Approved Proposals FY22

Following are the approved user proposals for the annual Community Science Program (CSP), FICUS JGI-EMSL, CSP Functional Genomics and CSP New Investigator calls.

Community Science Program

Proposer	Affiliation	Proposal Title	Proposal Description
Bowen, Jennifer	Northeastern University	Microbial controls on carbon cycling and storage resulting from salt water intrusion in tidal fresh, brackish, and saline marshes	The push of saltwater into fresher reaches from sea level rise results in the replacement of plant communities with salt tolerant species. This global-scale disturbance disrupts established plant-microbe interactions, alters the structure of soil microbial communities, and fundamentally changes controls on soil carbon cycling and storage. The goal of this research is to characterize changes in the genetic potential of microbes that control soil carbon cycling and storage along salinity and elevation gradients in a river-estuary system with documented shifts in salt-tolerant wetland vegetation.

Colwell, Frederick	Oregon State University	Defining microbial functional capabilities across high-latitude, glacially impacted, wetland landscapes	Globally, wetlands provide crucial ecosystem services but are stressed by a changing climate. We propose to study microbial communities, and their genes, that live on Alaska's glacially dominated Copper River Delta. Home to iconic fish and waterfowl, the Delta hosts microorganisms dependent on glaciers and the nearby ocean, and that cycle carbon and iron in the wetland sediments. We will study how these microbes cycle carbon, the factors that control their presence, and the relationship of microbes to glacier proximity yielding data broadly useful for studying high latitude wetlands.
de Vries, Ronald	Westerdijk Fungal Biodiversity Institute (Netherlands)	Mining the unknown part of fungal genomes by combining machine learning with multi-omics and functional characterization	Developing efficient processes for plant biomass utilization (e.g., for production of food and feed, pulp and paper or biofuels) remains challenging due to the structural complexity and variability of this biomass. This project aims to identify a large number of these missing genes in five well-studied reference fungi to get a more complete picture of the overall process of plant biomass conversion and the diversity in approaches fungi use to achieve this. The results will provide a more complete picture of the genes involve in plant biomass conversion and will enable more efficient strain engineering to obtain the next generation of fungal cell factories for biotechnology.

DeAngelis, Kristen	University of Massachusetts Amherst	Using genomics to understand microbial adaptation to soil warming	Healthy soils require a diverse and abundant microbial community. The earth's climate is warming, and long-term warming has many ecosystem effects including increased greenhouse gas emissions and accelerated soil carbon loss. Our recent research shows that chronic warming is irreversibly altering how microbes interact with their environment, potentially accelerating soil carbon loss. These irreversible effects should have genetic or genomic signatures, and our proposal is to combine genome sequencing with metabolomics of bacteria and fungi to describe these changes.
Dick, Gregory	University of Michigan	Metagenomic and metatranscriptomic insights into the role of microbial interactions in the cycling of carbon and nutrients during toxic cyanobacterial bloomse	The proposed project strongly aligns with DOE's interests and mission to study inter-organism interactions and microbes and communities involved in elemental cycling and secondary metabolites. Although microbial processing of biogeochemistry in lakes plays a substantial role in water quality, which is threatened under continued eutrophication and climate change, the microbial communities underpinning these processes have been understudied and thus controls on the fate of carbon and the production of greenhouse gases are not well understood.

Gawryluk, Ryan	University of Victoria (Canada)	Adapting ultra-low input long read sequencing methods to predatory algae in a complex culture system	Recently, a completely new group of species were discovered that belong to the same eukaryotic supergroup as plants, along with green and red algae. Surprisingly, these organisms – known as Rhodelphis – are the opposite of what one would expect of a plant relative: they do not harness energy through photosynthesis, but actively hunt other microbial cells. Elucidating the gene content and structure of Rhodelphis will have wide-ranging implications for the origin and evolution of plants, including the genomic consequences of losing photosynthesis.
Jesus, Edeson	EMBRAPA (Brazil)	Unveiling the functional potential of microbial communities of the Amazon forest floor through metagenomics	The soil organic layers play an essential role in the tropical forest's nutrient cycling. In this project, we will use metagenomics to understand how the microbial interactions in these layers contribute to diversity estimation and element nutrient cycles in a scenario still little explored. A forest in the Eastern Amazon and an adjacent pasture will be our model systems. We aim to promote awareness about the importance of preserving the Amazon forest and point to alternative ways of taking advantage of its biodiversity in a context in which it has been threatened by increasing deforestation.

Krukenberg, Viola	Montana State University	Exploring the microbial methane cycle in terrestrial geothermal environments	Microbially mediated methanogenesis and methane oxidation are key processes in the global carbon cycle and control the atmospheric levels of the potent greenhouse gas methane. This project will explore the microbial methane cycle in terrestrial geothermal environments. We will use metagenome, metatranscriptome and single cell genome sequencing to identify novel methanogens and characterize their taxonomic and functional diversity, metabolic activity and impact on biogeochemical element cycles.
Mengiste, Tesfaye	Purdue University	Whole genome resequencing of 400 sorghum core subset germplasm collection	Availability of whole genome sequences are critical for crop improvement. Identification of genets that control critical traits is facilitated by knowledge on the variations in DNA sequences of diverse plant resources. Sorghum bicolor is a plant with high potential for biofuel production. This proposal is to sequence diverse set of sorghum germplasm that may carry important traits including high biomass, high sugar, tolerance to stress such as drought and cold. This work will expedite the discovery of genes regulating processes in stress tolerance and biomass production.

Myburg, Alexander	University of Pretoria (South Africa)	Eucalypt genomic resources for woody biomass production and carbon drawdown	We will perform large-scale genome sequencing of a group of fast-growing tree species (eucalypts) that are a sustainable source of carbon and energy rich biomass globally, with high relevance to the DOE mission in sustainable biofuels and bioproducts. Eucalypts are widely grown as feedstocks for lignocellulosic and other biorefinery products. Their prevalence in the vast, carbon dense woodlands of Australia and their high potential for landscape restoration and new afforestation for carbon drawdown make eucalypts relevant to the DOE mission on global carbon cycling.
Nelson, Andrew	Boyce Thompson Institute (Cornell University)	Molecular basis of natural rubber biosynthesis in Parthenium argentatum (Guayule)	This proposal represents a joint effort by private and public research interests to understand and enhance the rubber biosynthesis pathway (RBP) in Parthenium argentatum (guayule), a drought-tolerant shrub cultivated in the American Southwest. Guayule is truly a multi-use commodity crop; guayule also accumulates high levels of resins with commercial application and is an ideal feedstock for biofuel generation. By developing genomic resources and understanding how the environment influences the RBP, we hope to unlock guayule's full potential as a renewable source of plant-based products.

Preston, Jill	University of Vermont	Development of the grass subfamily Pooideae as a powerful comparative genomics model for temperate crop and biofuel development	The use of warm-season grasses for the harvest of renewable biofuels is greatly contributing to local demand for renewable energy sources. However, effort is still required to diversify these crops in order to (1) deal with increasingly variable environments globally, and (2) develop perennial biofuel species that are carbon neutral. Here, we develop genomic resources in cool-season grasses to decipher key differences between annual and perennial species. This will allow for the discovery of genes that will enhance sustainable biomass, and add to burgeoning knowledge on plant diversification.
Purcell, Alicia	Northern Arizona University	Quantifying the ecophysiology of growing microbes responding to warming along a productivity gradient of the Marr Ice Piedmont Glacier, West Antarctic Peninsula	The Antarctic Peninsula is warming, expanding terrestrial environments. Glacier forefield ecosystems are home to diverse microbial communities that are responsible for carbon and nutrient cycling and plant development. Using metagenomics enabled qSIP, metatranscriptomics, and metabolomics, we aim to understand how warming impacts in situ microbial growth rates and activity. Our project will quantify and elucidate the metabolism of individual microbes that facilitate carbon and nutrient processes in a climate sensitive ecosystem.

Read, Betsy	Cal State University San Marcos	The Haptophyte Genome Project	Haptophyte microalgae contribute a major portion of the world’s photosynthetic activity with more than 400 species. They inhabit freshwater and marine ecosystems and exhibit remarkable morphologic and metabolic flexibility. They are able to produce spectacular calcium carbonate cell coverings, delicate organic scales, powerful toxins, unusual lipids; and can also elicit predatory tendencies, form massive blooms, be widely distributed, and thrive in harsh environments. To unravel the genomic underpinnings of these incredible algae we will sequence the genomes of 35 diverse species.
Roth, Melissa	UC Berkeley	Deciphering the role of master regulators in carbon flow for enhanced lipid production	Photosynthetic organisms are promising sources for sustainable solutions to help meet the growing global needs for energy and products, but there are currently practical limitations. Our research focuses on master regulators in algae that naturally produce high amounts of the preferred biofuel precursor triacylglycerols (TAG), and seeks to understand how carbon is converted into TAG production. Through identifying essential factors that are critical for high TAG, this research will enable redesign and engineering of algae and other organisms for improved biofuel and bioproduct production.

Vallon, Olivier	Centre National de la Recherche Scientifique (France)	A Chlamydomonas pan-genome	The land plants that make up our forests and produce most of our food have tiny relatives, called green algae. Their study allows us to learn more on how plants carry out photosynthesis, the only way nature can withdraw CO2 from the atmosphere, to build living matter. Among these inconspicuous organism, the unicellular Chlamydomonas reinhardtii is a key model organism, because of its ease of manipulation. It has been used in laboratories since 1945 and has allowed many discoveries. Our project will explore the natural biodiversity of this species and discover new functions for its many genes.
Wilkins, Michael	Colorado State University	Impacts of changing wildfire regimes on soil microbiome succession and function	This work aims to understand how soil microbiomes in fire-adapted ecosystems (montane coniferous forest, chaparral shrubland) respond to low and high severity wildfire. While studies have reported changes in the composition of soil microbiomes following wildfire, here we will determine how these shifts affect carbon and nitrogen cycling in burned soils. We will access recently burned soils in California and Colorado, and use novel “pyrocosm” apparatus. Combined metagenomic, metatranscriptomic, and metabolomic analyses will offer unique insights into soil microbiomes in burned ecosystems.

FY 2022 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Proposals

Proposer	Affiliation	Proposal Title	Proposal Description
Baldrian, Petr	Institute of Microbiology of the Czech Academy of Sciences (Czech Republic)	Effects of plant functional diversity on the ecosystem responses to forest harvesting	Forests maintain the global carbon balance and play an important ecological role in raw materials. This project will analyze and compare the functioning of forest soil microbiomes following various tree harvesting schemes. Understanding these effects is critical because harvested forest stands may become temporary carbon sources through greenhouse gas emissions.
Blenner, Mark	University of Delaware	Plastic Degrading Microbial Communities from Insect Larvae Guts	Insect microbial consortia degrade plastics more rapidly than microbial isolates. While several bacterial members of these communities have been isolated, the full set of microbes and their specific pathways responsible for biodegradation have not been elucidated. This research will examine the role for microbial interactions in plastic degradation.

Kroeger, Marie	Los Alamos National Laboratory	Temporal Dynamics of Microbial Traits – Driving Divergent Patterns of Carbon Flow During Surface Litter Decomposition	Climate change projections show that microbially driven surface litter decomposition rates will increase with rising temperatures as more carbon is released into the atmosphere and less is stored in soils. This project will build a foundation of research to identify microbial effect traits that create substantial variations in carbon cycling.
Master, Emma	University of Toronto (Canada)	Functional and structural analysis of microbial expansin-related proteins that transform lignocellulosic biomass	Bringing together functional genomics, structural biology, and materials science techniques, this project will evaluate the untapped potential of microbial expansin-related proteins on lignocellulose organization for production of bio-based chemicals and materials.
Merchant, Sabeeha	University of California Berkeley	Systems analysis of a microbial phototroph-heterotroph symbiosis	Phytoplankton rely on the sun for energy but change their metabolic strategy at night. This project will exploit a system with reduced complexity, established reference organisms with well-described physiologies, and a suite of methodologies to improve understanding of trophic interactions and diel patterns.

Meredith, Laura	University of Arizona	Belowground genotype-phenotype controls on nitrogen use efficiency of a sorghum bioenergy crop	Plant-microbe interactions drive nitrogen transformations in soil. This research will address critical barriers to observing rhizosphere nitrogen transformations in real-time by using below-ground measurements of volatile metabolites. The project will provide a detailed understanding of inter-organismal interactions that drive nitrogen transformations and loss in soils.
Miesel, Jessica	Michigan State University	Investigating interactions between soil microbial communities and soil organic matter dynamics along climate and vegetation gradient	Organic matter in soils is critical to nutrient cycling and climate change. As the primary agents of decomposition, soil microbes are key to soil organic-matter. turnover. The project uses NEON soil samples, utilizing EMSL and JGI facilities to better understand the mechanisms controlling soil organic matter persistence within and across ecosystems.
Nuccio, Erin	Lawrence Livermore National Laboratory	Beneficial Partners: Context Dependent Mycorrhizal Resource Exchange in Bioenergy Cropping Systems	The plant microbiome critically impacts plant health and productivity. This project will examine the resource exchange between Panicum hallii, a model grass species related to the bioenergy flagship plant switchgrass, and two mycorrhizal fungi, demonstrating how drought

			alters the benefit of fungi to the plant host.
Roden, Eric	University of Wisconsin-Madison	Tracking the degradation of fresh particulate organic matter in permeable riverbed sediments using FT-ICR-MS and metagenomic/ metatranscriptomic sequencing	This project combines Fourier-transform ion cyclotron resonance mass spectrometry with metagenomic/transcriptomic sequencing and metabolomics to track the transformation and degradation of fresh, photosynthetically derived particulate organic matter in permeable riverbed sediments influenced by hydrologically-driven transport of solutes and colloidal particulate organic matter.
Ruff, Emil	Marine Biological Laboratory	Assessing the contribution of sediment bioirrigation to the oxidative removal of methane from a fluvial wetland	Wetlands are the largest natural source of the greenhouse gas methane. This project investigates the microbiome of the insect burrows in freshwater sediments and studies aerobic methanotrophy in the burrow walls. The project will assess the path of methane carbon through the food web and the contribution of bioirrigation to methane removal.

Zheng, Jianqiu	PNNL	Leveraging a reciprocal soil transplant experiment to illuminate soil biogeochemical responses to moisture and salinity disturbance	Coastal ecosystems are highly dynamic systems undergoing high rates of natural variability and anthropogenic changes. Researchers will use EMSL and JGI resources to attain molecular-level understandings of biogeochemical transformations that underpin emergent ecosystem functions, which can then be captured in process models to advance the predictability of the Earth system.
Zimmerman, Amy	Pacific Northwest National Lab	Resolving taxon-specific contributions to nutrient cycling in soil microbial communities through stable isotope enabled multi-omics	Combining multiple omics approaches, this project will quantify taxonomically. resolved growth, substrate use, and functional allocation phenotypes, within diverse soil communities, in response to nitrogen source and temperature. This research will contribute to a framework for predicting how shifts in microbial community composition and physiology regulate nutrient cycling in soils.

CSP Functional Genomics

Proposer	Affiliation	Proposal Title	Proposal Description

Baer, Julia	University of California, Santa Cruz	The molecular evolution of bloom-forming toxic Pseudo-nitzschia in response to ocean warming	This project aims to predict the evolutionary changes of the toxic diatom Pseudo-nitzschia in response to a warming ocean and to investigate the molecular mechanism of acclimation of Pseudo-nitzschia to irregular warming conditions. The marine environment is changing at multiple timescales, with secular ocean warming and the abnormal occurrence of largescale heatwaves. To predict how Pseudo-nitzschia will respond to ocean warming, we will compare the genetic transcripts of toxic Pseudo-nitzschia strains adapted to either ambient cold temperatures or anomalously warm temperatures.

Bhat, Aditi	Brookhaven National Laboratory	Understanding the genotype-by-genotype basis of heavy metal tolerance in Medicago-rhizobia symbiotic interactions	Symbiotic interactions between legume host plants and nitrogen fixing bacteria (rhizobia) have profound impacts on soil quality and plant health and even separately, they have a huge potential for bioremediation of toxic soils. Our experiments will quantify the transcriptional changes inside nodules that are occupied by highly tolerant rhizobia compared with non-tolerant rhizobia. The data generated from this proposal will accompany transcriptomic data we have from free-living host plants and rhizobia. In addition, by incorporating CRAGE engineered biosynthetic gene clusters (BSGs), we will have a high-powered biological system that can be used to optimize microbe mediated tolerance and nitrogen fixation to further advance our understanding of plant-microbe interactions and abiotic stress.

Campbell, Robert	The University of Tokyo	Mining and exploiting histidine kinase sensor domains for construction of a massive catalog of green fluorescent protein-based biosensors for detection of biofuel, bioproduct, metal ion, and metabolite targets	We propose to revolutionize the field of biosensor development by creating an unprecedented catalog of biosensor prototypes that will utilize and exploit the seemingly limitless diversity of prokaryotic sensor histidine kinase (HK) proteins. Building upon the established framework of the Citron1 and Citroff1 biosensors, we now propose to create a massive catalog of structurally analogous biosensors with a diverse range of target specificities. As many of these sensor domains are fully or partially uncharacterized, we will screen the catalog against a wide range of possible target molecules to discover new biosensor prototypes while also defining the target specificity for these sensor domains.

Finkelstein, Ilya	University of Texas-Austin	Beyond CRISPR: Functional metagenomic discovery of programmable anti-phage systems	In this proposal, we will test the hypothesis that prokaryotes encode novel (non-CRISPR) programmable defense systems that can be leveraged for biotechnological applications. We hope to functionally validate the highest-confidence guided defense systems from our bioinformatics survey. Successful completion of this project will lead to the discovery of new guided anti-phage systems. These systems will further the DOE mission of understanding and manipulating diverse prokaryotic organisms and will also lead to new biotechnology tools.

Glasgow, Anum	Columbia University	Computational design of allosteric transcription factors to control PET degradation	Prokaryotic organisms are estimated to comprise 14% of all biomass on Earth and almost 40 times the biomass of all animals. In addition to representing enormous carbon stores, bacteria and archaea serve an essential role in fixing atmospheric nitrogen, accounting for 96-99% of natural nitrogen fixation. Understanding the factors that influence the population dynamics of these microorganisms is vital to understanding the biosphere. In particular, bacteriophages (phages), viruses that prey upon prokaryotes, drive the evolution of microbial communities in many ways. Broadening our understanding of how prokaryotes resist phages is necessary to predict and exploit microbial dynamics.

Moeller, Marie Sofie	The Technical University of Denmark	High throughput screening of binding modules to improve the efficiency of enzymatic degradation of synthetic polymers and polysaccharides	Our project will focus on the engineering of enzymes for more efficient use of available sources of carbon. Enzymatic degradation of plastics will allow for recycling of an important resource, either for production of high quality virgin plastic, or more valuable bioproducts. Polysaccharides from enzymatic degradation of plant biomass can also serve as feedstocks for production of biofuels and other bioproducts. Because of the complex composition of biomass, or the mixed nature of plastic products to be recycled, a large diversity of enzyme solutions is also required. This project will both identify binding domains for these engineering projects, and produce large amount of data for future data scientists to predict enzyme function from sequence data, and further accelerate enzyme discovery.

Nikel, Pablo Iván	The Novo Nordisk Foundation Center for Biosustainability	Paving the way towards new-to-Nature fluorinated bioproducts	We want to test combinatorial pathway libraries to identify the ideal combination of enzyme variants and their expression to produce fluorochemicals. Expression optimization is, however, required to produce biotechnologically relevant titers of fluorochemicals. With the help of the JGI, we will characterize and exploit functional biofluorination and F-PHA pathway parts and modules that lead to biotechnologically-relevant titers and yields of new-to-nature fluorinated molecules for the pharma and material sectors.

North, Justin	The Ohio State University	Rewiring the bacterial ethylene cycle through genome and virome functional gene discovery	This project employs construction of bacterial gene expression vectors with synthesized SAM hydrolase or alcohol dehydrogenase genes mined from virome and metagenome databases that are poised to enhance bacterial ethylene synthesis. These constructs will then be employed to screen for genes and gene products that enhance ethylene synthesis in the industrially amenable microbe, Rhodospirillum rubrum, engineered for maximal ethylene yields from renewable CO2. Results from these screens later will be translated to the lignocellulose degrading bacterium, Clostridium cellulolyticum, for maximal ethylene synthesis from renewable lignocellulosic biomass.

Parkinson, Elizabeth	Purdue University	Evaluation of the Gamma-Butyrolactone Repressors of Streptomyces Natural Product Biosynthetic Gene Clusters	Natural products (NPs) are a bountiful source of medicines, agricultural products, and chemical tools. Bioinformatics data suggest hundreds-of-thousands of novel NPs remain to be discovered from Streptomyces. Unfortunately, many NPs are not produced under standard laboratory conditions. This project will focus on evaluation of transcription factor repressors of NP BGCs and the bacterial hormones that release these repressors, thus resulting in activation of production of NPs. Specifically, we are interested in studying TetR-like repressors (GBLRs) that are predicted to bind γ-butyrolactones (GBLs). The work proposed here will lay the foundation for the prediction of BGC activating molecules based on the sequence similarity of predicted receptors.

Salis, Howard	Pennsylvania State University	Massively Parallel Experiments to Develop a Predictive Biophysical Model of Transcription Rate across Cellular Conditions	Transcription is a fundamental gene expression process, responsible for all RNA production, and yet our field has not yet developed sequence-to-function biophysical models capable of predicting the transcription initiation rate of arbitrary bacterial promoter DNA sequences, particularly when cells are grown in different conditions. Here, we propose to apply systematic design, massively parallel experiments, next-generation sequencing, and machine learning to develop predictive thermodynamic models of bacterial transcription initiation – a “Promoter Calculator” – that will transform how we reverse-engineer natural genetic systems and forward-engineer new genetic systems across changing cellular and environmental conditions.

CSP New Investigator

Proposer	Affiliation	Proposal Title	Proposal Description

Brennan, Georgina	Institute of Marine Sciences (ICM-CSIC)	Exploring plastic and evolutionary changes in wild aquatic microbes exposed to simulated global change	Microbes grow in large populations and reproduce quickly. This may allow them to adapt to environmental stressors relatively quickly, yet, we do not have a clear understanding of how wild microbial communities will react to global change both in the short-term early acclimation response and the long-term evolution response. Our team seeks to obtain metatranscriptomic, metagenomic and long-read sequences to explore how ecologically important aquatic microbes respond to elevated temperatures and invasion events, using a multigenerational, mesocosm experiment.
Burgos, Asdrubal	University of Guadalajara	Assessment of genome complexity for the cactus crop Opuntia ficus-indica and its diploid relative Opuntia basilaris	This project focuses on low-pass short read sequencing to gather information on the genome complexity of the cactus crop Opuntia ficus-indica (L.) Mill., which has already been used successfully for biofuel production, and its relative Opuntia basilaris. The comparison of both genomes will provide an evolutionary view of the adaptation to hard environments and how the number of copies per gene would help to tolerate stressful environments.

Cvetkovska, Marina	University of Ottawa	Investigating the basis of heat sensitivity in the Antarctic green alga Chlamydomonas sp. UWO241: a multi-omics approach	The perennially ice-covered lakes of the McMurdo Dry Valleys in Antarctica have long been studied as extreme habitats for life, and recently as sentinels of climate change. Minor fluctuations in air temperature can greatly alter the balance of liquid water and ice, which translates to significant changes in salinity and light availability. How cold-tolerant extremophiles (psychrophiles) will respond to environmental change is difficult to predict. Decreased salinity and increased light due to a melting ice sheet has been shown to result in algal blooms in polar regions, but the effects on algal physiology are not known. A system-wide investigation could help understand how acclimation to different salinity and light levels affects heat resilience of the psychrophilic alga UWO241.
Hackmann, Timothy	University of California, Davis	Using stable isotope labeling to unravel a new pathway of glycolysis in bacteria	Glycolysis is called the universal metabolic pathway because nearly all cells use it to metabolize glucose. It is thus surprising that several bacteria from several phyla and several environments have been found missing enolase, a key enzyme of glycolysis. This suggests there is a new pathway of glycolysis that bypasses enolase, is widely distributed, but is not yet known.
Hess, Nancy	Pacific Northwest National Laboratory	1000 Soils Project – Database of molecular measurements to inform soil organic matter	The 1000 Soils Project uses collaborations with AmeriFlux, NEON, and individual researchers to collected paired intact cores for analysis at EMSL and JGI. This proposal focuses on advanced soil physical, chemical and biological characterization of soil cores to

		cycling at a continental scale	complement measurements provided by existing ecological networks.
Huberman, Lori	Cornell University	Investigating transcriptional and metabolic mechanisms used by filamentous fungi to distinguish between multiple nutrient sources during lignocellulose degradation	To exploit resources in plant biomass, fungi prioritize the use of nutrients that promote rapid growth. Preferred carbon sources require minimal energy to metabolize. Metabolism of nonpreferred carbohydrates requires production of necessary enzymes and transporters. Distinguishing between preferred and nonpreferred carbohydrates is known as carbon catabolite repression (CCR). While some regulators of CCR are characterized, others are unknown. In this proposal, we aim to identify genetic mechanisms of CCR using the filamentous fungus Neurospora crassa.
Li, Xu	North Carolina State University	Field Pennycress seed coat and embryo development transcriptome analysis	Field Pennycress is a rapidly domesticated biofuel crop that also serves as a cover crop in the Midwest. The efficiency of seed oil extraction is limited by seed mechanical resistance, which is highly related with cell wall lignin deposition. However, the developmental regulation of lignin biosynthesis during seed coat maturation is largely unknown. This project involves RNA sequencing to investigate the transcriptome changes in the seed coat and embryo tissues separately during Pennycress (Thlaspi arvense) seed maturation process.

Malkin, Sairah	University of Maryland	Examining the partitioning of microbial metabolic potential in suspended particles and the sediments across oxygen gradients of the Chesapeake Bay	This project aims to examine the complex role of oxygen depletion on the partitioning of microbial metabolic processes related to carbon cycling through an examination of metagenomes associated with suspended particles and sediments of the Chesapeake Bay. The Chesapeake Bay functions both as a repository for carbon fixed locally and in the greater watershed, and as a major incinerator, producing large quantities of CO2, and biogenic methane.
Oliverio, Angela	Syracuse University	Toward a spatially explicit, genome-resolved understanding of litter decomposition	The land carbon sink absorbs nearly a third of annual anthropogenic CO2 emissions. Terrestrial ecosystems are therefore critical for global carbon cycling, but complex processes control rates of carbon fluxes. One such process is litter decomposition, a crucial pathway by which carbon moves from vegetation to soil. This project aims to resolve the complex role of microbial communities in controlling rates of decomposition through an examination of the metagenomes, metatranscriptomes, and metabolomes associated with the breakdown of leaf litter across National Ecological Observatory Network (NEON) sites.

Peng, Xuefeng (Nick)	University of South Carolina	Transcriptional studies of anaerobic metabolisms of fungi isolated from salt marsh sediments	Salt marshes are characterized by high primary productivity and sediments rich in organic contents. The annual carbon burial rate in salt marshes globally parallels that of tropical, boreal, and temperate forests combined. Microbial degradation of salt marsh biomass in sediments plays an important role in controlling the recycling and burial of organic matter. This project focuses on transcriptional profiling of fungal strains isolated from salt marsh sediments located in the North Inlet-Winyah Bay National Research Reserve, South Carolina.
Pingault, Lise	University of Nebraska-Lincoln	Transcriptomic networks mediating sorghum tolerance to sugarcane aphids	Sorghum (Sorghum bicolor L.) is among the important cereal crops in the world, and a model for C4 grass bioenergy crops. Sorghum is a significant food source for humans, a chief ingredient in livestock feed, and is a source of a wide range of manufactured products. However, this crop is susceptible to insect pests that can dramatically decrease its yields. The goal of the project is to understand the transcriptomic adaptation of tolerant sorghum genotype (JGI flagship plant) in response to pest attack.

Ramirez, Kelly	University of Texas at El Paso	Characterizing rhizosphere metagenomes to support dryland restoration goals	In the Chihuahua Desert of the American Southwest, drylands degradation (sometimes referred to as “desertification”) results in the conversion of the historical perennial grasslands to woody shrubs which can lead to soil erosion, loss of biodiversity, and loss of soil nutrients and carbon. Documenting changes to the soil and rhizosphere microbiome are important not only from a conservation perspective but also to better understand microbial controls on plant productivity and carbon cycling potential across state changes and ultimately the dryland ecosystems.
Rinke, Christian	The University of Queensland; Australian Centre for Ecogenomics	The impact of marine microbial lineages on carbon and nutrient cycling in a subtropical river ecosystem	Freshwater ecosystems are carbon processing hotspots, fuelled mainly by dissolved organic carbon (DOC) that is introduced via carbon transfer from terrestrial systems. Within Australia, the Brisbane River estuary is one of the few subtropical river ecosystems for which carbon emissions have been assessed. We propose to explore the microbial contribution to carbon and nutrient cycling in the Brisbane River estuary, a subtropical system that produces high methane (CH4) and nitrous oxide (N2O) emissions.

Rodriguez-Rojas, Luis M	Universität Innsbruck	Prokaryotic Microdiversity in Hot Springs of the Yellowstone National Park and Genomic Determinants of Biogeographic Distributions	The study of microbial biogeography has been, until recently, limited in both breath and resolution. Genomic analysis of certain model microbial groups has resolved differences below the species level, with this resolution corresponding to a diversity of realized niches (ecotypes). However, a wealth of studies using amplicon-based profiling suggests that biogeographic patterns – and therefore potentially corresponding ecotype diversity – may be common but still sparsely resolved. This study focuses on the prokaryotic communities of several hot springs in Yellowstone National Park (YNP) at within-species resolution.
Seyler, Lauren	Stockton University	Characterizing variations in microbial carbon cycling capabilities in salt marsh sediment from the northern Atlantic Coastal Plain	Salt marshes are an intriguing habitat for ecological study because they provide continuous gradients of conditions. Vegetative zones tend to be dominated by a single species of halotolerant grass; conversely, salt marsh microbial communities are staggeringly complex. To understand microbial community composition, this project aims to generate high-quality metagenome assembled genomes (MAGs) from microbial communities in salt marsh sediment cores taken from three different vegetative regimes in the Mullica River estuary near Jerry Creek in New Jersey.

Silveira, Cynthia	University of Miami	Viral control of green and purple sulfur bacteria in euxinic lakes	Viral lysis also affects biogeochemical cycles through the cycling of organic carbon. Viruses may exert the same type of impact on anoxygenic phototrophs. The project aims propose to sequence metagenomes from five stratified freshwater lakes in the Pacific Northwest that harbor green and purple sulfur bacteria (GSB and PSB). These anoxygenic phototrophs that couple carbon fixation with sulfur oxidation. The team's synergistic approach aims to reveal the relationship between the geochemical signatures of anoxygenic phototrophs and their viruses in stratified freshwater lakes.
Trubl, Gary	Lawrence Livermore National Laboratory	Unraveling the biology of soil viruses and their response to environmental change	VViruses alter the soil ecosystem by killing microbial hosts and rewiring their metabolism, which impacts transformations of carbon and whether it is respired away as CO2 versus retained as cell biomass or soil organic compounds. This suggests that viruses may be important for understanding global carbon cycling. By killing certain soil microbes, viruses both stop the metabolic activity of these microbes and release all the cellular organic compounds and nutrients to the environment. For this proposal, soil viruses were sampled from incubations with and without water, and with and without phosphate to characterize changes in viral activity, capabilities, and the fate of the soil carbon under these different environmental conditions.

Yeh, Ellen	Stanford University	Metabolic integration of a nitrogen-fixing endosymbiont within a photosynthetic diatom	Microscopic cyanobacteria and algae dominate the 50% of global photosynthesis that occurs in marine and fresh waters. Diatoms account for 40% of marine photosynthesis and undergo seasonal blooms critical for carbon sequestration. How these aquatic microorganisms couple photosynthesis and nitrogen fixation is largely unknown. Epithemia and related diatoms contain “spheroid bodies” that are in fact nitrogen-fixing cyanobacterial endosymbionts. Estimated at a mere 12 million years ago (Mya), this is the most recent documented endosymbiosis and an unparalleled opportunity to watch endosymbiosis evolution “in action.”
Yoon, Suad	Okinawa Institute of Science and Technology	Linking belowground variation in root nodulation to the aboveground metabolome in the tropical legume Crotalaria.	Plants in the genus Crotalaria (Fabaceae) fix atmospheric nitrogen through a symbiosis with root-nodulating rhizobia. In this association, and independent of nitrogen availability, rhizobia are critical for pyrrolizidine alkaloid production — a class of metabolites which defend leaves against herbivory and are active against pathogenic nematodes. Crotalaria plants can be experimentally manipulated to cease production of pyrrolizidine alkaloids by preventing their colonization by rhizobia via growth in a gnotobiotic substrate. The generality of this mechanism requires further investigation. This project focuses on analyzing 50 polar metabolite plant samples from the genus Crotalaria.