Dimensions of Biodiversity

NATIONAL SCIENCE FOUNDATION

Projects

2010-2017

CO-FUNDED BY

IMAGE CREDIT

THIS PAGE

- A Manpreet Dhami
- B Jim Bever
- C Carlos Garcia-Robledo
- D Daniel R. Matute
- E Abigail Bryson

FRONT COVER

- F Daniel R. Matute
- G A. Jonathan Shaw, D. J. Weston, & Collaborators
- H Claire S. Chialvo
- I Santiago Ramirez
- J Jim Bever
- K Britta Hamberger
- L Manpreet Dhami
- M Joel L. Sachs

FIELD SITES

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Canada
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ACKNOWLEDGMENTS

Many NSF staff members, too numerous to mention individually, assisted in the development and implementation of the Dimensions of Biodiversity competitions that resulted in the projects described herein. We thank and congratulate the Dimensions of Biodiversity investigators for their creativity and achievements in the research and coordination activities that these projects represent. We thank Mina Ta, Design Specialist, for her important contributions to the abstract booklet. Finally, we are grateful to AAAS Science and Technology Policy Fellows Drs. Sara Chun, Sean M. Watts, Karen Alroy, Rachel S. Meyer, and Catherine L. Malone who were most helpful in the strategic planning for the Dimensions of Biodiversity program and the production of this abstract booklet.

About the Program

The Dimensions of Biodiversity program is now in its 8th year of research support to characterize the least-well-known aspects of the diversity of life on Earth. The National Science Foundation (NSF) funded 8 new projects in fiscal year 2017 bringing the total number of funded projects to 96.

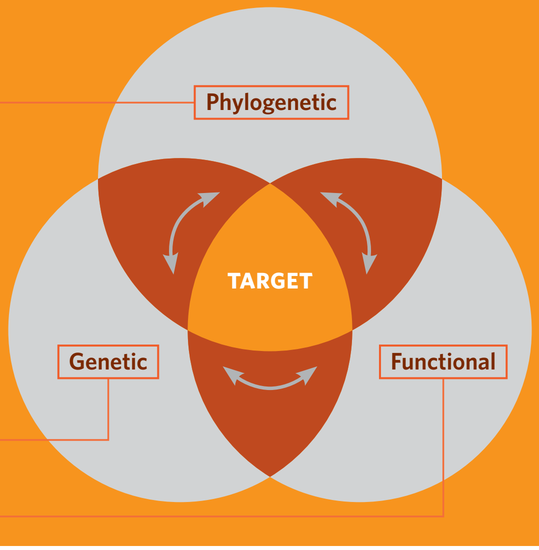
> *These awards showcase the creativity of scientists and the power of biology to understand the rules by which communities of organisms form, interact, and change through time. These projects examine global scale gradients in biodiversity and the eco-evolutionary feedbacks between coexisting species and their environments in novel and transformative ways.*
>
> **James Olds**
> Assistant Director
> NSF's Biological Sciences Directorate

The majority of the planet's biological diversity has yet to be explored. With estimates of existing global species hovering around 12 million — although some estimates suggest there are as many as 1 billion microbial species (Locey & Lennon 2016, PNAS) — at most only about 15% have been described to date, there is a bounty of exciting discovery to be made that can have major impacts on human wellbeing, technology, food security, and the health of planet Earth.

Beyond taxonomic investigation of the planet's species, **genetic** diversity within even a single species can be vast. The tremendous variation among domestic dog breeds illustrates this: genetic diversity of populations can express major differences in appearance, behavior, lifespan, and metabolic physiological adaptations to radically different selection pressures. The Dimensions of Biodiversity program is a platform for exploration of species and population-level diversity, recognizing that genetic diversity is best understood in a **phylogenetic** context to reveal how biodiversity is shaped over time. For instance, researchers using a phylogeny can ask: *Why* have some species endured time while others did not? *What* interactions, conditions, or events provided opportunities for diversification? And of peak interest is *how* do genetic distances that separate species in phylogeny relate to the different roles, appearances, life histories, and behaviors we observe? Despite centuries of study, we still have much to learn about the origin, maintenance, and function of diversity.

The **functional** roles of all these aspects of diversity are hardly understood. Dimensions researchers are making the

STREAMS OF ACTIVITY	2020 GOALS
Research	An integrated understanding of the key but unknown dimensions of biodiversity on earth
Cyberinfrastructure	Informatics and infrastructure that support accessible, interoperable information capability for dimensions of biodiversity
Collections	Digitization of collections and enhanced physical infrastructure to link to cyberinfrastructure and leverage the enormous investments of the past
Workforce	A diverse, interdisciplinary, globally-engaged, scientific workforce capable of transforming and communicating our understanding of biodiversity on Earth
Synthesis	Scientific analyses and syntheses that generate and disseminate useful information for scientists, educators, decision makers and the public
APPROACH	Planning & partnering → Baselining & synchronizing → Assessing progress → Aligning investments with emerging priorities



> *This research will help us understand, for example, the incredible diversity of marine life and how it functions. In a time of changing seas, that knowledge is of great importance in comprehending, and conserving, the species in Earth's vast oceans.*

Roger Wakimoto
Assistant Director
NSF's Geosciences Directorate

connections from genetic diversity to gene function, and from the expression of traits to their effects on our environment. Researchers are pioneering investigations on what impact the feedback from those environmental functions have on species and communities, while others are assessing the impacts of diversity on ecosystems over time. The projects supported through the Dimensions of Biodiversity program have applied *creative integration* of phylogenetic, genetic, and functional studies to ask grand questions about life on Earth that single-discipline studies cannot approach.

Addressing the substantial knowledge gaps in our understanding of biodiversity requires new thinking and a *coordinated* effort among several sub-disciplines of biology. The Dimensions of Biodiversity program is actively developing the workforce and partnerships necessary for the unique human- and cyber-infrastructure challenges of an interdisciplinary network of researchers. Dimensions previously partnered with NASA to fund projects that use remote sensing technologies to expand biodiversity investigations across broad spatial and temporal scales. Current international partnerships with the National Natural Science Foundation of China (NSFC) and The São Paulo Research Foundation (FAPESP) support the exchange of students and scientists, joint research projects, and university partnerships. Through these developments and intellectual partnerships, this program is redefining the way we understand the evolutionary and ecological significance of biodiversity in today's changing environment, and in the deep geologic past.

	PARTNERS	PROJECTS	OTHER NSF	GEO/OCE SHIP COSTS	GEO/OCE SCIENCE	BIO	NASA (N)	US TOTAL	CHINA (C)	BRAZIL (B)
2010		16		$2.9M	$9.3M	$18.9M		$31.1M	¥750k	
2011		12	$6.5M	$1.5M	$2.5M	$17.5M		$28.0M	¥610k	
2012	C, B, N	14	$3.2M	$168K	$2M	$22.8M	$720k	$29M	¥6M	R$2.8M
2013	C, B, N	13			$1M	$21.7M	$2.5M	$25.2M	¥3M	R$2.7M
2014	C, B	12			$1M	$22.5M		$23.5M	¥3M	R$3.1M
2015	C, B	10		$3.6M	$2.5M	$17.7M		$23.8M	¥3M	
2016	C, B	11				$20.3M		$20.3M		R$7.2M
2017	C	8				$17.93M		$17.93M	¥3M	

Broader Impacts

Dimensions of Biodiversity Projects have innovative outreach activities. Some examples and concepts connected to these activities are given here in the broad categories of citizen science, databases and cyberinfrastructure, undergraduate and graduate education, and K-12 education.

CITIZEN SCIENCE

Dimensions projects connect the public with...

- R Programming
- Field Guides
- Symbiotic Organisms
- Taxonomic Thesaurus
- Remote Sensing
- Decision Makers
- Terrestrial Mammals
- Fungal Ecologists
- Biodiversity Gradients
- Herbaria
- Plant-Microbe Interactions
- Intertidal Zone
- Cryptobiotic Crusts
- Climate Gradients
- Vascular Plants
- Soil Experimental Treatments
- Carbon Monitoring
- Environmental Engineering
- New Image Analysis Techniques

DATABASE & CYBERINFRASTRUCTURE

Through Dimensions, projects are connected with...

- Arthropod Diversity
- Extreme Weather Events
- Worm Biology
- Amphibian Traits
- Museums
- Oxygen Minimum Zone
- Flowering Plants
- Paleobiology
- Predictive Ecology
- Satellite Imagery
- Protein Fingerprints
- Parallel Sequencing
- Plant Traits
- Single Cell Genomics
- Parasitoid wasps
- Phylogenetic frameworks
- Deep Subsurface
- Coral Reefs
- Extinction Risk
- Soil Organic Matter

UNDERGRADUATE & GRADUATE EDUCATION

Through Dimensions, students are connected with projects on...

- Herbaria
- Copepods
- Microbiomes
- Symbioses
- Fungi
- Genomics
- Isotope Ratios
- Sensory System Evolution
- Gene Expression
- Extinction Risk
- Phytoplankton
- Adaptive Radiation
- Science Festivals
- Oxygen Minimum Zone
- Nutrient Cycling
- Plant Pathogens
- Deep Shale
- Nutrient Ratios
- Dry Valleys

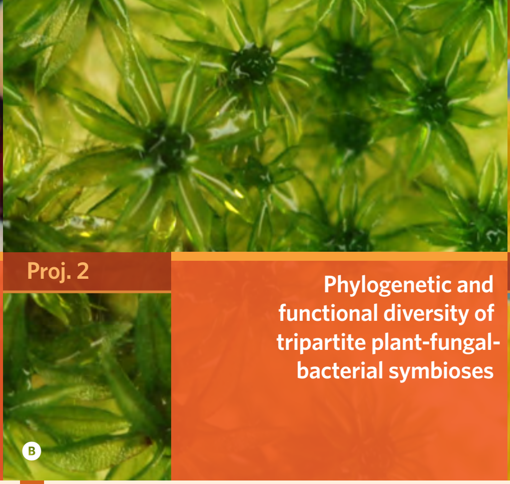
K-12 EDUCATION

Through Dimensions, educators and students are connected with...

- Coastal Ecosystems
- Microbial Sciences
- Mathematical modeling
- Nitrogen Cycling
- Trophic Interactions
- Genetic Architecture
- Lesson Plan Workshops
- Elevation Ranges
- Color Pattern Divergence
- Drought Tolerance
- Adaptive Radiation
- Video Game Design
- Weather Station Data
- Plant Mating Systems
- Soil Organic Matter
- Wild Nightshades
- Avian Malaria
- The Pacific Northwest

Proj. 1

US-China: Microbe eco-evolutionary feedbacks as drivers of plant coexistence and diversity gradients

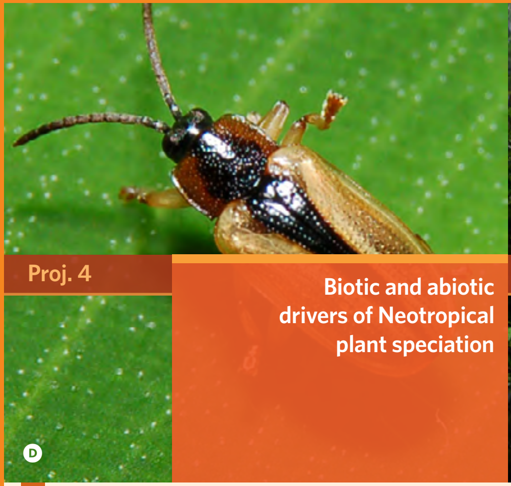


Proj. 2

Phylogenetic and functional diversity of tripartite plant-fungal-bacterial symbioses

Proj. 3

Assembly and function of nectar microbial communities

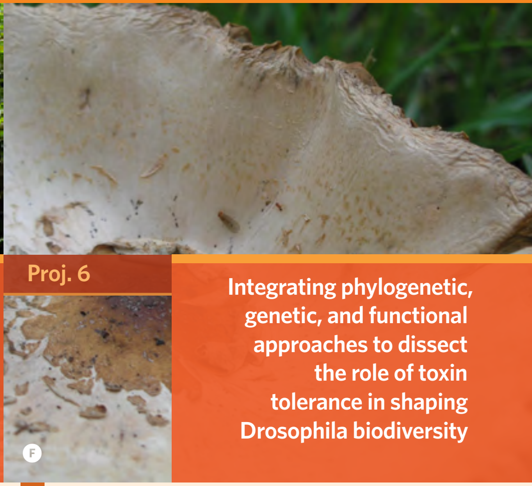


Proj. 4

Biotic and abiotic drivers of Neotropical plant speciation

Proj. 5

Tropical niche conservatism in *Drosophila*: Testing the genetic and functional constraints on diversification



Proj. 6

Integrating phylogenetic, genetic, and functional approaches to dissect the role of toxin tolerance in shaping Drosophila biodiversity

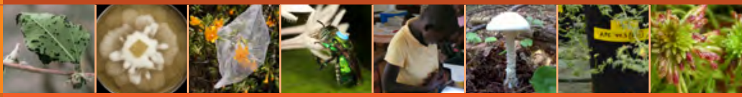
Proj. 7

Elucidating the drivers of mutualism variation in host-symbiont metapopulations

Proj. 8

Genome structure and adaptive evolution in peatmosses (*Sphagnum*): Ecosystem engineers

Abstracts
2017



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Ⓐ Jim Bever Ⓑ Britta Hamberger Ⓒ Manpreet Dhami

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Ⓖ Joel L. Sachs Ⓗ A. J. Shaw & D. J. Weston

Proj. 1 / 8

US-China: Microbe eco-evolutionary feedbacks as drivers of plant coexistence and diversity gradients

US TEAM
James Bever
Helen Alexander
Bryan Foster
Peggy Schultz
Benjamin Sikes
University of Kansas Center for Research Inc
(1738041)

Yaniv Brandvain
University of Minnesota, Twin Cities
(1737827)

Diane Byers
Illinois State University
(1737864)

CHINA TEAM
Xiaoyong Cui
Yanbin Hao
Yanfen Wang
University of Chinese Academy of Sciences

Baoming Ji
Beijing Forestry University

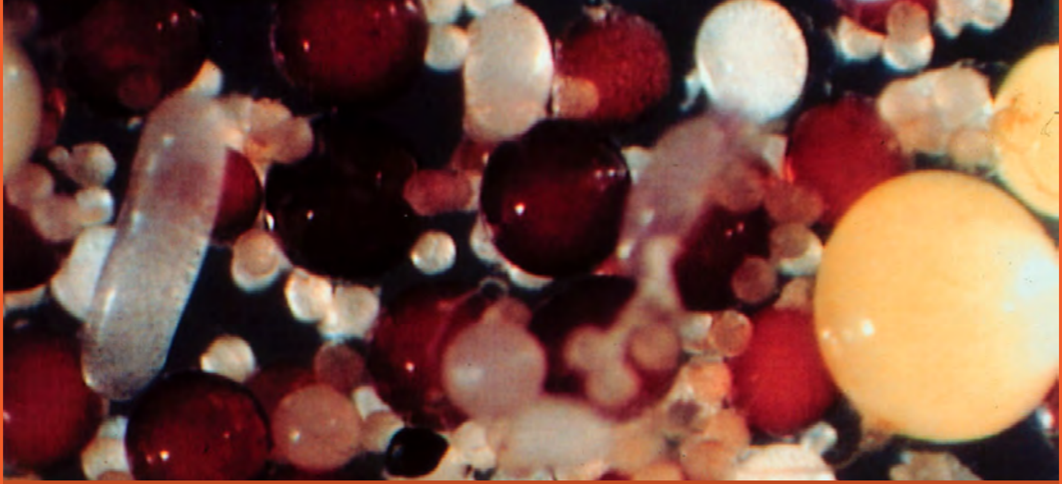
Feihai Yu
Taizhou University

Pathogens, by suppressing abundant plant species, may increase levels of diversity in plant communities. Alternatively, diverse plant communities may maintain high productivity by limiting pathogen spread. This project tests whether pathogens determine the patterns of plant diversity and productivity of plant communities across precipitation gradients in North American and Asian grasslands.

Grasslands around the world vary tremendously in the wealth of species they harbor, their biodiversity. Native grasslands are often very species-rich, with richness increasing with increasing annual precipitation and declining following disturbance such as agriculture. These patterns of diversity can have important consequences because diverse grasslands have been shown to be more productive and more resilient to unpredictable events like drought or flooding. It is essential to understand the processes that govern both the patterns of plant diversity and the benefits of plant diversity to better manage grassland habitats. Such knowledge could generate new directions for sustainable management of rangelands and improve the yield and resilience of degraded agricultural and native ecosystems. The natural forces that create and maintain the rich diversity of plant species coexisting in grasslands are still not known. Recent research suggests that microscopic organisms in the soil, such as plant pathogens, are crucial to maintaining diversity. This project tests whether plant disease determines and regulates natural patterns of plant diversity.

Pathogens can build up and limit plant productivity. Because many pathogens are specialized on their hosts, pathogens are predicted to spread most rapidly in grasslands with many individuals of the same plant species (e.g. monoculture) and with low genetic diversity. Pathogen build up within monocultures creates opportunities for invasion by other plant species, thereby increasing plant diversity. High levels of precipitation are also expected to facilitate pathogen spread, both because life cycles of many pathogens depend on moisture and because pathogen dispersal increases with plant density.

The dependence of pathogen dynamics on plant diversity and precipitation and the consequences of pathogen build up on plant productivity and diversity will be tested through a coordinated set of field observations, field manipulations, and greenhouse assays. Specifically, patterns of plant and pathogen diversity, patterns of plant resistance due to genetic diversity, and patterns of ecological and evolutionary feedback will be tested across the parallel rainfall gradients in the central United States and China. Rainfall manipulations in experimental plant communities will test environmental dependence of plant species coexistence, productivity benefits of plant diversity, and the role of pathogens as drivers of these processes. These empirical studies will be integrated with mathematical models to generate predictions of patterns and benefits of plant biodiversity, as well as predictions of vulnerabilities of grasslands to environmental perturbations. This project will support training of the next generation of scientists through direct engagement of undergraduates and faculty mentors at universities, colleges and community colleges across Illinois, Missouri, and Kansas in a collaborative research and education network and through summer programs focused on regional biodiversity.



^ The majority of prairie plant species have associations with beneficial soil fungi called arbuscular mycorrhizal (AM) fungi. Researchers on this project have found that AM fungi from prairie remnants are more beneficial to prairie plants than AM fungi that dominate following agriculture.

CREDIT: JIM BEVER

^ The prairie blazing star, *Liatris pycnostachya*, is a common forb in the mesic prairies of Illinois. Here it is pictured with Illinois tick trefoil *Desmodium illinoense*.

CREDIT: JIM BEVER

^ Project members identifying plant species within a remnant prairie in Illinois.

CREDIT: JIM BEVER

^ Wild annual sunflower (*Helianthus annuus*) occurs in open areas and prairies across the east-west precipitation gradient; it is commonly infected by the sunflower rust (*Puccinia helianthi*).

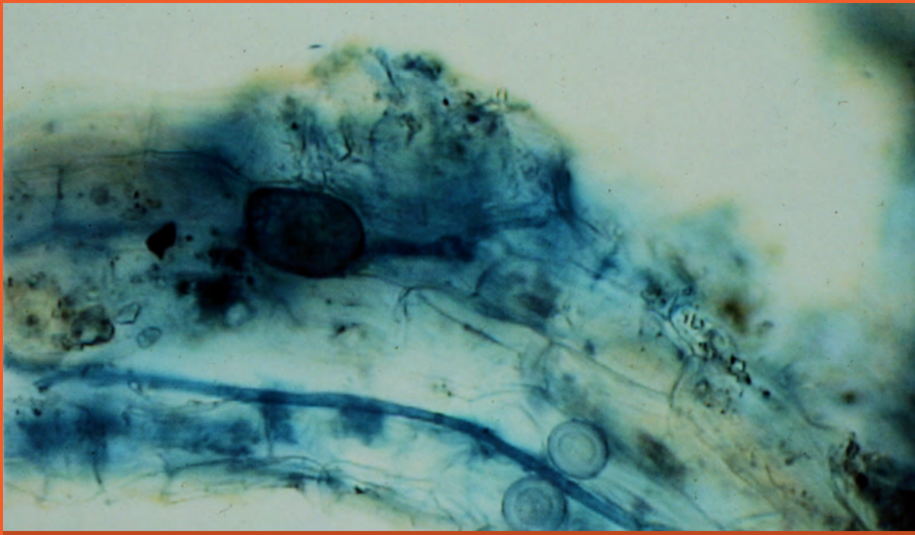
CREDIT: HELEN M. ALEXANDER

^ High forb diversity is typical of prairie remnants in Illinois. Here, *Dalea purpurea* (purple prairie clover), *Eryngium yuccifolia* (rattlesnake master), and *Euphorbia corollata* (flowering spurge) are shown flowering.

CREDIT: JIM BEVER

^ Rosin weed, *Silphium integrifolium*, is a common prairie forb distributed from Illinois to central Kansas. This project will test whether selection pressure from pathogens on *Silphium* increases with precipitation and whether eastern populations have responded by evolving greater resistance to pathogens.

CREDIT: JIM BEVER



^ Structures of several species of fungal and oomycete pathogens are stained blue in this cleared root. Root pathogens can exert strong negative effects on plant growth rate and are often host-specific in their effects. Their accumulation on plant species can limit the success of conspecifics, thereby contributing to high diversity in plant communities.

CREDIT: JIM BEVER

Proj. 2 / 8

Phylogenetic and functional diversity of tripartite plant-fungal-bacterial symbioses

Gregory Bonito
Bjoern Hamerger
Kevin Liu
Patrick Edger
Michigan State University
(1737898)

The transition of plants from an aquatic to terrestrial environment is hypothesized to have been facilitated by diverse Mucoromycota fungi, some of which harbor intracellular bacteria. This project aims to discover the basis for symbioses between plants, fungi and bacteria, and their co-evolution over 500 million years of divergence.

This project will investigate the diversity, evolution and ecological functions of a diverse lineage of fungi, the Mucoromycota. These fungi are industrially important for lipid production and as biofertilizers in agricultural systems. Fungi belonging to the Mucoromycota have co-evolved with plants through innovations that include mycorrhizal and endophytic growth within plant tissues and have been implicated in the colonization of land. Intriguingly, many Mucoromycota are plant growth promoters, and carry, within their cells, bacterial endosymbionts (or endobacteria) belonging to lineages of bacteria known only from fungi. This research will investigate the role of endobacteria on their fungal host's growth and metabolism and the impact of endobacteria on fungal-plant interactions. A culture collection of Mucoromycota fungi with vouchered isolates will be populated and curated during this research. Reference DNA barcodes and genome sequences will be integrated into sequence-based classifiers serving as a resource for the broader community. This project will also result in a short-course on "Computational Thinking in Biodiversity and Evolutionary Research" and an assessment of traditional agriculture and cultural practices that affect Mucoromycota fungi in the soil. This cross-disciplinary research will also provide diverse education and training opportunities for postdocs, graduate and undergraduate students.

To accomplish these goals, investigators will compare and analyze entire holobiont (plant-fungal-bacterial) genomes to identify symbiosis traits that have co-evolved in plant-fungi-bacteria partners. Metatranscriptomics will be used to assess the impact of bacterial endosymbionts on the function of their fungal host and their ability to interact with plants. Changes in host plant phenotype, metabolome, transcriptome, and resilience to abiotic stress will be assessed through bioassay experimentation. The phylogenetic dimension will integrate evolution and genomics to provide a robust phylogenomic framework and new computational tools for estimating co-evolutionary and horizontal gene transfer processes between Mucoromycota and their bacterial endosymbionts. The genetic dimension will apply genomic and metatranscriptomic studies of plant-fungal-bacterial symbionts, selected with guidance provided by the phylogenomics, to identify critical genes involved in symbiotic interactions. The functional component will dissect the role of candidate genes for plant host fitness in the context of different plant-fungal-bacterial partners and abiotic stressors. Together this integrated research will foster interdisciplinary collaborations to provide novel insights into the diversity, evolution, and functioning of tripartite multi-kingdom symbiosis.

Soil fungus *Mortierella elongata* growing in pure culture on malt extract agar (MEA).

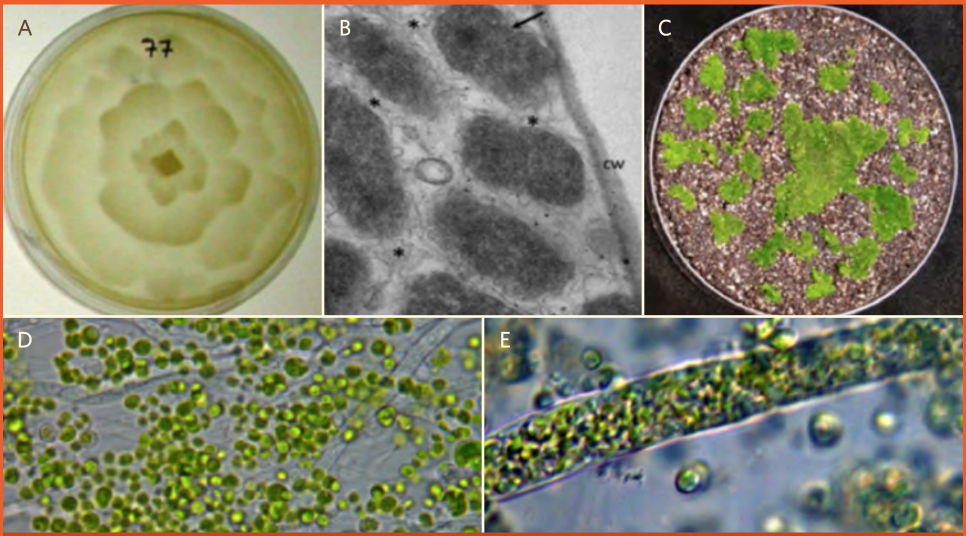
CREDIT: ABIGAIL BRYSON, MICHIGAN STATE UNIVERSITY

Soil fungus *Mortierella apina* isolate growing in pure culture.

CREDIT: ABIGAIL BRYSON, MICHIGAN STATE UNIVERSITY

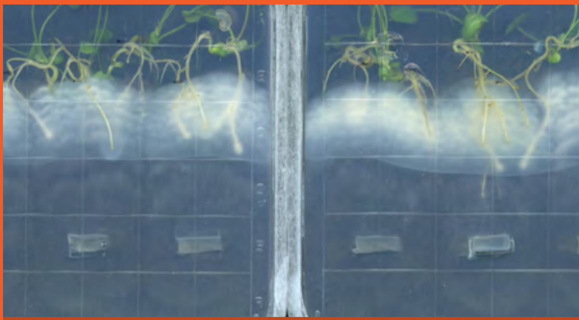
Transmission electron micrograph of *Mycoavidus* endobacteria (dark elongated cells) growing within the mycelium of *Mortierella* (isolate AD003).

CREDIT: ALESSANDRO DESIRO, MICHIGAN STATE UNIVERSITY



Symbioses under study: A) Soil fungus *Mortierella elongata* in 'pure culture' hosts intracellular bacteria. B) Intracellular endobacteria within *M. elongata*. C) Earth moss *Physcomitrella patens* growing with a novel species of *Mortierella* under abiotic drought stress. D) Freshwater green alga *Chlorella sorokiniana* and *M. humilis* after 1 week association. E) Endosymbiosis of the marine algae *Nannochloropsis oceanica* by *M. elongata* under long-term carbon-limited incubation.

CREDIT: GREGORY BONITO, ALESSANDRO DESIRO, ZHI-YAN DU AND BRITTA HAMBERGER, MICHIGAN STATE UNIVERSITY

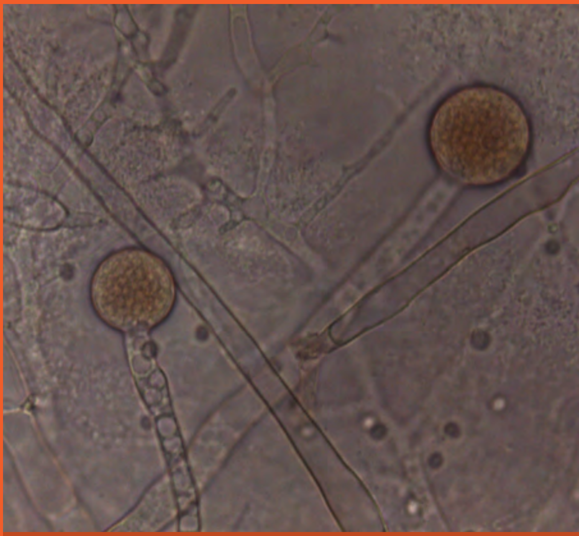


Pure culture isolates of *Mortierella* growing on malt extract agar show the morphological diversity of these fungi.

CREDIT: GREGORY BONITO

Magellan's peat moss *Sphagnum magellanicum* growing in pure culture.

CREDIT: BRITTA HAMBERGER, MICHIGAN STATE UNIVERSITY



Sporangia of fungus *Umbelopsis* (isolate AD052).

CREDIT: ALESSANDRO DESIRO, MICHIGAN STATE UNIVERSITY

Proj. 3 / 8

Assembly and function of nectar microbial communities

Tadashi Fukami
Stanford University
(1737758)

Adina Howe
Iowa State University
(1737765)

This research examines the genetic, phylogenetic, and functional diversity of the microorganisms that colonize floral nectar and how these dimensions of microbial diversity influence the mutually beneficial relationship between flowering plants and the animals that visit flowers as pollinators such as bees and hummingbirds.

The goal of this project is to study the ecology of microorganisms that are found in floral nectar. The results will be used to understand how the following three dimensions of biodiversity affect one another: genetic diversity of the most common species of nectar-colonizing yeast; species diversity of the bacteria that also colonize nectar; and functional diversity of the yeast and bacteria in their effects on the chemical characteristics of nectar and the consequences for pollination success and seed production. Although focused on a specific group of microorganisms, the primary research question addressed in this project is a general one: what are the factors that determine which "alternative stable state" is realized? Ecosystems are said to be in alternative stable states when final community membership depends on the order and timing in which species arrive. By regarding floral microbial communities as miniature ecosystems, the investigators will consider interactions among the three biodiversity dimensions as factors affecting alternative stable states. Ecological researchers usually assume that the regional pool of species that supplies immigrants to local communities is stable and unaffected by local communities. This project will relax this commonly held, but unrealistic, assumption by asking the following specific questions in tandem: how is the regional diversity of nectar-colonizing microbes is modified by the seasonal timing of flowering; how is local microbial diversity within flowers is shaped by hummingbird-assisted dispersal from the regional species pool; and how does local microbial diversity in turn affects regional diversity by altering hummingbird-assisted dispersal? This study will help to understand biodiversity as both a cause and consequence of alternative stable states. Through this project, the investigators will train high-school and graduate students and postdoctoral fellows as researchers. Candidates from underrepresented minority groups (African American, Hispanic, Native American, women) will be actively recruited. The investigators will also use this research as a learning material in the workshops they will offer to undergraduate students on scientific computing. In addition, this research will broaden the knowledge base for ecosystem management under climate change. Climate-induced shifts in flowering are considered a major threat to conservation of plant-pollinator mutualism, but few previous studies considered nectar microorganisms in this context. A combination of field observations, field experiments, and laboratory experiments will be conducted on nectar microbes associated with a hummingbird-pollinated shrub – the sticky monkey flower, *Mimulus aurantiacus* – in California. The results will then be used to build a simulation model of plant-hummingbird-nectar microbe interactions to achieve theoretical synthesis of the empirical data. The researchers will integrate the biodiversity dimensions by studying four ways in which the dimensions interact: how yeast genetic diversity and bacterial phylogenetic diversity are both influenced by flowering phenology; how yeast genetic diversity and bacterial phylogenetic diversity suppress each other through antagonistic priority effects within floral nectar; how yeast genetic diversity and bacterial phylogenetic diversity alter hummingbirds' foraging preference by modifying nectar chemistry as a result of growth in nectar, thereby affecting functional diversity of flowers in terms of nectar chemistry, pollination success, and seed production; and how functional diversity of flowers feeds back to affect yeast genetic diversity and bacterial phylogenetic diversity via altered dispersal of yeast and bacteria across flowers.

Anna's hummingbird, *Calypte anna*, visiting sticky monkey flowers, *Mimulus aurantiacus*, at Jasper Ridge Biological Preserve in California.

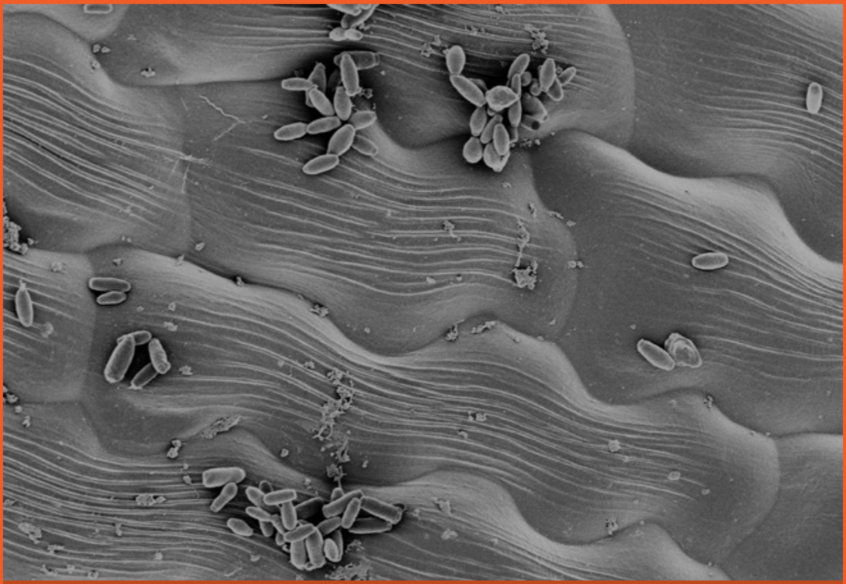
CREDIT: KAORU TSUJI, TREVOR HEBERT AND TADASHI FUKAMI, STANFORD UNIVERSITY

Sticky monkey flowers, *Mimulus aurantiacus*, bagged to study how flower-visiting animals affect the development of microbial communities in nectar.

CREDIT: NONA CHIARIELLO, STANFORD UNIVERSITY

Immediately after mistnetting Anna's hummingbirds, *Calypte anna*, they are fed with sterile sugar water and released. The remaining sugar water is used to identify species of bacteria and yeasts on the bird's beak and tongue that are potentially being transported by the bird from flower to flower.

CREDIT: NONA CHIARIELLO, STANFORD UNIVERSITY



Scanning electron micrograph of cells of the nectar-inhabiting yeast, *Metschnikowia reukaufii*, attached to petal cells of a sticky monkey flower that contains nectar (gold).

CREDIT: MANPREET DHAMI, STANFORD UNIVERSITY

Scanning electron micrograph (false-colored) of cells of the nectar-inhabiting yeast, *Metschnikowia reukaufii* (blue), attached to petal cells and trichomes of the sticky monkey flower that contains nectar (gold). Scale bar 5 µm.

CREDIT: MANPREET DHAMI, STANFORD UNIVERSITY

Many species of nectar-inhabiting yeast can be distinguished based on colony shape, as in *Metschnikowia reukaufii* (bumpy colonies) vs. *Candida rancensis* (smooth colonies) on this agar plate.

CREDIT: TESS GRAINGER, UNIVERSITY OF TORONTO

Proj. 4 / 8

Biotic and abiotic drivers of Neotropical plant speciation

Kathleen Kay
University of California,
Santa Cruz
(1737889)

Jennifer Funk
Chapman University
(1737878)

Santiago Ramirez
University of California, Davis
(1737771)

Dena Grossenbacher
California Polytechnic
State University
(1737848)

Carlos Garcia-Robledo
University of Connecticut
(1737778)

This team will explore the evolutionary causes of plant diversity in the tropical wet forests of Costa Rica and Panama using a recent radiation of spiral gingers. They will examine whether speciation is driven by adaptation to environmental conditions like temperature, precipitation and soil type, or to pollinators, herbivores, and ant mutualists.

Plants are the foundation for terrestrial biodiversity, and the forests of Central and South America house more types of plants than anywhere else in the world. Over evolutionary time, this diversity of plants is produced by speciation, the process whereby one set of populations becomes reproductively and genetically isolated from related populations. Two evolutionary hypotheses for high tropical speciation rates have been proposed. First, because the climate is relatively stable year-round, organisms may not evolve the ability to tolerate a wide range of climates and, therefore, will not disperse widely. Local populations may then become isolated from their relatives and gradually become new species. Alternatively, interactions between plants and other organisms, such as pollinators and herbivores, may vary from place to place, such that a population adapted to one biological community will grow and reproduce poorly when exposed to another. In this way, there may be natural selection for plants in different locations to become different species. This research uses spiral gingers in the monocot genus *Costus* in Costa Rica and Panama to test these hypotheses about tropical speciation. Spiral gingers occupy a wide range of habitats, extending from lowlands to montane forests and from dense understory to forest edges, with different temperature, water, and soil conditions. They interact with orchid bee and hummingbird pollinators, highly specialized beetles that feed on young leaves, and ants that provide protection from herbivores in exchange for nectar. This work integrates phylogenetic studies, broad scale observational approaches, focused field experiments (reciprocal transplants and direct manipulations of interacting organisms and abiotic factors), and genetic mapping. It will determine how plants interact with, and adapt to, pollinators, herbivores, ant protectors, and climatic conditions across their geographic ranges, and it will test the long-standing hypothesis that speciation is caused by traits and genes that have positive effects in one environment but negative effects in other environments.

This project will advance scientific knowledge of the causes of biodiversity by testing longstanding hypotheses about speciation mechanisms in tropical forests. Moreover, the research will greatly increase basic knowledge of how plants cope with different environments and how they interact with pollinators and herbivores in tropical ecosystems that are rapidly changing due to human influences. The team of investigators will provide mentored scientific research experiences for postdoctoral fellows, graduate students, and at least 50 undergraduate students, and they will focus their student recruiting on underrepresented minorities. They will work to increase international capacity in biodiversity science by teaching field courses for Latin American students, training local research assistants at each field site, and organizing an international research symposium in Costa Rica, and they will broadly communicate their experiences and results to the general public in the United States.

^ Undergraduate students at La Selva Biological Station.

CREDIT: CARLOS GARCIA-ROBLEDO

^ Larva of *Cephaloleia histrionica*, an insect herbivore of *Costus*.

CREDIT: CARLOS GARCIA-ROBLEDO

^ *Cephaloleia dorsalis*, an insect herbivore of *Costus*.

CREDIT: CARLOS GARCIA-ROBLEDO

^ Euglossine bees are common pollinators of many species of Neotropical *Costus*.

CREDIT: SANTIAGO RAMIREZ

^ Euglossine bees are common pollinators of many species of Neotropical *Costus*.

CREDIT: SANTIAGO RAMIREZ

^ Impact of herbivory on a *Costus* leaf.

CREDIT: CARLOS GARCIA-ROBLEDO

^ Hermit hummingbirds are common pollinators for many species of Neotropical *Costus*.

CREDIT: KATHLEEN KAY

^ *Costus malortieanus* (Costaceae).

CREDIT: CARLOS GARCIA-ROBLEDO

Proj. 5 / 8

Tropical niche conservatism in *Drosophila*: Testing the genetic and functional constraints on diversification

Daniel R. Matute
Allen H. Hurlbert
University of North Carolina,
Chapel Hill
(1737752)

This research integrates phylogenetic, experimental, and genetic inferences to provide the most comprehensive evaluation to date of the tropical niche conservatism hypothesis for explaining large scale diversity gradients using *Drosophila*.

A general pattern that natural historians have observed and quantified is that tropical regions harbor more biodiversity than temperate regions. This pattern holds across all taxonomic groups. This difference in levels of biodiversity has fascinated biologists for hundreds of years and has inspired a large number of hypotheses regarding their origin and maintenance. Despite this widespread interest, biologists still debate why there are so many species in the tropics and why most tropical groups of organisms rarely diversify into temperate areas of the planet. Two of the leading hypotheses for the striking difference in biodiversity between tropical and temperate habitats is that tropical climates have been stable for a long time (~30-40 million years), allowing the time needed for the number of species to accumulate, and that the evolution of cold tolerance is inherently difficult and has happened relatively rarely. The latter idea is known as the tropical niche conservatism hypothesis. Even though the idea of niche conservatism makes intuitive sense, the hypothesis has little direct support. This research will provide an explicit test of the factors underlying differences in biodiversity between tropical and temperate regions. This is an important and timely test because it will help us understand how biodiversity evolves and how we can best conserve that biodiversity.

Tests of the tropical niche conservatism hypothesis have been correlative in nature and have involved demonstrations of a strong phylogenetic signal in traits reflecting thermal preference, identifying differences in richness-environment relationships between subclades, correlating the richness in a region with the time since the clade colonized the region, and correlating the richness of a clade with clade age. Unfortunately, evolutionary processes other than niche conservatism can also explain these patterns. This research will integrate phenotypic, phylogenetic, genetic, and genomic data to provide the most comprehensive test of the role of niche conservatism and the ability of organisms to adapt to novel thermal environments in generating the latitudinal species gradient. The researchers will leverage the species rich, and globally distributed genus, *Drosophila*, to conduct these tests. The project involves (1) the generation of a new genus-wide phylogeny of *Drosophila*, (2) the analysis of the evolution of thermal performance traits for hundreds of species across the genus, (3) experimental tests of the evolvabilty of the thermal niche in both tropical and temperate *Drosophila* clades, and (4) the identification and testing of the genes controlling thermal niche evolution. Ultimately, the integration of these data will allow the researchers to make the strongest possible inferences about whether and how tropical niche conservatism is responsible for global diversity gradients and how species evolve under changing thermal environments.

^ Water stream at La Delfina, Dagua, Valle del Cauca, Colombia. This area remained largely unsampled for insects until recently due to the Colombia conflict.

CREDIT: DANIEL R. MATUTE

^ Sãotomean children (Bom Sucesso) visit an improvised laboratory setting in the Botanical gardens of São Tomé e Principe. In many cases, our research provides the first instance of access to scientific literacy for the local community.

CREDIT: DANIEL R. MATUTE

^ Early morning in the humid mountain forest of Nova Moka, Equatorial Guinea.

CREDIT: DANIEL R. MATUTE

^ Female (left) and male (right) of *Drosophila teissieri*, an African endemic species that dwells in humid Parinari forest.

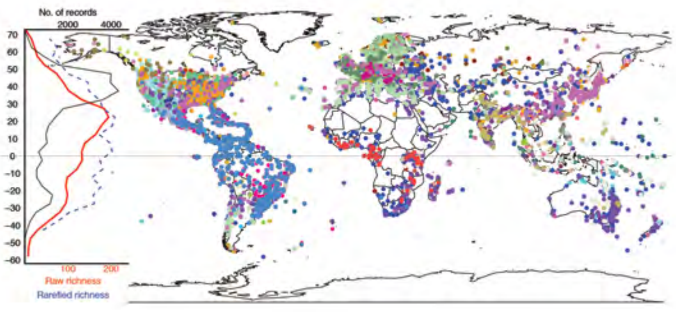
CREDIT: DANIEL R. MATUTE

^ Female of *Drosophila santomea*, an endemic species to São Tomé, a volcanic island off coast Gabón.

CREDIT: DANIEL R. MATUTE

^ The Colombian Andes near Dagua, Valle del Cauca, Colombia. Even though the Andes are a hotspot of biodiversity, the Northern range has not been systematically sampled for *Drosophila* in almost half a century.

CREDIT: DANIEL R. MATUTE



^ The distribution of *Drosophila* species across the globe follows a similar distribution to other taxonomic groups with a higher species diversity in the tropics.

CREDIT: DANIEL R. MATUTE

Proj. 6 / 8

Integrating phylogenetic, genetic, and functional approaches to dissect the role of toxin tolerance in shaping *Drosophila* biodiversity

Laura Reed
Clare Chialvo
University of Alabama, Tuscaloosa
(1737869)

Thomas Werner
Michigan Tech
(1737877)

Kelly Dyer
University of Georgia
(1737824)

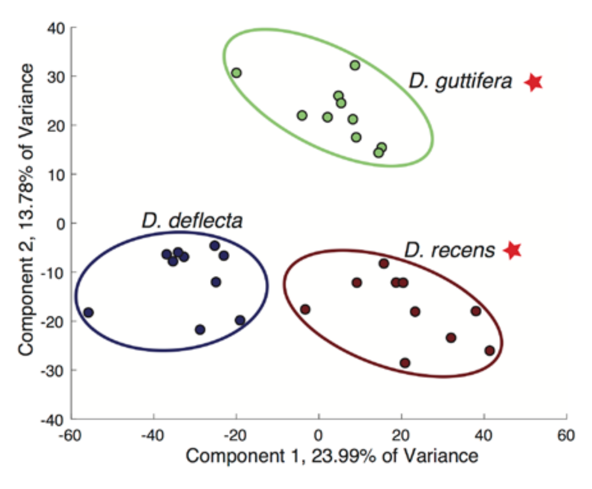
This team will study how novel traits emerge and shape biodiversity. Their research will characterize the evolution of a unique biochemical adaptation, which is tolerance to toxic mushrooms, and study how genetic and ecological mechanisms of toxin tolerance shape diversity within mushroom-feeding flies of the genus *Drosophila*.

Novel adaptations have long fascinated scientists and the public. These traits can allow organisms to escape from selective pressures, such as predation, and make use of new ecological niches. While much work has been done to understand the evolution of novel morphological structures, far less is known about the evolution of novel biochemical adaptations. Questions of particular interest relating to biochemical adaptations are: How do these traits arise if they are costly to the individuals who harbor them? How is the trait maintained when selection is variable within and between populations? What impact does a biochemical adaptation have on the biodiversity of the lineage in which it appears? The project team aims to address these questions by examining the evolution of tolerance to potent mushroom toxins in mushroom-feeding *Drosophila*.

Many flies in the genus *Drosophila* are classified as generalist feeders on both non-toxic and toxic fleshy mushrooms. They can also tolerate high doses of cyclopeptide mushroom toxins that are deadly to most other multi-cellular organisms. This research will test the hypotheses that: 1) tolerance to these toxic cyclopeptides evolved multiple times; 2) the genetic mechanism of tolerance is not the same in all species; and 3) trade-offs between the physiological costs of tolerance and the benefits of access to a low-competition resource maintain tolerance.

The first aim of the project is to characterize the mechanisms of tolerance and examine their evolution within different fly species. The project team will address this aim by using metabolomic and transcriptomic analyses within a phylogenetic framework. Second, the genetic basis of variation in toxin tolerance will be assessed using artificial selection experiments and whole genome sequencing of several *Drosophila* species. Together, these lines of inquiry will indicate whether independent acquisitions of toxin tolerance have a convergent genetic basis. Finally, the functional role of ecological selection on tolerance will be examined to determine the forces driving the evolution of this novel trait. In sum, this research will provide an in-depth evolutionary, ecological, and physiological assessment of a costly and novel biochemical adaptation and its impact on biodiversity.

Included in this project are activities designed to increase public scientific literacy and biodiversity awareness that will facilitate the inclusion and training of K-12 instructors and students, particularly from underrepresented minorities. In addition, the project team will use the results of this research to develop inquiry-based activities for use at local middle and high schools. Undergraduate and graduate students involved in this project will receive interdisciplinary training, and some of these students will visit other team members' labs to experience new research environments and to gain a deeper understanding of the research. Finally, this research will generate photographic identification guides for insect species associated with mushrooms that will be freely available for use by both scientists and the broader public.



A principal component analysis of metabolite profiles for three species fed a non-toxic diet. It illustrates that the profiles of different species are distinct and that these data can be used in the phylogenetic analysis. Stars indicate species that exhibit a novel biochemical trait, cyclopeptide tolerance.

CREDIT: CLAIRE SCOTT CHIALVO

An undergraduate student (Kelsey Lowman) at the University of Alabama prepares larval samples for metabolite extraction for NMR analysis.

CREDIT: THOMAS WERNER

Drosophila falleni female: A mushroom-feeding species in the *quinaria* group that is tolerant of cyclopeptide toxins and found in eastern North America.

CREDIT: THOMAS WERNER

Drosophila tripunctata feeding on a mushroom in Tuscaloosa, Alabama.

CREDIT: CLAIRE SCOTT CHIALVO

Newly collected mushroom-feeding *Drosophila* in an agar vial.

CREDIT: THOMAS WERNER

Brelahn Wyatt, an undergraduate student at the University of Alabama, collecting fly larvae from a laying chamber for use in a survival assay.

CREDIT: CLAIRE SCOTT CHIALVO

Frost's Amanita (*Amanita frostiana*): A non-lethal species of *Amanita* that hosts mushroom-feeding *Drosophila*.

CREDIT: THOMAS WERNER

Destroying angel mushroom: One of the toxic species of *Amanita* that mushroom-feeding *Drosophila* use as a developmental host.

CREDIT: THOMAS WERNER

Proj. 7 / 8

Elucidating the drivers of mutualism variation in host-symbiont metapopulations

Joel Sachs
University of California, Riverside
(1738009)

Jeffrey H. Chang
Oregon State University
(1738028)

Soil bacteria provide key benefits to crops and wild plants, but the range of effects can vary dramatically, even harming some hosts. Here, researchers use legumes and their nitrogen-fixing bacteria to study the genetic, ecological, and evolutionary drivers of variation in symbioses. Understanding these interactions is key for the maintainance and diversification of biodiversity and for advancing sustainable agricultural practices.

Symbiotic bacteria transform how plants and animals interact with their environment. These bacteria can enhance host growth and reproduction, increase tolerance to stress, and improve outcomes for hosts in interactions with competitors and pathogens. But symbioses vary greatly in their effects on host health and fitness. Little is understood about the forces that shape this variation and drive the spread of symbionts that interact but fail to benefit the host. Here, researchers use the relationship between native California legumes and nitrogen-fixing *Bradyrhizobium* bacteria to study the drivers of variation in symbioses. The project will sample interacting plants, bacteria, and soil across California, and use a combination of genetic, genomic, and experimental approaches. The research will determine the magnitude of benefits the bacteria provide to the host, what bacterial genes facilitate benefit or exploitation of the host, and how the host responds and defends itself against ineffective symbionts. The project will train undergraduate and graduate students as well as two postdoctoral fellows. The researchers will educate local farmers on plant-microbe interactions and soil amendments and generate and curate a collection of plant and bacterial variants that will be made freely available to other researchers. This project will provide insights into the parameters that influence symbiosis and help guide how microbes can be better deployed to increase productivity of agricultural systems and promote health of humans and the planet.

The native legume, *Acmispon strigosus*, is pictured in Anza Borrego Desert State Park in Southern California.

CREDIT: JOEL L. SACHS

A closeup of the native legume, *Acmispon strigosus*, in Anza Borrego Desert State Park in Southern California.

CREDIT: JOEL L. SACHS

Graduate student Kenjiro Quides collecting *Acmispon strigosus* at UC Riverside.

CREDIT: JOEL L. SACHS

The native legume, *Acmispon strigosus* is pictured in Anza Borrego Desert State Park in Southern California.

CREDIT: JOEL L. SACHS

Wildflowers in Anza Borrego Desert State Park.

CREDIT: JOEL L. SACHS

A field site at UC Riverside after a wet winter season.

CREDIT: JOEL L. SACHS

Graduate Student Camille Wendlandt recording GPS locations in Burns Pinon Ridge Reserve, near Yucca Valley, California.

CREDIT: JOEL L. SACHS

Inbred seed lines of *Acmispon strigosus* being grown at a UC Riverside greenhouse pictured with postdoc John Regus, graduate student Camille Wendlandt, and undergraduate Jonathan Lyu.

CREDIT: JOEL L. SACHS

Acmispon strigosus forms root nodules with *Bradyrhizobium* bacteria that fix nitrogen for the host plant.

CREDIT: JOEL L. SACHS

Proj. 8 / 8

Genome structure and adaptive evolution in peatmosses (*Sphagnum*): Ecosystem engineers

A. Jonathan Shaw
David Weston
Duke University
(1737899)

David T. Hanson
University of New Mexico
(1737951)

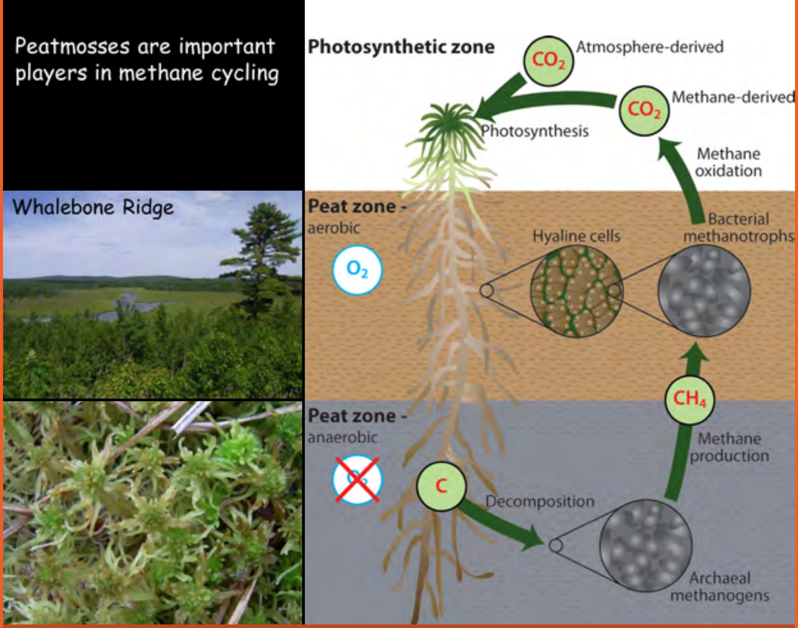
Christopher P. Bickford
Kenyon College
(1737825)

Peatmosses (*Sphagnum*) dominate many wetland habitats and engineer their own niches, allowing dozens of species to co-occur. The accumulation of peat (partially decomposed plant material) has profound impacts on biogeochemical cycles and therefore global climates. This project seeks to link inter- and intraspecific analyses to better understand how evolutionary processes that occur within species scale up to underlie the global diversification of peatmosses.

Sphagnum (peatmoss) is both a plant genus and an entire ecosystem. *Sphagnum*-dominated peatlands cover vast expanses of the Northern Hemisphere boreal zone in poorly drained landscapes where production outstrips decomposition, promoting the buildup of partially decomposed plant material — peat. Community ecologists have studied peatlands for many decades because the plant communities are relatively simple and as many as 15-25 *Sphagnum* species can co-occur, sorting themselves relative to environmental gradients such as local pH, nutrient abundance, and height above the water table. Coexisting peatmoss species don't just display niche differentiation, they create those niches. Species that occupy microsites raised above the water table (so-called "hummock" species), for example, tend to decompose slowly, building up peat (their own dead tissues), raising the growing plants above surrounding vegetation. More recently, *Sphagnum*-dominated peatlands have garnered renewed interest because these same biotic processes that promote the accumulation of peat, result in huge quantities of carbon storage. It is estimated that northern peatlands occupy about 10% of the terrestrial land surface but store 25-30% of the entire terrestrial carbon pool.

This project seeks to integrate evolutionary and ecological perspectives on peatmoss diversity. Through inter- and intra-specific comparative analyses of genome structure, morphology, and physiology, researchers seek to link gene structure and function to niche differentiation and global biogeochemistry.

Although they dominate boreal wetland ecosystems, *Sphagnum* occurs throughout the world, including many tropical regions. These biogeographic and ecological features facilitate research on questions related to evolution of plant traits that promote niche differentiation, and to the accumulation of vast quantities of carbon. This project uses whole genome sequencing of approximately 100 species, including those native to northern, tropical, and Southern Hemisphere regions. Researchers will seek to identify genes and genome regions related to environmental change and utilize the fact that *Sphagnum* has spread from boreal to tropical latitudinal zones independently, in multiple lineages, to tease apart lineage-specific from more general evolutionary processes. In a second component of the project, researchers turn attention to intra-specific patterns and processes, utilizing one species, *S. magellanicum*, which is distributed from the subarctic to tropical regions. Plants sampled along a latitudinal gradient will be grown to assess physiological responses to manipulated environmental conditions. RNA sequencing will be used to measure gene expression responses to the experimental treatments and complement these analyses with whole genome sequencing of some 100 plants sampled across the ecological diversity characterizing this species. Specific hypotheses about gene expression responses relative to genomic differentiation across the range of *S. magellanicum* will be tested to ask how evolution within one widespread species compares to evolutionary processes that underlie the diversification of the whole genus *Sphagnum*. The project includes training of undergraduate, graduate students, and post-docs, with a focus on underrepresented groups.

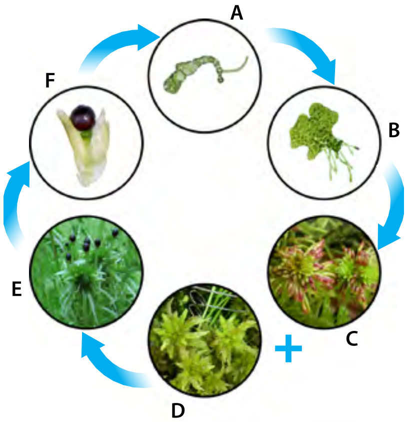


The role of peatmosses (*Sphagnum*) and peatlands in the methane cycle. Methane is an important greenhouse gas.

CREDIT: A. JONATHAN SHAW, D. J. WESTON, DUKE UNIVERSITY, AND COLLABORATORS

Campbell Lake and surrounding peatland, Anchorage, Alaska.

CREDIT: A. JONATHAN SHAW, D. J. WESTON, DUKE UNIVERSITY, AND COLLABORATORS

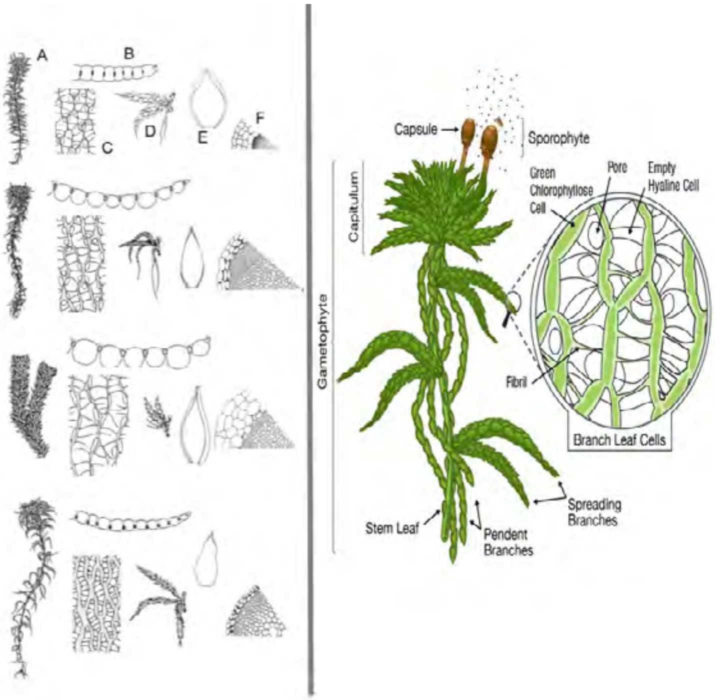


Sphagnum life cycle. A) Young protonema with a single rhizoid. B) Mature thalloid protonemata with rhizoids. C) Male gametophore. D) Female gametophore. E) Female gametophyte bearing multiple sporophytes. F) Mature sporophyte (round, brown capsule, bearing meiotically-derived spores) borne on a short pseudopodium (mostly surrounded by perichaetial leaves).

CREDIT: SHAW AJ, ET AL. (2016)

Two peatmoss species, *Sphagnum pulchrum* (yellow) and *S. magellanicum* (red).

CREDIT: A. JONATHAN SHAW, D. J. WESTON, DUKE UNIVERSITY, AND COLLABORATORS



Generalized anatomical features of a *Sphagnum* plant (right) and interspecific variation in functionally important traits (left).

CREDIT: A. JONATHAN SHAW, D. J. WESTON, DUKE UNIVERSITY, AND COLLABORATORS

Proj. 1

Diversification of sensory systems in novel habitat: Enhanced vision or compensation in other modalities?

Proj. 2

Time after time: Adaptive seasonal timing drives the sequential origin of community biodiversity

Proj. 3

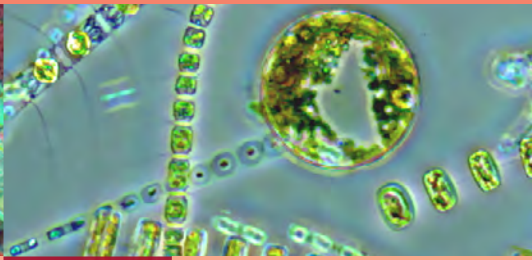
US-BIOTA-Sao Paulo: Scales of biodiversity—Integrated studies of snake venom evolution and function across multiple levels of diversity

Proj. 4

The evolution of novel interactions within a network of plant, insect and microbial biodiversity

Proj. 5

Evolutionary ecology of sponges and their microbiome drives sponge diversity on coral reefs



Proj. 6

Genetic, functional, and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients

Proj. 7

Predicting biodiversity vulnerability to climate change: Integrating phylogenetic, genomic, and functional diversity in river floodplains

Proj. 8

Secondary metabolites as drivers of fungal endophyte community diversity

Proj. 9

Desiccation and diversity in dryland mosses

Proj. 10

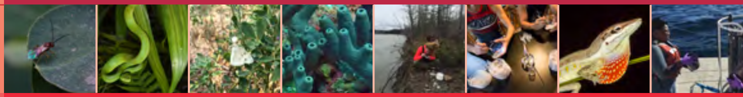
Landscape genomics of an adaptive radiation using ultra-high resolution genetic, morphometric, and spatial analysis

Proj. 11

Functional and genomic diversity in vitamin B_1 metabolism and impacts on plankton networks and productivity

Updates

2016



< | *CREDIT*

Ⓐ Janette W. Boughman Ⓑ Hannes Schuler Ⓒ Christopher L. Parkinson

< | *CREDIT*

Ⓓ Lauren Lucas Ⓔ Deborah J. Gochfeld Ⓕ Stephanie Anderson

< | *CREDIT*

Ⓖ Amanda DelVecchia Ⓗ Priscila Chaverri Ⓘ Theresa Clark

< | *CREDIT*

Ⓙ Ian J. Wang Ⓚ Jacques Descloitres

Diversification of sensory systems in novel habitat: Enhanced vision or compensation in other modalities?

Janette Boughman
Gideon Bradburd
Michigan
State University
(1638778)

Deborah L. Stenkamp
Michigan
State University
(1638567)

Johann 'Hans' A. Hofmann
University of Texas, Austin
(1638861)

Icelandic stickleback fishes provide a compelling testing ground and lots of statistical power to investigate how evolutionary change in sensory systems facilitates survival and persistence of species in rapidly changing environments.

Update

The team had a very successful field season collecting fish and environmental data for 10 populations from across Iceland. Researchers also generated functional data on sensory contributions to predator avoidance for these populations, and RNA-seq data for brain regions underpinning each sensory system. They are in the midst of analyzing genomic data to determine population history, as well as the influence of both ecology and drift on genomic variation. These efforts generated training opportunities for a postdoctoral scientist, two graduate students, two technicians, and 7 undergraduates. Preparations for the second field season is underway.

Top: The glacial lake Blautaver is on the Tungnaá River that drains Iceland's largest glacier Vatnajökull and is in Iceland's central highland region. It is one of the high elevation glacial lakes in the study.

Bottom: PI Janette Boughman collecting spectral data on Frostastaðavatn, a clear spring fed lake in the central region of the highlands renowned for its vivid blue and green coloration.

CREDIT: JANETTE BOUGHMAN

Postdoc John Phillips sampling fish in a Höfðavatn, a clear lagoon separated from the ocean by a natural sea wall in northern Iceland.

CREDIT: JANETTE BOUGHMAN

Time after time: Adaptive seasonal timing drives the sequential origin of community biodiversity

Jeffrey L. Feder
University of Notre Dame
(1638997)

Daniel Hahn
University of Florida
(1639005)

Gregory Ragland
Kansas State University
(1638951)

This research project will study rapid evolution of a new agricultural pest, the apple maggot fly, and a community of coevolving parasitoid wasps to understand how diversification in one lineage can help generate greater diversity across trophic levels.

Update

In 2017 researchers made substantial progress towards understanding how seasonal timing can drive diversification of both specialist fruit-feeding flies and the community of parasitoid wasps that attack them. In the first full year of the project, they have made large field collections of each of the fly and wasp species for population genetic and functional genomic work, including careful tissue dissection across diapause development. They have begun sequencing previously collected samples and also published a series of papers from literature reviews and opinion pieces to meta-analyses of both the existing data and data culled from the literature.

Publications

Denlinger DL et al. (2017) Keeping time without a spine: what can the insect clock teach us about seasonal adaptation? *Phil Trans Roy Soc B* 372: 1734–1742

Feder JL, et al. (2017) Barnacles, barrier loci, and the systematic building of species. *J Evol Biol* 30: 1494–1497

Feder JL, et al. (2017) "Speciation, Process of" In: *Encylopedia of Biodiversity* (Guy Bush, Ed.). pp. 620–628. Elsevier Press

Feder JL, SP Egan (2017) "Sympatry and Patterns of Genetic Differentiation in Sympatry" In: *Brenner's Encyclopedia of Genetics*. pp. 604–606. Elsevier Press

Ragland GJ, Keep E (2017) Comparative transcriptomics support evolutionary convergence of diapause responses across Insecta. *Physiol Entomol* 42: 246–256

Ragland GJ et al. (2017) A test of genomic modularity among life-history adaptations promoting speciation with gene flow. *Mol Ecol* 26: 3926–3942

Top: A parasitoid wasp searching for snowberry fly larvae to parasitize.

CREDIT: HANNES SCHULER, UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES VIENNA

Bottom: Edgewater High School students use curriculum developed through the project.

CREDIT: MARGARITA HERNANDEZ, CENTER FOR PRE-COLLEGIATE EDUCATION AND TRAINING, UNIVERSITY OF FLORIDA

A hawthorn fly preparing to lay eggs within a hawthorn fruit where the larvae will feed, grow, and sometimes be parasitized by hawthorn wasps.

CREDIT: HANNES SCHULER, UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES VIENNA

US-BIOTA-Sao Paulo: Scales of biodiversity — integrated studies of snake venom evolution and function across multiple levels of diversity

US TEAM

H. Lisle Gibbs
Ohio State University
(1638872)

Chris L. Parkinson
University of Central Florida
(1638879)

Darin Rokyta
Florida State University
(1638902)

BRAZIL TEAM

Inácio Azevedo
Erika Hingst-Zaher
Ana Moura
Instituto Butantan,
Sec. Estado Da Saúde

Hussam Zaher
Museu de Zoologia,
Universidade São Paolo

Understanding how groups of organisms have become exceptionally species-rich requires identifying the features and mechanisms that promote diversification. This research assesses the role that venom diversity, from the genetic to the functional level, has played in the diversification in front and rear-fanged venomous snakes from North, Central and, South America.

Update

This extremely active year was facilitated by 3 planning meetings; one in-person and two virtual. Collecting trips to Mexico and Honduras to acquire venom and tissues from front (venomous) and rear fanged (potentially venomous) snakes resulted in samples from 251 individuals across 5 snake families. Lastly, significant progress was made in establishing laboratory and data analysis protocols (including development of a new bioinformatics tools and pipelines) and 129 transcriptomes have been sequenced for the project.

^ Andrew Mason and Erich Hofmann, two Ph.D. students in Chris Parkinson's Lab at Clemson University, and collaborator Professor Carlos Augusto Andiono from UNAH-VS, tube a *Bothriechis marchi* specimen for venom collection in Honduras.

CREDIT: CHRISTOPHER L. PARKINSON

^ Palm-pitvipers are a group of arboreal vipers that range throughout Middle America. This species, March's Palm-Pitviper (*Bothriechis marchi*) is native to the mountains of northern Honduras and southern Guatemala. This individual was collected by Dr. Chris Parkinson.

CREDIT: CHRISTOPHER L. PARKINSON

^ Arboreal snakes of the genus *Sibon* have large jaw muscles for extracting snails from their shells. This species, *S. nebulatus* (the Cloudy Snail Eater) is common in high elevation rainforest across Central and into South America. This individual was found active at night in a cloud forest in central Honduras.

CREDIT: ERICH P. HOFMANN, CLEMSON UNIVERSITY

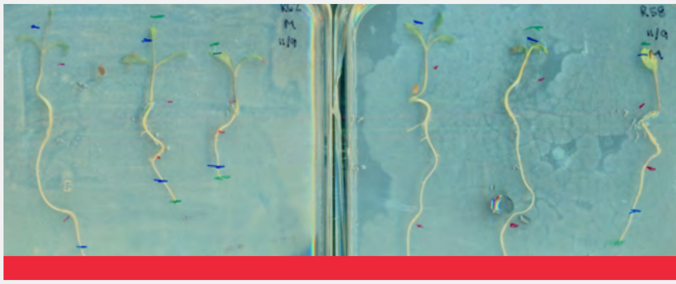
The evolution of novel interactions within a network of plant, insect and microbial biodiversity

Zachariah Gompert
Utah State University
(1638768)
Christian A. Buerkle
University of Wyoming
(1638602)
Craig D. Dodson
Matthew Forister
University of Nevada
(1638793)

James Fordyce
Sarah L. Werner
University of
Tennessee Knoxville
(1638922)

Chris C. Nice
Texas State University,
San Marcos
(1638773)

This project investigates the relationship between multiple components of biodiversity and the evolution of novel interactions among plants, insects, and microbes to answer the fundamental question: what role does biodiversity play in the evolution and maintenance of novel interactions?



Alfalfa seedlings being inoculated with microbial communities for experiments at the University of Tennessee.

CREDIT: ZACH GOMPERT

Update

The team visited over 30 field locations in the western USA to collect trait and genetic data on the insect and microbial communities associated with feral alfalfa. Team members were able to isolate and culture bacterial and fungal microbes from alfalfa samples. These isolates will be used in forthcoming manipulative experiments. Large caterpillar rearing experiments with the focal insect herbivore, the Melissa blue butterfly, revealed genetic differences among individual plants affect their suitability as hosts and indicated that host suitability was determined, in part, by plant genetic variation for leaf toughness.

Publications

Chaturvedi S, *et al.* (2017) Sources of variation in the gut microbial community of *Lycaeides melissa* caterpillars. *Sci Rep* 7: 11335

Gompert Z, Mock KE (2017) Detection of individual ploidy levels with genotyping-by-sequencing (GBS) analysis. *Mol Ecol Resources* 17: 1156–1167

Lebeis SL (2017) Plant microbiome identification and characterization. *Curr Prot Plant Bio* l2: 135–146

Marion ZH, *et al.* (2017) Pairwise beta diversity resolves an underappreciated source of confusion in calculating species turnover. *Ecology* 98: 933–939

An interaction (predation) between a spider and Pierid butterfly on alfalfa at the team's Verdi, NV field site.

CREDIT: ZACH GOMPERT

Alfalfa supports a diverse insect community, including the Melissa blue butterfly. This photo is taken at the team's field site in Kingston Canyon in the Toyiabe Range, Nevada.

CREDIT: ZACH GOMPERT

Postdoc Zach Marion at the University of Nevada pilots a drone to obtain an aerial photograph of the team's Reno, NV alfalfa field site.

CREDIT: ZACH GOMPERT

Proj. 5 / 11

Evolutionary ecology of sponges and their microbiome drives sponge diversity on coral reefs

Michael P. Lesser
Matthew MacManes
Kathleen Morrow
David C. Plachetzki
University of
New Hampshire
(1638296)

Deborah J. Gochfeld
Marc Slattery
University of Mississippi
(1638289)

The goal of this project is to investigate the symbiosis between marine sponges and their microbiome and to understand how these relationships drive the evolution and ecology of sponge diversity on coral reefs across the Caribbean basin.

Update

One year into the project, sponges have been sampled in Curacao and Belize with future trips planned for the Cayman Islands and the Florida Keys. Over 125 species with multiple replicates have been analyzed for both sponge species identification and its associated microbiome to date. Additionally, five sponge genomes are being sequenced and researchers are currently developing the analytical framework for a co-evolutionary analysis of sponges and their microbiome.

V Diverse sponge community showing several species on a reef with low coral and high algal/cyanobacterial mat coverage near St. Croix, US Virgin Islands.

CREDIT: DEBORAH J. GOCHFELD

Proj. 6 / 11

Genetic, functional, and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients

Elena G. Litchman
Christopher A Klausmeier
Michigan
State University
(1638958)

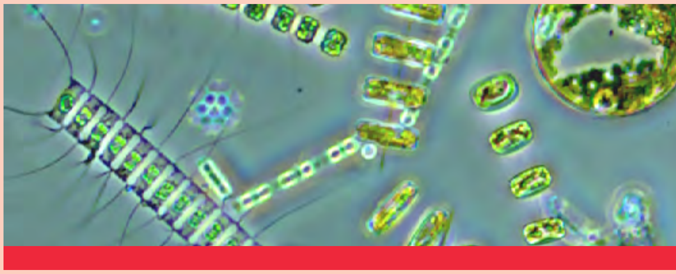
David A. Hutchins
University of
Southern California
(1638804)

Tatiana Rynearson
University of
Rhode Island
(1638834)

The project will combine field sampling, experiments, and mathematical models to understand and predict how marine phytoplankton communities will respond to changing temperature and nutrient regimes.

Update

Field work during this first year focused on the project's temperate site, Narragansett Bay (NB), RI. Three field sampling and two temperature shift experiments were conducted, resulting in the isolation of numerous species and strains of diatoms, cyanobacteria, and picoeukaryotes into culture. The team has begun measuring the thermal response curves of diatom species within the genus *Skeletonema*. These will be compared across species, seasons, and the genotypes within species, in order to investigate whether these diatoms effectively "subdivide" the NB thermal niche.



V A diverse phytoplankton community from Narragansett Bay, RI.

CREDIT: STEPHANIE ANDERSON, UNIVERSITY OF RHODE ISLAND, GRADUATE SCHOOL OF OCEANOGRAPHY

Predicting biodiversity vulnerability to climate change: Integrating phylogenetic, genomic, and functional diversity in river floodplains

Gordon H. Luikart
Brian K. Hand
Jack A. Stanford
University of Montana
(1639014)

River floodplains are among the most biodiverse, yet endangered, landscapes on earth. This study will advance understanding of biodiversity of arthropod communities (insects and crustaceans) in river floodplains (and the inter-connected aquifers) using innovative modeling and conceptual frameworks.

< Field crew members collect emerging adult stoneflies from pit fall traps installed in the banks of the Flathead River in the Kalispell valley.

CREDIT: GARRETT FRANDSON, FLATHEAD LAKE BIOLOGICAL STATION

Update

In the past 10 months the team chose focal study floodplains and sample sites in the North Fork, Middle Fork, and main Flathead Rivers in Montana. At these sites, a variety of methods were used to sample over 14,000 riverine and aquifer stoneflies. They are continuing to identify individual stoneflies to species, have developed and verified DNA extraction protocols for stoneflies, and have begun DNA extractions. PIs are also currently working on a high-quality full genome assembly for *Paraperla frontalis*, which will likely be the first of its kind in the world for a stonefly species.

Publications

DelVecchia AG, Stanford JA, Xu X (2016) Ancient and methane-derived carbon subsidizes contemporary food webs. *Nat Comm* 7: 13163

^ Field crew member collects emerging adult stoneflies from vegetation along the Flathead River in the Kalispell valley.

CREDIT: GARRETT FRANDSON, FLATHEAD LAKE BIOLOGICAL STATION

^ Field crew members collect riverine stoneflies using a kick net in the Flathead River near Glacier National Park in the spring of 2017. By disturbing the substrate stoneflies float into the net and are collected for identification and genetic analyses.

CREDIT: RACHEL L. MALISON, UNIVERSITY OF MONTANA

^ The Nyack floodplain, located on the Middle Fork of the Flathead River. The Nyack floodplain is one of our focal sites where we study riverine and aquifer stoneflies.

CREDIT: AMANDA G. DELVECCHIA, NORTH CAROLINA STATE UNIVERSITY

Secondary metabolites as drivers of fungal endophyte community diversity

Jason C. Slot
Ana Paula Alonso
Ohio State University
(1638999)

Priscila Chaverri
University of Maryland,
College Park
(1638976)

The project investigates the chemical diversity of the coffee family (Rubiaceae) and its fungal endophytes and how this diversity impacts the composition and genome structure of plant microbiome communities.

Graduate students isolating fungal endophytes from Rubiaceae leaves.

CREDIT: E. ESCUDERO, UNIVERSIDAD DE COSTA RICA

Update

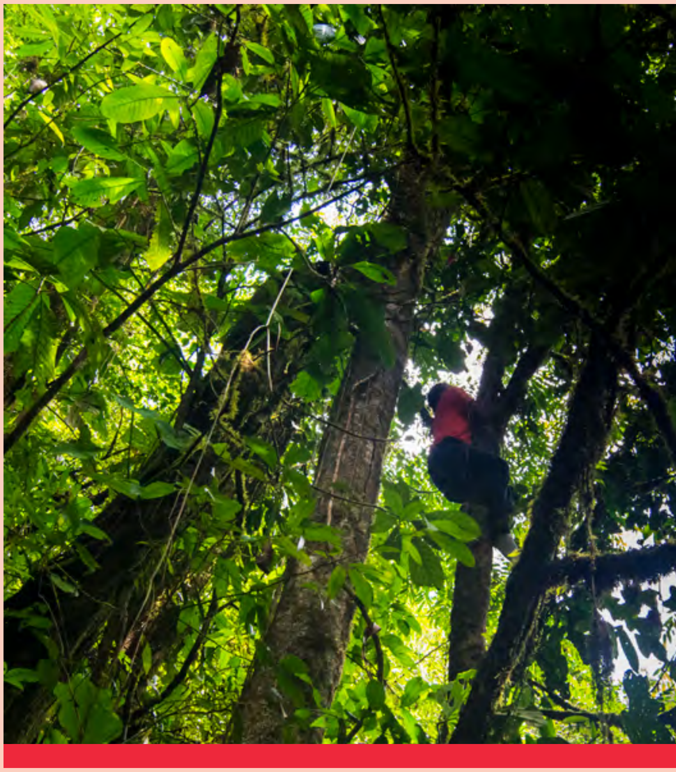
In the first year of the project, leaf specimens of the plant family Rubiaceae were collected from forests in Costa Rica. The collection contains species from multiple genera known for medically significant alkaloids. Fungal endophytes were investigated in 120 leaf samples by culturing and metabarcoding methods. 1500 endophytes have been isolated and are undergoing DNA barcoding. An additional 2000 putative species were identified by high-throughput, amplicon sequencing. Untargeted metabolomics has yielded approximately 200 compounds contributing to chemotypic differences among three Rubiaceae genera. A new metabolic gene cluster annotation pipeline was developed for analysis of forthcoming fungal endophyte genomes.

Publications

Gluck-Thaler E, Slot J (2018) Specialized plant biochemistry drives gene clustering in fungi. *ISME J* doi:10.1038/s41396-018-0075-3

Local botanist Pedro Suarez processing Rubiaceae plant vouchers.

CREDIT: E. ESCUDERO, UNIVERSIDAD DE COSTA RICA



Field assistant climbing a Rubiaceae tree to reach the leaves.

CREDIT: E. ESCUDERO, UNIVERSIDAD DE COSTA RICA

Desiccation and diversity in dryland mosses

Lloyd R. Stark
University of Nevada
Las Vegas

John C. Brinda
Missouri
Botanical Garden
(1638943)

Brent Mishler
University of
California-Berkeley
(1638956)

Kirsten Fisher
California State
University, Los Angeles
(1638996)

Kirsten K. Deane-Coe
St Mary's College
of Maryland
(1638955)

Matthew Bowker
Northern Arizona
University
(1638966)

Melvin Oliver
University of
Missouri-Columbia
(1638972)

This research will investigate the links between the genes, physiology, life stages, populations, and communities of *Syntrichia* mosses that have facilited their ability to thrive in dryland ecosystems.

Graduate student Cristina Rengifo, assisted by Spanish visiting scholar Angela LaFuente, prepares a new common garden experiment featuring *Syntrichia*. An existing reciprocal elevational transplant experiment of biocrusts can be seen in the background.

CREDIT: LLO STARK

Update

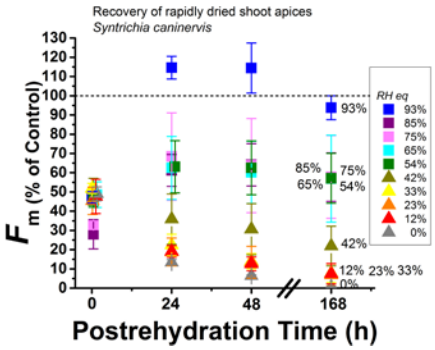
The team of 6 PIs focused on initiating experiments and protocols that will allow us to elucidate the elements of desiccation tolerance (DT, the ability to survive the complete absence of water) in adult plant individuals of the genus *Syntrichia* (a group of mosses distributed world-wide). They (i) completed the assembly and annotation of the genome of *Syntrichia caninervis* and established transcriptomes related to desiccation and rehydration; (ii) successfully cloned, decontaminated, and cultured 20 N. American species of *Syntrichia*; (iii) maintained, monitored and sampled moss tissue from an elevational transplant experiment in the field, cultured materials for a greenhouse experiment, and established a new common garden experiment; and (iv) initiated a lab experiment to evaluate the ecological strategy of DT in *Syntrichia* and assess the recovery environment for these plants.

Publications

Stark LR (2017) Ecology of desiccation tolerance in bryophytes: a conceptual framework and methodology. *Bryologist* 120: 130-165

PA screen shot from a genome browser depicting the structure of a small portion of the *S. caninervis* genome.

CREDIT: LLO STARK



How chlorophyll fluorescence (Fm) varies with postrehydration time and equilibrating relative humidity, in the moss *Syntrichia caninervis*.

CREDIT: LLO STARK

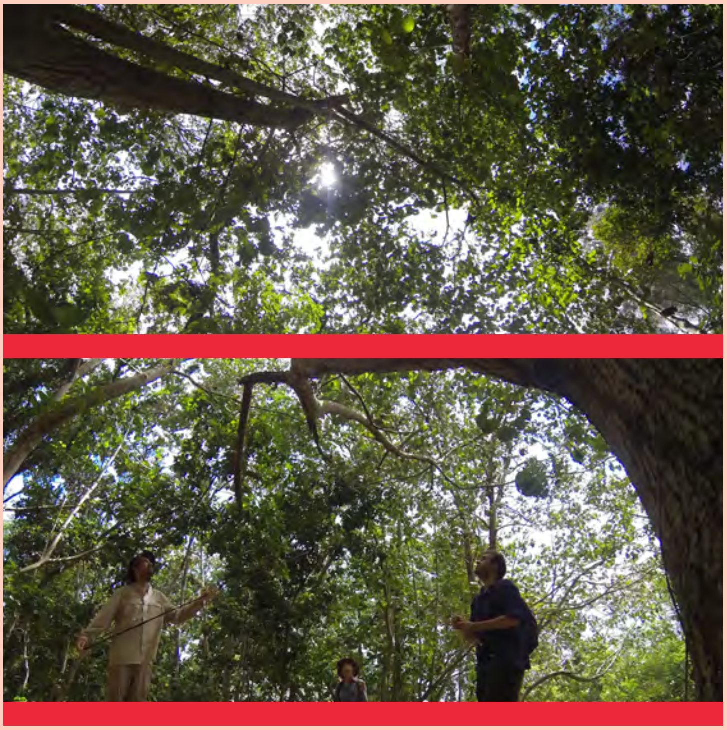
Landscape genomics of an adaptive radiation using ultra-high resolution genetic, morphometric, and spatial analysis

Ian J. Wang
University of
California, Berkeley
(1542534)

This project will integrate genetic, morphological, and environmental data to examine how ecological heterogeneity generates different levels of biodiversity in the adaptive radiations of *Anolis* lizards on the Greater Antilles.

Update

During the last project year, environmental data and over 500 specimens of *Anolis* lizards were collected from across Puerto Rico. Additionally, over 100 *Anolis* specimens from the Dominican Republic were collected to complete the sampling of the four target species from Hispaniola. Genomic and morphometric lab work is ongoing, with genomic libraries and CT-scans for hundreds of specimens constructed in the last year. These analyses suggest important morphological differences between populations in several species that are associated with different climates and habitats.



Top: The environmental data we are collecting include 3D scans of the habitat, from ground level to the forest canopy.

Bottom: The field team collecting *Anolis* lizard specimens and environmental data in Cambalache State Forest, Puerto Rico.

CREDIT: IAN WANG

Publications

Wogan GOU, Wang IJ (2017) The value of space-for-time substitution for studying fine-scale microevolutionary processes. *Ecography* https://doi.org/10.1111/ecog.03235

Top: Photo of the sharp-mouthed anole (*Anolis pulchellus*) from Puerto Rico.

CREDIT: IAN WANG

Bottom: Dominican giant anole (*Anolis baleatus*) from the Dominican Republic.

CREDIT: PHILIP SKIPWITH, UNIVERSITY OF CALIFORNIA, BERKELEY

Functional and genomic diversity in vitamin B_1 metabolism and impacts on plankton networks and productivity

Alexandra Z. Worden
Monterey Bay
Aquarium
Research Institute
(1639033)

Stephen J. Giovannoni
Oregon
State University
(1638928)

Research expeditions and experiments will explore the ecosystem implications of a recent discovery that ocean plankton engage in complex trafficking of component molecules, which can be assembled to make vitamin B_1. Various ‘omics science approaches and advanced chemical analyses will be integrated to develop a new paradigm of how molecule trafficking influences microbial diversity and phytoplankton carbon dioxide uptake.

Update

In 2017 two exciting cruises were undertaken, one transecting from the East Coast of the United States to the Sargasso Sea and the other in a productive region of the eastern North Pacific. Onboard experiments examined community responses to various precursor molecules involved in vitamin B_1 biosynthesis. Development of protocols for assaying low levels of these compounds in sea water have been a focus since Postdoctoral Fellow Chris Suffridge joined the project alongside ongoing analyses of the at-sea experiments. This year the team published several protocols and a first publication; the new research demonstrates that algae grow more efficiently on specific precursors than on the intact vitamin itself when given environmentally-relevant supply levels.

UCSC/MBARI graduate students Juliana Nzongo and Rachel Harbeitner sample from the niskin rosette aboard the R/V Western Flyer in the eastern North Pacific. They are investigating how the availability of different vitamin related compounds influences the microbial community. This region is highly productive and a major fishery. Results of our experiments here are being compared to those from experiments in the more nutrient poor Sargasso Sea.

CREDIT: CHARLOTTE ECKMANN, MONTEREY BAY AQUARIUM RESEARCH INSTITUTE

Publications

Gutowska MA, *et al*. (2017) Ecologically important marine haptophyte algae use exogenous pyrimidine compounds more efficiently than thiamin. *mBio* Vol 8: e01459-17

Top: Weather during the eastern US to the Sargasso Sea transect was a challenge, but exciting experiments showed a strong response of the microbial community transect to thiamin manipulation.

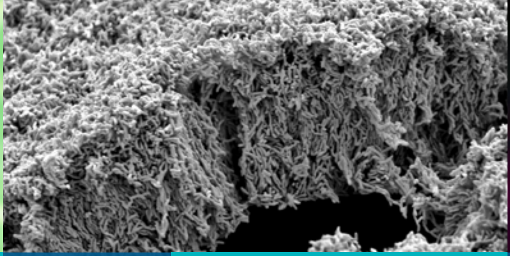
CREDIT: CAMILLE POIRIER, MONTEREY BAY AQUARIUM RESEARCH INSTITUTE

Bottom: OSU postdoc Chris Suffridge collecting vitamins from seawater on reverse phase columns.

CREDIT: STEVE GIOVANNONI

Proj. 1

Diversification dynamics of multitrophic interactions in tropical communities



Proj. 2

The phylogenetic and functional diversity of extracellular electron transfer across all three domains of life

Proj. 3

Life at extremes: Linking the phylogenetic and genomic diversity of ctenophores to ecophysiological adaptations in the deep sea

Proj. 4

The evolution of pollination syndrome diversity in *Penstemon*

Proj. 5

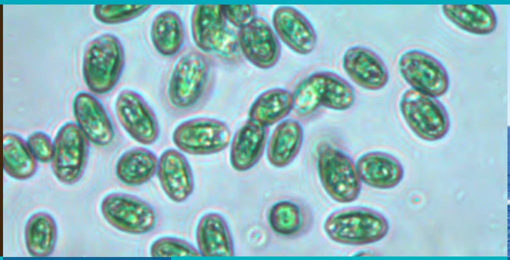
Biodiversity gradients in obligate symbiotic organisms: A case study in lichens in a global diversity hotspot

Proj. 6

Community genomic drivers of moss microbiome assembly and function in rapidly changing Alaskan ecosystems

Proj. 7

US-China: Allosomes and dioecy in plants as drivers of multi-level biodiversity



Proj. 8

Links between spectral irradiance and cryptophyte biodiversity in environments from ponds to oceans

Proj. 9

Diversity, assembly and function of microbial communities on suspended and sinking particles in a marine oxygen deficient zone

Proj. 10

Dynamical interactions between plant and oomycete biodiversity in a temperate forest

Updates
2015

< | *CREDIT*

Ⓐ Martha A. Condon Ⓑ Orianna Bretschger Ⓒ Steven H. Haddock

< | *CREDIT*

Ⓓ Carolyn Wessinger Ⓔ James C. Lendemer Ⓕ Verity Salmon

< | *CREDIT*

Ⓖ Lawrence B. Smart Ⓗ Steven Litaker Ⓘ YK, Shutterstock

< | *CREDIT*

Ⓙ Niklaus Grünwald

Diversification dynamics of multitrophic interactions in tropical communities

Martha A. Condon
Cornell College
(1542451)

Andrew A. Forbes
University of Iowa
(1542269)

Gaelen R. Burke
University of Georgia
(1542290)

Nina A. Theis
Elms College
(1542321)

Brian M. Wiegmann
North Carolina
State University
(1542395)

This project focuses on a species-rich tropical community of plants (Cucurbitaceae), tropical plant-feeding insects, and their predators (parasitic wasps). A major goal is to test the hypothesis that highly specific lethal interactions between herbivores and predators may explain patterns of diversity and diversification.

Update

This year began with a group meeting of all PIs (Burke attended via SKYPE) and some of the students, postdocs, and technicians. The team assessed progress and made plans for the upcoming year. During the past year, two major collecting trips were carried out: one to the Iquitos region of Peru and another to sites at different elevations in Ecuador. Researchers also began analysis of transcriptome data and made significant progress on the RADseq project. One manuscript was accepted for publication in BMC Evolutionary Biology, and one paper was presented at the annual meeting of the Entomological Society of America.

Publications

Ottens et al. (2017) Genetic differentiation associated with host plants and geography among six widespread species of South American *Blepharoneura* fruit flies (Tephritidae). *J Evol Biol 30* 4: 696

Scheffer et al. (2017) Phylogenetics of Australasian gall flies (Diptera: Fergusoninidae): Evolutionary patterns of host-shifting and gall morphology. *Mol Phy Evol* 115: 140-160

Winkler et al. (2017) Anatomy of a Neotropical Insect Radiation. *BMC Evol Biol* 18:30

^ Andrew Joseph (AJ), a Cornell College undergraduate, found the very first plant on our collecting trip in the Iquitos region of Peru. Left to right: Renata Harrison, AJ, Andrew Rasmussen.

CREDIT: MARTY CONDON

^ A voucher photograph of a female branch of *Gurania acuminata* at the Madre Selva field station run by Project Amazonas in the Iquitos region of Peru.

CREDIT: RENATA HARRISON, CORNELL COLLEGE

^ *Gurania eriantha* — one of the host plants of *Blepharoneura* and its parasitoids — at Santa Cruz, a field station run by Project Amazonas in the Iquitos region of Peru.

CREDIT: MARTY CONDON

The phylogenetic and functional diversity of extracellular electron transfer across all three domains of life

Peter Girguis
Harvard University
(1542506)

Orianna Bretschger
J. Craig Venter Institute, Inc.
(1542335)

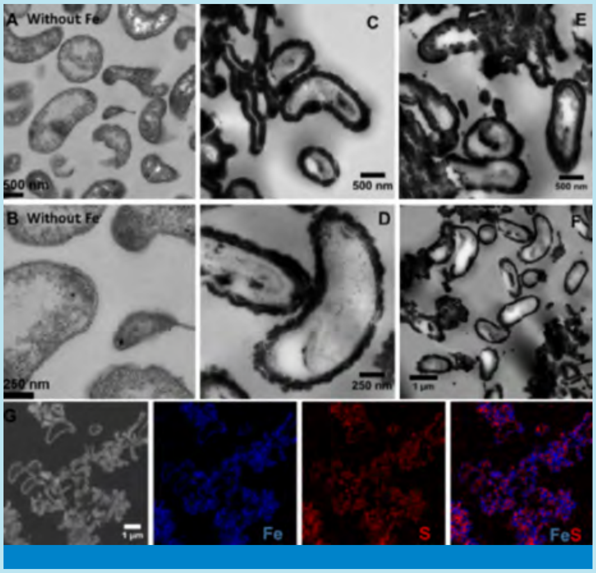
Mohamed Y. El-Naggar
University of Southern California
(1542527)

Jeffrey A. Gralnick
Daniel R. Bond
University of Minnesota, Twin Cities
(1542513)

Life harnesses energy primarily through the transfer of electrons within cells. However, some microorganisms harness energy by passing electrons to the outside of the cell in a process called extracellular electron transfer (EET). This project seeks to identify and characterize the full diversity of EET microbes and the mechanisms they use to transfer energy.

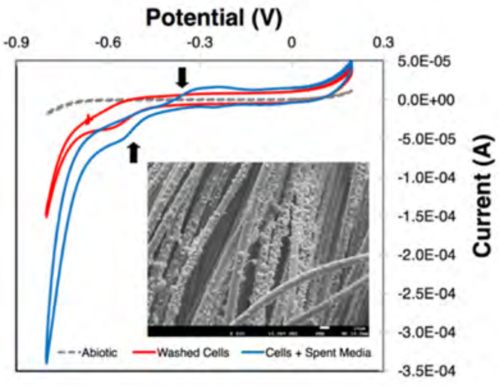
Update

All animals and many microbes harness energy by moving electrons from food (organic matter) to oxygen within the cell. We now know that some microbes can move electrons to solid compounds such as rust (iron oxides) located outside the cell. This remarkable process is called extracellular electron transfer and is the focus of this project. The team is cataloging the diversity of this capacity across all domains of life and have already discovered new microorganisms that use such mechanisms to harness energy and fix carbon. They are also working with the Harvard museum to engage high school students in these discoveries.



^ In an effort to understand the role of extracellular electron transfer in sulfur and iron cycling, cells are grown without (A and B) or with (C through F) iron. These TEM images clearly show that cells grown in iron become encrusted in minerals. Panel G has an SEM image and elemental maps (EDS), from left to right: secondary electron image, iron map, sulfur map, and overlay of both maps.

CREDIT: PICARD ET AL. (2017)



^ *Top:* A dual-chamber electrochemical reactor to investigate extracellular electron transfer.

Bottom: Cyclic voltammetry confirms the extracellular electron transfer capability of the methanogen *Methanosarcina barkeri*; electron uptake is routed to methane production. Arrows point to two distinct pathways for electron uptake. Inset: *M. barkeri* cells attached to working electrode fibers.

CREDIT: ANNETTE ROWE & MOH EL-NAGGAR, UNIVERSITY OF SOUTHERN CALIFORNIA; PETER GIRGUIS

Life at extremes: Linking the phylogenetic and genomic diversity of ctenophores to ecophysiological adaptations in the deep sea

Steven H. Haddock
Monterey Bay Aquarium Research Institute
(1542679)

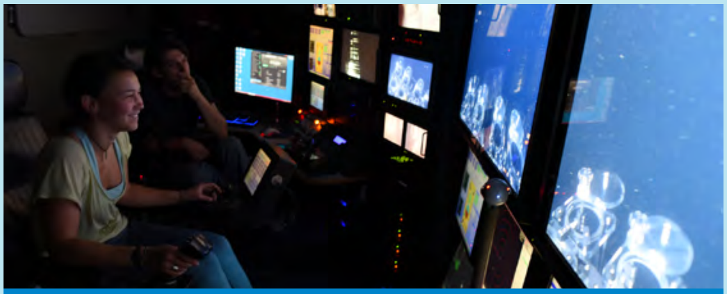
Joseph F. Ryan
University of Florida
(1542597)

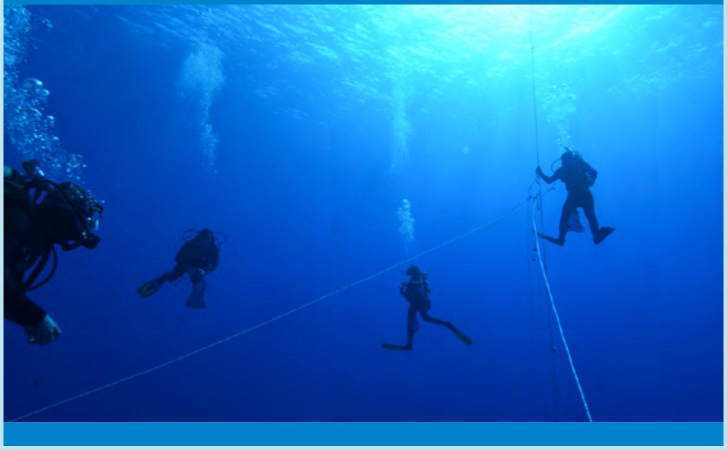
Erik V. Thuesen
Evergreen State College
(1542673)

DEEPC: Diversity, Evolution, and EcoPhysiology of Ctenophores — this project is investigating the genomic and physiological diversity that allow comb jellies to survive in the deep sea.

Update

In the last year, the DEEPC project has conducted field sampling off California and Hawaii, from the surface using SCUBA dives and from as deep as 4000 meters using submersibles and special trawl nets. They have cloned metabolic enzymes from deep and shallow comb jellies (ctenophores), expressed them to create large quantities of purified proteins, and assayed them for activity under a range of pressures. Bioinformatic analyses of 35 ctenophore transcriptomes has been carried out, including implementing different approaches to finding genes and specific amino-acid changes that are associated with adaptation to depth.

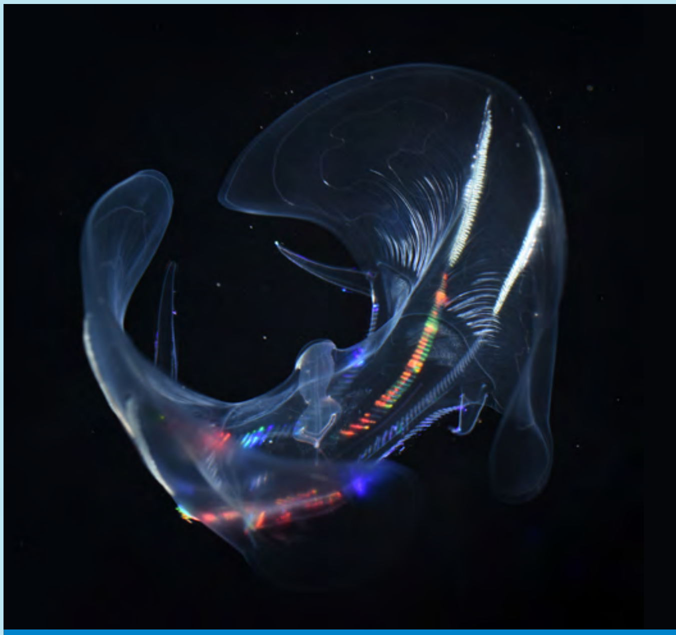




Top: During cruises on MBARI's R/V Western Flyer, the team uses a remotely operated vehicle to collect deep specimens down to 4000 meters. Collections require maneuvering a vehicle the size of a car so that an animal the size of a grape slides undamaged into the sampling tube.

Bottom: A team of blue-water divers collects ctenophores off the coast of Hawaii during an NSF-supported cruise aboard the Research Vessel Ka`imikai-O-Kanaloa. Blue-water diving in the open ocean allows researchers to collect and study fragile shallow species to compare with the deep ROV-collected specimens.

CREDIT: STEVEN HADDOCK



Top: Ocyropsis maculata is one of the most energetic of shallow-living ctenophores. Their many muscle fibers can be seen as striations in the lobes, which they flap to "fly" away during an escape response.

Bottom: Leucothea is a large (20 cm) ctenophore found only in shallow waters. They feed while swimming forward (up in this photo), with their lobes spread like the wings of a biplane.

CREDIT: STEVEN HADDOCK

The evolution of pollination syndrome diversity in *Penstemon*

Lena C. Hileman
Carolyn Wessinger
University of Kansas
Center for Research, Inc.
(1542402)

Mark D. Rausher
Duke University
(1542387)

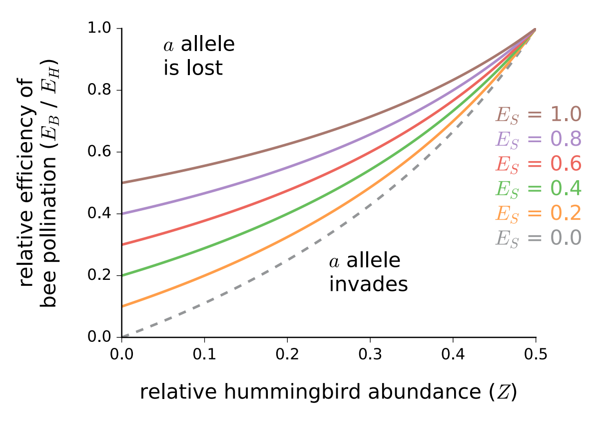
Floral diversity in terrestrial communities often reflects divergent pollination modes (e.g. bees, hummingbirds, butterflies, wind). This research examines ecological and genetic processes that may shape patterns of pollination syndrome diversity in the largest flowering plant genus endemic to North America.

Update

Facilitating all project aims, the team applied a pollen-culture protocol for improved Penstemon genome assembly. They assessed floral trait variation across a population with the ancestral bee-adapted pollination syndrome and found correlations to be parallel to the direction of natural selection, a feature that likely enables rapid pollinator shifts. They developed a population genetic model demonstrating that delayed self-fertilization can facilitate adaptation to hummingbird-pollination via recessive alleles like those that underlie flower color evolution. In addition to postdoctoral and graduate student training, six undergraduates received genuine research experiences, five were women, three underrepresented in STEM; contributing to a diverse scientific workforce.

Publications

Wessinger CA, Kelly JK (2018) Selfing can facilitate transitions between pollination syndrome. *Am Nat* 191: 582–594



^ Conditions where a hummingbird-attraction allele can invade a population otherwise fixed for a bee-attraction allele, expanded according to efficiency of delayed self-fertilization (ES). Lines show threshold values of the relative efficiency of bee-pollination below which the hummingbird allele can invade, as a function of the proportion of pollinators that are hummingbirds (Z).

CREDIT: CAROLYN WESSINGER

^ We assessed within-population flower trait variation in a large population of Penstemon virgatus located in Teller County, Colorado. This species displays the ancestral bee pollination syndrome.

CREDIT: CAROLYN WESSINGER

Biodiversity gradients in obligate symbiotic organisms: A case study in lichens in a global diversity hotspot

James C. Lendemer
New York
Botanical Garden
(1542639)

Erin A. Tripp
Nolan C. Kane
Christy M. McCain
University of
Colorado, Boulder
(1542387)

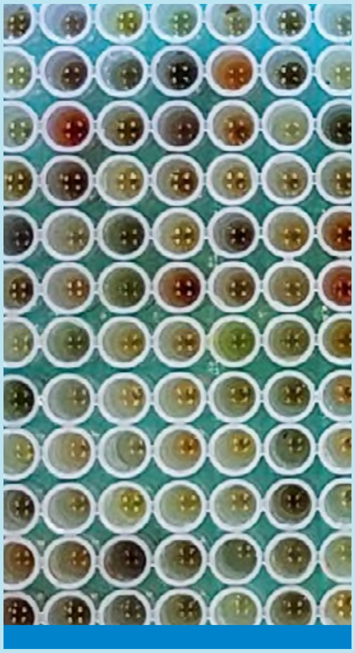
Diversity and distributions of obligate symbiotic organisms: lichens as a model system for deconstructing biotic and abiotic factors that drive major patterns in macroecology and macroevolution.

Update

Substantial education, research, and outreach progress was made. This included a lichen genome assembly course, biodiversity workshop, outreach events nationwide, and a new undergraduate/graduate course entitled *The Lichen Biome* that will be taught in 2018. Completed Alabama fieldwork generated >4,000 museum specimens and hundreds of environmental samples. These data are being synthesized to study biodiversity gradients and environmental impacts on diversity. Permits were obtained for Tennessee fieldwork. Five PhD students, the PIs, and numerous undergraduates assembled >500 lichen metagenomes, prepared the first broad study of lichen mitochondrial genomes, published new species, and continued capturing trait data to study functional diversity.

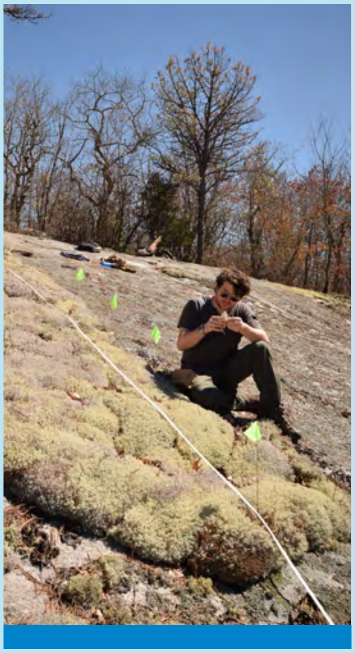
Publications

Lendemer JC, et al. (2017) Taxonomic delimitation of the eastern North American endemic lichen *Santessoniella crossophylla* (Pannariaceae). *J Torrey Bot Soc* 144(4): 459–468



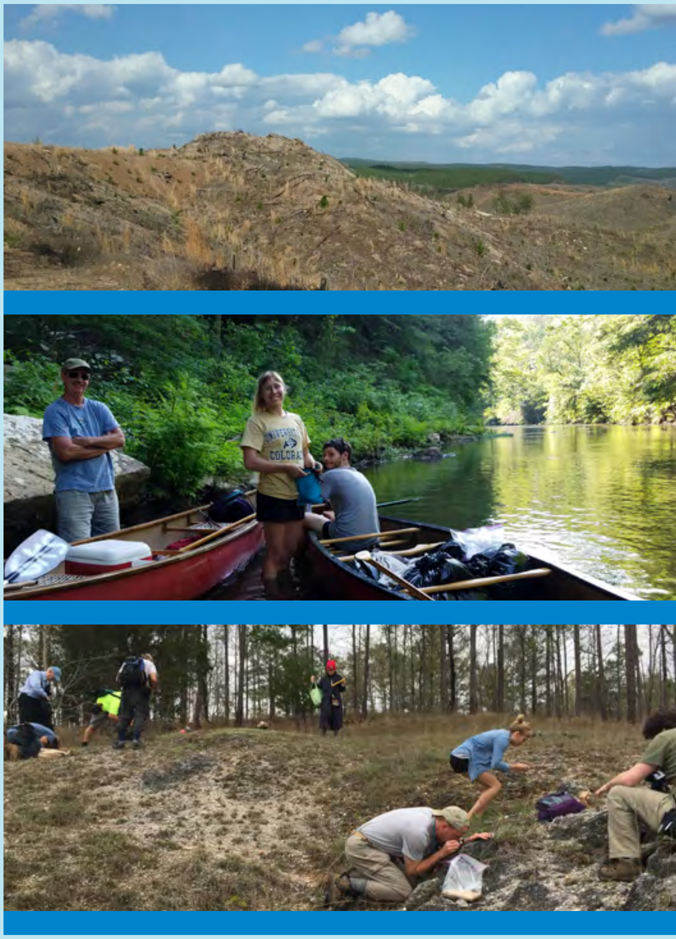
Diversity of lichen metagenome extractions in the Kane Lab at University of Colorado, Boulder.

CREDIT: KYLE KEEPERS, UNIVERSITY OF COLORADO



PhD student Jordan Hoffman from the City University of New York studying reindeer lichens on Whiterock Mountain, Nantahala National Forest, NC.

CREDIT: JAMES C. LENDEMER



Top: Highly disturbed habitat in Coosa County, Alabama.

Middle: PI-McCain admires an old growth tulip poplar in mature forest stands of the Sipsey Wilderness, Bankhead National Forest, Alabama.

Bottom: Participants in the 2017 Tuckerman Lichen Workshop at the Bibb County Glades, northern Alabama.

CREDIT: JAMES C. LENDEMER (TOP & BOTTOM); ERIN TRIPP (MIDDLE)

Community genomic drivers of moss microbiome assembly and function in rapidly changing Alaskan ecosystems

Stuart F. McDaniel
Jose M. Ponciano
University of Florida
(1542609)

Noah Fierer
University of Colorado, Boulder
(1542653)

Michelle C. Mack
Northern Arizona University
(1542586)

This team plans to model the role of bryophyte genetic and phylogenetic variation in driving the assembly and function of their associated microbial community, and model the interactions between these dimensions of biodiversity that influence Arctic and boreal ecosystem processes.

Update

The main project goals are to understand the feedbacks between environment, moss host genotype, and microbial community assembly and function across Alaskan biomes. Researchers have shown that mosses host a broader diversity of N-fixing microbes than was previously appreciated, and that moss species is a better predictor of bacterial community composition than site of origin (Holland-Moritz et al. submitted). To further evaluate this observation, they have begun to analyze more than 600 moss samples, representing 34 moss species from 23 sites that span a latitudinal gradient from the north slope of Alaska to Anchorage. They are now developing novel methods to evaluate the role of moss host phylogeny in shaping the bacterial community assembly and function.

Publications

Lewis, et al. (2017) Future directions and priorities for Arctic bryophyte research. *Arctic Sci* 3: 475-497

Lewis, et al. (2017) Bipolarity in Bryophytes and Lichens: A case study on the origin of the Magellanic sub-Antarctic endemic moss *Tetraplodon fuegianus* (Bryopsida: Splachnaceae). *Am J Bot* 104: 1651-1659

Top: Samantha Miller, Hannah Holland-Moritz, Julia Stuart, Dakshina Marlier, and Lily Lewis establish a transect across a bog near Girdwood, Alaska.
Bottom: Julia Stuart and Samantha Miller prepare a ^{15}N incubation experiment.
CREDIT: STUART F. MCDANIEL

A black spruce forest understory near Anchorage, Alaska, composed of sympatric *Hylocomium splendens* and *Pleurozium schreberi*.
CREDIT: STUART F. MCDANIEL

US-China: Allosomes and dioecy in plants as drivers of multi-level biodiversity

US TEAM

Matthew S. Olson
Texas Tech University
(1542599)

Stephen P. DiFazio
Luke M. Evans
West Virginia University
(1542509)

Kenneth M. Keefover-Ring
University of Wisconsin, Madison
(1542479)

Lawrence B. Smart
Cornell University
(1542486)

CHINA TEAM

Jianquan Liu
Sichuan University

Tongming Yin
Nanjing Forestry University

This research aims to understand how sex-specific differences in poplars and willows influence chromosomal evolution and the biodiversity of their associated insect communities in the U.S. and China, where these plants often play a dominant role in ecosystems.

Update

During the second year of the project, the team confirmed their hypothesis that the chromosomal locations of sex determination regions of willows exhibit extreme dynamism across species. They also implemented a new approach for determining the relationships among different poplar and willow species. Sexual dimorphisms in wild willow and poplar species were studied to understand how they influence genomic evolution. Finally, teams from the US and China convened at a symposium on "Sex Chromosome Evolution in Plants" at the International Botanical Congress 2017 in Shenzhen, China. The broader impacts focused on China-US collaborations and providing undergraduates with experiences in biodiversity-based research projects.

Publications

Carlson CH, et al. (2017) Dominance and sexual dimorphism pervade the *Salix purpurea* L. transcriptome. *Genome Biol Evol* 9: 2377–2394

Hawley PH, et al. (2017) Declawing the dinosaurs: A workshop that lowers teacher anxiety in the biology classroom. In: R Sokol-Chang, G Geher, DS Wilson, and H Head (Eds.), *Evolutionary studies: Darwin's roadmap to the curriculum*. Oxford Univ Press, New York, NY

Olson MS, et al. (2017) Breeding systems, mating systems, and gender determination in angiosperm trees. In: CA Groover and Q Cronk (Eds.) *Comparative and Evolutionary Genomics of Angiosperm Trees*. Springer Int Publishing, New York, NY

^ *Top:* Sampling sexually dimorphic traits on *Salix exigua* near Lincoln, New Mexico.

Bottom: Sampling *Salix purpurea* males and females for floral volatiles.

CREDIT: MATTHEW OLSON (TOP); LARRY SMART, CORNELL UNIVERSITY (BOTTOM)

^ *Top:* Chinese and US collaborators inspecting female fruit of *Idesia polycarpa*.

Bottom: Meeting among Chinese and US principal investigators at Sichuan University in Chengdu, China.

CREDIT: MATTHEW OLSON

^ *Top:* Sampling for chemical dimorphisms between males and females of *Slaix phlebophylla* on Murphy Dome in Alaskan alpine tundra.

Bottom: *Amauronematus spp.* sawfly pollinating *Salix phlebophylla* in Alaskan alpine tundra.

CREDIT: MATTHEW OLSON

Links between spectral irradiance and cryptophyte biodiversity in environments from ponds to oceans

Tammi L. Richardson
Jeffrey L. Dudycha
University of South Carolina
(1542555)

Cryptophytes are microscopic algae found in aquatic ecosystems. This project examines how color of the underwater light field influences the molecular evolution of cryptophyte light-capture genes, the spectral efficiency of their light absorption, and the taxonomic diversification and ecological distribution of cryptophyte species in nature.

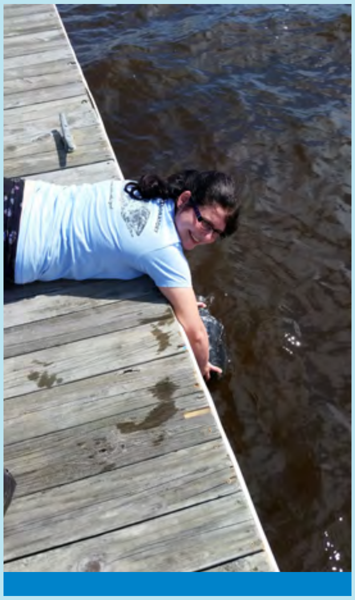
HTTP://WWW.BCO-DMO.ORG/PROJECT/655542

Update

Researchers continue to quantify pigment composition, absorption, fluorescence, and growth rates on >100 Cryptophyte strains grown under different light spectra. An initial phylogeny using rDNA sequences and the phenotypic data support the reclassification of one strain to a different genus, revision of phycobiliprotein (PBP) diversity within *Hemiselmis*, and the inclusion of previously unidentified pink strain in a clade of otherwise green strains. A discriminant analysis predicted 68.6% of the genetic clades using only photosynthetically usable radiation and PBP characteristics. Phylogenetic analysis shows that diversification of light capture in cryptophytes is associated with PBP characteristics, but not cell size or other photosynthetic pigments.

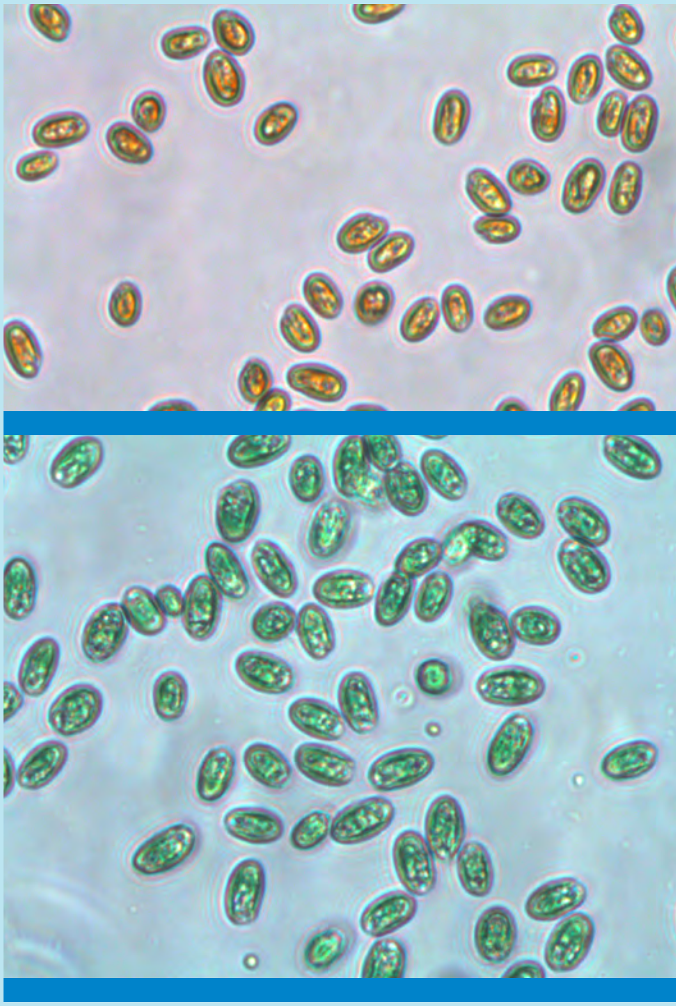
^ Graduate student Kristin Heidenreich collects water from forest ponds near the Belle W. Baruch Marine Field Laboratory (Georgetown, SC) in the search for new strains of freshwater cryptophytes.

CREDIT: RACHEL SCHOMAKER, UNIVERSITY OF SOUTH CAROLINA



^ Graduate student Kristin Heidenreich collects water from the Winyah Bay estuary, S.C., in search of new strains of estuarine/marine cryptophytes.

CREDIT: RACHEL SCHOMAKER, UNIVERSITY OF SOUTH CAROLINA



^ *Top:* Cells of *Rhodomonas salina* under light microscopy, 40x. Individual cell length is approximately 10 micrometers.

Bottom: Cells of *Chroomonas sp.* under light microscopy, 40x. Individual cell length is approximately 20 micrometers.

CREDIT: STEVEN LITAKER, UNIVERSITY OF SOUTH CAROLINA

Diversity, assembly and function of microbial communities on suspended and sinking particles in a marine oxygen deficient zone

Gabrielle Rocap
Curtis Deutsch
Allan H. Devol
Richard G. Keil
University of Washington
(1542240)

This project aims to improve our understanding of nitrogen cycling in an understudied marine microbial system, which can improve predictions for modeling oxygen availability and ocean productivity under future climate scenarios.

Update

Following significant preparation in the project's first year, this year the team conducted its first expedition off western Mexico. They collected sinking and suspended particles from two stations, near shore and offshore, in the oxygen deficient zone (ODZ). Molecular and geochemical tools are being used to determine the types of bacteria and activities thereof in the different niches (free-living, living on suspended particles, and living on sinking particles). They also evaluated changes in the size (per depth and per area) of the ODZ using chemical tracers. The expedition included five undergraduates (all women) who worked on their senior theses projects.

Researchers sample the oxygen deficient zone for marine bacteria and phytoplankton at different ocean depths.

CREDIT: GABRIELLE ROCAP

Office of Naval Research ship R/V *Thomas G. Thompson* is used to collect marine samples with the Rocap research team aboard. A variety of teachers and students are actively involved in the collection efforts.

CREDIT: GABRIELLE ROCAP

Publications

Fuchsman C, Devol A, Rocap, G (2017) Niche partitioning in the N cycling microbial community of an offshore oxygen deficient zone. *Front Microbiol* doi: 10.3389/fmicb.2017.02384

Many areas in the ocean are oxygen deficient, which leads microbes to convert nitrogen in the water into N2 gas. This process leaves the ocean depleted of nitrogen that is an element essential to sustain marine food webs. Climate change is predicted to exacerbate this problem. Many microbes operate in consortia in this N reduction process.

CREDIT: YK, SHUTTERSTOCK

Dynamical interactions between plant and oomycete biodiversity in a temperate forest

Brett M. Tyler
Oregon State University
Niklaus Grünwald
USDA-ARS
James Lutz
Utah State University
Margaret R. Metz
Lewis & Clark College
David K. Oline
Southern Oregon University
(1542681)

This project will examine the role of native oomycete plant pathogens in maintaining plant species diversity in an old growth forest in the Pacific Northwest. This information will improve management of natural ecosystems and diseases that occur within them.

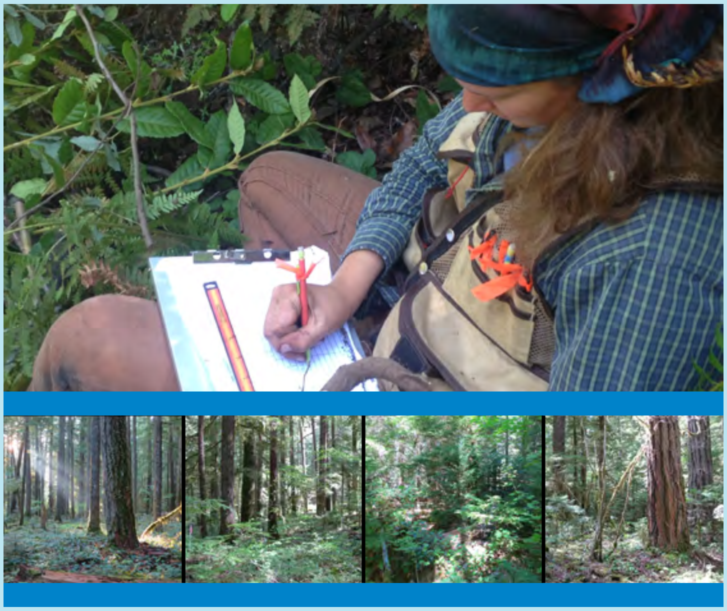
Update

The team completed a recensus of the woody stems in the Wind River Forest Dynamics Plot (WRFD), along with data entry and quality assurance, with the help of 4 undergraduate researchers from USU and SOU. An additional five USU undergraduate students received training in data management techniques and use of ESRI geospatial analysis. USU graduate student, Sara Germain, has been analyzing the growth and mortality data in the 2012-2016 period, primarily with spatial point pattern analyses and correlations with climate data, for a comprehensive paper on the demography of the WRFD. The team, led by post doc Felipe Albornoz, has continued to assess species diversity of plant-associated populations of oomycetes in the WRFD plot via culturing of isolates from conifer needles, soil, and roots.

Publications

Schappe T, et al. (2017) The role of soil chemistry and plant neighbourhoods in structuring fungal communities in three Panamanian rainforests. *J Ecol* 105: 569–579

Swenson NG, Jones FA (2017) Community transcriptomics, genomics, and the problem of species co-occurrence. *J Ecol* 105: 563–568



Top: Undergraduate researchers will conduct much of the forest research. Here, a senior biology major from Lewis & Clark College measures seedlings and forest regeneration.

Bottom: Four images from different parts of the Wind River Forest Dynamics Plot (**http://wfdp.org**) illustrate defining characteristics of this wet, temperate, old-growth ecosystem.

CREDIT: ALLISON SIMLER (TOP); JAMES LUTZ (BOTTOM)

Sudden oak death symptoms on tanoak caused by the oomycete *Phytophthora ramorum.*

CREDIT: NIKLAUS GRÜNWALD

Proj. 1

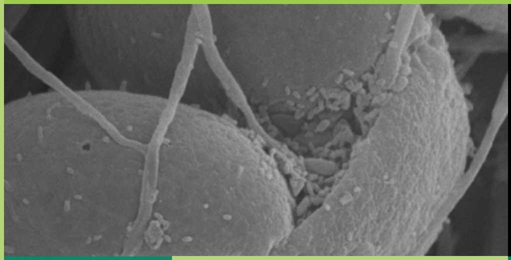
The macroalgal microbiome in space and time — maintaining primary producers in the Atlantic Rocky Intertidal Zone

Proj. 2

Discovering genomic and developmental mechanisms that underlie sensory innovations critical to adaptive diversification

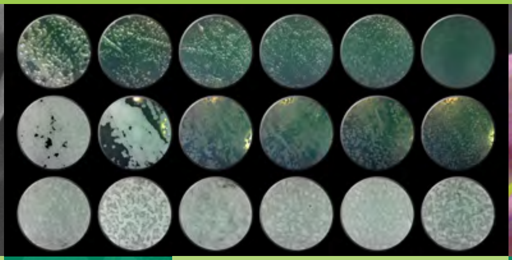
Proj. 3

US-BIOTA-São Paulo: Chemically mediated multi-trophic interaction diversity across tropical gradients



Proj. 4

Taxonomic, genetic and functional biodiversity of above-ground bacterial endophytes in subalpine conifers

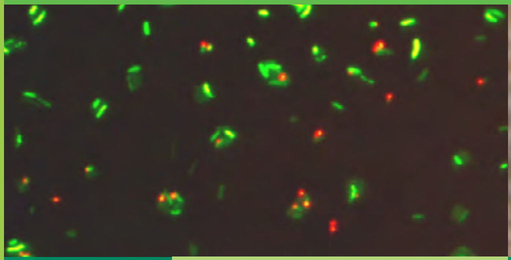


Proj. 5

The making of biodiversity across the yeast subphylum

Proj. 6

Molecular, ecological and evolutionary dynamics of carbon fixation and diversification in Agavoideae (Asparagaceae) and Oncidiinae (Orchidaceae)



Proj. 7

Collaborative Research: Microbial seed banks: processes and patterns of dormancy-driven biodiversity

Proj. 8

Identifying how the ecological and evolutionary interactions between host and symbiont shape holobiont biodiversity

Proj. 9

US-BIOTA-São Paulo: Collaborative Research: Integrating dimensions of microbial biodiversity across land use change in tropical forests

Proj. 10

US-China: How historical constraints, local adaptation, and species interactions shape biodiversity across an ancient floristic disjunction

Proj. 11

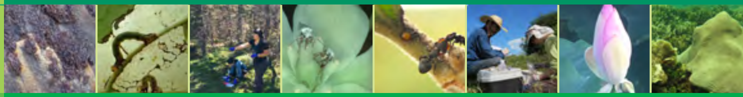
Coevolution of scleractinian corals and their associated microorganisms

Proj. 12

Dimensions: Collaborative Research: Genetic, phylogenetic, and functional microbial diversity in permanently frozen aquatic sediments over geological time

Updates

2014



< | CREDIT

Ⓐ Susan H. Brawley Ⓑ Karen E. Sears Ⓒ Lee Dyer

< | CREDIT

Ⓓ Paola Saldierna Ⓔ Dana A. Opulente & Amanda B. Hulfachor Ⓕ Katia Silvera

< | CREDIT

Ⓖ Sarah Cummins Ⓗ Scott Powell Ⓘ Klaus R. Nüsslein

< | CREDIT

Ⓙ Mark Whitten Ⓚ Ryan McMinds & Jerome Payet Ⓛ E.M. Rivkina

The macroalgal microbiome in space and time—maintaining primary producers in the Atlantic Rocky Intertidal Zone

Susan Brawley
Benildo de los Reyes
John Singer
University of Maine
(1442231)

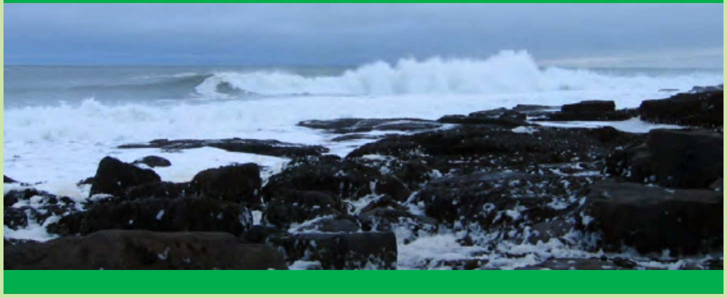
Hilary Morrison
Marine Biological Lab
(1442106)

This research examines the genetic, taxonomic, and functional aspects of the bacteria associated with several macroalgae that are prominent structural "bioengineers" of the intertidal food web.

Update

The team completed the North Atlantic collections of seaweeds *Fucus vesiculosus* and *Porphyra umbilicalis* over 11 stations across the species' biogeographic ranges. Sequencing (V4 16S rDNA tags) of summer samples across the 2-year study is nearly complete. A common garden experiment compared microbial structures recovered under several preparation techniques with analyses using the mothur pipeline versus minimum entropy decomposition (MED) for *Porphyra*. They have begun analysis of the transplant experiment done on the Maine shore in summer 2016. An appointed REU student participated at MBL in extractions of a supplemental set of samples from a species related to *Porphyra*.

Transplant experiments were carried out in the Maine intertidal zone, and research began to develop techniques for establishing axenic macrophytic material for reassociation experiments.



^ *Top:* Seaweed *Porphyra* patches in the barnacle zone at the northern-most site for host microbiome studies of *Porphyra* in the NE Atlantic (Norway, March 2017).

Bottom: Winter collection of *Fucus* and *Porphyra* for reconstitution studies of host and microbiome, Schoodic field site (Acadia National Park, Maine).

CREDIT: SUSAN H. BRAWLEY

^ *Top:* Temperature sensors at edge of *Porphyra* transect, Norway, March 2017.

Bottom: Collaborator Dr. Ladd Johnson (Université Laval) prepared *Fucus* microbiome samples near Peggy's Cove, N. S., March 2017.

CREDIT: SUSAN H. BRAWLEY

Discovering genomic and developmental mechanisms that underlie sensory innovations critical to adaptive diversification

Liliana M. Dávalos Álvarez
State University of
New York, Stony Brook
Stephen Rossiter
Queen Mary University
of London
(1442142)

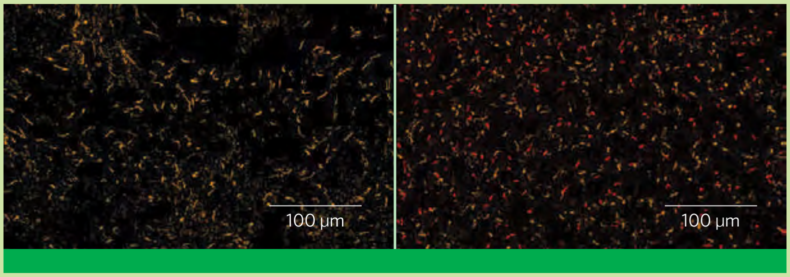
Elizabeth Dumont
University of
Massachusetts,
Amherst
(1442278)

Karen Sears
University of Illinois,
Urbana-Champaign
(1442314)

This international research team connects the evolution of sensory genes, developmental regulation, and morphological structures to the ecological and taxonomic diversity of New World noctilionoid bats, which exhibit a range of distinctive sensory adaptations, including multiple forms of echolocation, vision, and a variety of repertoires for volatile and pheromone olfaction.

Update

Through its Dimensions award, this team has discovered additional losses of pheromonal olfaction throughout the bat radiation, 13 in total, and more than in any other group of mammals. Although the evidence did not support a simple tradeoff with either volatile olfaction or other extreme sensory adaptations, ecological demands in New World leaf nosed and bent wing bats have maintained the vomeronasal system in these groups for tens of millions of years. In parallel, the team has completed collecting transcriptome data from sensory tissues and scaled up data collection through bait capture of sensory genes. During this year, the team has also capitalized on the most complete evolutionary trees of New World leaf nosed bats and relatives to develop the first methods to estimate recovery time for island faunas through natural rates of colonization and speciation after extinction. As the causes of extinction on the islands remain disputed, the team also advanced methods to determine timing of extinction, thereby clarifying the causes of this process. Together, these analyses revealed most extinction events occurred after human arrival and were likely caused by human activities, and the time to recover these losses is at least eight million years. News coverage in *Live Science*, *New Scientist*, and *Newsweek* has brought the research to the public. By uncovering the genetic basis of ecological specialization across mammals, as well as human influence on ancient landscapes, these findings highlight priorities for conservation based on both species and trait diversity and are likely to have practical applications for managing threatened ecosystems today.



Long- (yellow) and short-wave (red) cones—cells bearing photoreceptors—from two bat specimens, visualized using antibody staining and confocal microscopy on flatmounted retinas. Left, *Monophyllus redmani*, a nectar and flower specialist lives in large colonies deep in the darkness of caves, and their retinas show only long-wave cones. Right, *Artibeus jamaicensis*, a gregarious frugivore that roosts in abandoned buildings or the entrance of caves, has both long- and short-wave cones.

CREDIT: ALEXA SADIER, UNIVERSITY OF CALIFORNIA, LOS ANGELES

Publications

Cooke SB, et al. (2017) Anthropogenic extinction dominates Holocene declines of West Indian mammals. *Ann Rev Ecol Evol Sys* 48: 301–327

Valente L, Etienne R, Dávalos LM (2017) Recent extinctions disturb path to equilibrium diversity in the Caribbean. *Nat Ecol Evol* 1:0026, 1–7

Yohe LR, et al. (2017) *Trpc2* pseudogenization dynamics in bats reveal ancestral vomeronasal signaling, then pervasive loss. *Evolution* 71: 923–935

Diaemus youngi, the white-winged vampire bat, specializes on large birds, and is shown feeding on a chicken in Trinidad. Along with the common vampire bat, it is confined to the subtropics and tropics of the New World. They evolved a suite of specialized senses that enable them to detect where blood circulates on their prey, including heat sensors on their nose.

CREDIT: ALEXA SADIER, UNIVERSITY OF CALIFORNIA, LOS ANGELES

US-BIOTA-São Paulo: Chemically mediated multi-trophic interaction diversity across tropical gradients

(CO-FUNDED WITH FAPESP)

US TEAM

Lee Dyer
Christopher Jeffrey
Thomas Parchman
Lora Robinson
Angela Smilanich
University of Nevada, Reno
(1442103)

Scott Shaw
University of Wyoming
(1442110)

John Stireman
Wright State University
(1442134)

Eric Tepe
University of Cincinnati
(1442075)

BRAZIL TEAM

Jorge Massuo Kato
Antonio Salatino
Eny I. Segal Floh
Universidade de São Paulo

André Victor Freitas
Maysa Furlan
Universidade de Campinas

This research examines the diversity of plant chemicals that deter insect herbivory and how plant chemistry can affect the diversity and productivity of entire forests

Eois caterpillar herbivory on *Piper* contributes to tropical forest diversity.

CREDIT: TARA MASSAD, ORGANIZATION FOR TROPICAL STUDIES; ANDRÉ RANGEL, UNIVERSIDADE ESTADUAL DE CAMPINAS

Update

The team is documenting multiple dimensions of diversity of shrubs and vines in the genus *Piper* (Piperaceae) and examining associations between taxonomic, genetic, phytochemical, and interaction diversity on these shrubs. They have established novel experimental and observational methods for discovery of diversity for multi-trophic species assemblages on *Piper* communities at replicated sites along a tropical latitudinal gradient in the Neotropics. Their work has contributed to the systematics of focal genera, including *Piper* (Piperaceae), *Eois* (Geometridae), *Quadrus* (Hesperiidae), and parasitic Braconidae and Tachinidae. They continue the metabolomics approach to quantifying phytochemical diversity to address the question: What are the ecological causes and consequences of variation in phytochemical diversity?

Scenes from the Dimensions site at Fundo Genova, Chanchamayo, Peru. The site is characterized by wet forest, with copious rivers and waterfalls. *Hemeroplanes ornatus* (Sphingidae) feeds on a vine (*Fischeria panamensis*, Asclepiadaceae) embedded in a large mass *Piper* shrub. Katrin Arango, an REU student, and Lidia Sulca, a Peruvian collaborator, finish a *Piper* plot at the site.

CREDIT: LEE DYER

Publications

Blaschke JS, et al. (2018) Molecular phylogenetics and piercer evolution in the bug-killing flies (Diptera: Tachinidae: Phasiinae). Sys Entomol 43: 218–238

Araújo-Vilges KM, et al. (2017) Effect of piplartine and cinnamides on Leishmania amazonensis, Plasmodium falciparum and on peritoneal cells of Swiss mice. Pharmaceutical Biol 55: 1601–1607

Batista ANL, et al. (2017) The combined use of proteomics and transcriptomics reveals a complex secondary metabolite network in Peperomia obtusifolia. J Nat Products 80: 1275–1286

Belokobylskji SA, et al. (2017) Taxonomic revision of the Neotropical species of the braconid wasp genus Pedinotus Szépligeti, 1902 (Hymenoptera: Braconidae: Doryctinae). Zootaxa doi: 10.11646/zootaxa.4327.1.1

Shimbori EM, et al. (2017) A revision of the genus Andesipolis (Hymenoptera: Braconidae: Mesostoinae) and redefinition of the subfamily Mesostoinae. Zootaxa 4216: 101–152

Taxonomic, genetic and functional biodiversity of above-ground bacterial endophytes in subalpine conifers

Anna Carolin Frank
Lara Kueppers
University of California, Merced
(1442348)

Jennifer Pett-Ridge
Lawrence Livermore National Laboratory
(1442348)

This team seeks to determine the evolutionary and ecological significance of a novel symbiosis between pine trees and the nitrogen-fixing endophytic bacteria living inside their foliage. A deeper understanding of how biodiversity of endophytic bacteria affects the capability of forest conifers to fix nitrogen can solve a long-standing ecological mystery: where does the fixed nitrogen in conifer forests come from?

> Students at Sierra Foothill Charter School learning about scientific experiments and beneficial microbes.

CREDIT: DIANNE QUIROZ, UC BERKELY; CAROLIN FRANK; JILL HARRY, CATHEYS VALLEY

Update

The team continued work at the Ecological Staircase and the limber pine biogeographic range. An important part of this project was achieved this year as pine saplings were transplanted to a large labelling chamber and exposed to $15N_2$ gas for several weeks. Both foliage and roots were enriched in 15N at levels consistent with previous rate measurements. Now, the team can visualize 15N in pine needles using nanoSIMS and identify the microbes responsible. In the summer, RET teacher Erika Miranda joined the team in the field and lab and developed curriculum with PI Frank that is being taught in her 5-6th grade classroom.

Publications

Frank AC, et al. (2017) Transmission of bacterial endophytes. *Microorganisms* 5(70): 1–21

^ RET teacher Erika Miranda and PhD student Paola Saldierna taking lodgepole pine samples in Yosemite National Park.

CREDIT: DIANNE QUIROZ, UC BERKELEY; CAROLIN FRANK; JILL HARRY, CATHEYS VALLEY

^ The team labeled pine saplings and cuttings in a large box with $15N_2$ gas for three weeks.

CREDIT: DIANNE QUIROZ, UC BERKELEY; CAROLIN FRANK; JILL HARRY, CATHEYS VALLEY

The making of biodiversity across the yeast subphylum

Chris Hittinger
University of Wisconsin, Madison
Cletus Kurtzman
USDA
(1442148)
Antonis Rokas
Vanderbilt University
(1442113)

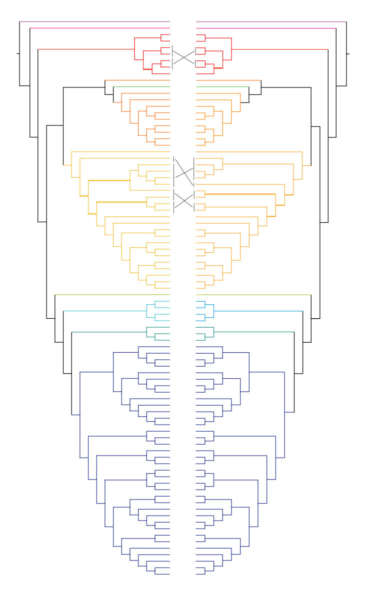
Yeasts of the ancient fungal subphylum Saccharomycotina employ many different resource utilization strategies to allow them to inhabit every continent and every major aquatic and terrestrial habitat. This project seeks to understand the diversification of yeasts by using information written in their genome.

Participating in a semester abroad, Martin Jarzyna, an undergraduate researcher in the Wild YEAST Program collected samples in hopes of isolating rare and new yeast species in the Brazilian wilds. He worked closely with a collaborator, Carlos Augusto Rosa, at the Universidade Federal de Minas Gerais, Brazil.

CREDIT: MARTIN JARZYNA, UNIVERSITY OF WISCONSIN, MADISON

Update

To determine how budding yeasts of the subphylum Saccharomycotina have diversified across their half-billion-year history, researchers are sequencing and analyzing the genomes of all known species and correlating genome content with ecologically relevant traits. They have already generated genome sequence data for more than 1000 yeast species and have begun high-throughput phenotyping. The team has published key computational infrastructure, a genome-based phylogeny for 86 species, taxonomic descriptions for four new species, more than 20 related manuscripts, and multiple review articles and book chapters and are preparing several manuscripts describing the first large batch of core results for the project.



Relationships of budding yeasts of the subphylum Saccharomycotina. Two trees with conflicting topologies are highlighted. Yeast families are color coded. Modified from Shen et al. (2016).

CREDIT: XING-XING SHEN, VANDERBILT UNIVERSITY

Publications

Hittinger CT, et al. (2018) Diverse yeasts for diverse fermented beverages and foods. *Curr Opin Biotechnol* 49: 199–206

Fidler AL, et al. (2017) Collagen IV and basement membrane at the evolutionary dawn of metazoan tissues. *eLife* 6: e24176

Haase MAB, et al. (2017) Genome sequence and physiological analysis of *Yamadazyma laniorum* f.a. sp. nov. and a reevaluation of the apocryphal xylose fermentation of its sister species, *Candida tenuis*. *FEMS Yeast Res* 17(3): fox019

King N, Rokas A (2017) Embracing uncertainty in reconstructing early animal evolution. *Curr Biol* 27: R1081-8

Kurtzman CP, Boekhout T (2017) Yeasts as Distinct Life Forms of Fungi. In: *Yeasts in Natural Ecosystems: Ecology* (Eds. Buzzini P, Lachance MA, Yurkov A) pp. 1–37. Springer International Publishing.

Ortiz JF, Rokas A (2017) CTDGFinder: A novel homology-based algorithm for identifying closely spaced clusters of tandemly duplicated genes. *Mol Biol Evol* 34: 215–29

Shen XX, et al. (2017) Contentious relationships in phylogenomic studies can be driven by a handful of genes. *Nat Ecol Evol* doi:10.1038/s41559-017-0126

Steenwyk J, Rokas A (2017) Extensive copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains. *G3: Genes, Genomes, Genetics* 7: 1475–85

Wisecaver JH, et al. (2017) A global coexpression network approach for connecting genes to specialized metabolic pathways in plants. *Plant Cell* 29: 944–59

Zhou X, et al. (2017) Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets. *Mol Biol Evol* 35(2): 486–503

Molecular, ecological and evolutionary dynamics of carbon fixation and diversification in Agavoideae (Asparagaceae) and Oncidiinae (Orchidaceae)

James Leebens-Mack
University of Georgia
Erin Dolan
University of Texas, Austin
Katia Silvera
University of California, Riverside
(1442199)

Victor Albert
State University of New York, Buffalo
(1442190)

This project compares the genomic basis of physiological adaptations to water limitation in agaves, yuccas and epiphytic orchids. Researchers will identify changes in gene content and function that have enabled evolutionary shifts from typical C3/C4 photosynthesis to Crassulacean Acid Metabolism (CAM), a rare strategy that makes sugar with less water and less concern about heat stress.

Update

This year has seen progress on characterization of diel cycles in photosynthetic physiology and transcriptional profiles for C3, CAM and intermediate species in the Agavoideae and the orchid genus *Erycina*. Transcriptional analyses of *Erycina* resulted in a master's thesis completion by Michelle Hwang at the University of Georgia.

Co-PI Katia Silvera accomplished significant physiological and RNA seq work on *E. pusilla* (CAM) and *E. crista-galli* (C3), in addition to collecting all tissues necessary for RNA seq analysis of both CAM and C3 *Rossioglossum* species and the C3 outgroup. Further, after adding 1,290 orchid species to her existing carbon isotope data set (now totaling 3,000 spp.), she has begun conducting a rigorous ancestral state reconstruction analyses. Finally, Silvera has measured stomatal conductance at multiple time intervals in 60 orchid species, including C3, CAM and intermediate species.

Publications

Unruh SA, et al. (2018) Phylotranscriptomic analysis and genome evolution of the Cypripedioideae (Orchidaceae). *Amer J Bot* doi:10.1002/ajb2.1047

Lin C-Se, et al. (2017) Concomitant loss of NDH complex-related genes within chloroplast and nuclear genomes in some orchids. *Plant J* doi: 10.1111/tpj.13525

Santiago L, et al. (2017) Functional strategies of tropical dry forest plants in relation to growth form and isotopic composition. *Environ Res Letters* doi:10.1088/1748-9326/aa8959

Yang X, et al. (2017) The Kalanchoë genome provides insights into the evolution of crassulacean acid metabolism. *Nat Plants* doi:10.1038/s41467-017-01491-7

Oncidium sotoanum (left) and *Oncidium sphacelatum* (right). Both are epiphytic C_3 species.
CREDIT: KATIA SILVERA

Yucca moths (*Tegeticula* spp.), obligate pollination mutualists to yuccas, are seen pollinating (moth on left) and injecting eggs into a yucca flower (moth on right).
CREDIT: OLLE PELLMYR, AS PUBLISHED IN SEGRAVES, KARI A. "BRANCHING OUT WITH COEVOLUTIONARY TREES." EVOLUTION: EDUCATION AND OUTREACH 3.1 (2010): 62-70. CREATIVE COMMONS LICENSE HTTP://CREATIVECOMMONS.ORG/LICENSES/BY/2.0

Microbial seed banks: Processes and patterns of dormancy-driven biodiversity

Jay Lennon
Kenneth Locey
Indiana University
(1442246)

Stuart Jones
University of Notre Dame
(1442230)

When faced with unfavorable conditions, many organisms enter a reversible state of reduced metabolic activity, or dormancy. This project focuses on how dormancy creates 'seed banks', which are important reservoirs of taxonomic, genetic, and functional biodiversity of microbial communities.

Update

The team has been focusing on how and why dormancy varies among microbes as a result of life history trade-offs. Specifically, they are 1) testing for life history tradeoffs between dormancy and physiological and genomic characteristics by comparing survivorship during prolonged dormancy across a phylogenetically disparate collection of soil bacteria using a traits-based approach, 2) testing predictions regarding the nature of dormancy as a cell-cell communicated response that affects pathogen suppression, plant-soil feedbacks, and ecosystem processes using signaling molecules to directly manipulate microbial seed banks, and 3) developing and testing theoretical predictions regarding the contribution of seed banks to geographic patterns of taxonomic and phylogenetic diversity using communities of soil bacteria from systems with contrasting disturbance histories.

Agricultural landscape at the Kellogg Biological Station Long-Term Ecological Research site.

CREDIT: KURT STEPNITZ, MICHIGAN STATE UNIVERSITY

Publications

Long H, et al. (2018) Evolutionary determinants of genome-wide nucleotide composition. *Nat Ecol Evol* 2: 237–240

Shoemaker WR, Lennon JT (2018) Evolution with a seed bank: the population genetic consequences of microbial dormancy. *Evol App* 11: 60–75

Kuo V, et al. (2017) Whole genome sequence of the soil bacterium *Micrococcus* sp. KBS0714. *Genome Announc* doi: 10.1128/genomeA.00697-17

Lamit LJ, et al. (2017) Patterns and drivers of fungal community depth stratification in *Sphagnum* peat. *FEMS Microbiol Ecoly* doi: 10.1093/femsec/fix082

LaSarre B, et al. (2017) Microbial mutualism dynamics governed by dose-dependent toxicity and growth-independent production of a cross-fed nutrient. *ISMEJ* 11: 337–348

Lennon JT, Locey KJ (2017) Macroecology for microbiology. *Environ Microbiol Rep* 9: 38–40

Lennon JT, et al. (2017) Microbial contributions to subterranean methane sinks. *Geobiology* 15: 254–258

Locey KJ, et al. (2017) Microscale insight into microbial seed banks. *Front Microbiol* doi: 10.3389/fmicb.2016.02040

Shoemaker WR, et al. (2017) A macroecological theory of microbial biodiversity. *Nat Ecol Evol* doi:10.1038/s41559-017-0107

Identifying how the ecological and evolutionary interactions between host and symbiont shape holobiont biodiversity

Corrie Moreau
Field Museum of Natural History
(1442316)

Scott Powell
George Washington University
(1442256)

Jacob Russell
Drexel University
(1442144)

John Wertz
Calvin College
(1442156)

This project explores how the diversity and functional integration of social animals and their bacterial gut symbionts are shaped by historical and contemporary environmental interactions. Lessons learned from this unique system will help researchers to understand the rules governing a ubiquitous but poorly understood partnership—the symbiotic relationship between animals and their gut bacteria.

Update

In the 2016-2017 year, the *Cephalotes*-holobiont biodiversity team completed their massive collection efforts for the genus across its diverse geographic and habitat ranges. Reduced representation genome sequencing has been completed and the phylogenomic inference and comparative analyses are underway. The team published 11 papers related to this project and continues to pursue functional characterization through *in vitro*, *in vivo*, and genomic inferences. Nitrogen-recycling has been characterized as a major feature of *Cephalotes'* gut microbiota. This symbiotic function appears conserved throughout the genus and across a broad geographic range. Symbiotic gut bacteria have, thus, likely played a substantial role in the success of *Cephalotes* ants and their radiation into the arboreal canopy.

Two *Cephalotes borgmeieri* workers in the Brazilian cerrado share nectar after one has finished feeding at a nearby extrafloral nectary (round plant structure to left). Extrafloral nectar is an abundant, sugar-rich food source in the canopy of most tropical habits.

CREDIT: SCOTT POWELL

Publications

Blanchard BD, Moreau CS (2017) Defensive traits exhibit an evolutionary trade-off and drive diversification in ants. *Evolution* 71: 315–328

Hu Y, et al. (2017) By their own devices: invasive Argentine ants have shifted diet without clear aid from symbiotic microbes. *Mol Ecol* 26: 1608–1630

Lin JY, Hobson WJ, Wertz JT (2017) *Saccharedens versatilis* gen. nov., sp. nov., a sugar-degrading member of the *Burkholderiales* isolated from *Cephalotes rohweri* ant guts. *Int J Sys Evol Bio* 67:1–8

Moreau CS, Wray BD (2017) An empirical test of reduced-representation genomics to infer species-level phylogenies for two ant groups. *Insect Sys Div* 1(2): 1–8

Moreau CS, Rubin BER (2017) Diversity and persistence of the gut microbiome of the giant Neotropical bullet ant. *Integ Comp Biol* 57(4): 682–689

Powell S, et al. (2017) Context-dependent defences in turtle ants: resource defensibility and threat level induce dynamic shifts in soldier deployment. *Funct Eco* l31: 2287–2298

Pringle EG, Moreau CS (2017) Community analysis of microbial sharing and specialization in a Costa Rican ant-plant-hemipteran symbiosis. *Proc Roy Soc B* 284: 20162770

Russell JA, Sanders JG, Moreau CS (2017) Hotspots for symbiosis: function, evolution, and specificity of ant-microbe associations from trunk to tips of the ant phylogeny (Hymenoptera: Formicidae). *Myrmecological News* 24: 43–69

Wills BD, et al. (2017) Correlates and consequences of worker polymorphism in ants. *Ann Rev Entomol* 63: 575–598

Winston ME, Kronauer D, Moreau CS (2017) Early and dynamic colonization of Central America drives speciation in Neotropical army ants. *Mol Ecol* 26: 859–870

Winston ME, et al. (2017) Novel approach to heritability detection suggests robustness to paternal genotype in a complex morphological trait. *Ecol Evol* 7(12): 4179–4191

US-BIOTA-São Paulo: Integrating dimensions of microbial biodiversity across land use change in tropical forests

(CO-FUNDED WITH FAPESP)

US TEAM

Jorge Rodrigues
University of California, Davis
(1442214)

Brendan Bohannan
University of Oregon, Eugene
(1442109)

Klaus Rudolf Nüsslein
University of Massachusetts, Amherst
(1442183)

Scott Saleska
Joost van Haren
University of Arizona
(1442152)

BRAZIL TEAM

Sui Mui Tsai
Dernando Andreote
Plinio Camargo
University of São Paulo

The deforestation of tropical forests for agriculture affects the production and consumption of methane, a potent greenhouse gas. The team seeks to identify the microorganisms involved in methane production and consumption, their physiologies and genetics, and their contribution to the flow of methane from Amazon soils to the atmosphere.

University of California, Davis graduate student Rachel Danielson and PI Jorge Rodrigues collecting soil samples in the Amazon rainforest converted to pasture.

CREDIT: KLAUS NÜSSLEIN

Update

The research team has conducted four sampling expeditions to the Amazon rainforest. They performed the deepest metagenomic sequencing to date of Amazonian soils of pristine rainforest and pastures. The molecular level results indicated the methane-consuming microorganisms were significantly affected by land use change, with a decrease in the relative abundance of genes encoding the particulate methane monooxygenase, a key enzyme responsible for consumption of this important greenhouse gas. Additionally, results indicated changes in methanotrophic life history strategy with forest-to-pasture conversion. While stress tolerator life strategies were observed in forest soils, disturbance specialist (ruderal) life strategies were found in pastures. The team collected gas samples in situ and is currently quantifying genes associated with methanotrophy and methanogenic microbial communities.

Old growth rainforest logs removed from primary Amazon rainforest in Rondonia, Brazil.

CREDIT: KLAUS NÜSSLEIN

Publications

Meyer KM, et al. (2017) Conversion of Amazon rainforest soil to agriculture alters community traits of methane-cycling organisms. *Molecular Ecology* 26: 1547–1546

University of Arizona PI Joost van Haren performing real time methane gas measurements in the Amazon rainforest.

CREDIT: KLAUS NÜSSLEIN

US-China: How historical constraints, local adaptation, and species interactions shape biodiversity across an ancient floristic disjunction

(CO-FUNDED WITH NSFC)

US TEAM

Pamela Soltis
Jeremy Lichstein
Douglas Soltis
Eric Triplett
University of Florida
Michelle Mack
University of Arizona, Flagstaff
(1442280)

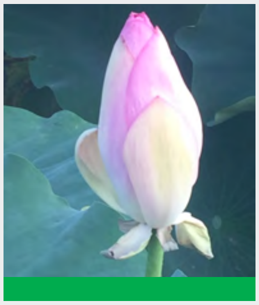
Jack Gilbert
University of Chicago
(1442309)
Jenny Qiuyun Xiang
North Carolina State University
(1442161)

CHINA TEAM

Fu Chengxin
Zao Yunpeng
Qi Zhechen
Zhejiang University

Chen Zhiduan
Chu Haiyan
Chinese Academy of Sciences

In this collaborative project, U.S. and Chinese scientists are conducting analyses of plant and microbial diversity in forests in both the U.S. and China to discover the factors that shape biodiversity through space and time. These forests may be geographically separated, but they share more similarities than many proximate forests.



Sacred lotus, *Nelumbo nucifera*, cultivated in the Wuhan Botanical Garden, Wuhan, China is native to tropical Asia. The closest relative of *N. nucifera* is *N. lutea*, which is native to eastern North America. *Nelumbo* is one of ~65 genera of plants that exhibit a disjunction between eastern Asia and eastern North America.
CREDIT: PAMELA S. SOLTIS

HTTP://WWW.USA-CHINA-BIODIVERSITY.ORG

Update

The highlight of the past year was an extended trip to China for the US team. A project meeting at Zhejiang University in Hangzhou, China, enabled face-to-face sharing of results and development of plans for collaborative analyses and publications. Following the meeting, the joint US-China team visited Tianmushan, with its high species diversity and large numbers of Eastern Asia-Eastern North American disjuncts and the spectacular Shennongjia National Park in western Hubei Province. The trip culminated in a symposium on the Eastern Asia-Eastern North American floristic disjunction at the International Botanical Congress in Shenzhen, China. Data collection on microbial diversity, functional traits, and phylogenetics is ongoing.

Shennongjia National Park, in western Hubei Province, China, is one of the field sites for this Dimensions of Biodiversity project. The US-China collaborative team took a joint field trip to this site in July, 2017.
CREDIT: PAMELA S. SOLTIS

Publications

Lu LM, et al. (2018) Evolutionary history of the angiosperm flora of China. *Nature* 554: 234–238

Yu Y, et al. (2017) Whole-genome duplication and molecular evolution in *Cornus* L. (Cornaceae) — Insights from transcriptome sequences. *PloS ONE* 12(2): e0171361

Collaborators on the project meet at Zhejiang University to discuss results and plan future research.
CREDIT: PAMELA S. SOLTIS

Coevolution of scleractinian corals and their associated microorganisms

Rebecca Vega
Oregon State University
(1442206)

Mónica Medina
Pennsylvania State University
(1442206)

The Global Coral Microbiome Project examines the distribution of coral-associated microbes across the phylogenetic, geographic and anatomical diversity of coral reefs. This project investigates whether the composition of coral microbial communities helps to explain the coral vulnerability through studying trans-continental ecosystems, and sampling genome sequences and metabolites of key coral bacteria.

HTTP://CORALMICROBES.ORG | HTTP://MARINESTUDIES.OREGONSTATE.EDU/GLOBAL-CORAL-MICROBIOME-PROJECT

Update

The Global Coral Microbiome Project aims to characterize and compare the microbiome from all 21 major coral clades. All coral samples have been collected, their bacterial DNA has been extracted and 16S amplicon sequencing has been completed on over three fourths of the coral sample collection. Additionally, 11 bacterial strain genomes have been sequenced. Data analysis on a subset of coral samples from Australia has been completed, and data analysis on the remainder of samples is ongoing. The team plans to investigate metabolic diversity, and codiversification of host and microbiome coevolution and to predict coral susceptibility to bleaching, disease, and extinction.

Publications

Pizarro V, et al. (2017) Unraveling the structure and composition of Varadero Reef, an improbable and imperiled coral reef in the Colombian Caribbean. *Peer J* 5:e4119 doi:10.7717/peerj.4119

Rippe JP, et al. (2017) Population structure and connectivity of the mountainous star coral, *Orbicella faveolata*, throughout the wider Caribbean region. *Ecol Evol* 7: 9234–9246

Thompson LR, et al. (2017) A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* 551: 457-463

Corals sampled to investigate their microbiomes from the Varadero reef in Colombia. This reef is scheduled to be destroyed due to the creation of a shipping channel in the next year.

CREDIT: MÓNICA MEDINA

Dimensions: Genetic, phylogenetic, and functional microbial diversity in permanently frozen aquatic sediments over geological time

Tatiana Vishnivetskaya
Benjamin Fitzpatrick
Alice Layton
Karen Lloyd
Susan Pfiffner
University of Tennessee, Knoxville
(1442262)

Tullis Onstott
Princeton University
(1442059)

This research project addresses the long-pondered question of whether microbes embedded in permafrost are dead (or fossils), representing ancient communities preserved through time, or are living communities that have continued to evolve since becoming buried.

HTTP://CEB.UTK.EDU/PERMAFROST-MICROBIOLOGY
2017 FIELD WORK VIDEOS | HTTPS://WWW.YOUTUBE.COM/WATCH?V=SEUL9TKARW0

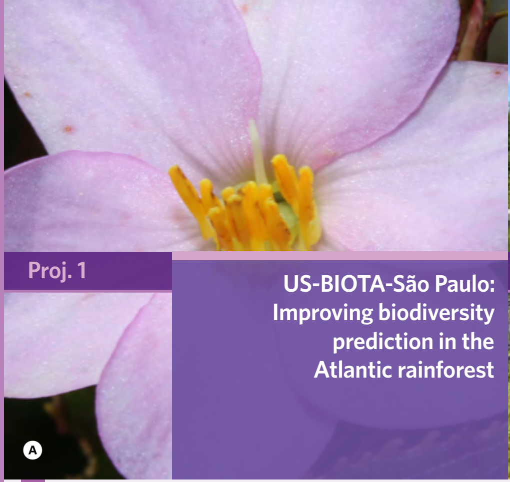
Update

This year the team collected 22-m core of permafrost of marine sediment along the coast of the East Siberian Sea. This core combined with previous cores collected from a different location on the Kolyma lowland represent both freshwater and marine sediments with freezing ages of 3 kyr to 3 myr. Sequencing of extracellular and intracellular DNA from these samples combined with amino acid racemization and 14C analyses will potentially distinguish the extinct from the extant microbial communities and delineate their evolution over that timespan. The team produced mini-documentaries about the permafrost collection sites on the Kolyma lowland.

Publication

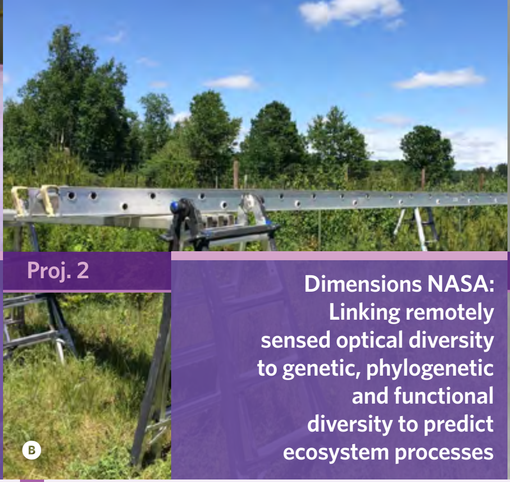
Edwards CR, et al. (2017) Draft genome sequence of uncultured upland soil cluster gammaproteobacteria gives molecular insights into high-affinity methanotrophy. *Gen Announc* 5(17): e00047–17

^ Numerous rivers flowing into the East Siberian Sea are relatively short with a high right bank.
CREDIT: E.M. RIVKINA, IPBPSS, PUSHCHINO, RUSSIA



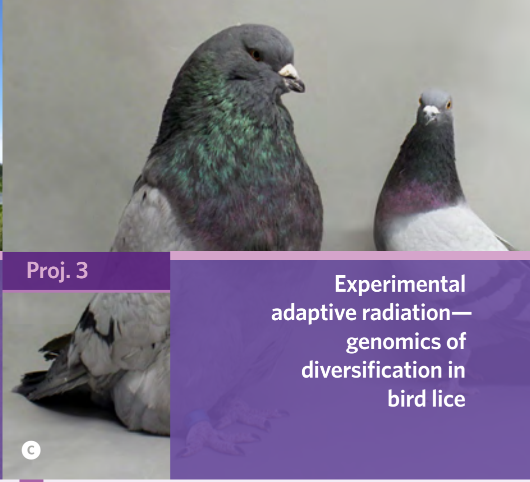
Proj. 1

US-BIOTA-São Paulo: Improving biodiversity prediction in the Atlantic rainforest



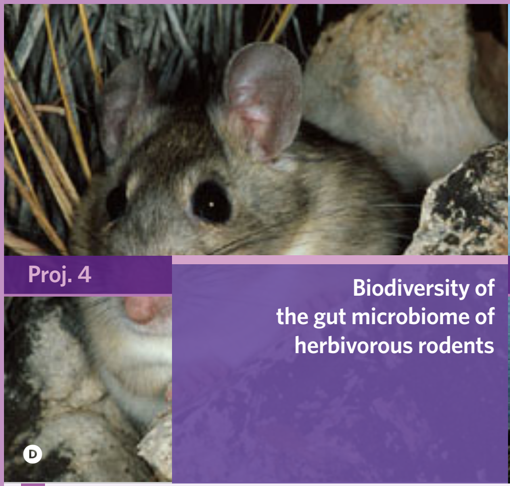
Proj. 2

Dimensions NASA: Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes



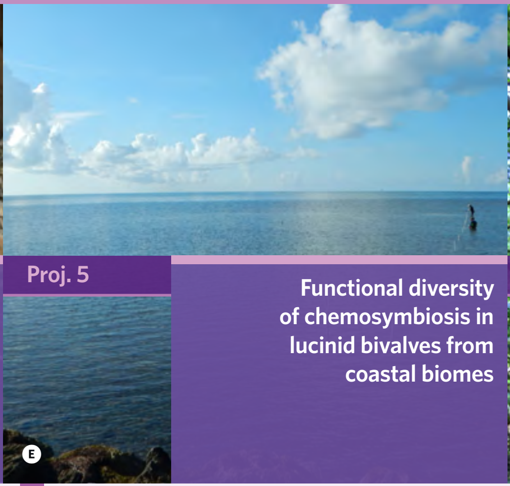
Proj. 3

Experimental adaptive radiation—genomics of diversification in bird lice



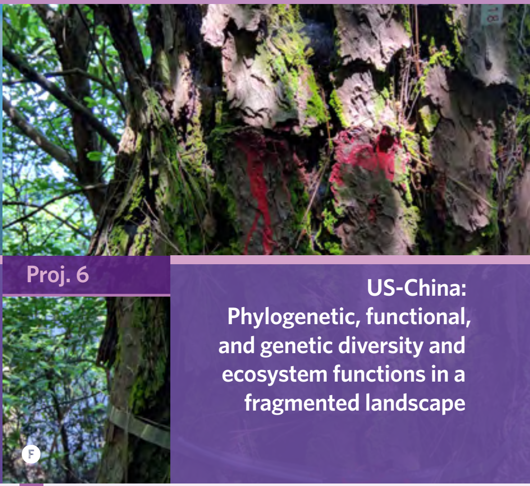
Proj. 4

Biodiversity of the gut microbiome of herbivorous rodents



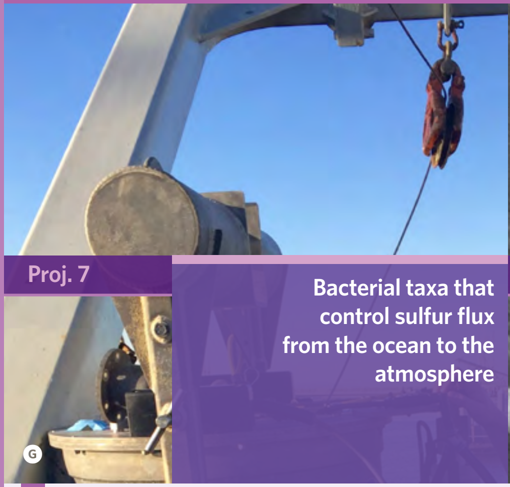
Proj. 5

Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes



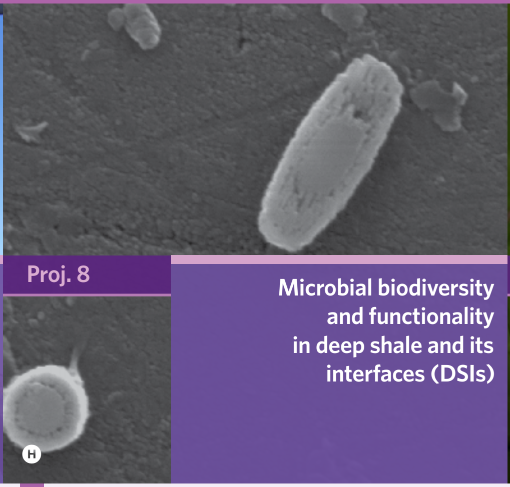
Proj. 6

US-China: Phylogenetic, functional, and genetic diversity and ecosystem functions in a fragmented landscape



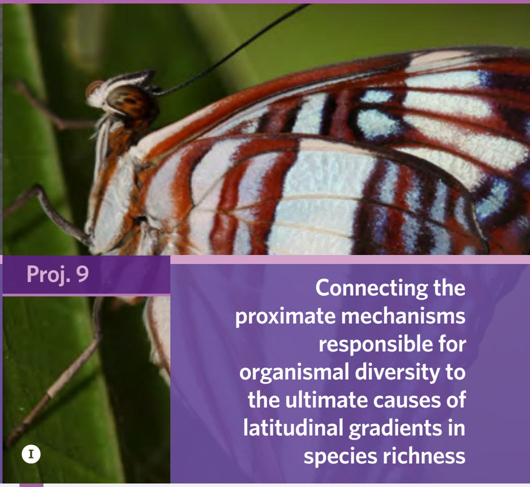
Proj. 7

Bacterial taxa that control sulfur flux from the ocean to the atmosphere



Proj. 8

Microbial biodiversity and functionality in deep shale and its interfaces (DSIs)

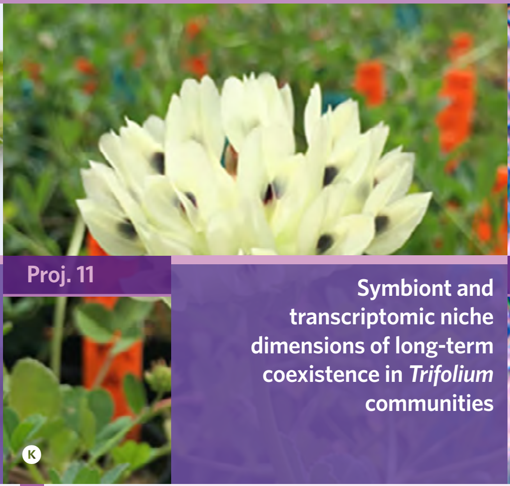


Proj. 9

Connecting the proximate mechanisms responsible for organismal diversity to the ultimate causes of latitudinal gradients in species richness

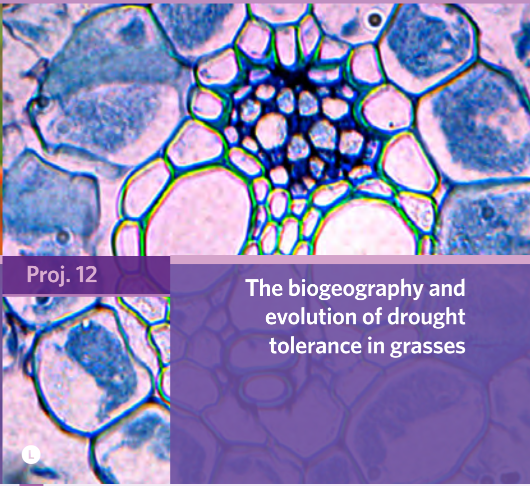
Proj. 10

Landscapes of Linalool: Scent-mediated diversification of flowers and moths across western North America



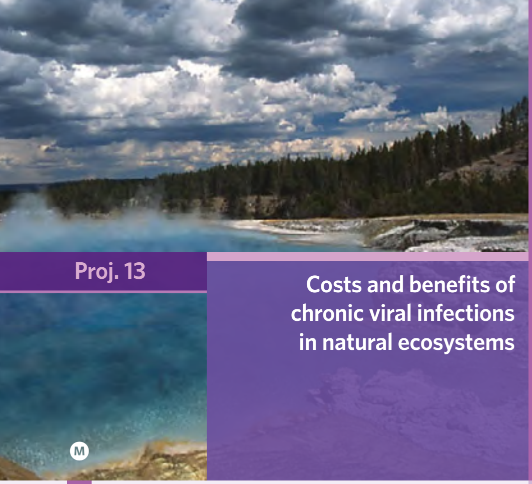
Proj. 11

Symbiont and transcriptomic niche dimensions of long-term coexistence in *Trifolium* communities



Proj. 12

The biogeography and evolution of drought tolerance in grasses



Proj. 13

Costs and benefits of chronic viral infections in natural ecosystems

< | *CREDIT*

Ⓐ Fabian A. Michelangeli
Ⓑ Anna K. Schweiger
Ⓒ Sydney A. Stringham

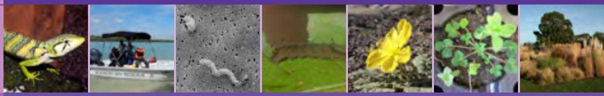
Ⓜ Mark J. Young

Updates

2013

< | *CREDIT*

Ⓓ Denise M. Dearing
Ⓔ Annette S. Engel
Ⓕ Lin Jiang



< | *CREDIT*

Ⓖ Brent Nowinski
Ⓗ David Cole
Ⓘ Keith Willmott

< | *CREDIT*

Ⓙ Tania Jogesh
Ⓚ Andrew Siefert
Ⓛ Joe Craine

US-BIOTA-São Paulo: Improving biodiversity prediction in the Atlantic rainforest

(CO-FUNDED WITH FAPESP)

US TEAM

Ana C. Carnaval
Michael J. Hickerson
Kyle McDonald
CUNY City College
(1343578)

Fabian A. Michelangeli
William W. Thomas
New York Botanical Garden
(1343612)

BRAZIL TEAM

Cristina Yumi Miyaki
Ricardo Pinto-da-Rocha
Francisco Cruz
Universidade de São Paulo

This project aims to develop a framework for predicting spatial patterns of biodiversity in the highly diverse environment of the Brazilian Atlantic Forest. Models are being constructed by integrating numerous types of data including remote sensing, meteorological, locality, phylogenetic, functional, biotic interaction, and paleoenvironmental data.

Update

The team advanced on goals to describe the Atlantic Forest's (AF) environment and biota by synthesizing available data, generating novel and relevant environmental information, and visualizing previously unexplored patterns and hypotheses. The group is building a paleorecord of historical changes in the AF range and putting together contemporary climatologies of the forest based on remote sensing data and microclimate data using hygrobuttons. Additionally, PIs established a protocol for genomic-scale data collection, enabling them to test hypotheses of concerted (community-scale) responses to the environmental gradients that they are describing at multiple temporal scales. Furthermore, progress was made on creating a spatial model of turnover, diversity, and endemism of AF species and lineages. Finally, the NYBG focused this year primarily on generating next gen sequencing data from multiple plant families.

The complex topography of Brazil's coast, where the Atlantic Forest is distributed.
CREDIT: FABIAN A. MICHELANGELI

Publications

Peres EA, et al. (2018) A short-range endemic of Southeastern Atlantic Rain Forest shows deep signature of historical events: phylogeography of the harvestmen *Acutisoma longipes* (Arachnida: Opiliones). *Biodiv Sys* 16: 171–187

Camacho A, Rusch TW (2017) Methods and pitfalls of measuring thermal preference and tolerance in lizards. *J Thermal Biol* 68: 63–72

Chiessi C (2017) Long-term vegetation, climate and ocean dynamics inferred from a 73,500 years old marine sediment core (GeoB2107-3) off southern Brazil. *Quat Sci Rev* 172: 55–71

Coronato-Ribeiro A, Pinto-Da-Rocha R (2017) Systematic revision and cladistic analysis of the genus *Metalibitia* Roewer, 1912 (Opiliones, Cosmetidae, Cosmetinae). *Zootaxa* doi:10.11646/zootaxa.4291.2.1

DaSilva MB, et al (2017). Historical relationships of areas of endemism of the Brazilian Atlantic rain forest: a cladistic biogeographic analysis of harvestman taxa (Arachnida: Opiliones). *Curr Zool* 63: 525–535

Hara MR, et al. (2017) Revision of *Thaumatocranaus* Roewer 1932, with description of two new species (Opiliones: Laniatores: Gonyleptoidea). *Zootaxa* 4254: 457–472

Lipshutz SE, et al. (2017) Behavioral response to song and genetic divergence in two subspecies of white-crowned sparrows (*Zonotrichia leucophrys*). Mol Ecol 26 (11) 3011–3027

CONTINUE >

May R, Catenazzi A, et al. (2017) Divergence of thermal physiological traits in terrestrial breeding frogs along a tropical elevational gradient. *Ecol Evol* 7: 3257–3267

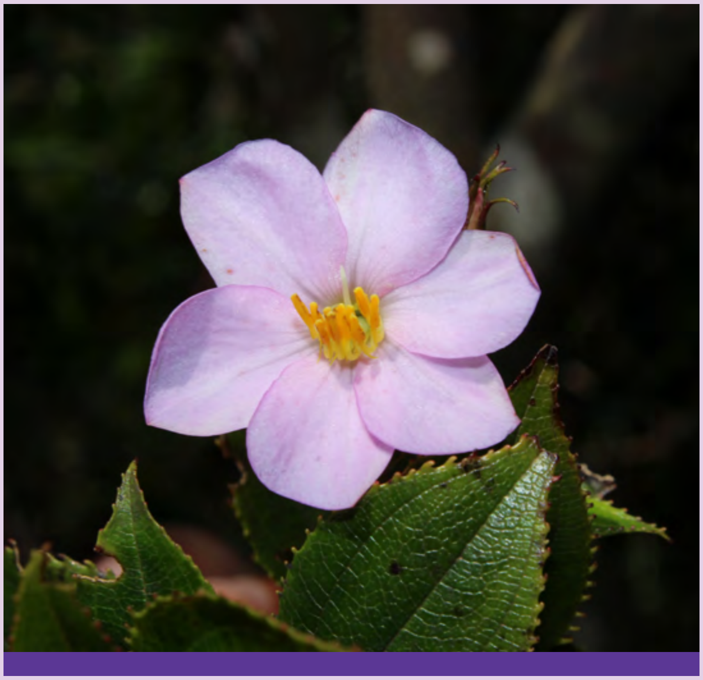
Novello VF, et al. (2017) High-latitude forcing of the South American monsoon from last glacial maximum to the Holocene. *Sci Rep* 7: 44267 DOI: 10.1038/srep44267

Orrico VGD, et al. (2017) Integrative taxonomy supports the existence of two distinct species within *Hypsiboas crepitans* (Anura: Hylidae). *Salamandra* 53(1): 99–113

Pinto-da-Rocha R, Bragagnolo C (2017) Cladistic analysis of the family Nomoclastidae with descriptions of a new genus and eight new species (Opiliones, Laniatores). *Invert Sys* 31: 91–123

Prates I, et al. (2017) Biogeographic links between the southern Atlantic Forest and western South America: rediscovery, re-description, and phylogenetic relationships of two rare montane anole lizards from Brazil. *Mol Phyl Evol* 113: 49–58

Xue AT, Hickerson MJ (2017) Multi-DICE: R package for comparative population genomic inference under hierarchical co-demographic models of independent single-population size changes. *Mol Ecol Resources* 17(6): e212–e224



^ *Behuria mouraei*, known only from two other collecting trips (the last one dating back to the 1930s), is a species restricted to the Eastern Brazilian mountains. By studying narrowly distributed species like this one, we will be able to understand the complex biogeographic patterns of the many biological groups that live in the Atlantic Forest.

CREDIT: FABIAN A. MICHELANGELI

^ *Polychrus marmoratus*, the many-colored bush anole, a lizard from South American rainforests.

CREDIT: IVAN PRATES, CUNY CITY COLLEGE

Dimensions NASA: Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes

(CO-FUNDED WITH NASA)

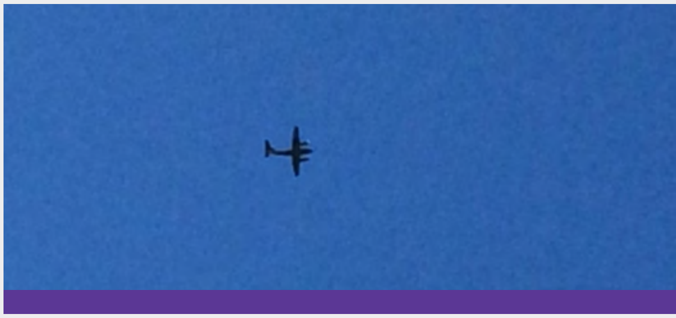
Jeannine M. Cavender-Bares
Sarah Hobbie
Rebecca Montgomery
University of Minnesota, Twin Cities
(1342872)

Michael D. Madritch
Appalachian State University
(NSF 1342827)

Philip A. Townsend
Richard Lindroth
University of Wisconsin, Madison
(1342778)

Arthur I. Zygielbaum
John Gamon
University of Nebraska, Lincoln
(1342823)

Remote sensing methods for monitoring the Earth's biodiversity are being applied to experimental manipulations of plant diversity. This allows scientists to examine the linkages between plant biodiversity, soil microbe diversity, and ecosystem function at multiple scales of spatial resolution.



> NASA AVIRIS flight over Cedar Creek Ecosystem Science Reserve.

CREDIT: ANNA K. SCHWEIGER, UNIVERSITY OF MINNESOTA

Update

The team obtained hyperspectral data, via remote sensing, and ground level measurements of plant properties across individuals, species, and communities. An automated tram was developed to scan vegetation across manipulated and natural systems. Spectral models for a range of leaf traits were constructed for use with vegetation survey data to scale plant chemical and structural characteristics to the community level. They are expanding efforts to link soil chemistry to remote sensing data across a range of systems. Preliminary data showed promise for detecting oak wilt, a fungal disease, from spectroscopy data. Two Native American undergraduates were trained through NSFs Broadening Participation program and presented their work at the 2016 American Indian Science and Engineering Society Meeting.

^ Platform for continuous monitoring of plant function and diversity using a high resolution imaging spectrometer in the Cedar Creek Forest and Biodiversity (FAB) experiment.

CREDIT: ANNA K. SCHWEIGER, UNIVERSITY OF MINNESOTA

Publications

Wang R, (2018) The spatial sensitivity of optical diversity-biodiversity relationship: an experimental test in a prairie grassland. *Ecol Appl* 28: 541–556

Cavender-Bares J, et al. (2017) Harnessing plant spectra to integrate the biodiversity sciences across biological and spatial scales. *Am J Bot* 104(7): 966–969

Cotrozzia L, et al. (2017) Using foliar spectral properties to assess the effects of drought on plant water potential. *Tree Physiol* 37: 1582–1591

Deacon NJ, et al. (2017) Genetic, morphological, and spectral characterization of relictual Niobrara River hybrid aspens (*Populus x smithii Boivin*). *Am J Bot* 104: 1878–1890

Meireles JE, Schweiger AK, Cavender Bares J (2017) Spectrolab: Class and methods for hyperspectral data. R package version 0.0.2

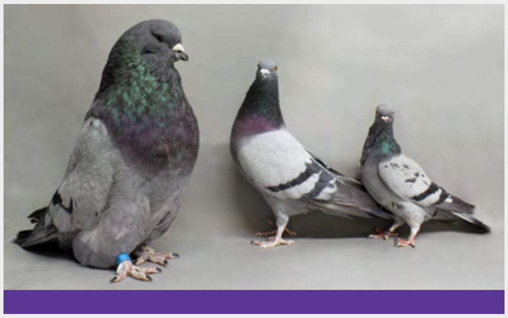
Stavros EN, et al. (2017) ISS observations offer insights into plant function. *Nat Ecol Evol* 1(7): pp.s41559-017. doi:10.1038/s41559-017-0194

Experimental adaptive radiation—genomics of diversification in bird lice

Dale H. Clayton
Sarah E. Bush
Michael D. Shapiro
University of Utah
(1342600)

Kevin P. Johnson
University of Illinois,
Urbana-Champaign
(1342604)

This project will expand the understanding of adaptive radiation using bird-specific ectoparasites as a model system. The researchers are conducting experimental studies that link phylogenetic, genomic, phenotypic, and functional data in order to clarify how micro-and macro-evolutionary processes influence the generation of biodiversity.



< Variation in the body size of rock pigeons (*Columba livia*). Lice were transferred to giant runts (left), the largest domesticated breed of pigeon, wild-caught feral pigeons (center), and figuritas (right), the smallest domesticated breed of pigeon.

CREDIT: SYDNEY A. STRINGHAM, UNIVERSITY OF UTAH

Update

Great progress on the genome assembly has been made by the Shapiro lab over this year with an annotated genome for the wing louse *Columbicola columbae* nearly complete. Experimental work in the Clayton-Bush lab has been moving forward where collected data on lice that have been exposed to different host breeds for approximately 50 generations. In the Johnson lab, phylogenomic analysis of 61 species of pigeons and doves was completed. This major accomplishment was based on data from 6,000 protein coding single copy orthologs and produced extremely well resolved and well supported trees. In preliminary comparisons with the published phylogenomic tree of *Columbicola*, several potential host switching events were identified, as well as a significant number of cospeciation events.

^ Variation in the size and color of lice in the genus *Columbicola*.

CREDIT: : SCOTT M. VILLA, UNIVERSITY OF UTAH

Publications

Allen JM, et al. (2017). Phylogenomics from whole genome sequences using aTRAM. *Sys Biol* 66: 786–798

Boyd BM, et al. (2017). Primates, lice and bacteria: Speciation and genome evolution in the symbionts of hominid lice. *Mol Biol Evol* 34: 1743–1757

Boyd BM, et al. (2017) Phylogenomics using target restricted assembly resolves intrageneric relationships of parasitic lice. (Phthiraptera: Columbicola). *Sys Biol* 1–16

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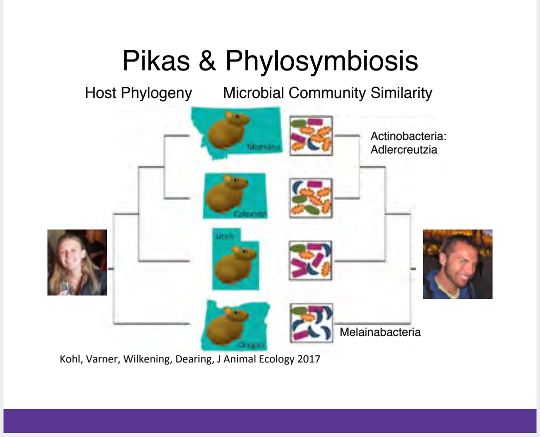
McNew SM, et al. (2017) Epigenetic variation between urban and rural populations of Darwin's finches. *BMC Evol Biol* 17: 183

Sweet AD, et al. (2017) A complete molecular phylogeny of *Claravis* confirms its paraphyly within the small New World ground-doves (Aves: Peristerinae) and implied multiple plumage state transitions. *J Avian Biol* 48: 459–464

Sweet AD, et al. (2017). Comparative cophylogenetics of Australian phabine pigeons and doves (Aves: Columbidae) and their feather lice (Insects: Phthiraptera). *Int J Parasitol* 47: 347–356

Biodiversity of the gut microbiome of herbivorous rodents

Denise M. Dearing
Colin Dale
Robert B. Weiss
University of Utah
(1342615)



Kohl, Varner, Wilkening, Dearing, J Animal Ecology 2017

This project sets out to understand how the evolution and environment of the gut microbiome in herbivorous mammals has helped create a biodiversity hotspot of microbial organisms that in turn may influence the physiology of the host mammal. This work will improve understanding of the metabolism of toxins and diet plasticity in mammals. It has potential applications for improving the health of the human microbiome.

< Evolutionary history plays a role in structuring the gut microbiome of pikas (*Ochotona princeps*).

CREDIT: DENISE DEARING

Update

Researchers have been investigating the diversity and function of gut microbial communities in herbivores, using small mammals as model organisms to advance understanding of these complex relationships. Through microbial transplant studies, they demonstrated that full community transplants persist longer than transplants of single toxin degrading microbes. Their comparative gene expression studies in woodrats (*Neotoma spp.*) and lab rats (*Rattus norvegicus*), with and without toxin metabolizing microbiomes, revealed species specific responses to toxin exposure. This highlights the complexity of the interactions between host and microbial pathways. In examining how evolutionary history and diet influences these microbial communities in the herbivorous pika, *Ochotona princeps*, they found support for the phylosymbiosis hypothesis i.e., that phylogeny plays a key role in structuring gut microbe communities. The team is further investigating phylosymbiosis in multiple species of woodrats that feed on a variety of toxic diets (see diagram). For the third summer, they led a summer camp for middle schoolers that introduced 11 students to the gut microbiome and microbiology through video game design.

^ Belly Bugs instructors Sara Weinstein and Rodolfo Martinez-Mota checking out a student's microbiome game and providing feedback on how microbes eat in the wild.

CREDIT: TESS STAPLETON, UNIVERSITY OF UTAH

Publications

Dearing MD, Kohl KD (2017) Beyond Fermentation: other important services provided to endothermic herbivores by their gut microbiota. *Integr Comp Bio* 57(4): 723–731

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Kohl KD, Dearing MD (2017) Intestinal lymphatic transport: an overlooked pathway for understanding absorption of plant secondary compounds in vertebrate herbivores. *J Chem Ecol* 43: 290–94.

Kohl KD, et al. (2017) Gut microbial communities of American pikas (Ochotona princeps): evidence for phylosymbiosis and adaptations to novel diets. *J Anim Ecol* 87(2): 323–330

Miller, A.W., Dale, C. and Dearing, M.D. (2017) Microbiota diversification and crash induced by dietary oxalate in the mammalian herbivore, *Neotoma albigula*. *mSphere* 2(5): e0048-17

Miller, A.W., Dale, C. and Dearing, M.D. (2017) The induction of oxalate metabolism in vivo is more effective with functional microbial communities than with functional microbial species. *mSystems* 2(5): e00088-17

Ridenhour BJ, et al. (2017) Modeling time-series data from microbial communities. *ISME J* 11: 2526–2537

Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

Annette S. Engel
University of Tennessee, Knoxville
(1342785)

Laurie C. Anderson
South Dakota School of Mines and Technology
(1342721)

Barbara J. Campbell
Clemson University
(1342763)

Organisms that live within another species (endosymbionts) are common within bivalves, a type of mollusk. These endosymbionts offer chemical nutrients to the host in a relationship called chemosymbiosis. This project explores uncharacterized coastal marine biomes to investigate the phylogenetic, genetic, and functional dimensions of biodiversity in modern and ancient lucinid bivalve chemosymbioses.

HTTP://ANNETTESUMMERSENGEL.COM/DIMENSIONS

Update

Fieldwork in the Bahamas and Florida continues to generate new ecological information and taxonomic inventories for the presence (and absence) of lucinids and their symbionts in seagrass, mangrove, and bare sand habitats. This year, field research to new areas of Florida, ranging from pristine to heavily impacted by anthropogenic activities, uncovered new taxonomic records. Some of the field areas were impacted by major hurricanes this year, which will provide future information about lucinid population resiliency and recovery. Graduate and undergraduate students continue to characterize morphometrics data of landmarks inside shells, as well as host and endosymbiont diversity from environmental samples, metagenomes, and metatranscriptomes.

^ Broc Kokesh (Masters student) and Brooke Long (Doctoral Candidate) cataloging lucinid bivalve specimens in the James E. Martin Paleontology Research Laboratory at South Dakota School of Mines and Technology, Rapid City, SD.

CREDIT: BROOKE LONG, GEOLOGY AND GEOLOGICAL ENGINEERING, SOUTH DAKOTA SCHOOL OF MINES AND TECHNOLOGY

^ *Top:* Volunteers from Team Ocean helped explore nearly pristine habitats for lucinids in Rookery Bay Reserve, Florida.

Bottom: Staff at the Keys Marine Lab, Florida, assisted with sampling lucinid populations off carbonate shoals and banks.

CREDIT: ANNETTE SUMMERS ENGEL

US-China: Phylogenetic, functional, and genetic diversity and ecosystem functions in a fragmented landscape

(CO-FUNDED WITH NSFC)

US TEAM

Lin Jiang
Georgia Tech
Research Corporation
(1342754)

Jianguo Wu
Arizona State University
(1342757)

CHINA TEAM

Ming-jian Yu
Zhejiang University

Zhihong Xu
Zhejiang Agriculture and
Forestry University

Jianbo Lu
Hangzhou Normal University

Xiao-yong Chen
East China Normal University

The major goal of this project is to use the Thousand Island Lake (TIL) region of Southern China as an idealized model of habitat fragmentation to study the ecological determinants of multiple dimensions of biodiversity of woody plant and arthropod assemblages, and their linkage to ecosystem functions.

Research scientist Jiaqi Tan (left) and Ph.D. student Xiang Yang (right) retrieving litterbags from a litter decomposition experiment on one of the TIL islands.

CREDIT: JIAQI TAN, GEORGIA TECH

Update

The team continued the collection and analyses of data on plants, arthropods, and soil microbes on the Thousand Island Lake islands. The second plant survey was completed in 2017. Functional trait measurements on common woody plant species are almost completed, and their growth is being monitored periodically; population genetic analysis is being conducted for representative species. A new litter decomposition experiment was implemented in Nov 2016 and completed in Nov 2017. Soil microbes were sampled again in May 2017 to gauge their temporal and spatial variation. Tens of thousands of insect individuals were collected, and their identification is ongoing.

Publications

Chen S, et al. (2018) Plant diversity enhances productivity and soil carbon storage. *PNAS* 115: 4027–4032

Lv K, et al. (2018) Habitat fragmentation influences gene structure and gene differentiation among the *Loxoblemmus aomoriensis* populations in the Thousand Island Lake. *Mitochondrial DNA A DNA Mapp Seq Anal* 29: 222–227

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Yang X, et al. (2018) Nitrogen Nitrogen fertilization, not water addition, alters plant phylogenetic community structure in a semi-arid steppe. *J Ecol* 106: 991–1000

Gan X, et al. (2017) When to use what: Methods for weighting and aggregating sustainability indicators. *Ecol Indicators* 81: 491–502

Li T, Xu ZH (2017) A new species of *Loboscelidia* (Hymenoptera: Chrysididae: Loboscelidiinae) from China. *Entomotaxonomia* 39:1 63–168

Liu Z, et al. (2017) Habitat Loss and Fragmentation During Urbanization. In: *Lectures in Modern Ecology (VIII): Advances in Community, Ecosystem and Landscape Ecology* (Y. Gao, J. Wu eds.) Higher Education Press, Beijing

Ma ZY, et al. (2017) Climate warming reduces the temporal stability of plant community biomass production. *Nat Comm* 8: 15378. doi: 10.1038/ncomms15378

Ojima MN, Jiang L (2017) Interactive effects of disturbance and dispersal on community assembly. *Oikos* 126: 682–691

Peng C, et al. (2017) CeO2 nanoparticles alter the outcome of species interactions. *Nanotoxic* 11: 625–636

Pu Z, (2017) Predator-prey coevolution drives productivity-diversity relationships in planktonic systems. *Am Nat* 189: 28–42

Tan J, et al. (2017) Spatial storage effect promotes biodiversity during adaptive radiation. *Proc Roy Soc B* 284: 20170841

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Tong X, et al. (2017) Habitat fragmentation alters predator satiation of acorns. *J Plant Ecol* 10: 67–73

Wilson MC, et al. (2017) A review of the economic, social, and environmental impacts of China's South-North Water Transfer Project: a sustainability perspective. *Sustainability* 9: 1489

Wu J (2017) Landscape Ecology. In: *Encyclopedia of Ecology 2nd ed.* (Brian Fath, ed.), ElsevierPress

Wu J (2017) Seascape Ecology and Landscape Ecology: Distinct, Related, and Synergistic. In: *Seascape Ecology* (Simon J Pittman, ed.), Wiley-Blackwell Publ

Yang Z, et al. (2017) Daytime warming lowers community temporal stability by reducing the abundance of dominant, stable species. *Glob Chg Biol* 23: 154–163

Zhang Q, Wu J (2017) Research advances in the relationship between functional diversity and ecosystem function. In: *Lectures in Modern Ecology (VIII): Advances in Community, Ecosystem and Landscape Ecology* (Y Gao, J Wu eds.) Higher Education Press, Beijing

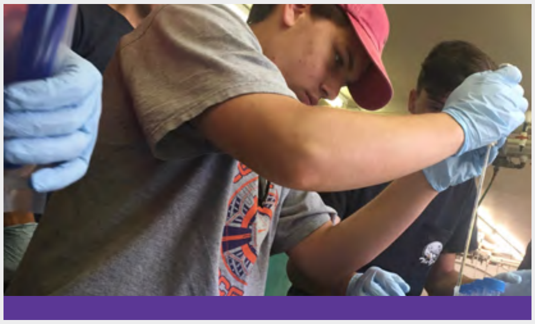
Bacterial taxa that control sulfur flux from the ocean to the atmosphere

Mary Ann Moran
William Whitman
University of Georgia
(1342694)

James Birch
Christopher Scholin
Monterey Bay
Aquarium Research
Institute
(1342734)

Ronald Kiene
University of South
Alabama
(1342699)

This project seeks to understand how the regulation of dimethylsulfoniopropionate (DMSP) metabolism in marine bacteria affects the climate-relevant sulfur cycle between the ocean and the atmosphere. The goal is to understand how the diversity and community structure of microbial life impacts the fate of oceanic and atmospheric chemicals.



> High school students isolate marine bacteria on a field trip to the University of Georgia Marine Institute in April 2017. Back in their classroom, students learn molecular biology concepts through laboratory exercises designed around the bacterial strains.

CREDIT: FRANK XAVIER FERRER-GONZÁLEZ, UNIVERSITY OF GEORGIA

Update

Model system experiments with co-cultured marine microbes have identified a suite of novel organic sulfur metabolites that are released by phytoplankton into seawater and rapidly cycled by heterotrophic bacteria. Although sulfur is plentiful in seawater in the form of sulfate, and not considered to limit microbial activity, the PIs conservatively estimate that these dissolved organic sulfur compounds are supporting a quarter of bacterial secondary production. The metabolic fate of the reduced sulfur moiety after assimilation by bacteria varies by metabolite and can be directed to the biosynthesis of S-containing biomolecules or oxidized for energy or released in an incompletely oxidized state.

^ Model systems consisting of DMSP-producing phytoplankton and DMSP-degrading bacteria test hypotheses on the role of this compound as a sulfur source, compatible solute, and antioxidant.

CREDIT: FRANK XAVIER FERRER-GONZÁLEZ, UNIVERSITY OF GEORGIA

Publications

Lavoie M, et al. (2018) Do polar diatoms take up a quantitatively important fraction of dissolved dimethylsulfoniopropionate? *Aquatic Microb Ecol* doi: 10.33354/ame01871

Landa M, et al. (2017) Bacterial transcriptome remodeling during sequential co-culture with a marine dinoflagellate and diatom. *ISME J* 11: 2677–2690

Lizotte M, et al. (2017) Dimethylsulfoniopropionate (DMSP) and dimethylsulfide (DMS) cycling across contrasting biological hotspots of the New Zealand Subtropical Front. *Ocean Sci* 13: 961–982

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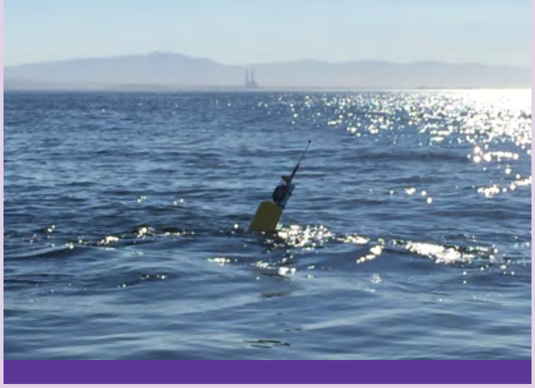


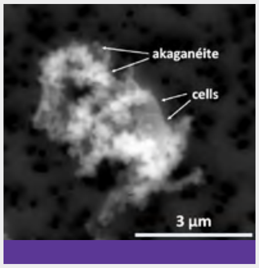
^ The Environmental Sample Processor deployed in Monterey Bay, CA, for autonomous sampling of bacteria transforming DMSP during a Fall, 2016 phytoplankton bloom.

CREDIT: BRENT NOWINSKI, UNIVERSITY OF GEORGIA

Microbial biodiversity and functionality in deep shale and its interfaces (DSIs)

Paulam J. Mouser
David Cole
Michael Wilkins
Kelly Wrighton
Ohio State University
(1342701)

Shikha Sharma
West Virginia University
Research Corporation
(1342732)



This project will characterize the diversity of microbes living at deep shale interfaces, identify the origin of these microbes within geologic time, and assess how this community is adapting to changing environments. With increased hydraulic fracturing, these deep shale environments may be particularly at risk for biodiversity change.

< Scanning Electron Microscopy (SEM) image of microbial cells and akaganéite (β-FeO(OH,Cl)) precipitates from a hydraulically fractured well in the Marcellus shale, WV.

CREDIT: PROF. DAVID COLE

Update

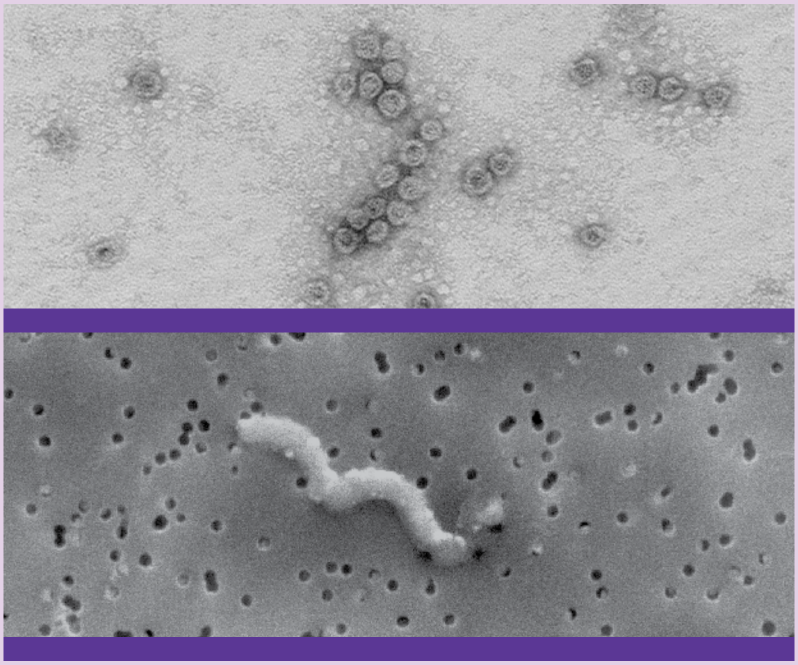
Throughout 2017, the team continued to collect and analyze samples from cores and produced fluids from hydraulically fractured shale wells at the Marcellus Shale Energy and Environmental Laboratory site in Morgantown, WV. Additionally, in January 2017, samples were collected from well piping positioned ~2,000 m below ground surface for cultivation and biomarker analysis. Dozens of salt-tolerant taxa have been isolated from the system, including *Frackibacter*, an obligate fermenter and newly discovered genus that may be native to fractured shales. Laboratory experiments confirming key fermentation, methanogenic, and xenobiotic-degrading metabolisms identified in genomic data as well as viral lysis mechanisms are underway.

Publications

Akondi R, et al. (2017) A modified lipid extraction method for deep subsurface shales. *Front Microbiol* doi: 10.3389/fmicb.2017.01408

Booker AE, et al. (2017) Sulfide generation by dominant colonizing *Halanaerobium* microorganisms in hydraulically fractured shales. *mSphere* 2(4): 00257-17

Booker AE, et al. (2017) Draft genome sequences of multiple *Frackibacter* strains isolated from hydraulically fractured shale environments. *Gen Announc* 5: e00608-17



^ *Top:* Viral particles generated from the lysis of a Halanaerobium bacterium that colonizes hydraulically-fractured shales.

Bottom: Scanning Electron Microscopy (SEM) image of Arcobacter sp. isolated from fluids produced from a hydraulically fractured well in the Marcellus shale, WV.

CREDIT: MICHAEL WILKINS (TOP); SUE WELCH, OHIO STATE UNIVERSITY (BOTTOM)

^ Field crew members pull the production tubing from thousands of feet below ground in preparation for natural gas production logging at the Marcellus Shale Energy and Environment Laboratory (MSEEL) in Morgantown, WV.

CREDIT: ANDREA HANSON, OHIO STATE UNIVERSITY

Connecting the proximate mechanisms responsible for organismal diversity to the ultimate causes of latitudinal gradients in species richness

Sean P. Mullen
Trustees of
Boston University
(1342712)

Adriana D. Briscoe
University of California,
Irvine
(1342759)

Ryan I. Hill
University of the Pacific
(1342706)

Marcus R. Kronforst
University of Chicago
(1342790)

Keith R. Willmott
University of Florida
(1342705)

This project connects genetic, molecular, and cellular mechanisms underlying adaptive variation within species to the ultimate causes of higher-order species diversity. Using the radiation of neotropical *Adelpha* butterflies, this team integrates phylogenetic and genomic insights about the evolution of adaptive traits with data from the ecology and natural history of the butterflies.

Update

In this very active year, a series of large-scale field experiments were conducted to test core predictions of Batesian mimicry theory at both temperate and tropical sites and examine geographic variation in predation intensity across an expansive latitudinal gradient at both low and mid-elevation predator communities. Work in Costa Rica and Ecuador focused on characterizing niche breadth and biotic interactions and discovering new natural histories. Improvements in the *Limenitis* reference genome enabled the investigation of genome-wide patterns of introgression and selection related to color pattern evolution among North American species of *Limenitis* as well as characterization rates of molecular evolution across the Adelpha phylogeny using RNAseq. Libraries are being made from RNA isolated from eye+brain, legs, mouthparts, and antennae of *Adelpha* and/or *Limenitis* and de novo transcriptomes assembly is ongoing. Lastly, investigation of species boundaries in the *A. serpa* group is nearly complete and examination of *A. serpa*, a species with very wide host breadth, indicates a lack of cryptic species.

^ Ultimate instar of *Adelpha naxia naxia*. Observations in southwest Costa Rica have added significantly to the information of this little known species. Our descriptions of the immature stages and knowledge of their food plants will help in understanding species groups and interpreting patterns of evolution within the genus.

CREDIT: R.I. HILL AND C.E. RUSH, UNIVERSITY OF THE PACIFIC

Publications

Finkbeiner SD, et al. (2018) Frequency-dependence shapes the adaptive landscape of imperfect Batesian mimicry. *Proc Roy Soc B* doi: 10.1098/rspb.2017.2786

Finkbeiner SD, et al. (2017) Complex dynamics underlie the convergent evolution of imperfect Batesian mimicry. *Evolution* 71(4): 949–959

Mazo-Vargas A, et al. (2017). Macro-evolutionary shifts of WntA function potentiate butterfly wing pattern diversity. *PNAS* 114: 10701–10706

Rossato DO, et al. (2017) Subtle variation in size and shape of the whole forewing and the red band among comimics revealed by geometric morphometric analysis in *Heliconius* butterflies. *Ecol Evol* 8: 3280–3295

Rush CE, Hill RI (2017) Life history descriptions for *Adelpha naxia* and *A. nea* from Costa Rica. *J Lepid Soc* 71(4): 249–260

Southcott L, Kronforst MR (2017). A neutral view of the evolving genomic architecture of speciation. *Ecol Evol* 7: 6358–6366

Westerman EL, et al. (2017). Does male preference play a role in maintaining female limited polymorphism in a Batesian mimetic butterfly? *Behav Process* 150: 47–58

Zhang W, et al. (2017) Tracing the origin and evolution of supergene mimicry in butterflies. *Nat Comm* doi: 10.1038/s41467-017-01370-1

Landscapes of Linalool: Scent-mediated diversification of flowers and moths across western North America

Krissa Skogen
Jeremie B. Fant
Norman Wickett
Chicago Botanic Garden
(1342873)

Rachel A. Levin
Amherst College
(1342805)

Robert A. Raguso
Cornell University
(1342792)

We commonly think of floral scent for its role in attracting pollinators, but it can also be a cue for floral and seed predators. This project integrates chemical ecology and comparative genomics to explore the impact of past selective pressures on current patterns of diversity in non-model organisms: evening primroses, hawkmoths, bees, and micromoths.

HTTP://ONAGMOTH.ORG

Update

The team has progressed in phylogenetic studies, behavior and fitness experiments, and chemical analysis of floral volatiles. Tribal-wide sequencing has been conducted for most Onagreae taxa, leveraging the ability to use herbarium material, and a phylogeny for *Oenothera* section *Pachylophus* was completed. To test the functional role of the documented geographic variation in (R)-(-) linalool emission by flowers of *O. harringtonii*, a series of phenotypic selection studies have been designed, regressing linalool emissions against seed fitness and *Mompha* seed predation at four populations. These experiments complement the manipulative field experiment at La Junta and laboratory bioassays with captive *Hyles lineata* hawkmoths where choice assays with naïve moths are ongoing. One new such experiment will test whether this volatile elicits changes in egg laying behavior.

Publications

Broadhead GT, et al. (2017) Diel rhythms and sex differences in the locomotor activity of hawkmoths. *J Experim Biol* 220: 1472–1480

Jogesh T, et al. (2017) Herbivory as an important selective force in the evolution of floral traits and pollinator shifts in a clade of evening primroses, *Oenothera* sect. *Calylophus* (Onagraceae). *AoB Plants* 9(1): plw088

Rhodes MK, et al. (2017) Pollinator identity and spatial isolation influence multiple paternity in an annual plant. *Mol Ecol* 26(16): 4296–4308

^ *Oenothera primiveris* flowering in Eureka dunes, Death Valley National Park. Flowers in California are large and hawkmoth-pollinated, whereas flowers east of Nevada are smaller and self-compatible. *O. primiveris* is one of 16 taxa where we have measured intraspecific floral trait variation in relation to biotic interactions.

CREDIT: TANIA JOGESH, CHICAGO BOTANIC GARDEN

Symbiont and transcriptomic niche dimensions of long-term coexistence in *Trifolium* communities

Sharon Y. Strauss
University of California, Davis
(1342841)

Maren Friesen
Michigan State University
(1342793)

This project expands on a long-term record of clover (*Trifolium*) species distributions to examine the role of genetic variation in rhizobial root symbionts in biological nitrogen fixation and clover coexistence.

Update

The project team continues long-term field data collections of 8 coexisting annual *Trifolium* species and their rhizobial symbionts. This year they sequenced 45 rhizobial genomes and tested symbiotic effectiveness of 32 strains in the greenhouse. Nodule sequencing identified rhizobial strain occupancy in two experiments manipulating competition in the field and in the greenhouse; rhizobial identity was found to impact invasion fitness in the greenhouse (manuscript in revision) and the impact of drought on coexistence was also explored. Two syntheses on mutualism were published, and PIs compiled a legume-wide database of nodulation status and the relationship between nodulation and diversification (in press, Ecology).

Publications

Afkhami ME, et al. (2018) Symbioses with nitrogen-fixing bacteria: Nodulation and phylogenetic data across legume genera. *Ecology* 99: 502

Barker J, et al. (2017) Synthesizing perspectives on the evolution of cooperation within and between species. *Evolution* 71(4): 814–825

Clark TJ, et al. (2017) Modeling mutualisms: challenges and opportunities for data integration. *Ecol Lett* 20(9): 1203–1215

Experiment manipulating rhizobial strain and *Trifolium* species associations.
CREDIT: MAREN L. FRIESEN & SHARON Y. STRAUSS

Top: *Trifolium* fucatum greenhouse experiment.
Bottom: *Trifolium* community in the field.
CREDIT: MAREN L. FRIESEN & SHARON Y. STRAUSS

The biogeography and evolution of drought tolerance in grasses

(CO-FUNDED WITH NASA)

Mark Ungerer
Jesse Nippert
Kansas State University
Lynn Clark
Iowa State University
(1342787)

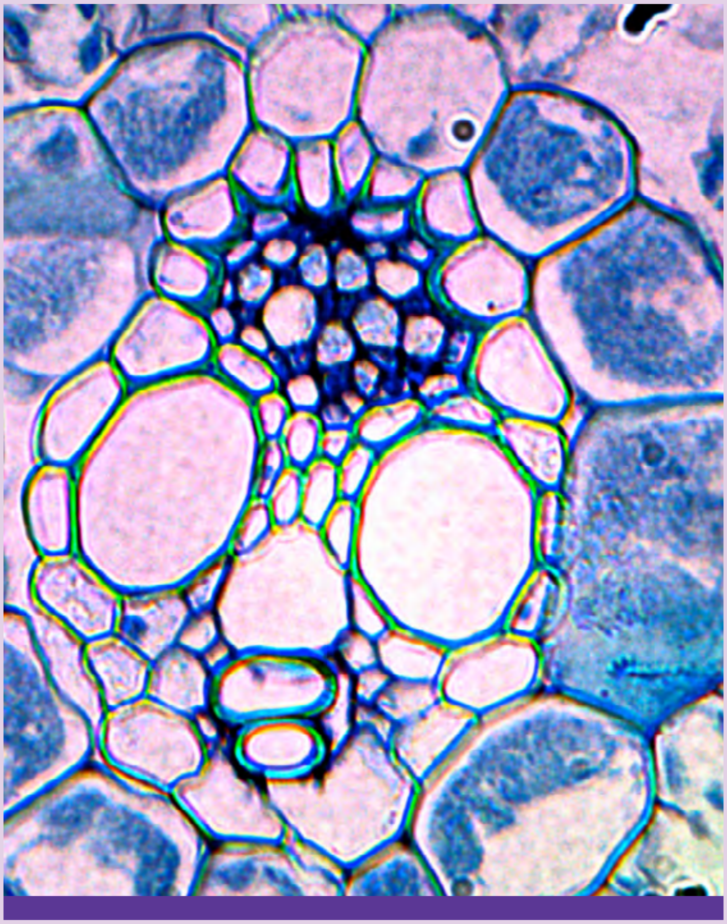
Melvin R. Duvall
Northern
Illinois University
(1342782)

Christopher J. Still
Oregon
State University
(1342703)

The goal is to understand the dimensions of biodiversity of drought tolerance in grasses. This project examines interspecific variation in drought tolerance among related species, intraspecific variation in drought tolerance of geographically widespread species, and physiological and genomic aspects of the evolutionary transition from C3 to C4 photosynthesis.

Update

This year the team performed expanded species sampling within the grass family of physiological responses to drought stress as well as population-level responses of common and broadly distributed C4 grasses in North America. They additionally initiated experiments focused on elucidating how wild grasses experience drought stress at different life stages. These latter experiments integrate physiological responses, thermography and multi-interval transcriptomics.



Xylem within these vascular bundles undergoes strong selection for physiological drought tolerance.

CREDIT: JOE CRAINE, KANSAS STATE UNIVERSITY

Publications

Duvall MR, et al. (2017) Grass plastomes reveal unexpected paraphyly with endemic species of Micrairoideae from India and new haplotype markers in Arundinoideae. *Am J Bot* 104: 286–295

Griffith DM, et al. (2017) Multi-century stasis in C3 and C4 grass distributions across the contiguous United States since the industrial revolution. *J Biogeo* 44: 2564–2574

Griffith DM, et al. (2017) Comment on "The extent of forest in dryland biomes". *Science* 358

Various grasses from around the world planted at Kew Gardens, UK.

CREDIT: JOE CRAINE, KANSAS STATE UNIVERSITY

Costs and benefits of chronic viral infections in natural ecosystems

Mark J. Young
Montana State University
Joshua Weitz
Georgia Institute of Technology
Rachel Whitaker
University of
Illinois, Urbana-Champaign
(1342876)

Microbial communities in the hot springs of Yellowstone National Park are prone to chronic viral infections, and this project investigates the genetic and functional basis of those infections. The study of this tractable hot spring model system can broaden our understanding of biodiversity and clarify the ways in which viruses influence the composition of microbial communities over time.

Update

During year four, continued analysis of a detailed virus-host association network from single cells isolated directly from the study hot spring provided direct evidence that (nearly) all cells are interacting with multiple viruses and the possibility that cells are simultaneously infected by multiple viruses. Model development to study the evolutionary ecology of host-virus interactions, ranging from pathogenic to commensal, based on the concept of predator-parasite duality, has begun. Transcriptomic and proteomic analysis led to identification candidate RNA transcripts and proteins packaged within vesicles specifically triggered by virus-cell interactions. PIs hypothesize that vesicle formation is an anti-viral response and could serve as a population-based communication system. Lastly, genetic and structural characterization of the founding member of the recently discovered archaeal viral family, MTIV, was completed.

Publications

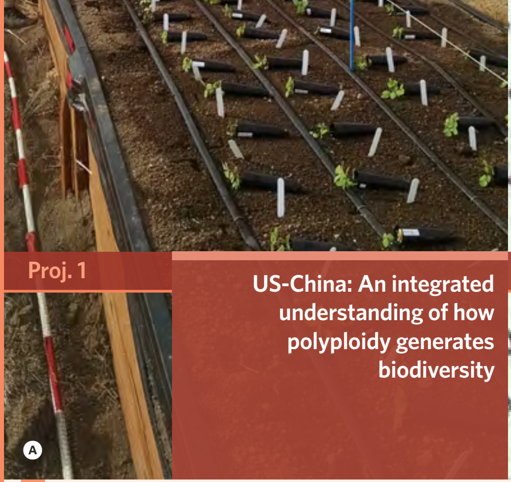
Munson-McGee J, et al. (2017) A virus or more in (nearly) every cell: ubiquitous virus-host interactions in extreme environments. *ISME J* doi: 10.1038/s41396-018-0071-7

Uldahl K, et al (2017) SMV1, an extremely stable thermophilic virus platform for nanoparticle trafficking in the mammalian GI tract. *J Appl Micro* 123(5): 1286–1297

Wagner C, et al. (2017) Isolation and characterization of *Metallosphaera* turreted icosahedral virus (MTIV), a founding member of a new family of archaeal viruses. *J Virol* 91: e00925-17

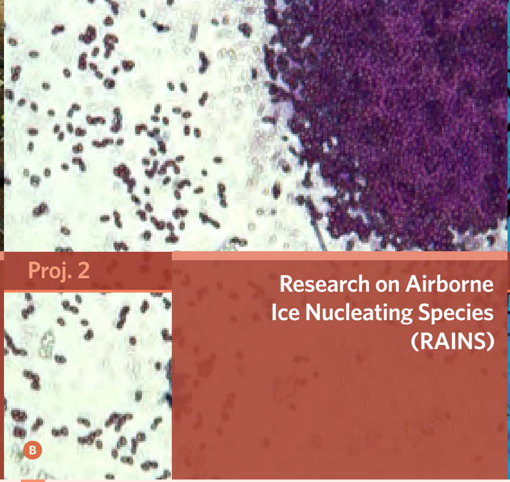
^ A boiling Yellowstone mud hot spring sampled for this project.
CREDIT: MARK J. YOUNG

^ Typical high temperature Yellowstone hot spring.
CREDIT: MARK J. YOUNG



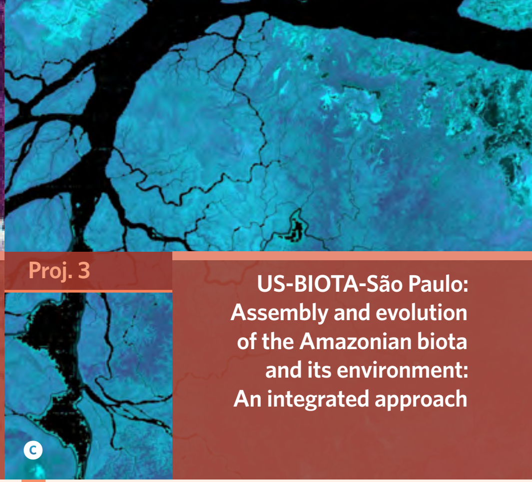
Proj. 1

US-China: An integrated understanding of how polyploidy generates biodiversity



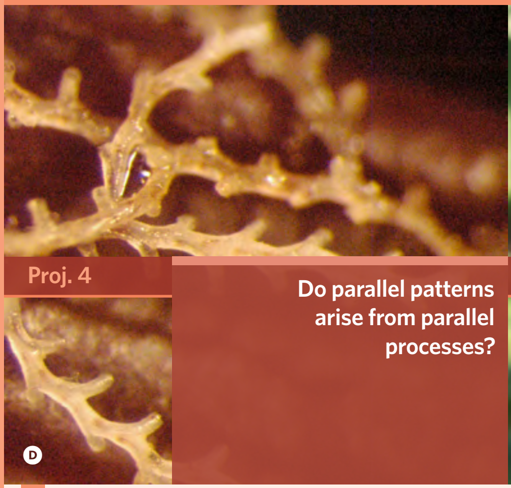
Proj. 2

Research on Airborne Ice Nucleating Species (RAINS)



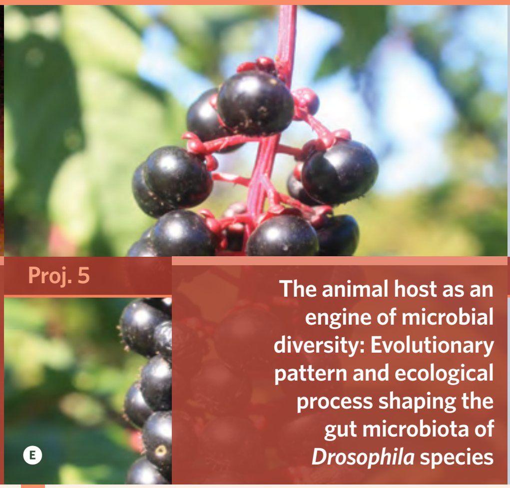
Proj. 3

US-BIOTA-São Paulo: Assembly and evolution of the Amazonian biota and its environment: An integrated approach



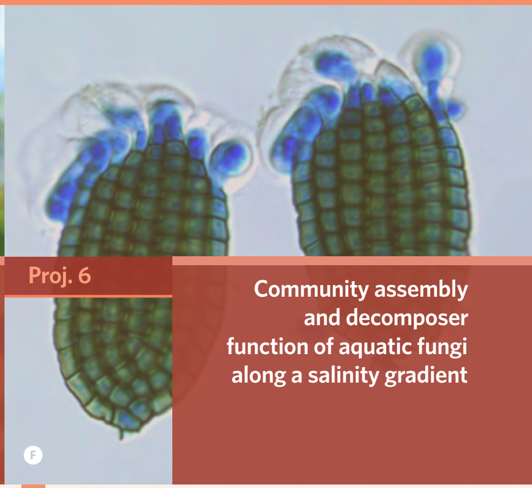
Proj. 4

Do parallel patterns arise from parallel processes?



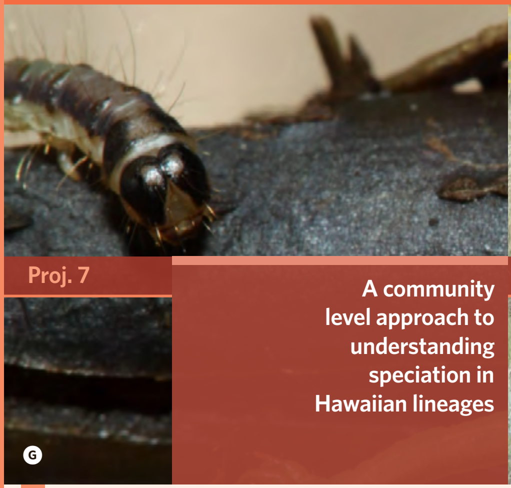
Proj. 5

The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of *Drosophila* species



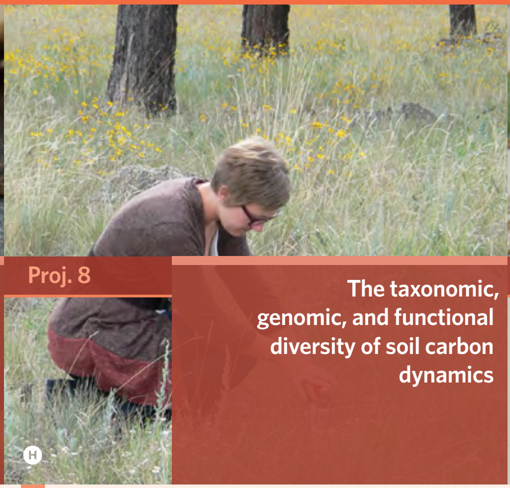
Proj. 6

Community assembly and decomposer function of aquatic fungi along a salinity gradient



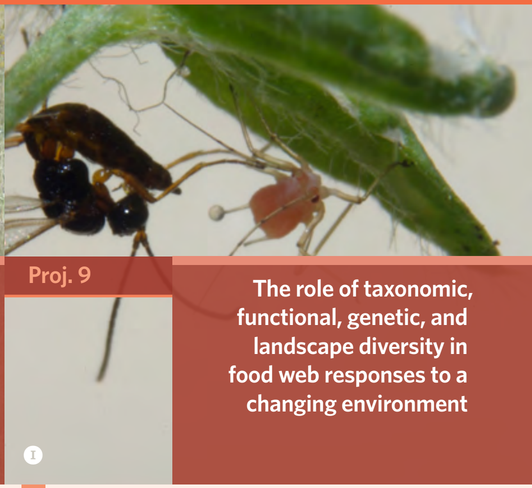
Proj. 7

A community level approach to understanding speciation in Hawaiian lineages



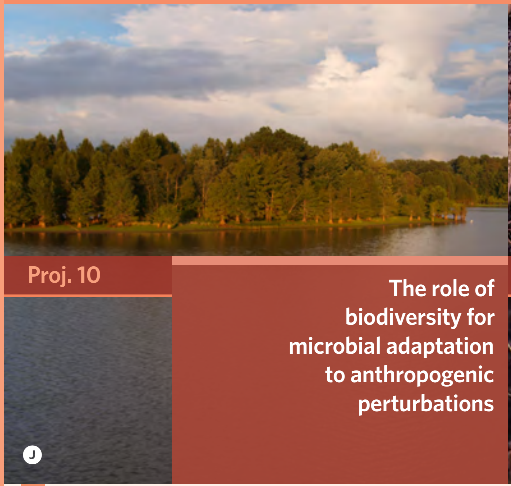
Proj. 8

The taxonomic, genomic, and functional diversity of soil carbon dynamics



Proj. 9

The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment

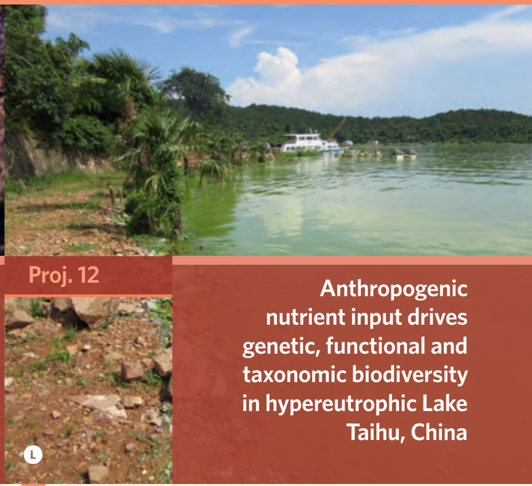


Proj. 10

The role of biodiversity for microbial adaptation to anthropogenic perturbations

Proj. 11

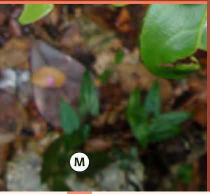
Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia



Proj. 12

Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China

Proj. 13



US-China: Disentangling the components of tree biodiversity: Integrating phylogenies, functional traits and transcriptomes

< | *CREDIT*

- Ⓐ Aaron Liston
- Ⓑ Brent Christner
- Ⓒ Joel Cracraft

- Ⓜ Nathan Swenson

Updates

2012

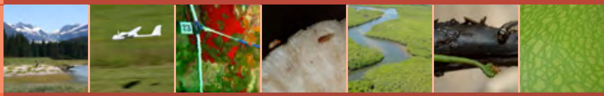
Proj. 14

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity

< | *CREDIT*

- Ⓓ Michael N. Dawson
- Ⓔ Gabrielle Brind 'Amour
- Ⓕ Astrid Hersilia Ferrer Correa

- Ⓝ Gert van Dijken



< | *CREDIT*

- Ⓖ Karl Magnacca
- Ⓗ Paul Dijkstra
- Ⓘ Anthony Ives

< | *CREDIT*

- Ⓙ K. Konstantinidis & D. Tsementzi
- Ⓚ Thomas E. Martin
- Ⓛ Hans Paerl

US-China: An integrated understanding of how polyploidy generates biodiversity

(CO-FUNDED WITH NSFC)

US TEAM

Tia-Lynn Ashman
University of Pittsburgh
(1241006)

Richard Cronn
USDA Forest Service Pacific Northwest Research Station

Aaron Liston
Oregon State University
(1241217)

CHINA TEAM

Ming Dong
Jiliang Pang
Hangzhou Normal University

Jumin Li
Shisheng Ke
Taizhou University

Minghua Song
Chinese Academy of Sciences

Polyploid species have undergone recent whole genome duplications. This project examines the role that polyploidy has played in the evolution of strawberry species, using species in US and in China as models. The strawberry genus, Fragaria, with generally small genomes and cytogenetic compatibility, is ideal for exploring patterns of genetic diversity arising from polyploidization.

Eagle Glacier and River, Juneau Alaska, a high latitude site of *Fragaria chiloensis*.

CREDIT: ARLO MIDGETT

HTTP://WILDSTRAWBERRY.ORG

Publications

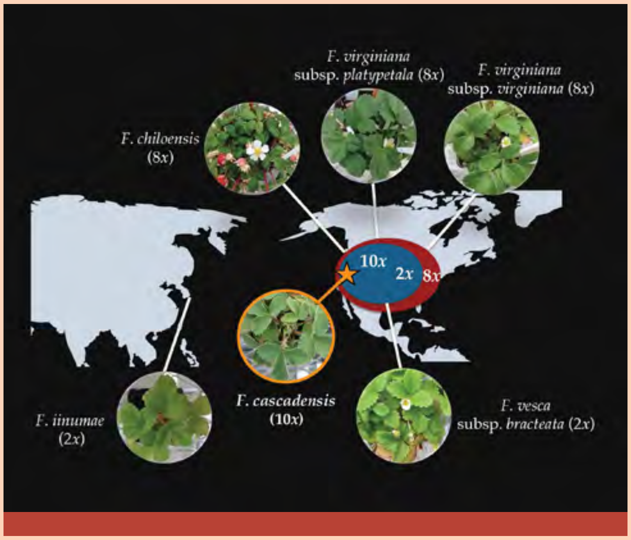
Wei N, Ashman T-L (2018) The effects of host species and sexual dimorphism differ among root, leaf and flower microbiomes of wild strawberries in situ. *Sci Rep* 8(1): 5195

Forrester N, Ashman T-L (2017) The direct effects of plant polyploidy and the legume-rhizobia mutualism. *Ann of Bot* 121(2): 209–220

Kamneva OK, et al. (2017) Evaluating allopolyploid origins in strawberries (*Fragaria*) using haplotypes generated from target capture sequencing. *BMC Evol Biol* 17(1): 180

Wei N, et al. (2017) Present-day sympatry belies evolutionary origin of a high-order polyploid. *New Phytol* 216: 279–290

Wei N, et al. (2017) Genetic mapping and phylogenetic analysis reveals variation in sex chromosomes of the Virginian strawberry. *J Heredity* 108: 731–739



Geographic distribution of *Fragaria cascadensis* and its potential ancestors.

CREDIT: NA WEI, UNIVERSITY OF PITTSBURGH

Planting the strawberry common garden in Bend, Oregon.

CREDIT: AARON LISTON

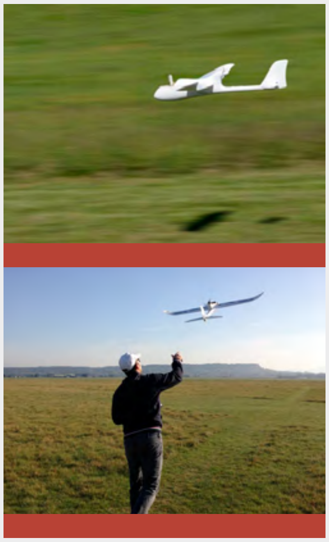
Research on Airborne Ice Nucleating Species (RAINS)

Brent Christner
University of Florida
(1643288)

Ken Aho
Idaho State University
(1241069)

David Sands
Cindy Morris
Montana State University
(1241054)

Boris Vinatzer
David Schmale
Virginia Tech University
(1241068)



This project examines the diversity and activity of airborne microbes that catalyze the formation of ice crystals in the atmosphere. RAINS seeks to understand the role of microbial ice nucleation in atmospheric microbial dispersal, and ultimately, precipitation generation.

Top: A water-resistant unmanned aerial vehicle (UAV) developed through the Schmale lab to collect samples in the lower atmosphere before, during, and after rain.

Bottom: A hand-launched drone taking off for an atmospheric sampling mission in Pujaut, France. The drone is equipped with a device to sample microorganisms in the lower atmosphere.

CREDIT: DAVID SCHMALE

Publications

Powers CW, et al. (2018) Remote collection of microorganisms at two depths in a freshwater lake using an unmanned surface vehicle (USV). *Peer J* 6: e4290

Coluzza I, et al. (2017) Perspectives on the future of ice nucleation research: research needs and unanswered questions. *Atmosphere* 8(8): 138

Failor KC, et al. (2017) Ice nucleation active bacteria in precipitation are genetically diverse and nucleate ice employing different mechanisms. *ISME J* 11(2): 2740–2753

Hanlon R, et al. (2017) Microbial ice nucleators scavenged from the atmosphere during simulated rain events. *Atmosph Environ* 163: 163: 182–189

Morris CE, et al. (2017) Mapping rainfall feedback to reveal the potential sensitivity of precipitation to biological aerosols. *Bull Am Meteorol Soc* 98(6): 1109–1118

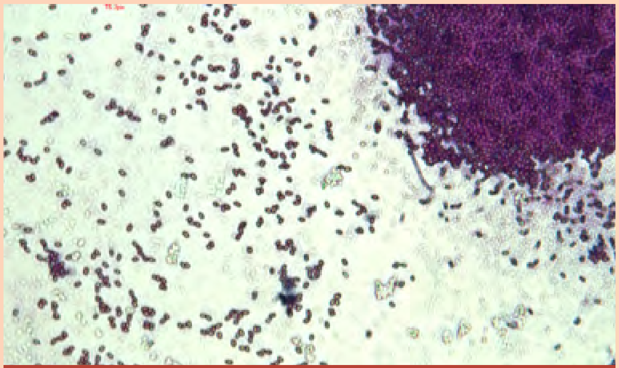
Pietsch RB, et al. (2017) Diversity and abundance ice nucleating strains of *Pseudomonas syringae* in a freshwater lake in Virginia, USA. *Front Microbiol* 8: 318

Striluk ML, et al. (2017) The effect of season and terrestrial biome on the abundance of bacteria with plant growth-promoting traits in the lower atmosphere. *Aerobiologia* 33: 137–149

Washburn QL, et al. (2017) Addition of zinc, manganese, and iron to growth media triggers antibiotic production in bacterial isolates from the lower atmosphere. *J Young Investigators* doi:10.22186/jyi.32.2.7-11

Sampling snowpack in late winter in the southern French Alps to isolate the ice nucleation active bacterium and plant pathogen *Pseudomonas syringae*.

CREDIT: CINDY MORRIS



Balloons floating into the stratosphere collect microorganisms that are brought back to the lab and studied. Some of them travel hundreds of kilometers through the air.

CREDIT: BRENT CHRISTNER

US-BIOTA-São Paulo: Assembly and evolution of the Amazonian biota and its environment: An integrated approach

(CO-FUNDED WITH NASA AND FAPESP)

US TEAM

Joel Cracraft
American Museum of Natural History
(1241066)

Christopher Dick
University of Michigan, Ann Harbor
(1240869)

Robert Guralnick
University of Florida
(1536140)

Kenneth Campbell
Los Angeles County Museum of Natural History
(1241042)

Andrew Brower
Middle Tennessee State University
(1241056)

John M. Bates
Field Museum of Natural History
(1241075)

Barbara Thiers
Scott Mori
New York Botanical Garden
(1241127)

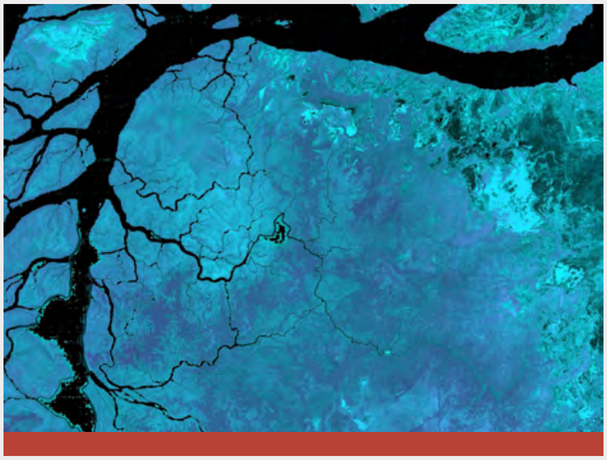
BRAZIL TEAM

Lucia Lohmann
Diogo Meyer
Francisco Cruz
Universidade de São Paulo

Andre Freitas
Universidade Estadual de Campinas

Jose Diniz Filho
Universidade Federal de Goias

This project seeks to understand the evolutionary and ecological history of Amazonia, the most diverse ecosystem on Earth. A goal is to build a comprehensive database of plants, birds and primates, which, together with phylogenetic, population genetic, remote sensing, geology, and Earth-systems modeling, will illuminate the historical development of Amazonian biota.



^ This image depicts the Amazon basin and was created with data from NASA's Shuttle Radar Tomography Mission combined with imagery from the Japanese Space Agency's Advanced Land Observing System (ALOS) Phased Array type L-band Synthetic Aperture Radar (PALSAR).

CREDIT: JOEL CRACRAFT

Publications

Garzón-Orduña, IJ, Brower AVZ (2018) Quantified reproductive isolation in *Heliconius* butterflies: implications for introgression and hybrid speciation. *Ecol Evol* 8(2): 1186–1195

Garzón-Orduña IJ, et al. (2018) Cracking the code: examination of species delimitations among *Hamadryas* butterflies with DNA barcodes suggests Caribbean cracker is *Hamadryas februa* Hübner (Nymphalidae: Biblidinae). *J Lepidopt Soc* 72(1): 53–73

Bemmels JB, et al. (2017) Filter-dispersal assembly of lowland Neotropical rainforests across the Andes. *Ecography* doi: 10.1111/ecog.03473

Bertelli, S (2017) Mexican land birds reveal complexity in fine-scale patterns of endemism. *J Biogeo* 44: 1836–1846

Brower AVZ, Garzón-Orduña IJ (2017) Missing data, clade support and "reticulation": the molecular systematics of *Heliconius* and related genera (Lepidoptera: Nymphalidae) reexamined. *Cladistics* 34(2): 151–166

Cracraft J, Claramunt S (2017) Conceptual and analytical worldviews shape differences about global avian biogeography. *J Biogeo* 44(4): 958–960

McMichael CH, et al. (2017) Comment on "Persistent effects of pre-Columbian plant domestication on Amazonian forest composition" *Science* 358 (6361): eaan8347

Mori SA, et al. (2017) Observations on the phytogeography of the Lecythidaceae clade (Brazil nut family). *Phytoneuron* 30: 1–85

Musher LJ, Cracraft J (2017) Phylogenomics and species delimitation of a complex radiation of Neotropical suboscine birds (*Pachyramphus*). *Mol Phyl Evol* 118: 204–221

Nazareno AG, et al. (2017) Minimum sample sizes for population genomics: An empirical study from an Amazonian plant species. *Mol Ecol Resourc* 17(6): 1136–1147

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Ribas C, et al. (2017) Biogeography and diversification of Rhegmatorhina (Aves: Thamnophilidae): implications for the recent evolution of Amazonian landscapes. *J Biogeo* 45(4): 917–928

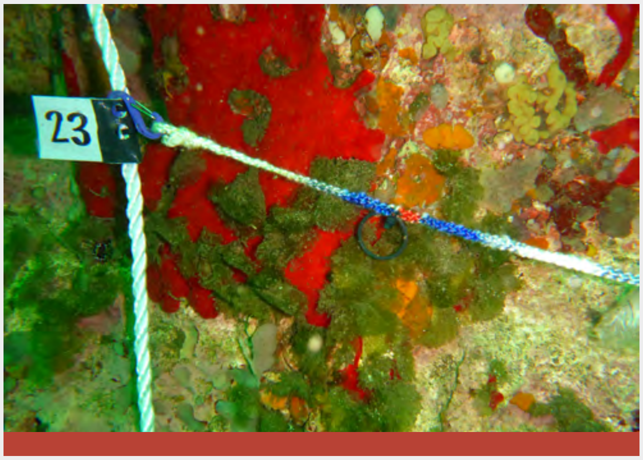
Schultz ED, et al. (2017) Systematics and biogeography of the *Automolus infuscatus* complex (Aves; Furnariidae): cryptic diversity reveals western Amazonia as the origin of a transcontinental radiation. *Mol Phyl Evol* 107: 503–515

Do parallel patterns arise from parallel processes?

Michael N. Dawson
John Beman
University of California, Merced
(1241255)

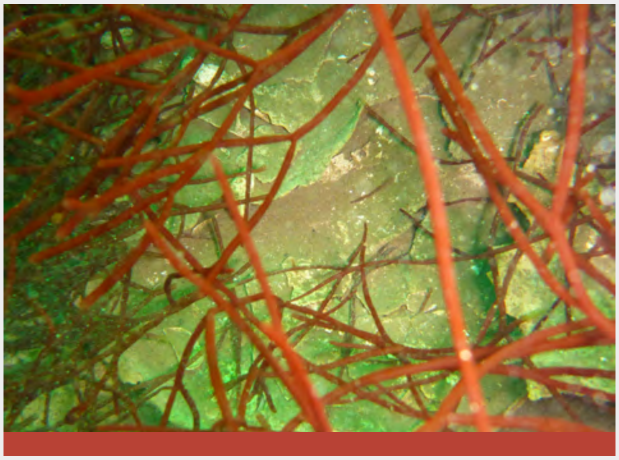
Julian P. Sachs
University of Washington
(1241247)

This project is to survey the dimensions of diversity of the organisms found in marine lakes, and investigate the processes that cause gains and losses in this biodiversity. Marine lakes formed as melting ice sheets raised sea level after the last glacial maximum and flooded hundreds of inland valleys around the world.



^ Benthic point intercept transects are used to quantify species abundance, cover, and richness.

CREDIT: MICHAEL N. DAWSON



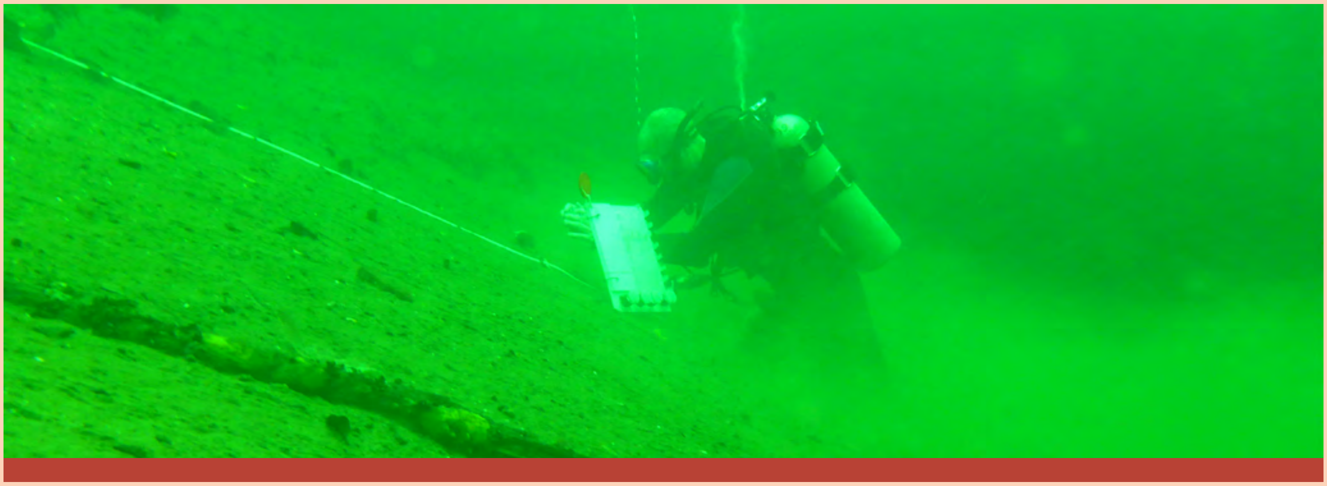
^ Dead coral under a bed of branching red alga may indicate a prior tipping point in the lake ecosystem.

CREDIT: MICHAEL N. DAWSON

Publications

Ladd S N, Sachs JP (2017) 2H/1H fractionation in lipids of the mangrove *Bruguiera gymnorhiza* increases with salinity in marine lakes of Palau. *Geochimica et Cosmochimica Acta* 204: 300–312

Wilson JM, et al. (2017) Primary production, community respiration, and net community production along oxygen and nutrient gradients: environmental controls and biogeochemical feedbacks within and across "marine lakes." *Front MarSci* doi: 10.3389/fmars.2017.00012



^ Surveys at ~25 m depth have an eerie ambience.

CREDIT: MICHAEL N. DAWSON

Proj. 5 / 14

The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of *Drosophila* species

Angela E. Douglas
Gregory Loeb
Cornell University
(1241099)

John Jaenike
University of Rochester
(1241099)

This project investigates the significance of mutually-beneficial interactions in promoting the diversity of bacterial communities and their animal hosts in fruit flies and their relatives.

Drosophila falleni female on a wild mushroom cap in Corbett's Glen Nature Park, Brighton, New York.

CREDIT: VINCENT G. MARTINSON, UNIVERSITY OF ROCHESTER

Publications

Inamine H, et al. (2018) Spatio-temporal heterogeneous population dynamics of gut bacteria inferred from fecal time-series data. *mBio* 9(1): e01453-17

Bost A, et al. (2017) How gut transcriptional function of *Drosophila melanogaster* varies with the presence and composition of the gut microbiota. *Mol Ecol* 27(8): 1848–1859

Martinson V, et al. (2017) Community structure of gut microbiotas within and among sympatric wild *Drosophila species*. *Ecol Lett* 20(5): 629–639

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Proj. 6 / 14

Community assembly and decomposer function of aquatic fungi along a salinity gradient

Astrid Hersilia Ferrer Correa
James Dalling
Katy Heath
University of Illinois,
Urbana Champaign
(1241212)

Diverse groups of freshwater and marine fungi remain to be described from tropical waters. This project examines the roles of aquatic fungi in the decomposition of wood along salinity gradients in Panamanian coastal rivers, asking how gene expression patterns among diverse fungi influence the rate and trajectory of wood decay in water.

Mouth of the Boca Grande River, Coiba Island, Panama. Aquatic fungi are being studied at this site and two undisturbed rivers.

CREDIT: KEVAN MANTELL

HTTP://PUBLISH.ILLINOIS.EDU/AQUATICFUNGI

A community level approach to understanding speciation in Hawaiian lineages

Rosemary Gillespie
John Harte
Patrick O'Grady
Rasmus Nielsen
University of California, Berkeley
(1241253)

Daniel Gruner
University of Maryland, College Park
(1240774)

Kerry Shaw
Cornell University
(1241060)

Donald Price
University of Hawaii, Hilo
(1241228)

The arthropod communities on Hawaiian islands that differ in age have different natural histories and may express different patterns and rates of evolution. This research will transform our thinking of how biodiversity is impacted by the dynamic community.

Publications

Berry A, Gillespie RG (2018) Island Evolution & Biodiversity. In: *The Routledge International Handbook of Island Studies* (Godfrey Baldacchino, ed.) Taylor & Francis Group LLC, USA

Gillespie RG, et al. (2018) Repeated diversification of ecomorphs in Hawaiian stick spiders. *Curr Biol* 28(5): 941–947

Gillespie RG, Will K (2018) Biodiversity of Arthropods on Islands. In: *Insect Biodiversity: Science and Society* (RG Foottit and PH Adler, eds.) Wiley-Blackwell Publ

Kennedy S, et al. (2018) Stable isotopes reflect substrate properties and trophic ecology in spiders along a Hawaiian chronosequence. *Peer J* doi: 10.7717/peerj.4527

Krehenwinkel H, et al. (2018) The effect of DNA degradation bias in passive sampling devices on metabarcoding studies of arthropod communities and their associated microbiota. *PloS one* 13(1): e0189188

Claridge EM, et al. (2017) Stepping-stones across space and time: repeated radiation of Pacific flightless broad-nosed weevils (Coleoptera: Curculionidae: Entiminae: *Rhyncogonus*). *J Biogeo* 44(4): 784–796

Gillespie RG, et al. (2017) The Theory of Evolutionary Biogeography. In: *The Theory of Evolution* (S Scheiner, D Mindell, eds.) University of Chicago Press. Chicago, IL

Gillespie RG, et al. (2017) Ancient biogeography of generalist predators on remote oceanic islands. *J Biogeo* 44(5): 1098–1109

Graham N, et al. (2017) Island ecology and evolution: challenges in the Anthropocene. *Environ Conserv* 44(4): 323–335

Harte J, et al. (2017) Metabolic partitioning across individuals in ecological communities. *Glob Ecol Biogeo* 26(9): 993–997

Krehenwinkel H, et al. (2017) A cost efficient and simple protocol to enrich prey DNA from extractions of predatory arthropods for large scale gut content analysis by Illumina sequencing. *Meth Ecol Evol* 8: 126–134

Krehenwinkel H, et al. (2017) Estimating and mitigating amplification bias in qualitative and quantitative arthropod metabarcoding. *Sci Rep* 7(1): 17668

Patiño J, et al. (2017) A roadmap for island biology: 50 fundamental questions after 50 years of The Theory of Island Biogeography. *J Biogeo* 44(5): 963–983

^ A Hawaiian carnivorous caterpillar, *Eupithecia palikea*.

CREDIT: KARL MAGNACCA

The taxonomic, genomic, and functional diversity of soil carbon dynamics

Bruce Hungate
Jane Marks
Egbert Schwartz
Paul Dijkstra
James Caporaso
Northern Arizona University
(1241094)

Lance Price
Translational Genomics Research Institute
(1241115)

This project examines the roles that taxonomic and genetic diversity of microbes play in the processing of new and old carbon in soils. Of particular interest is the concept of 'priming', where a pulse increase of carbon causes an acceleration in microbial-mediated soil organic matter degradation.

Publications

- Koch BJ, et al. (2018) Estimating taxon-specific population dynamics in diverse microbial communities. *Ecosphere* 9: e02090
- Mau RL, et al. (2018) Warming induced changes in soil carbon and nitrogen influence priming responses in four ecosystems. *Appl Soil Ecol* 124: 110–116
- Papp K, et al. (2018) Comparison of microbial ribosomal RNA synthesis and growth through quantitative stable isotope probing with $H_2{}^{18}O$. *Appl Environ Microbio* doi: 10.1128/AEM.02441-17
- Liu X-JA, et al. (2017) Labile carbon input determines the direction and magnitude of the soil priming effect. *Appl Soil Ecol* 109: 7–13
- Liu X-JA, et al. (2017) Increased plant uptake of native soil nitrogen with fertilizer addition – not a priming effect? *Appl Soil Ecol* 114: 105–110
- Morrissey EM, et al. (2017) Bacterial carbon use plasticity, phylogenetic diversity, and the priming of soil organic matter. *ISME J* 11: 1890–1899

^ Collecting soil for microbial diversity analysis.
CREDIT: PAUL DIJKSTRA

The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment

Anthony Ives
Volker Radeloff
University of Wisconsin, Madison
(1240804)

Kerry Oliver
University of Georgia
(1240892)

Jason Harmon
North Dakota State University, Fargo
(1241031)

Ives and colleagues are examining how genetic, taxonomic, ecological, and landscape diversity influence the control of agricultural pests by their natural enemies. They have accrued an array of remote-sensing ecological and molecular tools to examine this system, using aphids and pea family plants as the central interaction of interest.

> The parasitoid *Aphidius ervi* attacking a pea aphid.

CREDIT: ANTHONY IVES

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Barton BT, Harmon JP (2017) Editorial overview: Global change biology: everything connects to everything else. *Curr Opinl Insect Sci* 23: v-vii

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The role of biodiversity for microbial adaptation to anthropogenic perturbations

Konstantinos Konstantinidis
Jim Spain
Georgia Tech Research Corporation
Eberhard Voit
Georgia Institute of Technology
(1241046)

This project examines how low-abundance (rare) members of microbial communities enable community adaptation and resilience to disturbances and to the presence of new organic compounds such as petroleum hydrocarbons, pesticides, and antibiotics.

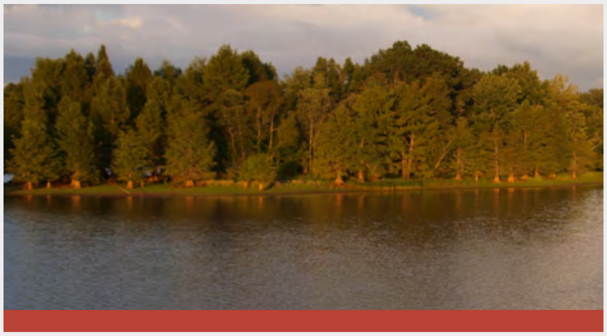

Photo of Lake Eufaula, Alabama.

CREDIT: K. KONSTANTINIDIS AND D. TSEMENTZI, GEORGIA TECH

Publications

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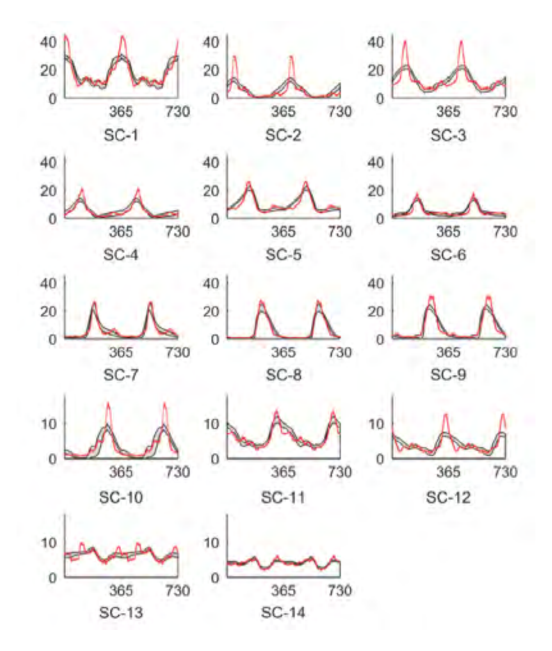

Time-dependent abundances of 14 bacterial sub-communities in Lake Mendota. Red lines: means of observed abundances collected between 2000 and 2011. Grey shading: ranges of abundances predicted by our ensemble of dynamical models. X-axis: days of a two-year period. Y-axis: abundances of the sub-communities (note different scales).

CREDIT: DAM P, ET AL. (2016)

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia

Thomas E. Martin
University of Montana
Robert Fleischer
Ellen Martinsen
Smithsonian Institution
(1241041)
Frederick Sheldon
Louisiana State University & Agricultural and Mechanical College
(1241059)
Robert G. Moyle
University of Kansas Center for Research Inc.
(1241181)

This project examines multiple factors that may contribute to the maintenance of elevational gradients in biodiversity, using diverse tropical bird fauna in Borneo as a model system. Bird blood parasites, nesting behavior, and other life history variables will be examined with genetic and environmental differentiation.

> *Yuhina*, an endemic species in Borneo, has a wide elevational distribution, potentially associated with the lower sensitivity to temperature of its embryos.

CREDIT: THOMAS E. MARTIN

Publications

Boyce AJ, Martin TE (2018) Contrasting latitudinal patterns of life-history divergence in two genera of new world thrushes (Turdinae). *J Avian Biol* 48: 581–590

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Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China

(CO-FUNDED WITH THE CHINESE MINISTRY OF SCIENCE & TECHNOLOGY)

Hans Paerl
University of North Carolina, Chapel Hill
(1240851)

Wayne Gardner
University of Texas, Austin
(1240798)

Steven Wilhelm
University of Tennessee, Knoxville
(1240870)

Ferdinand Hellweger
Northeastern University
(1240894)

Paerl and colleagues are examining the genetic diversity of microbial involved in production and nutrient cycling dynamics in a lake that experiences massive blooms of toxic cyanobacteria. They are linking diversity to the inputs and processing of nitrogen that is the cause of the toxic blooms.

> View of toxic cyanobacterial bloom on Lake Taihu, China.

CREDIT: HANS PAERL

Publications

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^ Close-up view of a cyanobacterial surface bloom at Lake Taihu, China, during June, 2016.

CREDIT: HANS PAERL

Proj. 13 / 14

US-China: Disentangling the components of tree biodiversity: integrating phylogenies, functional traits and transcriptomes

(CO-FUNDED WITH NSFC)

US MEMBERS

Nathan Swenson
Michigan State University
(1542549)

CHINA MEMBERS

Keping Ma
Zhanging Hao
Lixin Zhang
Lanzhu Ji
Chinese Academy of Sciences

A pioneer of the emergent community functional phylogenomics field, this study of tree biodiversity is developing a predictive framework that can address classic questions about the functional similarity of species, the dynamic functional responses of species to environmental stimuli and help us understand processes that generate and maintain forest diversity.

Samyda spinulosa sapling in the understory of the Luquillo Forest Dynamics Plot in Puerto Rico.

CREDIT: NATHAN SWENSON

Publications

Han B, et al. (2017) The role of transcriptomes linked with responses to light environment on seedling mortality in a subtropical forest, China. J Ecol 105(3): 592–601

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Proj. 14 / 14

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity

Jonathan Zehr
Zbigniew Kolber
University of California, Santa Cruz
(1241221)

Matthew Church
University of Hawaii
(1241263)

Kevin Arrigo
Stanford University
(1241093)

Genomics, molecular biology, and stable isotope tracers become tools to investigate how changes in the form and availability of nitrogen affect the dimensions of biodiversity in marine phytoplankton. Focusing on the North Pacific Subtropical Gyre, they use innovative nanomethodologies for characterizing seawater and a number of state-of-the-art methods for comprehensive community evaluation.

Samyda spinulosa sapling in the understory of the Luquillo Forest Dynamics Plot in Puerto Rico.

CREDIT: NATHAN SWENSON

Publications

Shilova IN, et al. (2017) Differential effects of nitrate, ammonium and urea as N sources for microbial communities in the North Pacific Ocean. *Limnol Oceanogr* 62(6): 2550–2574

Shilova I, et al. (2017) Differential effects of nitrate, ammonium and urea as N sources for microbial communities in the North Pacific Ocean. *Limnol Oceanogr* 62(6): 2550–2574

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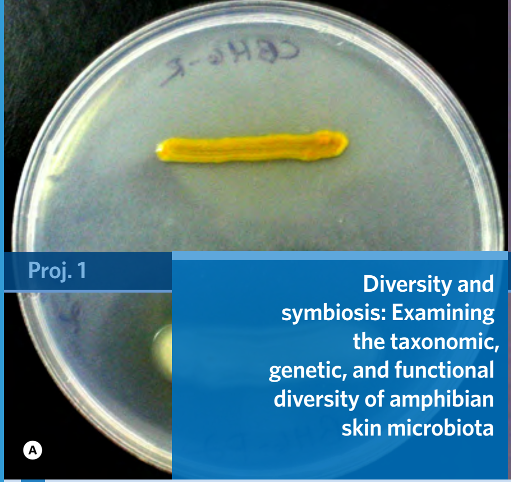
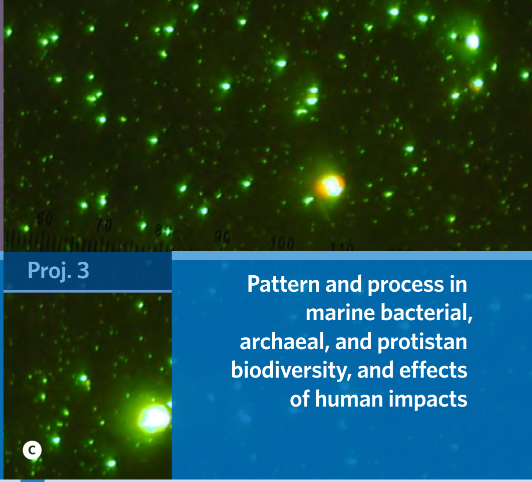


Proj. 1

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

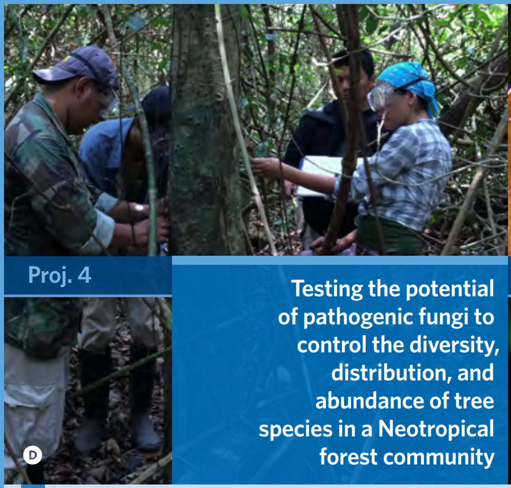
Proj. 2

US-China: International Research Coordination Network: A research coordination network for biodiversity of ciliates



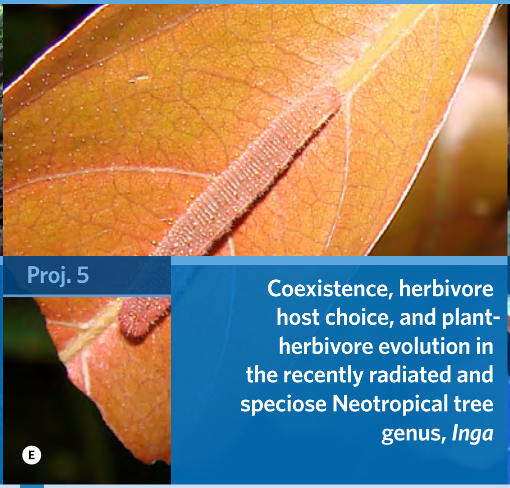
Proj. 3

Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts



Proj. 4

Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community

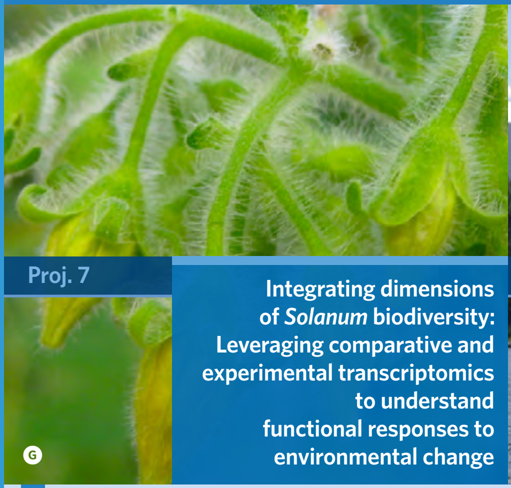


Proj. 5

Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga*

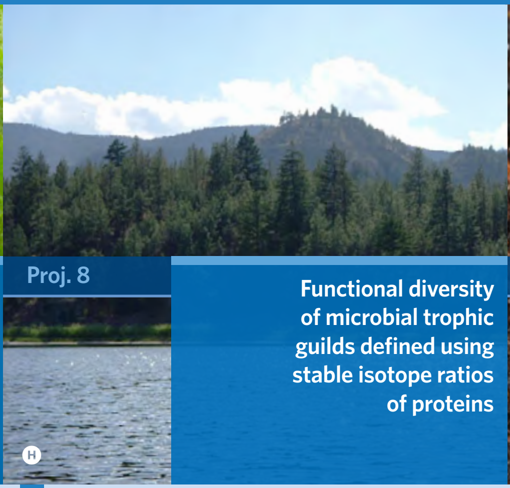
Proj. 6

Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton



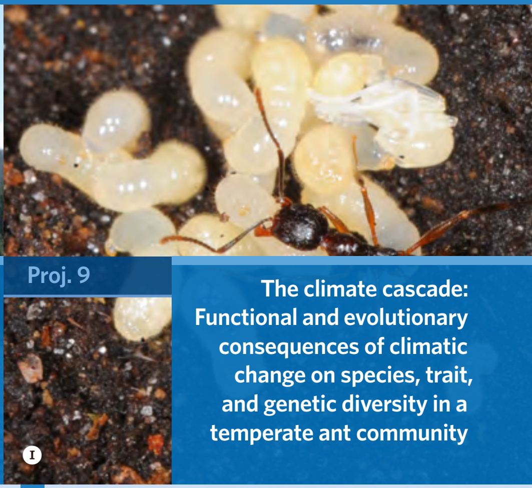
Proj. 7

Integrating dimensions of *Solanum* biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change



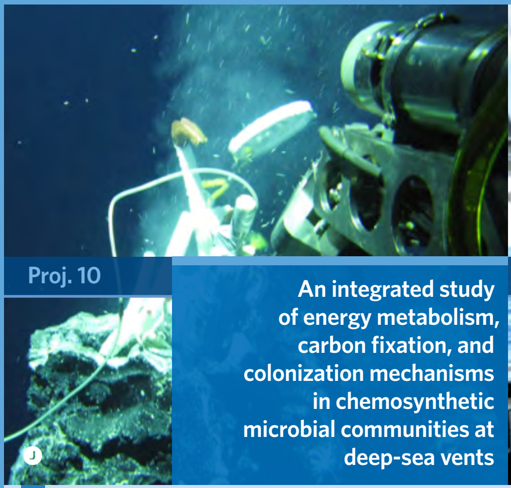
Proj. 8

Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins



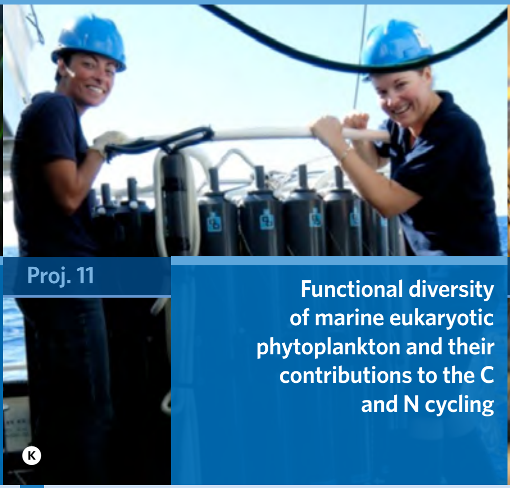
Proj. 9

The climate cascade: Functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community



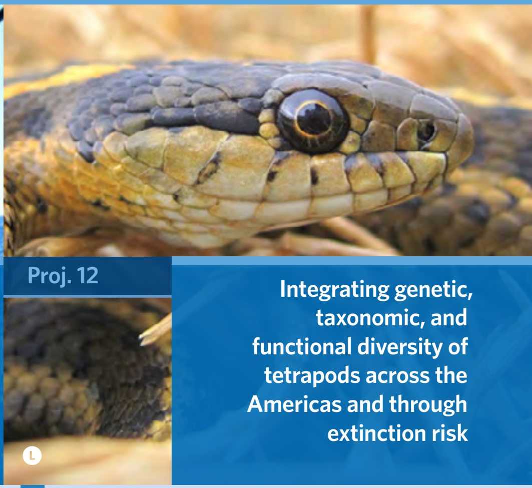
Proj. 10

An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents



Proj. 11

Functional diversity of marine eukaryotic phytoplankton and their contributions to the C and N cycling



Proj. 12

Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk

< | *CREDIT*

Ⓐ Jenifer Walke Ⓑ John Clamp Ⓒ Jed Fuhrman

Citations

2011

< | *CREDIT*

Ⓓ Gregory S. Gilbert Ⓔ Thomas Kursar Ⓕ Bart De Stasio

< | *CREDIT*

Ⓖ David Haak Ⓗ Jennifer Glass Ⓘ Aaron Ellison

< | *CREDIT*

Ⓙ Stefan Sievert Ⓚ Sarah Fawcett Ⓛ Geoffrey Hammerson

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

Lisa Belden
Roderick Jensen
Leanna House
Virginia Polytechnic Institute and State University
(1136640)

Reid Harris
James Madison University
(1136602)
Kevin Minbiole
Villanova University
(1136662)

This project investigates the diverse microbial communities on the skin of amphibian species and their role in controlling a critical disease that threatens amphibian biodiversity in the Neotropics.

Top: The red-eyed treefrog, *Agalychnis callidryas*, is found in Panamanian rain forests. The skin bacteria from this species and four additional species are being studied to determine how diverse communities of microbes provide protection from a lethal skin fungus (*Batrachochytrium dendrobatidis*).

CREDIT: BRIAN GRATWICKE, SMITHSONIAN CONSERVATION BIOLOGY INSTITUTE

Bottom: The bacterial species *Pseudomonas* spp. (lower streak) is found on amphibian skins and is shown inhibiting *Batrachochytrium dendrobatidis* (light colored lawn on the agar plate). The bacterial species at the top of the plate is a control that does not inhibit fungi.

CREDIT: JENIFER WALKE, VIRGINIA TECH

Publications

Rebollar EA, et al. (2018) The functional repertoire of the skin microbiome of the frog *Craugastor fitzingeri*: inferring potential bacterial-host-pathogen interactions from metagenomic data. *Front Microbiol* doi: 10.3389/fmicb.2018.00466

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Walke JB, et al. (2017) Dominance-function relationships in the amphibian skin microbiome. *Environ Microbiol* 19: 3387–3397

US-China: International Research Coordination Network: A research coordination network for biodiversity of ciliates

(CO-FUNDED WITH NSFC)

This project establishes an international research coordination network (IRCN) for the biodiversity of ciliates, including researchers from the US, Brazil, China, Germany, and the United Kingdom. This IRCN is an 'engine' for generating new ideas, projects, and procedures for archiving complex data needed to facilitate exploration of these important protists.

US TEAM

John Clamp
North Carolina Central University
(1136580)

Laura Katz
Smith College
(1136580)

Chris Lobban
University of Guam
(1136580)

CHINA TEAM

Xiaofeng Lin
South China Normal University, Guangzhou

Weibo Song
Ocean University of China, Qingdao

OTHER COUNTRIES

Micah Dunthorn
University of Kaiserslautern, Germany

Laura Utz
Pontificia Universidade Católica do Rio Grande do Sul, Brazil

Alan Warren
Natural History Museum London, United Kingdom

> *Diophrys sp*, a hypotrich.

CREDIT: JOHN CLAMP

Publications

- Clamp J, Lynn DH (2017) Investigating the biodiversity of ciliates in the 'Age of Integration'. *Eur J Protistol* 61(PtB): 314–322
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- Weiwei L, et al. (2017) Diversity of free-living marine ciliates (Alveolata, Ciliophora): faunal studies in coastal waters of China during the years 2011–2016. *Eur J Protistol* 61(PtB): 424–438
- Xumiao C, et al. (2017) The diverse morphogenetic patterns in spirotrichs and philasterids: researches based on five-year-projects supported by IRCN-BC and NSFC. *Eur J Protistol* 61(PtB): 439–452
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Proj. 3 / 12

Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

Jed Fuhrman
David Caron
Fengzhu Sun
John Heidelberg
William Nelson
University of
Southern California
(1136818)

This project compares heavily disturbed harbor regions and relatively pristine ocean habitat in the Los Angeles basin to better understand links between marine microbial diversity and ecosystem function. The team uses time series approaches in three coastal locations to evaluate relationships among microorganisms of different complex natural communities.

HTTP://BITBUCKET.ORG/CHARADE/ELSA
HTTP://WWW-RCF.USC.EDU/~FSUN/PROGRAMS/NGS-MC/NGS-MC.HTML

Publications

Ahlgren N, et al. (2017) Alignment-free d_2^* oligonucleotide frequency dissimilarity measure improves prediction of hosts from metagenomically-derived viral sequences. *Nuc Acids Res* 45(1): 39 –53

Berdjeb L, et al. (2017) Short-term dynamics and interactions of marine protist communities during the spring-summer transition. *ISME J* 3642–3661

Caron DA, et al. (2017) Planktonic food web structure at a coastal time-series site: I. Partitioning of microbial Abundance and Biomass. *Deep-Sea Res Part I: Oceanogr Res Papers* 121: 14–29

^ Sampling from a small boat near Catalina Island.

CREDIT: JED FUHRMAN

Proj. 4 / 12

Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community

Stephen Hubbell
Smithsonian Institution
Travis C. Glenn
University of Georgia
(1136626)
Gregory S. Gilbert
University of
California, Santa Cruz
(1136626)
Brant C. Faircloth
University of California,
Los Angeles
(1136626)

The abundance and diversity of tropical trees and fungal pathogens of trees are functionally interconnected with forest dynamics. This project tested a mechanistic hypothesis for why so many tropical tree species are rare (occur at low population density) in a well-studied tropical forest on Barro Colorado Island (BCI): Panama.

^ A crew of project interns collecting data on internal decay of mature living trees.

CREDIT: GREGORY S. GILBERT

Publications

Glenn TC, et al. (2017) Adapterama I: Universal stubs and primers for thousands of dual-indexed Illumina libraries (iTru & iNext). Mol Ecol Resour doi: 10.1101/049114

Young HS, et al. (2017) Introduced species, disease ecology, and biodiversity-disease relationships. *TREE* 32(1): 41–45

Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga*

Thomas Kursar
Phyllis Coley
University of Utah
(1135733)

This project studies interactions among members of the tree genus Inga (>300 species) and their insect herbivores at five sites in Central and South America. This work is shedding light on the coevolution of plants and herbivores and its influence on the ecology of the most diverse forest communities on Earth.

Publications

Coley PD, et al. (2018) Consequences of interspecific variation in defenses and herbivore host choice for the ecology and evolution of *Inga*, a speciose rainforest tree. *Oecologia* doi: 10.1007/s00442-018-4080-z

Dexter KG, et al. (2017) Dispersal assembly of rain forest tree communities across the Amazon basin. *PNAS* 114(10): 2645–2650

Endara M-J, et al. (2017) Coevolutionary arms race versus host defense chase in a tropical herbivore-plant system. *PNAS* 114(36): E7499–E7505

Schneider GF, et al. (2017) Current ambient concentrations of ozone in Panama modulate the leaf chemistry of the tropical tree *Ficus insipida*. *Chemosphere* 172: 363–372

Top: An unidentified herbivove ("bagworm") consuming *Inga bourgonii* (Nouragues, French Guiana).

Bottom: Herbivores preferentially consume tender, expanding leaves, such those of *Inga suberosa* (Reserva Ducke, Manaus, Brazil) shown here.

CREDIT: THOMAS KURSAR

Both: Ants are attracted to the sugary rewards provided in the nectaries of expanding leaves. These provide only carbohydrates and no protein. The plant benefits because ants also search for and consume herbivores, an excellent protein source for ants.

Top: Ants on *Inga umbratica* from Km41, Manaus, Brazil.

Bottom: Ants on *Inga longiflora* from Nouragues, French Guiana.

CREDIT: THOMAS KURSAR

Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton

Elena G. Litchman
Christopher A. Klausmeier
Michigan State University
(1136710)

Edward C. Theriot
University of Texas, Austin
(1136667)

Stephanie E. Hampton
University of California,
Santa Barbara
(1136637)

Lev Yampolsky
East Tennessee State
University
(1136706)

Marianne Moore
Wellesley College
(1136657)

This project studies the planktonic food web of the world's largest, oldest, and most biologically diverse lake—Lake Baikal in Siberia—to predict how native vs. non-native plankton will respond to accelerating environmental change in this system.

^ Under-ice sampling on Lake Baikal, Siberia. Periodically winds and underwater currents cause large ice slabs to form and rise up.

CREDIT: PAUL WILBURN, MICHIGAN STATE UNIVERSITY

Publications

Kremer CT, et al. (2017) Temperature- and size-scaling of phytoplankton population growth rates: Reconciling the Eppley curve and the metabolic theory of ecology. *Limnol Oceano* 62(4): 1658–1670

O'Donnell DR, et al. (2017) Nitrogen and phosphorus co-limitation of phytoplankton in Lake Baikal, Siberia: insights from the lake survey and nutrient enrichment experiments. *Limnol Oceanogr* 62(4): 1383–1392

Osmond MM, et al. (2017) When predators help prey adapt and persist in a changing environment. *Am Nat* 190: 83–98

Osmond MM, Klausmeier CA (2017) An evolutionary tipping point in a changing environment. *Evolution* 71(12): 2930–2941

Ozersky T, et al. (2017) Heavy metal burdens in Lake Baikal seals respond to decreased Eurasian atmospheric emissions. *Environ Sci Technol* 51(18): 10316–10325

Poste A, et al. (2018) Contemporary and historical mercury accumulation in the Lake Baikal seal: patterns, predictors and toxicological implications. *Environ Toxicol Chem* 37(5): 1476–1486

^ Processing samples from a bag experiment conducted in Baikal to determine what the dominant pelagic grazer (a copepod, *Epischura baikalensis*) eats.

CREDIT: BART DE STASIO, JR., BIOLOGY DEPARTMENT, LAWRENCE UNIVERSITY

Proj. 7 / 12

Integrating dimensions of *Solanum* biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change

Leonie Moyle
Matthew Hahn
David Haak
Indiana University
(1136707)

The project aims to generate an integrated understanding of natural adaptive trait variation in response to abiotic and biotic environmental variation in the wild tomato plant group *Solanum* sect. *Lycopersicum*. It highlights the role of drought and herbivore defense in driving remarkable diversity.

^ Tobacco hornworm *Manduca sexta* on densely hairy leaves and buds of wild species of *S. habrochaites*.

CREDIT: DAVID HAAK

Publications

Mendes FK, Hahn MW (2018) Why concatenation fails near the anomaly zone. *Syst Biol* 67: 158–169

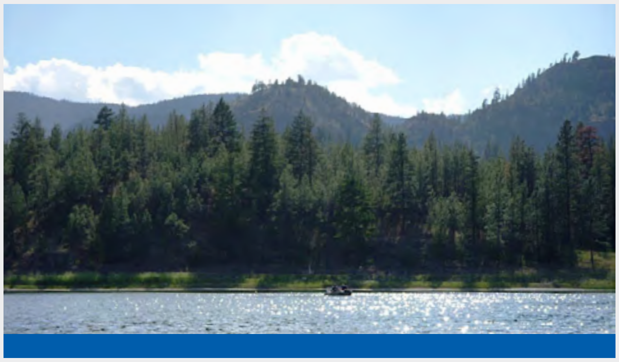
Haak DC, et al. (2017) Multilevel regulation of abiotic stress responses in plants. *Front Plant Sci* doi: 10.3389/fpls.2017.01564

Proj. 8 / 12

Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins

Ann Pearson
Peter Girguis
Harvard University
(1136484)
Jennifer Macalady
Pennsylvania State University
(1136218)

This project uses isotopic ratios of carbon, nitrogen, and sulfur from microbial metabolism to link guilds of microbes to their roles in biogeochemical processes. This novel approach is improving our understanding of the role of microbes in ecosystems.



^ Mahoney Lake, Penticton, BC Canada.

CREDIT: JENNIFER GLASS, ASU

The climate cascade: Functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community

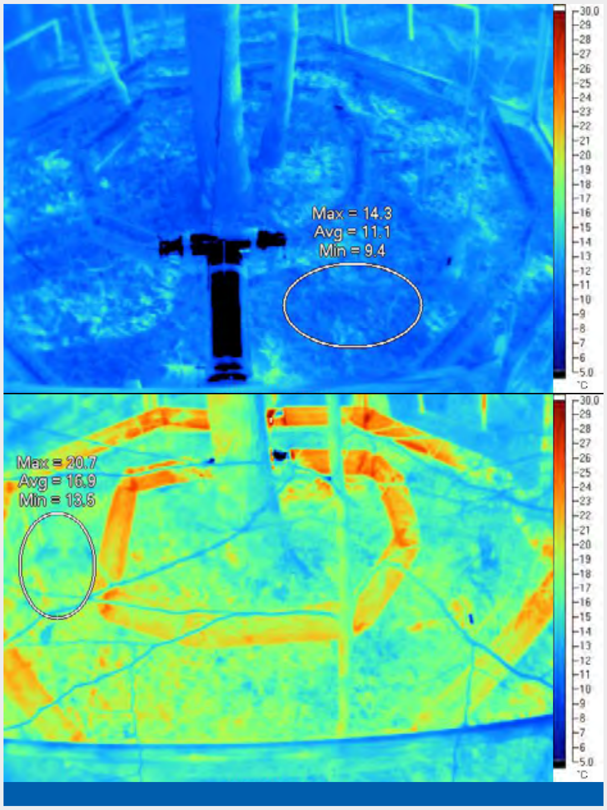
Nathan Sanders
University of Tennessee, Knoxville
(1136703)

Aaron Ellison
Harvard University
(1136646)

Robert Dunn
North Carolina State University
(1136717)

Sara Cahan
Bryan Ballif
Nicholas Gotelli
University of Vermont and State Agricultural College
(1136644)

Sanders and colleagues study adaptations to climate change in a common foraging ant in eastern US forests to understand the mechanisms that allow some species to adapt to shifts in climate rather than migrating or going extinct.



These images illustrate the levels of atmospheric warming achieved in the research chambers.
CREDIT: PAUL J. HANSON

Publications

CaraDonna PJ, et al. (2017) Interaction rewiring and the rapid turnover of plant- pollinator networks. *Ecol Lett* 20(3): 385–394

Helms Cahan S, et al. (2017) Modulation of the heat shock response is associated with acclimation to novel temperatures but not adaptation to climatic variation in the ants *Aphaenogaster picea* and *A. rudis*. *J Comp Biochem Physiol* 204: 13–120

One of the species in the *Aphaenogaster rudis* complex, the taxonomy and systematics of which is being disentangled with this Dimensions of Biodiversity project.
CREDIT: AARON ELLISON

Species in the *Aphaenogaster rudis* complex nest in and around damp, fungus-laden soil. These ants are some of the most important dispersers of seeds of "spring ephemerals" — the understory herbs such as Trillium, Bloodroot, and Winged Polygala.
CREDIT: AARON ELLISON

An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents

Stefan Sievert
Jeffrey Seewald
Craig Taylor
Woods Hole
Oceanographic Institution
(1136727)

Costantino Vetriani
Rutgers University
New Brunswick
(1136451)

Ramunas Stepanauskas
Bigelow Laboratory
for Ocean Sciences
(1136488)

Dionysios I. Foustoukos
Carnegie Institution
of Washington
(1136608)

Deep-sea hydrothermal vents, first discovered in 1977, are 'poster child' ecosystems where microbial chemosynthesis rather than photosynthesis is the primary source of organic carbon. This project establishes an interdisciplinary international research program to better understand the underlying microbiology and biogeochemistry in these poorly-understood deep-sea hydrothermal vent ecosystems.

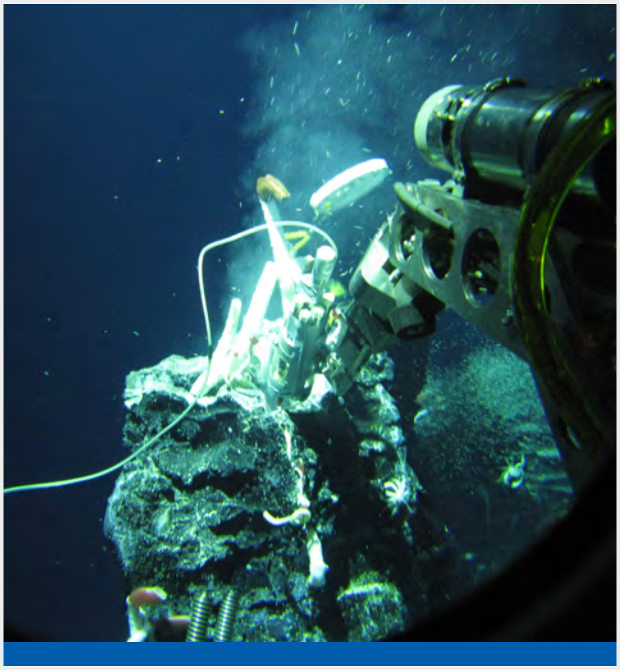


Photo of a diffuse-flow vent site on the East Pacific Rise called Crab Spa. It shows the submersible *Alvin's* manipulator arm holding a sensor developed by Nadine Le Bris that measures temperature, pH, and sulfide in situ. This site is being used by the authors and colleagues as a model system to gain insights into chemosynthetic processes at deep-sea vents.

CREDIT: STEFAN SIEVERT

Publications

Bergauer K, et al. (2018) Rather uniform organic matter processing by microbial communities throughout the Atlantic water column as revealed by metaproteomics. *PNAS* 115(3): e400–e408

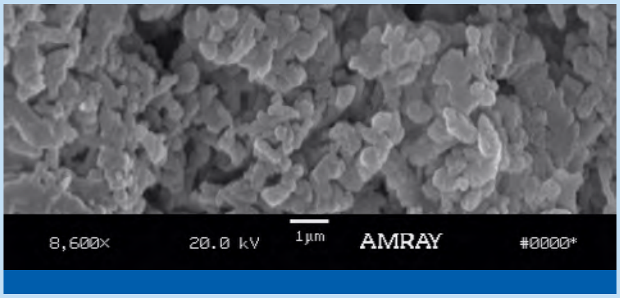
Munson-McGee JH, et al. (2018) A virus or more in nearly every cell in a Yellowstone hot spring. *ISME J* doi: 10.1038/s41396-018-0071-7

Bowers RM, et al. (2017) Genome standards for single amplified genomes and genomes from metagenomes of Bacteria and Archaea. *Nat Biotechnol* 35(8): 725–731

Jungbluth SP, et al. (2017) Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. *Peer J* 5: e3134

Mino S, et al. (2017) Endemicity of the cosmopolitan mesophilic chemolithoautotroph *Sulfurimonas* at deep-sea hydrothermal vents. *ISME J* 11(4): 909–919

Stepanauskas R, et al. (2017) Improved genome recovery and integrated cell-size analyses of individual, uncultured microbial cells and viral particles. *Nat Comm* doi:10.1038/s41467-017-00128-z



Scanning electron micrograph of chemosynthetic biofilm collected from a deep-sea hydrothermal vent.

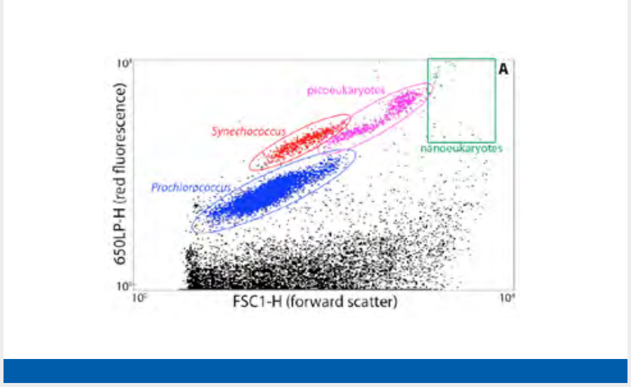
CREDIT: CONSTANTINO VETRIANI

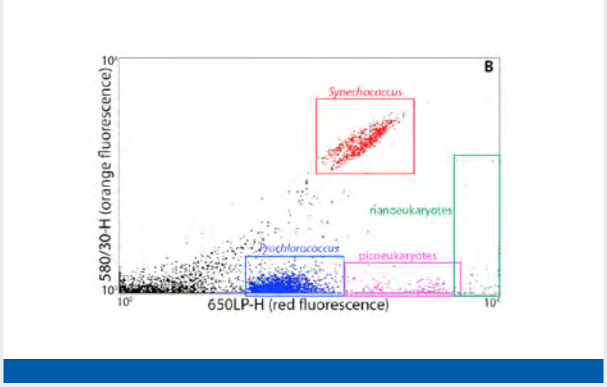
Functional diversity of marine eukaryotic phytoplankton and their contributions to C and N cycling

Bess Ward
Daniel Sigman
Princeton University
(1136345)

Andrew Allen
J. Craig Venter Institute, Inc.
(1136477)

This project uses two North Atlantic sites in two seasons to link genetic diversity and species composition of phytoplankton communities to the biogeochemistry of the surface ocean, tracking the complex changes occurring during late summer blooms of algae.





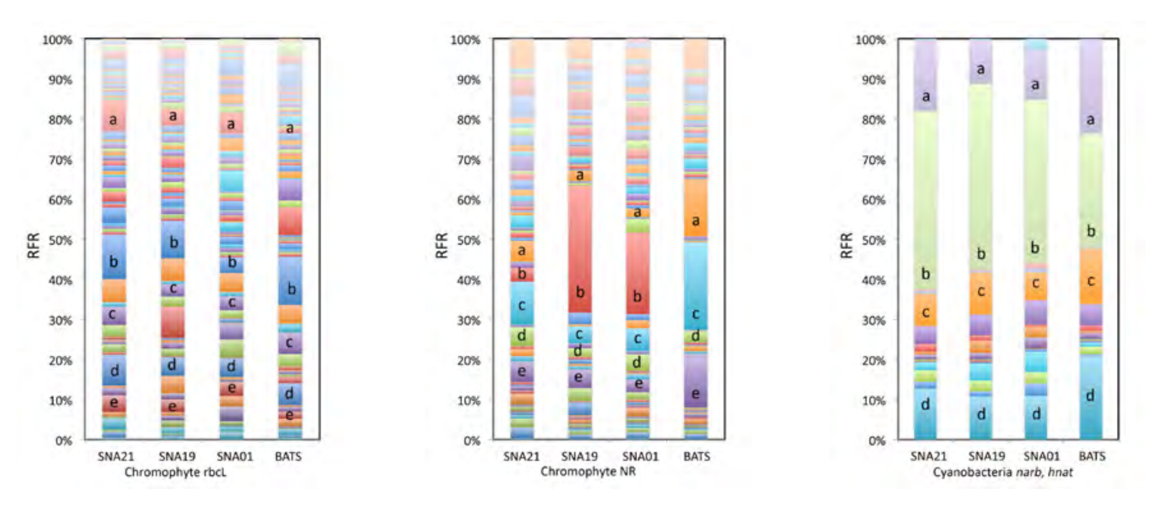
Left & Right: Scattergram of flow cytometry data showing differentiation between different groups of phytoplankton on the basis of size and autofluorescence.

CREDIT:
SARAH FAWCETT,
PRINCETON UNIVERSITY

HTTP://WWW.BCO-DMO.ORG/PROJECT/544343

Publication

Van Oostende N, et al. (2017) Variation of summer phytoplankton community composition and its relationship to nitrate and ammonium assimilation across the North Atlantic Ocean. *Deep-Sea Res Part I: Oceanogr Res Papers* 121: 79–94



Relative contribution of diverse archetypes to the phytoplankton community in the Subarctic North Atlantic (SNA) in May 2009 and at BATS in March 2009 analyzed on Phytoarray-2. The colors represent Relative Fluorescence Ratio, the fraction of total fluorescence due to each probe (average of two replicate arrays for each sample).

CREDIT: BESS WARD

Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk

Thomas Brooks
Bruce Young
NatureServe
Gabriel C. Costa
Federal University of Rio Grandedo Norte
(1136586)
Volker Radeloff
University of Wisconsin, Madison
(1136592)
Catherine Graham
State University of New York, Stony Brook
(1136705)
Stephen B. Hedges
Pennsylvania State University
(1455761)

This project has assembled a database of 13,000 land vertebrates of the Americas to investigate how changes in one dimension of biodiversity influences changes in others. Understanding how species composition influences the vibrant diversity of animal functional traits will improve understanding of how different communities are assembled and change over time.

Aspidoscelis sexlineata six-lined racerunner, Colorado, USA.

CREDIT: GEOFFREY A. HAMMERSON

Publications

Graham CH, et al. (2018) Phylogenetic scale in ecology and evolution. *GlobEcol Biogeo* 27(32): 175–187

Brum FT, et al. (2017) Global priorities for conservation across multiple dimensions of mammalian diversity. *PNAS* 114: 7641–7646

Davidson AD, et al. (2017) Geography of current and future global mammal extinction risk. *PLoS ONE* 12(11): e0186934

Gehara M, et al. (2017) Estimating synchronous demographic changes across populations using hABC and its application for a herpetological community from northeastern Brazil. *Mol Ecol* 26(18): 4756–4771

Graham L, et al. (2017) Future geographic patterns of novel and disappearing assemblages across three dimensions of diversity: a case study with Ecuadorian hummingbirds. *Divers Distrib* 23: 944–954

Hammerson GA, et al. (2017) Strong geographic and temporal patterns in conservation status of North American bats. *Biol Conserv* 212: 144–152

Holt BG, et al. (2017) Environmental variation is a major predictor of global trait turnover in mammals. *J Biogeo* 45(1): 225–237

Machac A, et al. (2017) Ecological controls of mammalian diversification. *J Biogeo* 27(1): 32–46

Marin J, et al. (2017) Evolutionary time drives global tetrapod diversity. *Proc Roy Soc B* doi: 10.1098/rspb.2017.2378

Oliveira BF, et al. (2017) AmphiBIO, a global database for amphibian ecological traits. *Nat Sci Data* 4: 170123

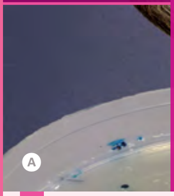
Oliveira EF, et al. (2017) Climatic suitability, isolation by distance and river resistance explain genetic variation in Brazilian whiptail lizard. *Heredity* 120(3): 251–265

Rapacciuolo G, et al. (2017) The signature of human pressure history on the biogeography of body mass in tetrapods. *Glob Ecol Biogeo* 26(9): 1022–1034

Young BE, et al. (2017) Are pollinating hawk moths declining in the northeastern United States? An analysis of collection records. *PLoS ONE* 12(10): e0185683

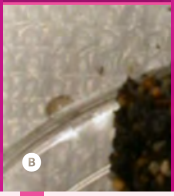
Zurano JP, et al. (2017) Morphological and ecological divergence in South American canids. *J Biogeo* 44: 821–833

Proj. 1



The microbial basis of animal speciation

Proj. 2

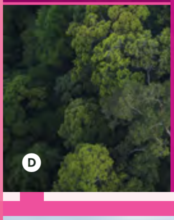


Deconstructing diversity and ecosystem function at multiple spatial and genetic scales in a keystone plant-microbe symbiosis

Proj. 3

Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?

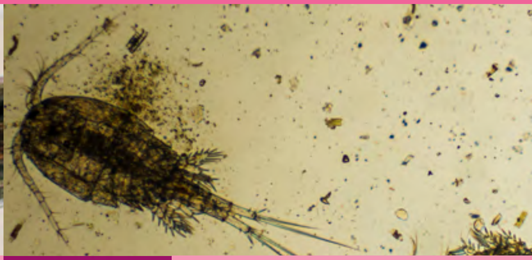
Proj. 4



US-China: Diversity and Forest Change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities

Proj. 5

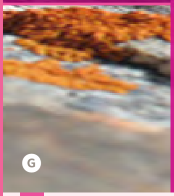
Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations



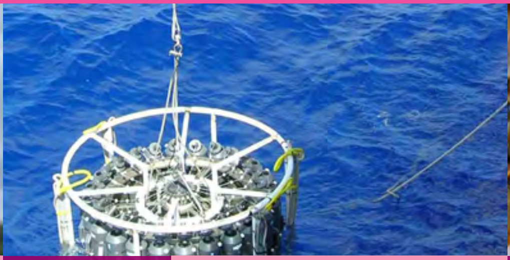
Proj. 6

Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

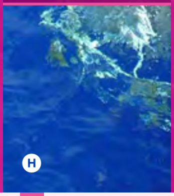
Proj. 7



An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests



Proj. 8

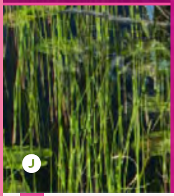


Biological Controls on the Ocean C:N:P ratios

Proj. 9

Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees

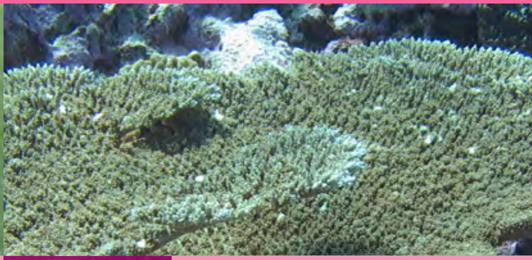
Proj. 10



Dimensions of Biodiversity Distributed Graduate Seminar

Proj. 11

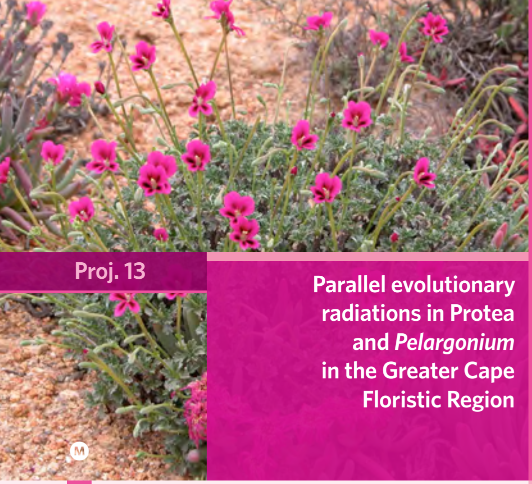
An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity to climate change



Proj. 12

Shedding light on viral dark matter—genetic, taxonomic, and functional diversity of coral reef viromes

Titles 2010



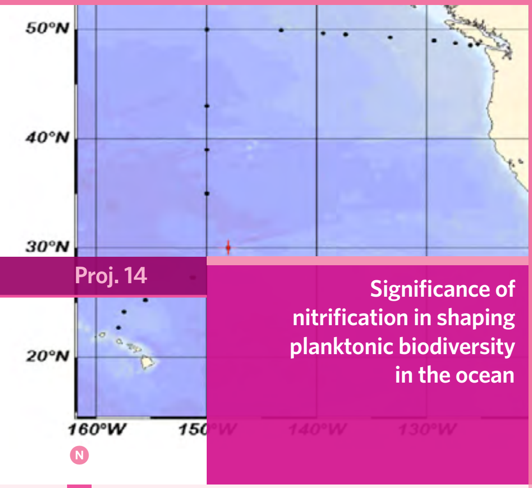
Proj. 13

Parallel evolutionary radiations in Protea and *Pelargonium* in the Greater Cape Floristic Region

< | ***CREDIT***

Ⓐ Robert Brucker & Seth Bordenstein
Ⓑ Kabir G. Peay
Ⓒ Bradley Cardinale

Ⓜ Carl D. Schlichting



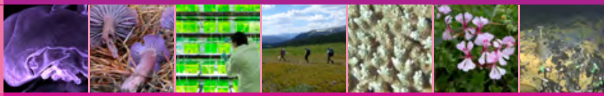
Proj. 14

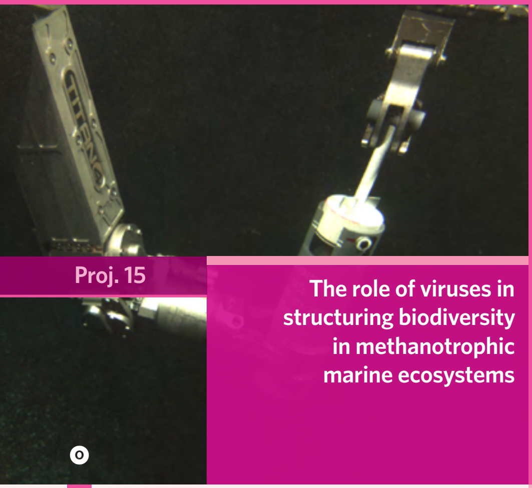
Significance of nitrification in shaping planktonic biodiversity in the ocean

< | ***CREDIT***

Ⓓ Christian Ziegler
Ⓔ Richard Lankau
Ⓕ iStock

Ⓝ Anitra Ingalls & David Stahl





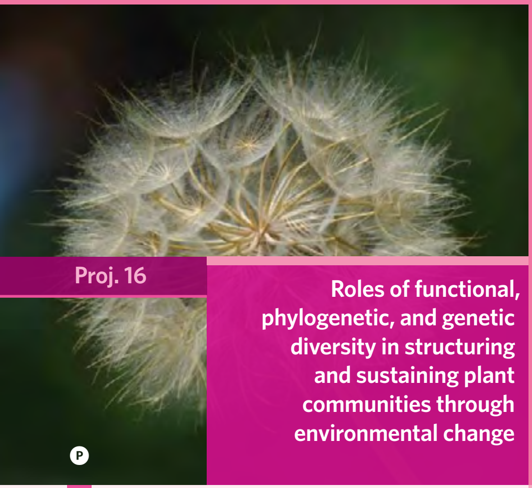
Proj. 15

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

< | ***CREDIT***

Ⓖ A. Elizabeth Arnold
Ⓗ Adam Martiny
Ⓘ Jay Evans

Ⓞ David Valentine



Proj. 16

Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change

< | ***CREDIT***

Ⓙ Jes Coyle, David Gonthier, Jonathan Moore & the Brookhaven National Lab
Ⓚ W. Chris Funk
Ⓛ Forest Rohwer

Ⓟ Gregory Sonnier

Proj. 1 / 16

The microbial basis of animal speciation

Seth Bordenstein
Vanderbilt University
(1046149)

The head of *Nasonia* wasp that was captured in detail by a scanning electron microscope. The image is false colored purple.

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN

Proj. 2 / 16

Deconstructing diversity and ecosystem function at multiple spatial and genetic scales in a keystone plant-microbe symbiosis

Thomas Bruns
John W. Taylor
University of California, Berkeley
(1046115)

Kabir G. Peay
Stanford University
(1249341)

Rytas Vilgalys
Duke University
(1046052)

Many of the fungi involved in ectomycorrhizal symbiosis produce conspicuous fruiting bodies, commonly known as mushrooms.

CREDIT: KABIR G. PEAY

Proj. 3 / 16

Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?

Bradley Cardinale
University of Michigan, Ann Arbor
(1046121)

Charles F. Delwiche
University of Maryland, College Park
(1046075)

Todd H. Oakley
University of California, Santa Barbara
(1046307)

Undergraduate research assistant maintains chemostats.

CREDIT: BRADLEY CARDINALE

Proj. 4 / 16

US-China: Diversity and Forest Change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities

(CO-FUNDED BY NSFC)

US TEAM

Stuart Davies
Richard Condit
W. John Kress
Helene Muller-Landau
Smithsonian Institution
(1354741)

Nathan Swenson
University of Maryland, College Park
(1354741)

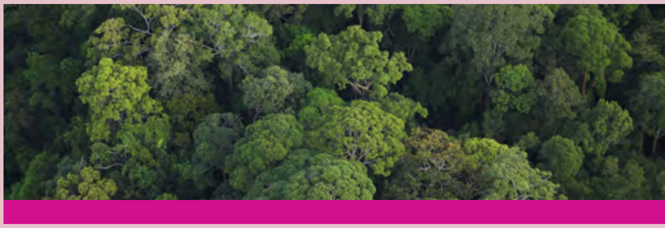
CHINA TEAM

Zhanqing Hao
Xugao Wang
Institute of Applied Ecology, Chinese Academy of Sciences (CAS)

Keping Ma
Xiangcheng Mi
Institute of Botany, CAS

Wanhui Ye
South China Botanical Garden, CAS

Min Cao
Jie Li
Xishuangbanna Tropical Botanical Garden, CAS



Canopy of the plot at Lambir, Malaysia.

CREDIT: CHRISTIAN ZIEGLER

Proj. 5 / 16

Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations

Richard Lankau
University of Wisconsin, Madison
(1552412)


External hyphae of arbuscular mycorrhizal fungi with spores growing around sycamore (*Platanus occidentalis*) roots.

CREDIT: RICHARD LANKAU

Proj. 6 / 16

Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

Carol Lee
University of
Wisconsin, Madison
(1046372)

Joana Carneiro da Silva
University of
Maryland, Baltimore
(1046371)


Copepods are a major food source for some of the world's most important fisheries, such as herring, anchovy, salmon and flounder.

CREDIT: ISTOCK

Proj. 7 / 16

An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests

Francois Lutzoni
Duke University
(1046065)

Georgiana May
University of
Minnesota, Twin Cities
(1045608)

Ignazio Carbone
North Carolina
State University
(1046167)

Anne Arnold
University of Arizona
(1045766)


Boreal lichens harbor a diverse array of secondary fungi (Endolichenic fungi).

CREDIT: A. ELIZABETH ARNOLD, UNIVERSITY OF ARIZONA

Proj. 8 / 16

Biological Controls on the Ocean C:N:P ratios

Adam Martiny
Steven Allison
University of
California, Irvine
(1046297)

Simon Levin
Princeton University
(1046001)

Michael Lomas
Bigelow Laboratory
for Ocean Sciences
(1303287)

Benjamin Van Mooy
Woods Hole
Oceanographic
Institution
(1303287)

Kun Zhang
University of
California, San Diego
(1046368)


A sampling rosette from R/V Atlantic Explorer Dimensions of Biodiversity project.

CREDIT: ADAM MARTINY

Proj. 9 / 16

Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees

Nancy Moran
University of Texas, Austin
(1415604)

Jay Evans
USDA Agricultural Research Service Beltsville Area
(1046153)

Honeybee workers and queen on the hive (*Apis mellifera*).
CREDIT: JAY EVANS

Proj. 10 / 16

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish
University of Washington
(1050680)

Collage representing dimensions of biodiversity with images contributed by student participants of the DBDGS program.
CREDIT: JES COYLE, DAVID GONTHIER, JONATHAN MOORE AND THE BROOKHAVEN NATIONAL LAB; GRAPHIC DESIGN BY CATHY SCHWARTZ

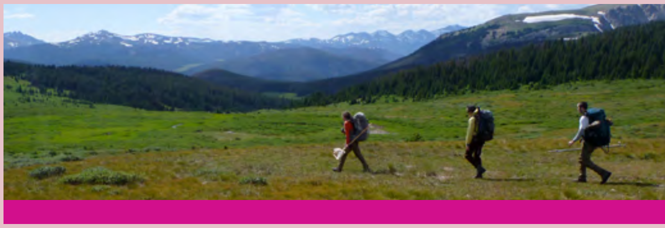
Proj. 11 / 16

An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity to climate change

LeRoy N. Poff
Boris Kondratieff
Cameron Ghalambor
William C. Funk
Colorado State University
(1046408)

Steven Thomas
University of Nebraska, Lincoln
(1045991)

Alexander Flecker
Joseph Bernardo
Kelly Zamudio
Cornell University
(1045960)



Students on their way to sample aquatic insects in streams in the Colorado Front Range for the ECOTRAC project.
CREDIT: KELLY ZAMUDIO

HTTP://WWW.EEB.CORNELL.EDU/EVOTRAC/WELCOME.HTML

Proj. 12 / 16

Shedding light on viral dark matter — genetic, taxonomic, and functional diversity of coral reef viromes

Forest Rohwer
Anca Segall
Robert A. Edwards
San Diego State University
(1046413)

Acropora corals.
CREDIT: FOREST ROHWER

Proj. 13 / 16

Parallel evolutionary radiations in *Protea* and *Pelargonium* in the Greater Cape Floristic Region

Carl D. Schlichting
Kent Holsinger
Cynthia Jones
John Silander
University
of Connecticut
(1046328)

Andrew Latimer
University of
California, Davis
(1045985)

Justin O. Borevitz
Australian National
University
(1242294)

Pelargonium peltatum.
CREDIT: CARL D. SCHLICHTING

Proj. 14 / 16

Significance of nitrification in shaping planktonic biodiversity in the ocean

David Stahl
Allan Devol
E. Virginia Armbrust
Anitra Ingalls
University
of Washington
(1046017)

James Moffett
University of
Southern California
(1046098)

Scanning electron micrograph of *Nitrosopumilus maritimus*, the first marine ammonia oxidizing archaeon isolated in pure culture.
CREDIT: DAVID STAHL

Proj. 15 / 16

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

David Valentine
University of California,
Santa Barbara
(1046144)

An incubator as first seen on the return to a second study site in 2013, showing substantial growth of microbial mats on the outer surfaces.
CREDIT: DAVID VALENTINE

Proj. 16 / 16

Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change

Donald M. Waller
Kenneth Cameron
Thomas Givnish
Kenneth Sytsma
University of Wisconsin,
Madison
(1046355)

Tragopogon sp, a typical example of a wind-dispersed species.
CREDIT: GREGORY SONNIER,
UNIVERSITY OF WISCONSIN, MADISON

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ALEXANDRIA, VIRGINIA 22314

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