and techniques for imaging and analyzing microbially mediated carbon cycling processes in terrestrial ecosystems.

Linking Systems Biology from Lab to Ecosystem Scale

The response of ecosystems to environmental change depends on the collective responses of many types of organisms whose functions are encoded in genomes. Although linking directly from genomes to global phenomena is not practical, many connections at intermediate scales are viable with integrated application of new systems biology approaches and powerful analytical and modeling techniques at the physiological and ecosystem levels. By adapting genome-enabled techniques to the investigation of microbial systems *in situ* or by using micro- or mesocosms, this research is providing the quantitative measurements and metabolic and regulatory models that ultimately could inform larger-scale biogeochemical models of microbial processes in the environment.

Research Funding

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