Approved Proposals FY24

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

FY 2024 Annual CSP Proposals

Proposer	Affiliation	Proposal Title	Proposal Description

Ahern, Olivia	Marine Biological Laboratory	Linking genes to models: Unraveling microbial food web connectivity through multi-substrate RNA stable isotope probing, omics, and metabolic models	Earth’s biogeochemical cycles result from interactions of individual microscopic organisms, but the exact mechanisms driving organic matter cycling in most ecosystems are still poorly characterized. This project focuses on tracking bacteria, viruses, and predators in actual ecosystems by using heavy isotopes of carbon. We can identify the bacteria that consume these heavy carbon isotopes by detecting it in their RNA. In turn, we can detect this heavy RNA from the predators that ate these bacteria. We can therefore understand how carbon is transferred between trophic levels within a real microbial ecosystem. Our proposed collaboration with the JGI aims to sequence the RNA from those tracking experiments and develop ecosystem models derived from the genomes of the organisms involved. Overall, this comprehensive approach combining multiple scientific disciplines will allow researchers to explore various aspects of microbial ecology, biogeochemistry, and ecological modeling at the intersection of these fields.

Corrales, Adriana	Society for the Protection of Underground Networks	Ectomycorrhizal functioning in under-explored ecosystems: using fungal genomes and soil metatranscriptomes to discover new mycorrhizal connections with nutrient cycling and climate stress in tropical and Mediterranean biomes	Underground, plant roots form symbiotic associations with mycorrhizal fungi – an important class of soil fungi that provide critical nutrients to plants across the world’s terrestrial ecosystems. There are a growing number of datasets that demonstrate the importance of ectomycorrhizal fungi to carbon sequestration and nutrient cycling. However, these datasets have been largely focused on the Northern Hemisphere. There is an urgent need for data from more diverse mycorrhizal lineages and under-sampled locations in the global south to understand how mycorrhizal communities shape biogeochemical cycles across the Earth. Unlike plants and animals, much of the living part of mycorrhizal fungi is hidden around ground, making it hard to identify species. Working with a new class of machine learning models, we are developing maps that can help predict the hotspots of ectomycorrhizal fungal across the globe. A number of these biodiversity hotspots are understudied tropical and Mediterranean ecosystems. These ecosystems are of extreme interest because the availability and cycling of phosphorus and nitrogen differ to those catalogued in well-studied temperate forests.

Cross, Hugh	National Ecological Observatory Network	Continental-scale metagenomics: leveraging the NSF National Ecological Observatory Network to advance understanding of terrestrial and aquatic microbial communities in response to land use and climate change	Our project aims to produce freely available metagenomics data of unprecedented scope to enable novel analyses and insights into microbial communities. We will leverage and combine resources from three entities: the continental scale, long-term ecological data from the National Science Foundation’s National Ecological Observatory Network (NEON), the unmatched sequencing capabilities of the DOE Joint Genome Institute (JGI), and the microbiome database and cutting edge data analysis pipelines of the National Microbiome Data Collaborative (NMDC). We propose to send DNA extracts from NEON soil and water samples to the JGI for sequencing. Then, genomic data will be shared with NMDC who will apply advanced bioinformatics techniques to determine the composition and function of microbes in NEON samples. The raw and processed data will be made available as soon as possible to enable new research and scientific insights. Microbial communities in the soil and water provide the machinery that runs terrestrial and aquatic nutrient cycles and are key to maintaining the flow of energy and materials through the ecosystem. By acquiring high quality genomic data from these communities and linking them

		with the wealth of NEON measurements from the surrounding ecosystems, this project will provide unmatched opportunities for researchers to explore the fundamental drivers of ecological change from local to continental scales.

DeMarche, Megan	University of Georgia	A canary-in-the-coal-mine for arctic and alpine communities under climate change: using genomics to leverage long-term datasets in *Silene acaulis*	One of the greatest challenges we face today is to understand how biological systems are impacted and will respond to climate change. Altered climate conditions affect how individuals grow, survive, and reproduce, and these changes scale up to affect whether populations are stable or in decline, where species occur, and how groups of species interact to form larger ecosystems. Yet few studies have the appropriate data to link climate effects on individuals to larger-scale outcomes such as population stability or species distributions that are most relevant for conservation and management decisions. This project is designed to meet this need, by creating crucial genomic resources for an ecologically important plant in arctic and alpine tundra communities. Silene acaulis, or moss campion, is a common and widespread tundra plant that has been intensively studied for decades to understand how climate affects individuals and populations across the species' latitudinal range, from arctic Alaska to central New Mexico. By carefully monitoring the performance of the same set of permanently marked, long-lived plants year after year, we have found that moss campion is strongly affected by climate change. This project will sequence the genomes of many

plants from our long-term study so that we can investigate how genomic variation influences individual responses to climate change, and incorporate this information into population models to predict how the species as a whole will be affected across its geographic range. By using genomics to leverage one of the longest and most comprehensive datasets on individual performance, moss campion can serve as a "canary-in-the-coal-mine" for arctic and alpine communities.

Emerson, Joanne	University of California, Davis	Scaling wetland viral impacts on methane cycling from single cells to ecosystems	Viruses in terrestrial wetland ecosystems are predicted to have substantial impacts on carbon cycling and biogeochemistry, yet our understanding of wetland viruses is limited to a handful of field sites. Leveraging peatland and other wetland samples from the USA, UK, France, and Denmark, we propose to perform approximately the same suite of DNA and RNA sequencing-based analyses on a cross-continental dataset to make direct comparisons of virus-host dynamics, host metabolic capacity, and gene expression in similar ecosystems across the globe. Just as 20-40% of the C in ocean microbial cells is estimated to cycle through viruses daily, we expect to find quantitative evidence for substantial cycling of terrestrial C through viruses in microbial food webs, as well as viral impacts on microbial metabolic processes underlying global methane emissions.

Hudson, Matthew	University of Illinois at Urbana-Champaign	A reference level pangenome of soybean founder lines	Our goal is to assemble a complete collection of genetic variations, called a pangenome, for different types of soybeans, including cultivated soybeans, wild soybeans, and their relatives. This will enable us to identify and catalog various structural differences in soybean genes at different levels. Additionally, we aim to gather information about specific gene variations that are currently used or have the potential to be used in soybean breeding. Ultimately, this project should enhance our ability to improve soybeans used in agriculture and adapt soybean varieties more rapidly to changes in the environment.

Keller, Megan	University of New Mexico	Potential carbon-degrading genes of saprotrophic compared to ectomycorrhizal fungi in a boreal forest may inform assessments of carbon cycling	The warming Arctic is exposing carbon from once-frozen soils to the atmosphere which could accelerate warming trends. The roles of diverse fungi in either slowing or fueling carbon loss to the atmosphere are poorly understood. This study uses a novel “community genomics” approach to infer the relative carbon degrading capabilities of diverse, co-existing fungi in a boreal forest, where a great deal of carbon resides belowground. The number and diversity of carbon-cycling genes within each genome will be used to determine the potential influence that symbiotic fungi have on carbon degradation compared to co-occurring free-living, decomposer fungi.

Kelliher, Julia	Los Alamos National Laboratory	Elucidating the molecular mechanisms underlying the novel phenomenon of fungal internalization of plant- and algal-derived chloroplasts	Fungi are capable of harboring a diverse microbiome within their cells, yet knowledge on how the fungal microbiome impacts the fungal host and its interactions with other organisms in complex communities remains limited. Previous studies conducted by our team have revealed that phylogenetically diverse fungi can frequently harbor chloroplasts, and that fungi are capable of internalizing chloroplasts at a surprisingly fast rate. This proposed work expands upon our previous work to investigate the genetic mechanisms underlying the internalization of chloroplasts in select fungi. Through comparative transcriptomic experiments, this work will examine how both fungal and chloroplast gene expression are altered when they are co-cultured together, and the temporal dynamics of their interactions over the course of several hours.

Kouvelis, Vassili	University of Athens (Greece)	Deciphering the genetic and metabolic plasticity of endophytic entomopathogens and fungicolous fungi of the order Hypocreales	Hypocrealean fungi present various modes of life, including parasitism, mutualism, commensalism and saprophytism. The order Hypocreales comprises over a hundred genera, and the diversity of mechanisms underlying these adaptations is of significant importance. Although extensive research has been conducted on the genetic and molecular mechanisms of entomopathogenicity for entomopathogenic fungi (EPF), little is known regarding their potential to colonize plants, living as endophytes. This proposal aims to address these knowledge gaps by analyzing the genetic mechanisms involved, the gene expression and secondary metabolites produced by these species during their host colonization. This research we will provide insights for (a) the optimal exploitation of endophytic entomopathogenic fungi (eEPF) as biofertilizers and biostimulants for their plant hosts, in addition to their established use as biological control agents against insect pests, and (b) the interaction among the MF and their fungal hosts. To achieve these objectives, a holistic approach integrating

			comparative genomics, transcriptomics and metabolomics will be employed. This will enable us to decipher the genes and mechanisms involved in endophytic and mycophilic modes of life. Thus, fundamental questions in the evolution of nutritional plasticity in economically important fungi will be addressed, developing the resources needed to understand the complexity between inter- and intra-kingdom interactions.

Kuehn, Seppe	University of Chicago	Understanding denitrifying soil microbiome response to environmental change	Researchers are increasingly discovering the fascinating potential of the microbiome in solving problems in the environment and agriculture. For example, microbial communities play significant roles in regulating global carbon and nitrogen cycles related to climate change, enhancing crop health for sustainable agriculture. Recent advances in DNA sequencing allow researchers to relate the microbiome's genomic composition (structure) to the metabolic activities (function) of these communities. To effectively manipulate the microbial communities toward beneficial metabolic functions, we need to infer design principles and strategies from these observed structure-function relationships. However, much of the successes in mapping structure to function mostly come from simplified systems or synthetic communities, rather than the fully complex natural communities such as soils. In the context of natural communities, efforts have sought to connect taxonomic or genomic composition to key process rates in soils, but these predictions remain poor. Therefore, With metagenomics data, we will bridge this gap by understanding the underlying microbial genetic components and their interactions that dictate

			soil microbiota’s metabolic response (function) to environmental change. Ultimately, this will enable us to predict and control microbial metabolism in soils in changing environments.
Mengiste, Tesfaye	Purdue University	Sorghum anthracnose genomics and elucidation of virulence genes	This project will provide the foundational knowledge and blueprint for future progress. Understanding the genetic makeup and DNA sequences of important fungal species is critical for the protection of biofuel crops from devastating fungal diseases. These will provide ways to build genetic resistance and avoid chemical disease control, thus reduce pesticide use and help maintain public safety and environmental quality.

Schwartz, Egbert	Northern Arizona University	High temporal resolution of transcripts and metabolites to analyze rapid responses of soil microbial communities to C and N addition	Carbon dioxide concentration in the atmosphere is increasing rapidly because humans are burning extremely large quantities of fossil fuels. Carbon dioxide is a greenhouse gas and traps heat in the atmosphere resulting in climate change. To limit climate change, and associated damage to human infrastructures, we must figure out how to take carbon out of the atmosphere and store it underground, including into soil organic matter. Our research has shown that many of the processes that lead to soil organic matter formation, including microbial growth and predation, are occurring much faster, on the time scale of hours, than previously thought. Yet all of the collected data sets are on a time scale of days, weeks, or even months. Here we propose to sample soils amended with a carbon source, on an hourly time scale so that we can elucidate microbial processes that lead to soil organic matter formation.

Shulman, Hannah	University of Tennessee at Knoxville	Impact of climate change on the plant-microbe N cycling network across time and space in montane ecosystems	Climate change is causing significant changes in mountain ecosystems. Warmer and drier conditions are affecting where plants grow and how they function. Our ongoing research in these high elevation areas has shown that nitrogen, an essential nutrient for plants, is influenced by different types of microbes that cycle nitrogen in specific seasons. Nitrogen availability also changes with increasing elevation, and this affects the ability of plants to expand their range in the mountains. We want to understand how climate change affects nitrogen over time and in different locations by studying genes, ecosystems, and the relationships between microbes and plants. To do this, we need to collect detailed information about plants, microorganisms, and the cycling of nutrients in different environments and under different climate change conditions.

Stone, Bram	Pacific Northwest National Laboratory	The role of microbial predation and cooperation on soil carbon turnover and sequestration measured through multi-omics networks	The aim of our research is to quantify how interactions between soil microorganisms affect the way that carbon is stored, lost, or transformed in the soil. Soils represent the largest global reservoir of terrestrial carbon and soil microorganisms (bacteria, fungi, protists) are the key agents of carbon recycling because they control decomposition. Our work proposes to extensively sequence which genes soil microbes use when interacting with other microbes. These data will be combined with concurrent stable isotope tracing experiments which track the movement of important elements (carbon and oxygen) into microbial cells.
Voriskova, Jana	Czech Academy of Sciences	Response of soil microbial communities to changing climate in Arctic tundra	The Arctic represents one of the most vulnerable ecosystems to climate change. Microbes are known to play key roles in determining the stability of soil carbon and its possible release into the atmosphere as carbon dioxide and methane. In our project we aim to comprehensively explore the response of microbial communities to predicted climate warming in tundra soil. Our goal will be achieved by combining long-term soil, vegetation and CO2 emissions data from climate manipulation experiment located in Greenland with

			sequencing data enabling detailed characterization of soil microbes.

FY 2024 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Proposals

Proposer	**Affiliation**	**Proposal Title**	**Proposal Description**
de Vries, Ronald	Westerdijk Fungal Biodiversity Institute (Netherlands)	Expanding synthetic biology tools by deeper understanding of Aspergillus niger primary metabolism	A deep understanding of metabolism is crucial for efficient and effective metabolic engineering strategies to develop novel or improved fungal cell factories for a range of biotechnological applications. In this project, researchers will use EMSL and JGI capabilities to discover and characterize novel enzymes and to obtain a new level of understanding of primary carbon metabolism in fungi.
Ernakovich, Jessica	University of New Hampshire	A high-resolution view of the plant-microbe-mineral interactions affecting C-cycling in thawed permafrost soils	Researchers aim to determine how plants, microbial activity, and organo-mineral associations influence permafrost soil carbon balance. Findings will be integrated into a modeling framework to resolve the interactions among plants, microbes, and minerals, which are critical to advancing fundamental understanding of

			biogeochemical processes in a warming and thawing Arctic.
Hatzenpichler, Roland	Montana State University	(Eco)Physiology of methanogens of the phylum Thermoproteota	In this project, scientists will study the physiology of newly discovered methanogens both in culture and in their native habitat. The team will address how these cells vary their gene expression and metabolomes under changing physiochemical and thermodynamic conditions.
Jakes, Joseph	USDA Forest Service, Forest Products Laboratory	Nanoscale multimodal analysis of brown rot fungal decay mechanisms for improved biomimetic lignocellulosic biorefinery processes	Researchers will use resources at EMSL, JGI, and APS to produce accumulative transcriptomic, chemical, composition, structural, and mechanical data that will be used to identify different decay stages in wood with their associated decay mechanisms and cell wall modifications.
Master, Emma	University of Toronto	Functional and structural analysis of microbial expansin-related proteins that loosen in lignocellulosic and chitin fiber networks	This project brings together functional genomics, structural biology, and advanced techniques in material science to evaluate the untapped potential of microbial expansin-related proteins in the production of bio-based chemicals and materials.

Saleska, Scott	University of Arizona	Integrating microbial meta-omics, isotopes and methane metabolites to connect belowground microbial processes to aboveground methane emissions in seasonally-inundated Amazonian floodplain forests.	This project builds on the first continuous whole-ecosystem measurements of methane emissions, via eddy covariance methods, from a seasonal inundated floodplain forest in the Amazon. Researchers will use metagenome and metatranscriptome sequencing and metabolomics to mechanistically identify the distribution of methane production and consumption activity in soils and tree stems, and how these components shift between wet and dry season in seasonally inundated forests, and between a floodplain forest and an upland terra firme forest.
Smertenko, Andrei	Washington State University	Systems Analysis of Embolism Resiliency in Grasses for Biofuel Production Under Marginal Environments	Water flows from roots to shoots through vessels composed of hollow dead cells. Specialized regions in the cell wall, known as pits, conduct water between vessels. Drought causes embolism of vessels leading to blockage of water movement. Pits contribute to the embolism spread between the vessels. This project aims at developing technology for containing embolism by optimizing pit morphology.

Smith, Heidi	Montana State University	Opening the black box of glacial carbon cycling – providing fundamental insight into impacts of a changing climate	In this project, scientists will study the physiology of newly discovered methanogens both in culture and in their native habitat. The team will address how these cells vary their gene expression and metabolomes under changing physiochemical and thermodynamic conditions. Roughly 104 petagrams of organic carbon are stored within ice worldwide. Glacial carbon originates from new atmospherically deposited material (including black carbon from wildfires) and in situ production by microorganisms. The metabolic strategies of carbon transformation within glacial systems are not well understood, yet critically affect adjacent and downstream aquatic ecosystems. This research will link microbial processing of discrete sources of organic carbon and its concomitant compositional shifts.

Stone, Bram	Pacific Northwest National Laboratory	The role of microbial predation and cooperation on soil carbon pathways measured through multi-omics	Researchers will conduct labeled isotope tracer incubations to follow the movement of plant and microbial carbon under different moisture and predator manipulations. Data from this experiment will be used to combine soil carbon processing more rigorously with organismal interactions. These data will thus address the critical knowledge gap of how and when microbial interactions accelerate soil carbon cycling.
Ziegler, Samantha	National Renewable Energy Laboratory	Structural and biochemical characterization of glycosyltransferase 47 family proteins from Spirodella to enable predictive biology	In this project, researchers are comprehensively studying cell wall synthesis enzymes found in the duckweed Spirodela polyrhiza to create a database that can be used to predict the functionality of similar proteins in other organisms. The data generated from this proposal will be used to create designer plants, with specified cell wall structures for bioproduction.
Zimmerman, Amy	Pacific Northwest National Laboratory	Linking multi-organism-environment interactions across lab and field scales to estimate viral contributions to soil C cycling	Researchers will conduct complementary field and laboratory-based experiments to generate the data necessary for baseline estimates of when and how much viruses contribute to soil carbon cycling. The team will generate some of the first quantitative data about rates of viral production in soil, shifts in soil carbon pools as a result of viral predation, and the degree

			to which natural soil viral communities vary over time.

CSP Functional Genomics

Proposer	Affiliation	Proposal Title	Proposal Description
Alper, Hal	University of Texas at Austin	Elucidation of novel plastizymes via a protein library based on a multi-omic statistical learning approach	Although previous reports have characterized plastics as persisting in the environment for decades or even centuries, scientists have more recently discovered microbes and enzymes capable of breaking down plastic at faster rates than previously expected. Although these breakthroughs are monumental, they still have not been fast enough to use them as products for recycling plastic or cleaning up contained waste sites. The use of environmental nucleic acid (e.g. DNA) sequence data, known as meta-omics, has recently opened a window into the activity of microbes that live on plastic. This has led to previously unobserved insights into which enzymes could be major players in plastic degradation, and potentially degrade plastic faster than our current biological agents. This research project looks to perform a functional screening of these previously untested enzymes with commonly used plastics, to test whether these proteins can truly degrade plastics at rates faster than previously described. This biotechnology would present an advancement towards our utilization of biological agents for industrial recycling, as well as furthering our understanding on

			how microbes in the environment are responding to plastic.
Bridwell-Rabb, Jennifer	University of Michigan	Illuminating the structure-function relationships in Chlorophyll metabolic enzymes	This proposal is focused on elucidating how light-absorbing photosynthetic pigments are built, modified, recycled, and degraded. This research is important because it will provide fundamental information about photosynthesis, one of the most important biological processes on Earth. Moreover, this proposal will elaborate upon how organisms adapt their lifestyles, metabolism, and chemistry to environments that vary broadly with respect to light and oxygen availability. This information is important for agricultural production, engineering of photosynthetic organisms for the production of biofuels or commodity chemicals, and the lifetimes of fresh and processed fruits and vegetables.
Culbertson, Alan	Iowa State University	Determination of physiological substrate of Sorghum ABC Transporters for improved bioenergy crops	Plants rely heavily on the transport of molecules into or out of their cells for normal growth and development. One of the major contributors to transporting small molecules across cell membranes is a family of proteins called ABC transporters. ABC transporters are present in all forms of life including bacteria, algae, plants, and humans. They are particularly enriched in plants with between 100-300 ABC transporter genes, depending on the species. The goal of this research proposal is to understand plant ABC transporters in the biofuel crop sorghum by determining what molecules they transport into or out of the cell and how they do it.

Hallam, Steven	University of British Columbia	Developing a high-throughput functional screening surface display platform for strategic metal recovery from environmental transcriptomes	Microorganisms represent one promising and versatile solution supporting sustainable metal recovery that can be readily tuned to site conditions. Specifically, this project will generate a much-needed high-throughput screening platform for selective metal binding on the surface of C. crescentus that is compatible with both FACS and microtiter plate based functional assays. We will demonstrate utility of this platform by screening copper-enriched, microbial community cDNA libraries for recovery and characterization of genes mediating selective copper binding. Once established, the platform will be applied to REE binding screens and can be readily extended to other strategic metals to drive microbial biotechnology innovation in support of the clean energy transition.
Miller, Scott	University of Montana	Identification of the Chlorophyll d synthase: Implications for far-red light photosynthesis by crops	Enhancing a plant’s ability to use far-red light (FRL) could increase the solar radiation available for productivity by 20%. By contrast, the cyanobacterium Acaryochloris marina, which makes a living the same way a plant does, has evolved a novel pigment, Chlorophyll d (Chl d), that enables it to grow solely with FRL. Our objective is to identify the enzyme(s) responsible for making Chl d from Chl a in A. marina. We have identified several plausible candidates for the “Chl d synthase” by comparing the genomes of more than fifty A. marina laboratory strains and those of their close relatives. The identification of the Chl d synthase is the first step toward improving crop light energy capture and conversion

			through FRL harvesting for both bioenergy and food.
Rajakovich, Lauren	University of Washington	Family-wide functional annotation of transcriptional regulator proteins for the discovery of microbial catabolic pathways	The goal of our research is to expand the experimental characterization of microbial metabolism occurring in different ecosystems with varied nutrient resources. This proposal combines bioinformatic approaches to categorize microbial genes involved in nutrient degradation with a high-throughput experimental functional screen. The resulting functional dataset will provide insight into the types of nutrients that microbes can degrade and improve our ability to predict metabolism of diverse microbes based on genetic information alone.
Scott, Kathleen	University of South Florida	Distribution of bicarbonate uptake ability among the ubiquitous and diverse SulP family transporters	SulP transporters are a huge and ancient protein family found in almost every organism, and they are responsible for moving molecules into and out of cells. Currently, the SulP family of transporters is in the top 1% of all protein families with respect to its abundance in organisms. Surprisingly, we have no idea what the vast majority of these transporters move into and out of cells; only a handful have been studied this way. Understanding which ones transport bicarbonate will help us understand how SulP transporters support the biochemistries of the many organisms in which they are found, which in turn will help us understand how these organisms function in nature and influence global element cycles. In addition, this work has the potential to be applied to the engineering of organisms that take up carbon dioxide and bicarbonate as the first

			step in synthesizing chemicals important to industry.
Voiniciuc, Catalin	University of Florida	Rapid Prototyping of Plant Hemicellulose Biosynthesis in Yeast	As the growing world population strives for sustainable solutions and diminishing use of fossil fuel, the importance of plant polysaccharides such as hemicelluloses has never been more critical. These complex carbohydrates, specifically β-mannans, hold immense potential for revolutionizing energy, materials, and food security. However, unlocking their full value requires overcoming the notable knowledge gaps surrounding their biosynthesis, which has been infamously difficult to genetically modify in plants. This project aims to leverage SynBio-driven strategies to screen and evaluate a diverse set of enzymes involved in β-mannan elongation and modification.
Zerbe, Philipp	University of California Davis	Functional characterization of terpenoid-biosynthetic networks in switchgrass, millet, maize and poplar toward bioenergy and bioproduct engineering.	Terpenoids comprise a diverse group of such chemicals and also have broad human uses as high-energy biofuels, food additives, fragrances and therapeutics. The proposed project aims to generate a systematic knowledge of the genes, enzymes and metabolic pathways involved in the biosynthesis of common and species-specific terpenoids that mediate environmental interactions in the major model plants switchgrass, maize, millet, and poplar. We will combine a customizable discovery pipeline with transcriptomics, metabolomics, and protein functional studies to gain a comprehensive understanding of the metabolic networks that plants employ to interact with and adapt to their environment.

FY 2024 CSP New Investigator Proposals

Proposer Name	Affiliation	Proposal Title	Proposal Description
Bulseco, Ashley	University of New Hampshire	Exploring the microbial response to salt marsh restoration and its connection to carbon and nitrogen cycling	Salt marshes are coastal wetlands that provide several important ecosystem services, including storm surge protection, nutrient removal, and carbon sequestration. Many of these ecosystem services are mediated by microbes. Despite their tremendous value, salt marshes (as well as their resident microbial communities) are lost at high rates as a result of land alteration, coastline development, nutrient enrichment, and climate change. A concerted effort has focused towards restoring these valuable ecosystems through techniques such as the removal of tidal restriction, however, we still have a limited understanding of how the microbial community responds to these restoration efforts. Data produced by this project will greatly expand our understanding of salt marsh microbes, their contribution to successful salt marsh restoration, and how they mediate important ecosystem services more broadly.

Conway, Jonathan	Princeton University	Metagenomic Sequencing of the Rhizosphere During Drought to Enable Engineering of Microbiome-Mediated Resilience	To adapt and fortify our agricultural systems against the challenges posed by extreme weather, a consequence of climate change, it is essential to delve into the dynamics of plant-microbe interactions during stresses such as drought. Intriguingly, certain microbes seem to become enriched on many plants during drought, and plants that harbor these microbes often fare better than those without them. However, the precise genetic mechanisms driving this microbial enrichment during droughts, and how it subsequently aids plants, remain largely undiscovered. In this research, we will analyze microbial communities in field-grown maize and soybean subjected to drought conditions. Through metagenomic sequencing of samples before, during, and after drought, we will analyze specific genes and microbial strains that are attracted to and thrive on plant roots during water scarcity. This comprehensive dataset will pave the way for subsequent genetic engineering studies aimed at unraveling how the microbiome aids plants in surviving drought stress.

Cusick, Kathleen	University of Maryland – Baltimore County	Draft genome and RNA-sequencing to examine the link between secondary metabolite synthesis and copper detoxification in the algal (dinoflagellate) species Pyrodinium bahamense	Dinoflagellates are an ancient and ecologically important group of microalgae with significant roles in biogeochemical cycling, harmful algal blooms, bioluminescence, and secondary metabolite production. They are key players in many environmental processes but sequencing of this group lags far behind that of other organisms due to their genome size, complexity, and uniqueness. Pyrodinium bahamense is a bioluminescent species that forms dense blooms along the coasts of Florida, Puerto Rico, and the Indo-Pacific and produces the secondary metabolite saxitoxin (STX). Many theories exist as to the function of STX in the algae that produce it, including as a predator deterrent; a pheromone; and for nitrogen storage. The draft genome of P. bahamense will expand genomic insights on dinoflagellates in general.

Erickson, Katie	UC Davis	Functional Impacts of a Chromosomal Inversion on Eelgrass (Zostera marina) Performance under Marine Heatwave Conditions	Seagrasses are important to “blue carbon,” or carbon stored in marine environments. Seagrasses serve as carbon sinks by sequestering carbon from the sediment into marine sediments. This process contributes significantly to mitigating global warming by reducing the amount of greenhouse gasses in the atmosphere. The species Zostera marina, known as eelgrass, is the most widely distributed seagrass in the northern hemisphere. Our work aims to understand how certain structural variants in eelgrass genomes impact their performance and survival across temperature treatments. We hope that our work will identify eelgrass genotypes that perform well under different temperature treatments.

Glodowska, Martyna	Radboud University	Rising Tides, Shifting Gases: Impacts of Salinization on Peatland Ecosystems	In this project, we address the pressing question of how the sea levels and increasing salinity, spurred by climate change, impact freshwater peatland ecosystems. Our study seeks to unravel the intricate connections between environmental shifts, microbial communities, biogeochemistry, and greenhouse gas emissions, with a specific focus on methane. The intrusion of saline seawater into freshwater environments poses a significant concern. However, the mechanisms driving these ecological changes remain elusive. Microorganisms play a central role in the methane cycling. Therefore, our research is dedicated to comprehending how these microbial communities respond to saltwater intrusion and how it affects the biogeochemistry of the ecosystem.

Korenblum, Elisa	The Volcani Center	Exploring the climate change effects on the rhizosphere microbiome functions of Brachypodium wild populations in Israel	Climate change has far-reaching consequences for plants, and one of the potential impacts is the alteration of microorganisms that inhabit the areas around their roots. These tiny organisms play vital roles in how plants take up nutrients and maintain their health. Here we are studying the effects of climate change on the community of microorganisms that reside near the roots of Brachypodium. These microorganisms have co-evolved with the Brachypodium roots under cycles of drought and rewetting for millions of years. The exploration of Brachypodium and its root microorganisms in the context of climate change holds significant potential. It might unveil the intricate ways in which plants and microorganisms cooperate, ultimately offering solutions to enhance crop productivity and strengthen plants against the strains of a changing environment.

Longley, Reid	Los Alamos National Laboratory	Genomics and transcriptomics of Mucoromycota and their endobacteria from arid grasslands	Bacteria and fungi are often the most abundant organisms in soil ecosystems worldwide. Interactions between these two groups of organisms have been understudied and the impact of these interactions on their environments and on ecosystem functioning are largely unknown. Interactions between bacteria and fungi are more common than previously thought. However, these interactions are often difficult to study in a laboratory setting as they can be fleeting and inconsistent. This work will form the basis of future studies which will assess the functions of bacterial-fungal interactions (BFI) in interactions with plants in arid ecosystems.
Maillard, Francois	Lund University	Deciphering the oxidative mechanisms of chitin degradation in ectomycorrhizal fungi: A legacy from brown rot ancestors?	This project aims to investigate how plant mutualistic fungi, known as ectomycorrhizal fungi, and closely related fungal decomposers break down a molecule called chitin, an important source of carbon and nitrogen in soil. Chitin is a component found in fungal cell walls and in the exoskeletons of arthropods. Understanding the mechanisms soil fungi use to degrade chitin could offer valuable insights into global carbon and nutrient cycling. Ultimately, the research could characterize a new step in the fungal degradation pathway of chitin and provide significant

			insights into fungal mechanisms that regulate forest nutrient and carbon cycling.
Martinez, Clara	University of Bayreuth	Community composition and elemental fluxes in cultured microalgae-bacteria assemblages	Marine unicellular algae (phytoplankton) are responsible for a critical fraction of the CO2 that is captured from the atmosphere and later stored in the depths of the ocean. These microscopic organisms are surrounded by and interact with bacteria, comparable to soil bacteria surrounding plant roots, albeit in a dilute and unstructured environment: the ocean. The influence of bacteria in algal physiology and their impact on carbon cycling has been acknowledged. However, neither the composition (which types of bacteria and in which proportions) nor the potential (which functions can theses bacteria perform) of such algal microbiomes is well understood. We will compare the microbiomes of closely-related phytoplankton cultures isolated from a broad set of locations, spanning from open ocean to coastal and estuarine environments. These comparisons (enabled by the standard conditions at which the cultures have been kept for decades) will allow us to address key questions in microbial ecology (such as the host specificity of microbiomes), and to infer which factors

			dominate in the shaping of algae-associated bacterial communities.
Martinez, Joaquin	Bigelow Laboratory for Ocean Science	Identifying the microbial and viral players that influence coastal phytoplankton bloom dynamics in the Gulf of Mexico	Phytoplankton (microscopic algae) are the major primary producers in aquatic ecosystems. Every year, vast phytoplankton species proliferation occurs in coastal waters and lakes worldwide. Phytoplankton are important ecological players by converting atmospheric CO2 to organic carbon, forming the base of aquatic food webs. In this project, we investigate the bacteria and viruses that interact with the red tide species Karenia brevis along the Florida Gulf Coast, investigate their genetic makeup, and advance mechanistic understanding of their interactions and biogeochemical consequences using omics tools. The data generated through this study will enable us to identify which bacteria and viruses with a direct impact on K. brevis fate are present, which are active, and what kind of metabolic products they produce at different times of the day and bloom stages. Ultimately, these data can be used to inform the role bloom-associated microbes play in carbon cycling.

McDonald, Mark	Argonne National Lab	Breaking the fast: investigating the relationship between microbial function and carbon degradation following permafrost thaw	The advancement of global warming and climate change has revealed negative consequences for the continually frozen permafrost soils of the northern arctic region. When these soils thaw under a warmer climate, the microorganisms present will begin consuming the previously frozen plant matter and carbon molecules present in the soil. This process will, in turn, release a large amount of carbon dioxide and methane gases into the atmosphere, perpetuating the cycle of climate change and global warming due to the effect these gases have on our atmosphere. There are several factors that contribute to how much carbon dioxide and methane are released following thaw of the permafrost, including the amount of carbon and nutrients, the types of minerals, and the type and potential activities of the microorganisms present in the soil. Our study aims to better understand how the microbes’ activities change when permafrost thaws under a warmer climate across a large region of permafrost-affected soils in Alaska.

Ruytinx, Joske	Vrije Universiteit Brussel	Radionuclide tolerance in the Suillus-Pinus ectomycorrhizal system	Suillus luteus is a fungal pioneer species that associates with pine trees. This species is particularly abundant in disturbed environments, including recently radionuclide contaminated areas. In this project we will investigate changes in genome sequence and regulation of S. luteus ectomycorrhizal symbionts that were exposed to the extreme environmental stress resulting from the Fukushima Dai-Ichi nuclear accident and assess their impact on pine health. We anticipate that this project will uncover fungal mechanisms important for radionuclide tolerance in plant hosts, and adaptation towards chronic irradiation. These findings will contribute to the development of remediation strategies, a better understanding of radionuclide cycling in forest ecosystems and improved models for risk assessment in chronic exposure conditions.

Simonsen, Anna	Florida International University	Effects of soil warming on plant rhizosphere microbiomes in tropical forests	Tropical forests have a huge influence on how major elements, such as carbon, nitrogen and phosphorus are cycled on earth, but are also highly sensitive to climate change. Given that soils in tropical forests are projected to experience an average of 4-5ºC warming increase to 1 m depth by the end of this century, the objective of this proposal will be to determine how warming affects the way soil microbes cycle nitrogen, carbon and phosphorus in a tropical rainforest. What this proposal will focus on is whether tropical trees, through microbial relationships on their roots, can mitigate any potential negative effects of soil warming by buffering against changes in the environment that might cause soil microbes to cycle nutrients differently.

Skoog, Emilie	University of California San Diego	Development of metagenomic and metatranscriptomic data for the discovery of novel biogeochemical processes in Orca Basin	Located in the Gulf of Mexico, Orca Basin is one of the largest deep-sea hypersaline anoxic basins (DHABs) in the United States. This work aims to identify novel microbial taxa, viral lineages, and metabolic diversity and activity within this DHAB and will determine the role of microbial host-virus relationships in biogeochemical cycling within Orca Basin and similar terrestrial environments. These results will allow us to quantify terrestrial biomass storage potential in this environment, determine the utility of terrestrial biomass storage as a viable carbon dioxide removal strategy, and understand anaerobic lignocellulose breakdown pathways, which may provide valuable insights into future biofuel production.

Sogin, Emilia	University of California, Merced	Seasonal effects on microbial carbon cycling within the seagrass rhizosphere and sediments	Coastal vegetative ecosystems, such as seagrass meadows, mangroves, and saltwater marshes, play an imperative role for global carbon cycling. Within the sediments, carbon is both stored as well as cycled between the plants and their microbiome. The intimate partnerships the plants have with the microorganisms that live within their soils have evolved both with each other as well as with their environment. Our proposal seeks to connect the interactions between host, microbiome, and environment, by focusing on the shifts in carbon metabolism by microorganisms living within the seagrass soils across the seasons. Specifically, our organism of study is the seagrass species Zostera marina, which is widespread across the northern hemisphere and is being developed as a model organism for these ecosystems.

Tabima, Javier	Clark University	Diversity and Evolution of Secondary Metabolism in a commensal cosmopotilan genus: Basidiobolus	Secondary metabolites are biologically synthesized compounds that allow organisms to have an evolutionary advantage in their environments. This project focused on understanding the diversity and origin of secondary metabolism in a understudied group of early divergent microfungi from the genus Basidiobolus. We aim not only to expand by increasing species diversity, but by adding samples from different hosts, geographic areas and evolutionary groups to identify novel and shared genes involved in secondary metabolism. This with the overarching goal of identifying novel biosynthetic compounds and their roles in the ecology, evolution and survival of the organism.

Turchetto Zolet, Andreia Carina	Federal University of Rio Grande do Sul	Microbiome of the Neotropical tree species Eugenia uniflora L (Myrtaceae): implications for evolution and conservation under a changing world	In this research project, we are interested in understanding the different types of tiny living organisms (microorganisms) in distinct ecosystems within the Atlantic forest (AF). We also want to investigate soil health and gas emissions in these areas. To do this, we will be using a functional genomics approach. We are also interested in learning how these microorganisms interact with native tree species in the region and how they have evolved and adapted to one another over time. By better understanding these relationships, we hope to gain insight into how we can protect and preserve the delicate balance of the AF ecosystem.
Vannette, Rachel	University of California, Davis	Genomic insights into the ecology and metabolism of a bee-associated lipophilic yeast	Species of yeasts that associate with bees grow in resource rich environments and metabolize complex triglycerides, similar to the precursors frequently used in biofuel production. This project is aimed at sequencing the genomes of four yeasts isolated from larval bees and their stored food to identify yeast adaptations to this environment and shed light on the enzymes involved in the metabolism of complex lipids. This project has the potential to shed light on the evolutionary relationships of these poorly understood Basidiomycete yeasts and

			facilitate more efficient biofuel production.
Winegar, Peter	University of California Berkeley	Whole Genome Sequencing, Assembly, and Annotation of Veratrum californicum and Veratrum nigrum	Many plants produce steroids and derivatives of steroids that have immense potential for use as therapeutics as well as non-hazardous pesticides, biofuels, and biomaterial building blocks. However, the use of these molecules is limited by the ability to obtain them from the plants that produce them in useful quantities. The proposed research will obtain annotated whole genome sequences for Veratrum californicum and Veratrum nigrum, facilitating the discovery of the biosynthetic pathways of steroid derivatives and enabling their scalable bioproduction in model plants and microorganisms.

Yanuka-Golub, Keren	The Institute of Applied Research, The Galilee Society.	Investigating microbial dynamics as a key factor for assessing the carbon and greenhouse gas budget of restored wetlands	Wetlands are considered among the most productive ecosystems on Earth. Due to oxygen-poor conditions, wetlands efficiently absorb carbon in the soil over long time periods. Moreover, they play a key role in water quality, flood control, water table replenishment and support wildlife biodiversity and natural habitats. Thus, these terrestrial ecosystems play an important part in the environment. However, they are also among the most vulnerable and sensitive habitats, often disturbed by human activity worldwide. The objective of the current study is to evaluate the potential of restored wetlands in Israel, as a case study, to serve as a sink for carbon, without becoming a net source of greenhouse gases.

Zhao, Jun	University of Florida	Coupling taxon-specific soil carbon sequestration to the recovery of nitrogen transformation after environmental disturbance	This research project aims to improve understanding of temporal succession of microbial species after disturbances in soil. One specific focus of the project is to identify groups of microorganisms that are crucial in recovering and sustaining the biogeochemical process of nitrification, a central link of the nitrogen cycle. As these nitrification-related microorganisms are known for conversion of ammonia to nitrate while fixing atmospheric carbon dioxide, we will estimate the contributions of different nitrifier groups to these biogeochemical processes, through powerful tools of stable isotope tracing techniques combining metagenomics and metatranscriptomics analysis.