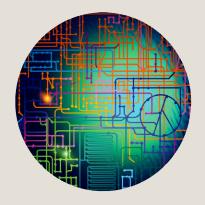
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The United States is committed to understanding the factors that influence climate change, reducing uncertainties in assessments of climate change, and developing strategies to mitigate change. Microbes in the earth's oceans and soils play a major role in the cycling of carbon and other elements. GTL seeks to understand this role to be able to predict the impacts of climate change on microbes and their responses to the resulting ecosystem shifts. This knowledge also will provide the basis for developing and assessing strategies for ocean- and soilbased carbon sequestration.

DOE Mission: Carbon Cycling and Sequestration

Understand Biosystems' Climate Impacts and Assess Sequestration Strategies

C.1.1. The Climate Change Challenge

Atmospheric greenhouse gas (GHG) concentrations have been increasing for about 2 centuries, mostly as a result of human (anthropogenic) activities, and now are higher than they have been for over 400,000 years. As shown in Fig. 1. Simplified Representation of the Global Carbon Cycle, p. 229, about 6 billion tons (gigatons) of carbon are released into the air by human activity each year, three-quarters from the burning of fossil fuels and the rest from deforestation and other changes in land use, with a small amount from cement production. Although the effects of increased levels of CO₂ on global climate are uncertain, many agree that a doubling of atmospheric CO₂ concentrations, predicted for the middle of this century by the Intergovernmental Panel on Climate Change (IPCC), could have a variety of serious environmental consequences.

Global climate change is a long-term energy and environmental challenge requiring major investments in targeted research and development (see Mission Science Goals and Challenges below). Gaining a greater knowledge of how carbon cycles through ecosystems is a critical element of the national strategy to understand climate and potential changes that might occur due to anthropogenic greenhouse gases and to develop solutions to reduce future increases in CO₂ (the most important

Mission Science Goals and Challenges

Mission Science Goals: Understand the microbial mechanisms of carbon cycling in the earth's ocean and terrestrial ecosystems, the roles they play in carbon sequestration, and how these processes respond to and impact climate change. Develop methods to relate genome-based microbial ecophysiology (functionality) to the assessment of global carbon-sequestration strategies and climate impacts.

Challenges: We are just beginning to understand the genetic and functional diversity of ocean and terrestrial ecosystems. They potentially contain millions of microbial species organized in extensive communities. We must understand both the global and molecular mechanistic behaviors of these large systems.

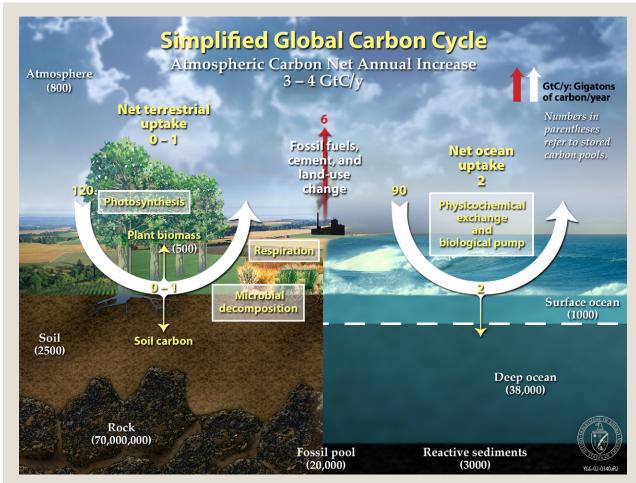


Fig. 1. Simplified Representation of the Global Carbon Cycle. The illustration depicts human-induced changes relative to the total cycle. [Graphic adapted from *Carbon Sequestration Research and Development (1999)*.]

GHG) and other GHGs (see sidebar, CCSP Calls for Carbon Cycle Data, this page). Understanding how climate affects both natural and managed "pools" (e.g., forest, agriculture lands) of carbon stored in global ecosystems and how these carbon "sinks" influence atmospheric concentrations of CO₂ will be important in reducing uncertainty in climate models and in understanding the long-term sequestration capacity of those pools (Carbon Sequestration 1999).

C.1.2. The Role of Microbes

Natural processes also contribute to the storage and cycling of carbon (Fig. 1, this page). The stability and sequestration of the vast pools stored in oceanic and terrestrial environments depend, in part, on the microbial world.

CCSP Calls for Carbon Cycle Data

The U.S. Climate Change Science Program (CCSP) is a multiagency effort to understand the earth's climate and predict how it will evolve under various greenhouse gas scenarios. The CCSP calls for development of information on the carbon cycle to assist in evaluation of carbon-sequestration strategies and alternative response options, the understanding of key "feedbacks" including biological and ecological systems, improved knowledge about the sensitivity of ecosystems to climate variability and change, and incorporation of such knowledge into climate models. Understanding how carbon dioxide and other by-products of energy generation affect the global environment requires research into how carbon (and, to a lesser extent, nitrogen, phosphorous, oxygen, and iron) cycle through ecosystems (see Appendix F. Strategic Planning for CCSP and CCTP, p. 249).

According to the American Society of Microbiology (King et al. 2001), "Microbes, responsible for transforming many of earth's most abundant compounds, cannot be ignored in the search for scientific solutions to adverse global changes.... Both the ubiquity of microbes and the delicacy of environmental balances contribute to [the planet's] sensitivity to disturbances in the microbial world."

Microbial energy transfer and material processing in the biosphere have been transforming the earth for over 3 billion years (see sidebar, Planet-Transforming Microbes Cycling Carbon, this page) and influencing climate on a global scale (Staley et al. 1997). Extremely diverse ocean and terrestrial microbial communities serve fundamentally different roles in the carbon cycle as primary photosynthetic producers of biomass in the ocean biological "pump" and as carbon and nutrient managers and decomposers in terrestrial systems (see Table 9. Microbial Community Characteristics in Diverse Earth Environments, p. 39). Microbes cycle immense volumes of carbon in the process of recycling most of earth's biomass: They can fix CO₂ by light-driven (photoautotrophy) and geochemically driven (lithoautotrophy) reactions, generate methane, produce CO₂ as they decompose organic matter, precipitate carbonate minerals, and catalyze the polymerization of plant polymers into recalcitrant pools of carbon in soil.

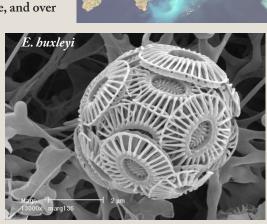
The DOE mission of global carbon management requires that we achieve a comprehensive understanding of terrestrial and marine microbial communities so we can learn the role that these communities play in carbon sequestration. We then must find ways to enhance their capabilities to develop microbe-based strategies for capturing and sequestering atmospheric CO₂ and to assess the potential effectiveness and adverse ecological impacts of proposed carbon-sequestration technologies. Microbial systems also have great potential as sensitive indicators of environmental change.

Natural cycles of carbon in the environment involve exchanges many times greater than anthropogenic emissions (see Fig. 1, p. 229). While anthropogenic emissions threaten to change the globe's climate gradually, secondary effects on natural ecosystems and disturbance of their much larger atmospheric exchanges could result in even larger shifts. Knowing the effects of anthropogenic emissions on natural cycles is important as part of the complete picture of carbon management on a global scale.

Planet-Transforming Microbes Cycle Carbon

Blooms of *Emiliania huxleyi*, captured by satellite, are shown just off the coast of the United Kingdom. Though microscopic, these carbon-cycling cocolithophores (bottom image) are present in such large numbers that they are visible from space—an indicator of their pervasiveness and thus influence on ocean ecosystems (top image). Their shells are made of calcium carbonate, and over

the ages their deposits have created the "White Cliffs of Dover" on the southern coast of England. Understanding the planet-transforming capabilities of these and other ocean microbes—that is, how they affect ocean ecosystems by cycling carbon and other important elements—is a focus of the GTL program. *E. huxleyi*'s genome is being sequenced by DOE's Joint Genome Institute. For more information, see www.noc.soton.ac.uk/soes/staff/tt/.



Top – Landsat 7 photo of July 24, 1999, by S. Groom, Plymouth Marine Laboratory Remote Sensing Group; bottom – J. Young, Natural History Museum, London

Investigating and understanding these ecosystems require probing numerous complementary functionalities in thousands of species and millions of genes, involving hundreds of thousands of proteins. In brief, goals and challenges in this mission follow (see Table 1. Carbon Cycling and Sequestration: Goals and Impacts, this page).

C.1.3. Microbial Ocean Communities

C.1.3.1. Photosynthetic Capabilities

Microbial communities living near the surface layers of oceans are the primary photosynthetic organisms driving the biological pump. Absorbing CO, and sunlight to produce most oceanic organic materials, the organisms make up the foundation of the marine food chain. Photosynthesis of such phytoplankton as diatoms, dinoflagellates, and cyanobacteria converts about as much atmospheric carbon to organic carbon in the ocean as plant photosynthesis does on land. Large variations in phytoplankton abundance, therefore, can greatly impact the oceans' ability to take up atmospheric carbon.

Oceans currently have a net absorption of about 2 Gt of carbon per year, offsetting about 30% of carbon emitted to the atmosphere by the burning of fossil fuels. Understanding the interactions and dynamics underlying this natural CO₃ sink is necessary to explain past shifts in global climate and to predict future environmental changes. Microbes drive these processes by converting atmospheric CO₂ into organic matter, some of which remains in the oceans (see sidebar, Carbon Cycling in the Oceans, p. 232).

Dominant organisms in surface waters include such cyanobacteria as Synechococcus species and Prochlorococcus marinus, which capture CO, and light to carry out photosynthesis. Prochlorococci now are thought to be the most abundant photosynthetic organisms on earth. Eukaryotic diatoms such as the recently sequenced Thalassiosira pseudonana also live in surface waters and convert CO, and other nutrients into hard silicates. This process carries organically complexed carbon to ocean depths, thus converting its relatively rapid cycling in surface waters (where it is returned to the atmosphere) to a considerably slower one in ocean sediments.

C.1.3.2. Strategies for Increasing Ocean CO, Pools

Ocean carbon-sequestration strategies aim to increase the deep ocean inventory of CO₂. Two approaches typically are considered: Direct injection of a CO₂ stream into the ocean interior depths and iron fertilization to enhance photosynthesis by phytoplankton in the biological pump and thus increase carbon uptake. The potential effectiveness and adverse impacts must be evaluated for both approaches. According to the CCTP strategic plan, due for publication in 2005: "A research portfolio is required that seeks to determine, via experimentation and computer simulations, the ability of the world's oceans to effectively store anthropogenic CO₂ without negative environmental consequences" [CCTP, www.climatetechnology.gov].

DOE has sponsored genomic sequencing of several of these organisms (see sidebar, Microbial Genomes Yielding Clues to Global Climate Change, p. 233). Additionally, recent GTL-sponsored metagenomic approaches have involved researchers sequencing DNA fragments isolated from samples taken from ocean (and terrestrial) environments. These studies have for the first time allowed direct insights into the makeup and functionality of these natural systems, revealing an amazing diversity. Analyses from Sargasso Sea samples, for example, turned up more than a million previously unknown genes, including almost 800 rhodopsins (the

Table 1. Carbon Cycling and Sequestration: Goals and Impacts

- Improved understanding of key feedbacks and sensitivities of biological and ecological systems and accelerated incorporation into climate models will reduce uncertainties in assessments of climate change.
- Knowledge of the carbon cycle will allow evaluation of carbon-sequestration strategies and alternative response options.
- Development of sensors and monitoring techniques and protocols will allow use of these sensitive ecosystems as sentinels for the effects of climate change.

Carbon Cycling in the Oceans: Solubility and **Biological Pumps**

Ocean processes regulate the uptake, storage, and release of CO, to the atmosphere. The total exchange of carbon between atmosphere and oceans is controlled by two principal processes: The solubility (or physical) pump and the biological pump.

The solubility pump is driven by physical processes. The solubility of CO, in water increases with lower water temperature, and the colder water sinks. This gradient, from lower CO, concentration near the surface to higher concentrations below about 500 m, helps draw CO, from the atmosphere into the oceans. The solubility pump, in combination with ocean circulation, results in net CO, emissions at the equator and net CO, drawdown at high latitudes. Changes to ocean circulation or stratification due to increased global warming from increased greenhouse gases are predicted to result in decreased ocean uptake of CO, by the ocean solubility pump.

The biological pump, whose activities are just being revealed, refers to the composite of biological processes occurring in ocean surface layers. These begin with the microbial photosynthesis of CO, into organic matter (much like land plants) and end with either the conversion of organic matter to CO, at different depths or with the deposition of a small fraction of organic material into sediments on the ocean floor. The biological pump's efficiency is a function not only of carbon fixation but also of the depth at which the organic carbon is remineralized to CO₂. Current models, which rely on incomplete carbon-cycle models having little biological input, suggest that if the biological pump were turned off today, atmospheric levels of CO, would rise to 680 ppm (~400 ppm higher than preindustrial levels and about 300 ppm higher than current levels). The ocean's future activity as a carbon sink is uncertain, however, because of potential (and currently uncharacterized) feedbacks among global climate change, ocean circulation, and microbial communities that actively cycle carbon. These natural ocean carbonsequestration processes extend beyond carbon to affect organic and inorganic pools of nitrogen, phosphorus, oxygen, and many other chemical species.

A key feature of ocean environments is the extremely slow recycling of mineral nutrients. Dead organisms from the photosynthetically active top of the water column sink into its depths and, ultimately, the ocean floor. They carry with them essential nutrients, mainly nitrogen and phosphorus, that are liberated in the darkness of the deep ocean. From there, upwelling currents take several thousand years to return the nutrients to warm surface waters. Consequently, primary production in the top of the water column is limited severely by the lack of mineral nutrients, whereas the nutrient-rich deep waters lack light energy for primary photosynthetic production.

light-absorbing antennae of microbes essential for photosynthesis) (Venter et al. 2004). Metagenomic studies of soil samples show an even greater amount of genetic material (Riesenfeld, Schloss, and Handelsman 2004). Results suggest that microbial communities have an extraordinarily wide range of mechanisms and pathways that could offer new applications to meet DOE carbon-management missions.

GTL will use these data as starting points for explorations into molecular processes underlying microbial photosynthesis. The goal is to ascertain fundamental principles of photosynthetic systems' molecular design. These principles will reveal the dynamics of carbon-assimilation pathways and those that degrade organic matter and ultimately either sequester carbon or return it to the atmosphere.

GTL research will enable us to begin identifying critical organisms and their capabilities and responses to stress. These data will provide the foundation for developing biological rate constants that can be incorporated into detailed models of carbon cycling. When these models are extended to the global ecosystem, the potential impact of carboncycle perturbations on climate-change models can be assessed. Ultimately, this knowledge will guide decisions about acceptable levels of change and hence acceptable atmospheric levels of GHGs.

In addition to elucidating carboncycling nuances, such detailed biological data can lead to the development of increasingly sophisticated microsensors that can detect changes in the levels of biomolecules (DNA, RNA, proteins, metabolites) and serve as indicators of microbial-community response to environmental stressors (see sidebar, Ocean Monitors, p. 234).

C.1.3.3. GTL's Vision for Ocean Systems

The GTL Knowledgebase ultimately will provide in silico models of microbial systems in oceans, with supporting data and experimental capabilities that can be used to inform policies and develop methods and applications relevant to DOE missions in carbon management.

C.1.3.3.1. Gaps in Scientific Understanding

Understanding carbon cycling and sequestration requires knowledge about the underlying mechanisms controlling microbiological systems. Investigations will include defining key players and their roles; determining how systems change as a function of climate, CO₂, nutrients, and biogeochemical cycles; and enabling predictions of atmospheric CO, and climate impacts on marine communities over time. Specifically, these analyses will enable us to begin exploring the following types of questions:

- What happens to carbon in the oceans, and how is it portioned among various life forms? How does this portioning vary in rate as a function of location, depth, salinity, nutrient availability, temperature, proximity to population centers and coastlines, currents, and seasons?
- How far do carbon and carbon dioxide migrate from their "points of entry" into the ocean, and what impacts their travel and processing?
- What are the elements of the biological pump?
- What happens to growth rates of phytoplankton as a function of carbon entry into the oceans in light of the variables noted above?
- What would happen to carbon absorption if growth rates for phytoplankton were altered either up or down?
- What are the dynamic community structures of ocean microbes, and how do they impact carbon processing?
- · How reversible would be the effects of actions that we might take to alter ocean carbon sequestration (and on what time scales)?

C.1.3.3.2. Scientific and **Technological Capabilities** Required

Defining communities and their genomic potential will require capabilities for rapid and accurate sequencing of single cells, key organisms, and environmental communities. Also needed are methods to perform comparative genomic analyses and capabilities for gene synthesis and manipulation. Specific needs include the following:

 Metagenomic approaches to aid in sifting through millions of genes and determining which proteins are produced by ocean communities and when.

Microbial Genomes Yielding Clues to Global Climate Change

Analyses of the first ocean microbes to be sequenced—a diatom and several cyanobacteria—are beginning to help investigators understand the physiological and genetic controls of photosynthesis and the cycling of carbon and nitrogen. The diatom T. pseudonana (images below) and species of Prochlorococcus and Synechoccus contribute to absorbing amounts of CO₂ comparable to all the world's tropical rain forests combined. GTL research on the molecular processes underlying the capabilities of these organisms can lead to more-accurate climate models and strategies for carbon sequestration. The diatom and three of the four cyanobacteria in these analyses were sequenced at the Joint Genome Institute and

funded by DOE (see also Falciatore and Bowler 2002). [Science 306, 79-86 (2004); Proc. Natl. Acad. Sci. USA 100, 10020-25 (2003); *Nature* 424, 1037-42 and 1042-47 (2003)]



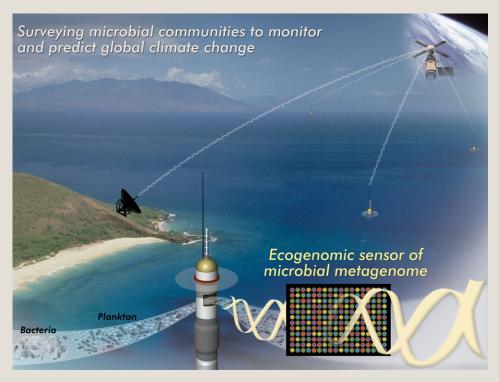
B. Palenik and D. Lee, Scripps Institution of Oceanography

- Capacity to make and study the proteins determined by the ocean's metagenome to understand ocean microbial functionality and processes. Because these microbes are essentially unculturable, protein analysis initially will be achieved only by synthesis directly from genome sequence. A high-throughput approach would permit simultaneous, highly parallel production and characterization tests on hundreds of thousands of proteins.
- Molecular tags (or affinity reagents) for proteins with established critical roles to use as probes for determining the structure and function of natural ocean ecosystems.
- New sampling and analysis tools to investigate the natural dynamics of relationships among microbial, biogeochemical, and physical processes.
- Technologies to measure environmental responses, including ecogenomic sensors of sentinel organisms; biochemical assays of cells, communities, and ecosystems; and environmental assays (see sidebar, Ocean Monitors, this page).
- Detailed studies of proteins, multimolecular machines, and metabolites to aid in understanding key microbial responses in terms of photosynthesis, transporters, and biomineralization processes; development of functional assays and technologies, including imaging, to measure system responses.
- Information on microbial mechanistic behaviors (cellular, community, ecosystem) for incorporation into more accurate climate models.
- Database of genes, pathways, microbes, and communities to explore the structure and function of ocean ecosystems, and, in particular, the roles of ocean microbes in carbon processing and their impact on global climate processes.

Ocean Monitors: Nanoscale Ecogenomic Sensors

Nanoscale environmental genomic sensors may one day be used to monitor microbial populations and their interactions with environmental processes, including those affected by climate change. The real-time approach envisioned by DOE for the National Oceanographic Partnership Program merges information from genome research programs with nanotechnologies and smart sensors.

The knowledge gained will enhance understanding of the genetic diversity and functions of microbial communities and help answer key questions about their influence on ocean and terrestrial biogeochemical cycles. Microbial sentinels of ecosystem changes may forewarn the approach of such events as red tide caused by an increase in Pfisteria species. (For more information on microbial sensing, see Klaper and Thomas 2004 and Belkin 2003.)



C.1.4. Terrestrial Microbial Communities

C.1.4.1. Influence on Plant Growth

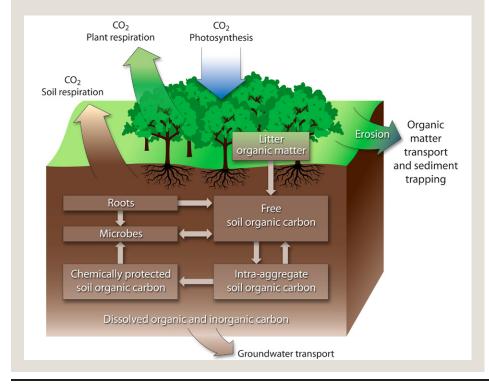
Terrestrial ecosystems absorb CO₂ directly from the atmosphere, mainly via plant photosynthesis. The carbon is stored in plant biomass and soil organic matter or respired back to the atmosphere. Terrestrial ecosystems can help reduce concentrations of CO, in the atmosphere by increasing carbon stores in biomass, soils, and wood products (see sidebar, Carbon Transformation and Transport in Soil, this page).

Some microbial populations influence carbon storage in plants by enhancing their growth through interactions with organic compounds around the root (the rhizosphere), by providing nutrients such as phosphorous and nitrogen, or by suppressing plant pathogens in the soil. Other microbial communities exert neutral or even harmful effects. A better understanding is needed of the molecular mechanisms that enable microbes to colonize root surfaces, interact with organic compounds in the rhizosphere, and cooperate with other organisms.

Microbes impact carbon storage in soils by transforming carbon in decaying plants into other forms of organic matter, with varying degrees of recalcitrance. Soils thus are a complex mixture of compounds having different residence times, with more-stable compounds being the most important for carbon sequestration because their turnover times can be hundreds to thousands of years. Soils contain about 75% of the carbon in the terrestrial ecosystem, and knowing more about the microbial processes taking place there will lead to a better understanding of long-term carbon storage in soils.

Carbon Transformation and Transport in Soil

These processes can result in sequestration of carbon in the soil as organic matter or in groundwater as dissolved carbonates, increased emissions of CO₂ to the atmosphere, or export of carbon in various forms into aquatic systems. [Source: The U.S. Climate Change Science Program: Vision for the Program and Highlights of the Scientific Strategic Plan, 2003, www.climatescience.gov/Library/stratplan2003/ vision/ccsp-vision.pdf]



Carbon dioxide is emitted from soils through soil respiration, a result of the metabolic activity of plant roots and soil microbes decomposing plant material and soil organic matter. Most plant material entering the soil is respired relatively quickly as CO₂; a small fraction becomes humus, which remains in soils for a longer time. Soil respiration is a major component of the global carbon cycle, returning nearly 10 times as much CO₂ to the atmosphere as emissions from fossil-fuel combustion (Rosenberg, Metting, and Izaurralde 2004). The shift in the ability of microbes to respire carbon to the atmosphere during environmental stresses such as climate change (e.g., more carbon is released by decomposition when

stress causes plants to die) is a serious complicating factor in determining the permanency of these pools for sequestration. Physical influences such as agricultural tillage practices and fire contribute greatly to the amount of carbon released to the atmosphere from soils. As we understand microbial species and specific processes that create recalcitrant forms of carbon and those that metabolize carbon rapidly to carbon dioxide, we can manage terrestrial ecosystems in better ways, including low-till and no-till agriculture.

C.1.4.2. Strategies for Increasing Stable Carbon Inventories

Gaining a fundamental understanding of biological mechanisms of carbon cycling and sequestration in an ecological context can help us understand and predict effects of climatic change on key ecological processes. Genomics and, even more so, proteomics and metabolomics will become valuable tools for developing a biological systems understanding and reducing uncertainty about effects of future (potential) climate changes on the terrestrial biosphere's structure and function. They also will be useful for increasing the likelihood of successful human responses to such climate-change contributors as carbon sequestration and ecosystem management (see sidebar, Integrated Assessment Program, this page).

Augmenting natural microbial activities may be a promising option to optimize the inventories of stable carbon forms. DOE has sponsored successful field experiments that remove uranium from contaminated groundwater by stimulating the growth of particular microbial communities known to precipitate (and immobilize) that contaminant. We also can envision potentially altering some plants (notably cellulosic energy crops needed to produce bioethanol) in ways that stimulate them to produce larger fractions of more-recalcitrant organic matter that would lead to increased carbon sequestration in the terrestrial biosphere (see sidebar, Poplar Tree Offers Potential for Greater Carbon Storage, p. 237). An added benefit could be improved soil quality because of increased carbon. Natural carbon fluxes are large, so even small forced changes resulting from sequestration strategies can be very significant.

C.1.4.3. Terrestrial Systems Vision

GTL science will generate the knowledge to incorporate, for the first time, models describing the global ecosystem into climate models to provide foundations for a more robust science base for policy and engineering. It also will enable evaluation of potential biology-based strategies for terrestrial carbon sequestration. The national goal is to develop these policies and strategies substantially over the coming decade (see Table 2. Carbon Cycling and Sequestration Challenges, Scale, and Complexity, p. 237).

C.1.4.3.1. Gaps in Scientific Understanding

Understanding the global ecosystem and its climatic effects requires learning about key microbial processes involved in carbon and nitrogen cycling, maintaining soil fertility, and increasing soil carbon content. Understanding how microbes and their ecosystems respond to a variety of environmental factors will allow for more accurate assessments and predictions of carbon inventories in terrestrial systems and their impacts on climate change to enable more-effective strategies to manage these inventories.

Integrated Assessment Program

DOE's Integrated Assessment (IA) of Climate Change Research Program combines simplified representations of the entire global climate system, emphasizing greenhouse gas (GHG) emissions and actions that would affect emissions. Integrated models are used to assess the value of technologies that result from research; these include new biotechnological approaches, for example, that improve biomass conversion and generate hydrogen, an expected result of the knowledgebase generated in the GTL program. IA research provides a foundation for subsequent policy analysis or decision making.

The IA Program addresses several of DOE's research priorities. The most immediate issue of interest is the role of energy production and associated GHG emissions in global climate change. Closely related is the question of climate change impacts—by extension, energy production impacts—on humans and their environment. The program thus brings together a major approach (integrated assessment), a global environmental problem (climate change), and the scientific challenges of interdisciplinary and modeling of multiscale complex systems.

As part of a broader science base for understanding effects of climatic change on terrestrial ecosystems, GTL systems biology will support studies on interactions among terrestrial ecosystems and on changes in atmospheric composition and the climate system. In particular, advanced hardware and software capable of rapidly sequencing genomes will provide the foundation for performing systems biology analyses and quantifying climate effects on key protein functions to understand the following:

How do microbes contribute to carbon transformation in soils, and what is their potential for sequestering
meaningful amounts of carbon (gigatons per year) in more stable forms? This knowledge will provide decision makers, including the public, with information on designing and evaluating options for responses to
potential climatic effects of future carbon-based energy production.

Poplar Tree Offers Potential for Greater Carbon Storage

An international team including the DOE Joint Genome Institute recently sequenced the genome of the black cottonwood or poplar tree (*Populus*). This research could be used to improve tree breeding and forest management practices that would enable significant quantities of carbon to be sequestered by this and, eventually, other trees. In addition, a significant fraction of carbon associated with a stand of trees is in soil organic-matter pools rather than in aboveground biomass or living roots. The poplar genome sequence information might be used to develop ways to enhance both the production and translocation of organic compounds from leaves

and shoots to roots and soil, where it might lead to long-term storage of carbon. In addition to carbon storage, poplar produces products and services of considerable value to humans and many ecosystems. Moreover, poplar trees are highly productive in many environments and have a wide ecological range or distribution.



- How do microbial genomes adjust mechanistically to climate change? This understanding will allow more realistic prediction of future climate-change effects (or explain effects of recent climate change) on the structure and functioning of ecosystems.
- What is the genomic-mechanistic basis for biological feedbacks to the climatic system brought about through the terrestrial carbon cycle? The potential exists for significant releases of CO₂ or CH₄ to the atmosphere in response to rising temperatures and changes in precipitation.
- With a "simple" understanding of the underlying biology of ecosystems, how can we develop a modeling framework to put systems biology information into a usable context for predicting feedbacks to climate and atmospheric CO₂?

Table 2. Carbon Cycling and Sequestration Challenges, Scale, and Complexity

Research and Analytical Challenges	Scale and Complexity
Analysis of ocean and terrestrial microbial-community makeup and genomic potential	Thousands of samples from different sites, consisting of millions of genes, thousands of unique species and functions
 Analysis of carbon and other cycling processes » Photosynthesis and respiration in oceans » Storage and decomposition in soil: microbial, fungal, and plant communities • Modeling and simulation of microbe biogeochemical systems 	 Functional analysis of enzymes involved—potentially tens of thousands; hundreds of regulatory processes and interactions; spatially resolved community formation, structure, and function Models at the molecular, cellular, and community levels incorporating signaling, sensing, metabolism, transport, biofilm, and other phenomenology into macroecosystem models

C.1.4. 3.2. Scientific and Technological Capabilities Required

Defining communities and their collective genetic functional potential requires both single-cell and community sequencing (in situ and in vitro), systems biology studies, and the ability to relate microbial activities to soil processes. Capabilities to accomplish these goals include:

- Methods to understand processes by which carbon is transformed into long-lived forms and to design technical and management strategies for enhancing advantageous processes and mitigating negative responses.
- Methods to measure biomolecular inventories correlated with environmental conditions; characterizations of microbial-system interactions with soils, rhizosphere, and plants; and imaging of microbial functional activities (e.g., proteomes and metabolomes) at cellular and community levels—all to understand processes that impact production of GHGs (CO₂, methane, nitrous oxide, and dimethyl sulfide).
- Methods to detect and measure microbial responses to manipulation of plant inputs to the carbon cycle, to human inputs to soils, and to other environmental changes.
- Methods to use microbes as sentinels of climate-induced change in the environment. Research will determine the biomarkers that correlate with specific environmental parameters. Biomarker signatures include combinations of RNAs, proteins, metabolites, and signaling elements; community genomic makeup brought about by population shifts; and functional assays (Tringe et al. 2005).