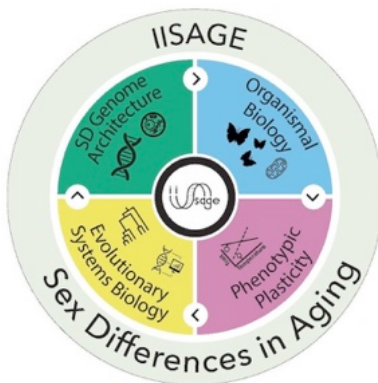
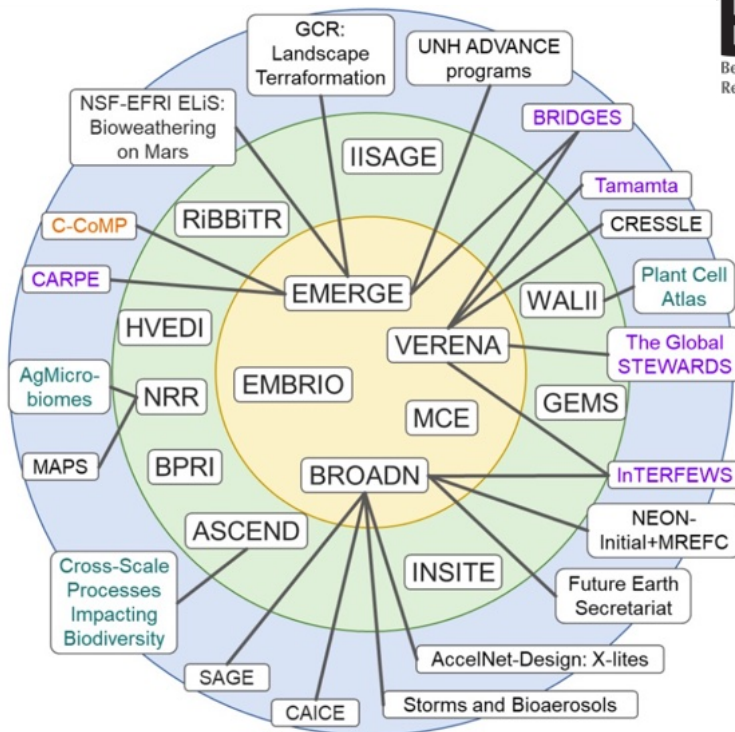
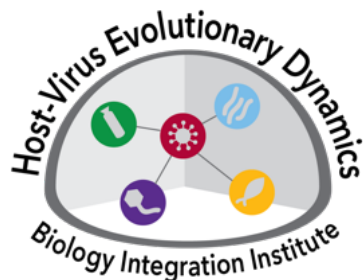
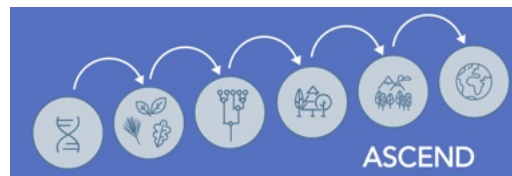
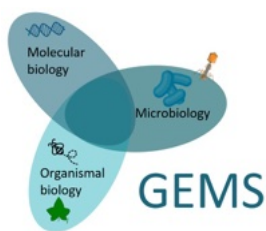


National Science Foundation
Directorate of Biological Sciences

Biology Integration Institutes 2024 Awardees Meeting

January 22-23, 2024

NSF Headquarters, Alexandria, VA





Biology Integration Institutes 2024 Awardees Meeting
National Science Foundation
Directorate of Biological Sciences

Zoom Link: https://nsf.zoomgov.com/webinar/register/WN_u1fC5pxYTb65fBzA8O8HWQ

Monday, January 22, 2024 (Times given for Eastern Standard Time), NSF Headquarters, Room E2030

7:30 am – 8:30 am	Coffee and light refreshments
8:30 am – 8:45 am	Statement of Purpose and Agenda Overview, Steve DiFazio Welcome from Susan Marqusee, Assistant Director, Directorate for Biological Sciences
8:45 am – 9:45 am	Presentations from the 2020 Institutes – Project Overviews (10 min per presentation). <u>Virginia Rich</u> – The EMERGE Institute: Identifying EMergent Ecosystem Responses through Genes-to-Ecosystems Integration at Stordalen Mire <u>Katy Heath</u> – GEMS: Genomics and Eco-evolution of Multi-scale Symbioses <u>Fabrizio Gabbiani</u> – Behavioral Plasticity Research Institute (BPRI): Transforming the Study of Phenotypic Plasticity through Biological Integration <u>Jeannine Cavender-Bares</u> – The Causes and Consequences of Plant Biodiversity Across Scales in a Rapidly Changing World
9:45 am – 11:15 am	Poster Session 1 and refreshments
11:15 am – 12:00 pm	Presentations from the 2021 Institutes Part 1 (10 min per presentation) <u>David Umulis</u> – Emergent Mechanisms in Biology of Robustness, Integration & Organization (EMBRIO) <u>Susan VandeWoude</u> – Regional OneHealth Aerobiome Discovery Network (BROADN) <u>Corinne Richards-Zawacki</u> – Uncovering Mechanisms of Amphibian Resilience to Global Change from Molecules to Landscapes
12:00 pm – 1:15 pm	Lunch (on your own)
1:15 pm – 2:00 pm	Presentations from the 2021 Institutes Part 2 (10 min per presentation) <u>Michael Lynch</u> – Mechanisms of Cellular Evolution <u>Ruben Ceballos</u> – Host-Virus Evolutionary Dynamics Institute (HVEDI) <u>Allison Miller</u> – New Roots for Restoration: Integrating Plant Traits, Communities, and the Soil Ecosphere to Advance Restoration of Natural and Agricultural Systems
2:00 pm – 3:00 pm	Presentations from the 2022 Institutes (10 min per presentation) <u>Michele Nishiguchi</u> – INSITE: Institute for Symbiotic Interactions, Teaching and Education in the Face of a Changing Climate <u>Sue Rhee</u> – Life Without Water: Protecting Macromolecules, Cells and Organisms During Dessication and Rehydration Across Kingdoms of Life <u>Nicole Riddle</u> – SAGE: Discovering the Mechanisms and Evolution of Aging Differences Between Females and Males <u>Colin Carlson</u> – Predicting the Global Host-Virus Network from Molecular Foundations
3:00 pm – 4:30 pm	Poster Session 2 and refreshments
4:30 pm – 5:00 pm	Biology Integration Institutes Research Coordination Network
5:00 pm – 5:30 pm	BII Administrative Session – Reed Beaman - Governing documents: (Broadening Participation Plan, Strategic Plan, Governance) - Project management expectations - Renewal policy
5:30 pm	Adjourn (Dinner on your own)

(continued on next page)

Tuesday, January 23, 2024 (Times given for Eastern Standard Time), NSF Headquarters, Room E2030

7:30 am – 8:30 am	Coffee and light refreshments
8:30 am – 9:30 am	Flash Talks by Early Career Researchers (3 min each, 1 each for 14 institutes)
9:30 am – 10:00 am	Integration Breakouts (and refreshments): Each group appoints a moderator and a notetaker. Notes are posted to a Google Docs folder. In-person only. (Extra space in room W2210, as needed) <ol style="list-style-type: none">1. Opportunities and challenges for early career researchers2. Budget management3. Publishing policy best practices4. Managing graduate students on integrated projects5. Project integration across institutions and disciplines6. How to recruit and engage undergraduate students to conduct multidisciplinary research7. Project management and adapting to challenges and opportunities8. Data management of projects with multiple working groups9. Assessment of efficacy and interdisciplinarity10. Connecting to solutions science, translational research11. Communicating substantively across disciplines12. Communication of science to the general public13. Safety & inclusivity & belonging science in the modern era14. Mentoring & supporting early career researchers
10:00 am – 11:00 am	Flash Talks by Early Career Researchers (3 min each, 1 each for 14 institutes)
11:00 am – 11:30 am	Highlights from Virtual Site Visits – Jennifer Weller
11:30 am – 12:00 pm	Breakout Summation and Closing Remarks (BII Working Group)
1:30 pm	Biology Integration Institutes Research Coordination Network Working Session (RCN Leads and Institute Liaisons)

Flash Talks, Session 1, Tuesday, 8:30 to 9:30 EST

No.	Institute	Name	Institution	Title (virtual talks in red and underlined)
1	BPRI	Liza Bessonova	Washington University, St. Louis	<u>Serotonergic amplification of odor-evoked neural responses maps flexibly onto behavioral outcomes</u>
2	ASCEND	J. Antonio Guzmán Q.	University of Minnesota	Integrating phylogenetic and spaceborne spectroscopy for mapping the distribution of communities at the large scale
3	ASCEND	Mariana Hernandez-Leal	University of Minnesota	Phenotypes in phylogeography: employing foliar spectral signatures to unravel the contribution of local adaptation in the diversification of live oaks.
4	EMERGE	Hannah Holland-Moritz	University of New Hampshire	Climate Feedbacks from Permafrost Thaw are Buffered by Functional Ecology and Community Assembly
5	EMERGE	Zhen Li	Lawrence Berkeley Labs	A framework for integrating genomics, microbial traits, and ecosystem biogeochemistry
6	GEMS	Laura Suttentfield	University of Illinois Urbana-Champaign	Phage-mediated resolution of genetic conflict alters the evolutionary trajectory of <i>Pseudomonas aeruginosa</i> lysogens
7	GEMS	Lilian Caesar	Indiana University	Her royal phages: how honey bee queen mobilome shapes the microbiome
8	BROADN	Ashley Miller	CSU-FC	Characterizing the aerial transmission of white pine blister rust disease
9	BROADN	Marina Nieto-Caballero	CSU-FC	Bioaerosol Sampler Comparison Over a Semi-Arid Grassland Site
10	EMBRIO	Linlin Li	Purdue	Integrating Artificial Intelligence in Computational Biology
11	EMBRIO	Weiwei Zhang	Purdue	Decoding Ca ²⁺ signatures and signaling to the actin cytoskeleton in plant immune response
12	HVEDI	Elizabeth Padilla	Interamerican University, Puerto Rico	Standardizing qPCR protocols for characterizing viruses and host across the HVEDI BII network
13	HVEDI	Ruth Plymale	Ouachita Baptist University	Standardization of virus workflow using Gordoniaphage, a HVEDI core virus system model
14	IISAGE	Jack Rayner	University of Maryland	Gene expression changes in bats with extreme sex-biased longevity

Flash Talks, Session 2, Tuesday 10:00 to 11:00 EST

No.	Institute	Name	Institution	Title (virtual talks in red and underlined)
1	NRR	Molly Hanlon	Danforth Plant Science Center	Root traits and root system allocation in perennial plants (put back-to-back with other NRR talk)
2	NRR	Stella Woeltjen	Danforth Plant Science Center	Developing in-field imaging methods for aboveground phenotyping of non-model species
3	MCE	Jeremy Wideman	Arizona State	The spatial proteome of <i>Tetrahymena thermophila</i>
4	VERENA	Greg Albery	Georgetown University	Global change and the last coronavirus pandemic
5	VERENA	Torre Lavelle	Georgetown University	Global change and the next influenza pandemic
6	IISAGE	Jamie Marks	Michigan State University	Mitochondrial function exhibits sex-specific aging among painted turtle (<i>Chrysemys picta</i>) populations
7	INSITE	Heather Stever	UC Merced	Understanding Hawaiian Insects in a Changing Climate
8	INSITE	Stephen Williams	UC Merced	A generalized model of the impacts of temperature on distinct types of symbiosis
9	RIBBITR	Jake Eisaguirre	UC Santa Barbara	Open Science: Catalyzing Positive Change in the Scientific Landscape
10	MCE	Kerry Geiler-Samerotte	Arizona State	<u>Single-cell investigation of the growth law in yeast and bacteria</u>
11	RIBBITR	Brandon Hoenig (Postdoc)		<u>Fungus Finders: Using CRISPR for rapid, field-deployable detection of amphibian fungal pathogens</u>
12	WALII	John F. Ramirez	University of Wyoming	<u>Identifying glass properties that distinguish desiccation tolerant and sensitive tissues in resurrection plants</u>
13	WALII	Sheila Ferer	California State University, Channel Islands	<u>Membrane damage and repair upon rehydration</u>
14	BPRI	Mehreen Tahir	Arizona State	<u>High protein diet promotes faster growth in locusts but also increases their susceptibility to <i>Metarhizium biopesticide</i></u>

Posters, by Institute

No.	Institute	Lead Author	University	Title
1	ASCEND	Artur Stefanski	University of Minnesota	All the light we cannot see: signatures of climate change in leaf spectra of trees
2	ASCEND	Brett Fredericksen	University of Minnesota	Heritability of hyperspectral data varies by site
3	ASCEND	Celso Olivera	University of Wisconsin-Madison	Phytochemical shifts in aspen during and following an invasive <i>Lymantria dispar</i> moth outbreak: Consequences for interacting disturbances
4	ASCEND	Ethan Butler	University of Minnesota	Estimating variation in global photosynthesis from genetic variation in the nitrogen content of Rubisco
5	ASCEND	J. Antonio Guzmán Q.	University of Minnesota	Tree diversity and composition predicts seasonal structural stability in a large-scale forest diversity experiment
6	ASCEND	Mariana Hernandez-Leal	University of Minnesota	Phenotypes in phylogeography: employing foliar spectral signatures to unravel the contribution of local adaptation in the diversification of live oaks.
7	ASCEND	Natalie Queally	University of Wisconsin-Madison	High frequency imaging spectroscopy data from SHIFT show phenological changes in trait expression in grazed landscapes
8	ASCEND	Ting Zheng	University of Wisconsin-Madison	Foliar traits from imaging spectroscopy inform variation in GPP from flux towers across NEON sites
9	BPRI	Erez Lieberman	Baylor College of Medicine	Multiple locust species lack a stable karyotype
10	BPRI	Fabrizio Gabbiani	Baylor College of Medicine	Single Cell Atlas of Locust Optic Lobe Across Phases
11	BPRI	Hojun Song	Texas A&M University	Time-Travel with Swarming Locusts: Molecular Snapshots of Phase Change across Time, Space and Evolution
12	BPRI	Millicent Oyugi	Texas A&M University	Using IDP to Enhance Interdisciplinary Research Skills and Career Readiness Among Behavioral Plasticity Research Institute Stem Graduate Trainees
13	BPRI	Millicent Oyugi	Texas A&M University	Challenges and Strategies for Implementing Interdisciplinary Biological Research Training in Collaborative Institutions
14	BPRI	Richard Dewell	Baylor College of Medicine	Single-cell transcriptomics of an identified looming-detection neuron in locusts identifies membrane ion channels critical for collision-avoidance behaviors
15	BPRI	Richard Dewell	Baylor College of Medicine	To jump or not to jump: Comparing effects of phenotypic plasticity on visual responses and behavior between desert locusts & grasshoppers
16	BPRI	Spencer Behmer	Texas A&M University	Three's a Crowd: how density and temperature guide nutrient regulation in a phenotypically plastic herbivore
17	BROADN	Adam Gillison	CSU-Pueblo	Functional Resistances of Airborne Bacteria that might Promote Survival in the Atmosphere
18	BROADN	Ashley Miller	CSU-FC	Characterizing the aerial transmission of white pine blister rust disease
19	BROADN	Brad Borlee	CSU-FC	Integrating BROADN research teams through an undergrad summer research program
20	BROADN	Jeni Cross	CSU-FC	A developmental evaluation framework for transdisciplinary teams and institutes
21	BROADN	Marina Nieto-Caballero	CSU-FC	Impact of Relative Humidity Shifts on Bioaerosols in a Colorado Grassland Site
22	BROADN	Mark Hernandez	CU-Boulder	What bacteria say when they fly: deciphering the airborne microbial stress response.
23	BROADN	Pankaj Trivedi	CSU-FC	Structure and Interactions of the Airborne Bacterial Communities
24	BROADN	Sonia Kreidenweis	CSU-FC	Bioaerosol sampling campaigns at the NEON Central Plains Experiment Range
25	EMBRIO	David Gazzo	Notre Dame	A Novel High Throughput Behavioral Platform for Characterization of Neurodegeneration.
26	EMBRIO	Linlin Li	Purdue	Integrating Artificial Intelligence in Computational Biology
27	EMBRIO	Weiwei Zhang	Purdue	Decoding Ca ²⁺ signatures and signaling to the actin cytoskeleton in plant immune response
28	EMERGE	Anne Mook	Colorado State University	Evaluation of Team Growth and Effectiveness
29	EMERGE	Ruth Varner	University of New Hampshire	EMERGE REU: Innovative approaches to undergraduate training in integrative ecosystem biology
30	EMERGE	Sarah Bagby	Case Western Reserve University	A Comprehensive Toolkit for Interdisciplinary Team Science
31	GEMS	Carla Cáceres	University of Illinois Urbana-Champaign	Genomics and Eco-evolution of Multi-Scale Symbioses in Aquatic Systems
32	GEMS	Katy Heath	University of Illinois Urbana-Champaign	Plasmids in bacteria in plants: Rhizobia as model multi-scale symbionts
33	GEMS	Laura Sutfenfield	University of Illinois Urbana-Champaign	CRISPR-Cas mediated drivers of <i>Pseudomonas aeruginosa</i> lysogen diversity
34	GEMS	Lilian Caesar	Indiana University	Her royal phages: how honey bee queen mobilome shapes the microbiome
35	GEMS	Nicholas Leonardi	University of Illinois Urbana-Champaign	GEMS Education and Outreach: Utilizing Research to Inform Curriculum and Professional Learning Design
36	GEMS	Rachel Whitaker	University of Illinois Urbana-Champaign	Co-evolutionary dynamics and diversity in microbial populations with CRISPR immunity
37	GEMS	Tiffany Tovey	UNC Greensboro	Using a Values-Engaged Educative Approach to Evaluate The GEMS Project: Critical Friendship to Support Project Improvement

Posters, by Institute

No.	Institute	Lead Author	University	Title
38	HVEDI	Nathan Reyna	Ouachita Baptist University	K-16 outreach and dissemination - BII: Host-Virus Evolutionary Dynamics Institute
39	HVEDI	Ruben Michael Ceballos	University of California Merced	Host-Virus Evolutionary Dynamics Institute: Progress
40	IISAGE	Anne Bronikowski	Michigan State University	The Integration Initiative: Sex, Aging, Genomics, Evolution - TRAINING PROGRAMS
41	IISAGE	Gerald Wilkinson	University of Maryland	Integration Initiative: Sex, Aging, Genomics, Evolution
42	IISAGE	Jamie Marks	Michigan State University	Mitochondrial function exhibits sex-specific aging among painted turtle (<i>Chrysemys picta</i>) populations
43	IISAGE	Nicole Riddle	University of Alabama at Birmingham	Challenges in cross-species comparisons of RNA-seq data
44	IISAGE	Peggy Biga	University of Alabama at Birmingham	IISAGE: Engaging the public through traveling outreach and community science to enhance understanding of sex-specific aging across the animal kingdom
45	INSITE	Daravuth Cheam	UC Merced	Effects of protozoan grazing on <i>Vibrio fischeri</i> biofilms outside the host
46	INSITE	Kaden Muffett	UC Merced	Developmental ramifications of a season-length heat event on <i>Exaiptasia</i>
47	INSITE	Michele Nishiguchi	UC Merced	INSITE: Harnessing Data to Predict Symbiotic Trajectories Under Climate Change
48	INSITE	Stephen Williams	UC Merced	Exploring the fluid dynamics of establishing symbiosis in the bobtail squid
49	MCE	Jeremy Wideman	Arizona State	The spatial proteome of <i>Tetrahymena thermophila</i>
50	MCE	Wayne Frasch	Arizona State	The evolution of biology's mode of energy production: ATP synthase
51	NRR	Allison Miller	Danforth Plant Science Center Saint Louis University	Above- and below-ground trait covariation in perennial, herbaceous species
52	NRR	Ben Sikes	University of Kansas	Can above-and below-ground phenotypic variation predict coexistence, diversity, and community productivity?
53	NRR	Eric von Wettberg	University of Vermont	Do root/shoot plant traits vary in monocultures vs. polycultures, and does this predict production?
54	NRR	Kris Callis-Duehl	Danforth Plant Science Center	Fostering a sense of belonging in pan-geographic training programs supporting historically excluded trainees.
55	NRR	Molly Hanlon	Danforth Plant Science Center	Root traits and root system allocation in perennial plants
56	NRR	Stella Woeltjen	Danforth Plant Science Center	Developing in-field imaging methods for aboveground phenotyping of non-model species
57	RIBBITR	Delia Basanta (Postdoc)	University of Nevada, Reno	Uncovering resilience mechanisms in the amphibian communities of Panama
58	RIBBITR	Jenny Cocciardi	University of Mississippi	Previous exposure to a fungal pathogen and its effect on thermal preference and survival in an endangered frog species
59	VERENA	Amy Sweeny	University of Sheffield	Virus-virus interactions and wildlife disease dynamics: utilizing surveillance data to investigate co-infection
60	VERENA	Briana Betke	University of Texas Austin	Defining anthropogenic roosting ability and its role in shaping viral outcomes in bats
61	VERENA	Emily Gallichotte	Colorado State University	COMET: A database of vector competence experiments with mosquito-borne viruses
62	VERENA	Lily Cohen	Icahn School of Medicine at Mount Sinai	Sampling strategies and pre-pandemic surveillance gaps for bat coronaviruses
63	WALLI	Bob VanBuren	Michigan State University	Exploring the cross kingdom evolutionary dynamics of desiccation tolerance
64	WALLI	Selena Rice	Michigan State University	Biomolecular design principles of water-responsive intrinsically disordered proteins
65	WALLI	Sue Rhee	Michigan State University	Physical and cellular properties of anhydrobiosis
66	WALLI	Sue Rhee	Michigan State University	Rehydration and recovery from desiccation: shades of protection and survival at the cellular level



Our first *in-person* annual workshop, spring 2023, hosted at the Biosphere 2 in Arizona.

Elevator Speech: The NSF-funded EMERGE Biology Integration Institute's goal is to enable predictive modeling of ecosystem response to change, using the model ecosystem of Stordalen Mire and a 'genes-to-ecosystems-to-genes' approach.

Keywords: ecosystems, genes-to-ecosystems, microbiome, climate change, modeling system feedbacks

Project Website: <https://emerge-bii.github.io>

Participants: <https://emerge-bii.github.io/people/>

Institute Objectives and Goals:

We seek to map the emergent genes-to-ecosystems-to-genes (G2E2G) response of communities to change, using a model ecosystem; to distill consequential findings into improved models; and, to share our transdisciplinary toolkit with others.

We undertake this via 5 goals: (i) To characterize how genes-to-ecosystems-to-gene feedbacks produce system outputs, under controlled *ex situ* conditions and in the field. (ii) To iteratively incorporate insights into models, particularly Biocrunch and ecosys. (iii) To build and disseminate the "EMERGE Toolkit" to accomplish this research. (iv) To engage diverse stakeholders via an integrated outreach program. (v) To train a suite of integrative biologists in the interdisciplinary G2E2G framework.

Integrating across Biology

The EMERGE BII is working to significantly impact the biological disciplines of ecosystem biology, ecology, and molecular biological sciences (microbiome meta-omics) in a convergent research and training framework that explicitly focuses on transdisciplinarity, science of team science, inclusion, and diversity.

Our organizational structure is designed to build convergent research and training, and we have achieved a measurable increase in network integration in our first 3 years. We periodically revise meeting and workshop structures to explore new axes of integration across our diverse team; one example is Keystone Integration Activities in in 2023 Annual Workshop which specifically interwove our disciplines, e.g. molecular chemistry and remote sensing, or gene regulation and ecosystem modeling.

The Institute norm for manuscript development is disciplinarily integrative, with clear support structures for multiple first and/or corresponding authors to acknowledge foundational intellectual investment from multiple teams.

The bulk of our ETO work shares G2E2G Integrative Biology training to reach diverse scientists across the country and internationally.

Education, Training & Outreach:

(i) Our Summer Program unites 30 instructors in training professional scientists (post-baccalaureate and above) over an intensive 2-week period, with ongoing cohort training through the following year, across 5 Core Competency areas, reaching 60 scientists over 3 years, and producing 3 manuscripts (McDonald et al, 2023 + 2 submitted). (ii) Our REU has engaged 14 Institute mentors to train 20 undergraduates over 2 years, in integrative Arctic biology research, with a culminating poster presentation at AGU's annual meeting. (iii) The broader EMERGE Team receives regular trainings in SciTS, DEI, & Mentoring, & "Deep Dive" trainings on key models and datasets. (iv) EMERGE co-hosted 2 internationally-attended webinar series: ECR Viromics, and OSU Microbiome Informatics. (v) EMERGE has developed an Interdisciplinary Team Science toolkit, along with informatics and wet-lab methods, and shares them via publications, webinars, and trainings, via a Learning Workshop at AGU-2023. (vi) We engage in diverse public outreach activities to athletes, faith communities, and K-12, and have been profiled by the press. (vii) We share science via BlueSky, X, & YouTube.

Broadening Participation Outcomes:

To build an inclusive and welcoming institute, EMERGE has implemented the Mentor Academy, and the Navigating Differences program, in the Summer Program; the Co-Directors co-led URGE (Unlearning Racism in GEosciences) pods at their respective institutions, and many Institute Leaders have continued or increased their own DEI trainings. We have held several institute-wide discussions of Title IX news events in biology, and put into action the collectively-identified best practices. We've specifically engaged our universities' Title IX offices as EMERGE partners.

To provide field safety for diverse team members, Dr. Sophie Burke led development of the EMERGE Field Safety Handbook, which has subsequently been implemented in field campaigns and the REU program, presented at AGU, and been adopted as a model by several other projects, groups, and UNH.

To diversify the Institute & its training programs, Co-Director Varner developed application support and evaluation pipelines designed to mitigate implicit bias; these are used for both the REU & Summer Program. We are also promoting professional development of diverse scientists within the Institute through a multi-pronged support & advancement plan.

Significant Research Results:

The foundational experimental and field science we have accomplished includes:

- Multi-decadal changes at the field site:
 - Carbon accumulation and flux (Holmes et al 2022)
 - Quantification of multi-decadal thaw and climate feedbacks (Varner et al, 2022).
- Thaw sequence changes:
 - Characterization of the shift in plant community composition, biomass, nutrient stoichiometry, and molecular composition with increasing permafrost thaw (Hough et al, 2022; Wilson et al, 2022).
 - Characterization of the multi-year habitat preferences, predicted host associations, and metabolic gene content, of DNA and RNA viral communities (Pratama et al, in review; Trubl et al, in prep), and establishment of new methods for characterizing RNA viral ecology & evolution (Zayed et al 2022, Dominguez-Huerta et al 2022).
- Incubations:
 - Execution of parallel multi-institution incubations of 2 thaw-stage habitats in 2022 and '23 to explore mechanistic G2E2G responses; data analysis ongoing.
 - Quantification of the tandem impacts of standard incubation experiments from site peat on microbiomes and DOC (Wilson et al, 2021).
 - Community and gas response to chemical perturbation (Cory et al 2022, Fofana et al, 2023), which provides specific hypotheses for the results of underway incubation experiments.
 - Completion of cross-team temperature-ramp experiments (Corey et al, submitted).
 - Experimental linkage of specific microbial lineages to the transformation of particular metabolites and plant substrates (Hough et al, in prep; Tfaily et al, in prep).
 - Successful enrichments of and genomic characterizations of target metabolisms (Smith et al in prep; Leu et al in prep) including a previously unknown breadth of phenolic-processing pathways in the Mire microbiome, representing a death knell for the phenolic latch paradigm (McGivern et al, in revision).
- Modeling:
 - Categorization of site genomes into Biocrunch's available functional guilds, and ongoing assessment of the distribution of additional metabolic functions not currently represented; we now have a strategy to incorporate the 3 As (Acclimation, Assembly, Adaptation). (Wu & Karaosz et al, in prep).
 - Sensitivity analysis of guild parameter variation in ecosys, for C cycling. Provided the forcing (T, water, C inputs, etc) to BioCrunch. Performed sensitivity analysis in ecosys of methane fluxes to microbial traits inferred from genome information (Li et al, in revision).
- Scaling:
 - Global drivers of peat organic matter chemistry (Verbeke et al, 2022)
 - Of microbiomes, plant communities, and C gas profiles from plot to landscape scale (Varner et al, in prep).
 - At the pan-Arctic scale (McCalley et al, in prep; Kuhn et al, submitted).
- Field:
 - Three years of successful collection of peat and geochemical samples at primary field sites, materials for incubations and bioreactors, and with paired aerial survey data.
 - Engaged new site collaborators, including with substantive co-leveraging of resources by sharing sample splits from our field campaign. These collaborative groups are examining at our site (with a range of funding sources): N-cycling (European), Fe-cycling (European), root-emissions relationships (DOE), and hydrology/ground stability (DOD).
- Identification of a differential temperature sensitivity of lake sediment microbiomes from different depths, implying larger CH₄ emissions as lakes warm than predicted from current (Li et al, in revision); overall habitat kinetics. (Emerson et al, 2021).
- Illumination & recovery of drivers of genetic diversity from the field microbiomes at our site and others (Roux et al, 2021; Guo et al in prep).

Project Management: Our Institute is organized into 9 Teams, with strategic cross-membership to engage integration, and regular monthly meetings. We have held 5 all-hands multi-day workshops (1 in person), and a number of all-hands short meetings for Consensus Planning Sessions, Deep Dives for knowledge-sharing, and Team Science trainings. Having developed overall & team-specific goals, and team-member roles & responsibilities, we have supported and coordinated progress on goals, and held one formal opportunity to adjust roles & responsibilities. We have managed substantial growth (~tripling the original ~30 named participants), developed a process for vetting new faculty members, and built an onboarding packet. Rapid growth is a testament to the potential impact of the science and the power of the nested field and experimental system developed, and establishing process for this growth was vital.

Future plans: This year our scientific analytical focus is on the multi-institution parallel incubation experiments performed in 2023, designed to mechanistically characterize how community gene expression, interactions, and diversity respond to environmental change via acclimation, assembly, and adaptation, and cumulatively produce system outputs. We are working to bring to closure diverse papers that characterize the *in situ* field site community responses to change. We will continue to train a suite of integrative biologists in the interdisciplinary G2E2G framework, through our REU and Summer Programs, and to disseminate the "EMERGE Toolkit" to the broader scientific community.

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

Publications can be found at <https://emerge-bii.github.io/publications>

Genomics and Eco-evolution of Multi-scale Symbioses (GEMS)

Heath, Katy · 2022049 · University of Illinois Urbana-Champaign · kheath@illinois.edu



Nested networks of symbiosis.

Elevator Speech: We live in a symbiotic world, governed by dynamics occurring at the molecular and cellular scales among nested layers of microbes and mobile genetic elements that scale up to generate ecological and evolutionary processes at the population, community, and ecosystem scales. A more predictive Biology in this era of unprecedented change is critical but requires reunification of biological subdisciplines and the strengths that come from changing STEM culture and STEM education in ways that make it more inclusive for diverse science and scientists.

Keywords: Microbes, viruses, bacteria, plants, animals, interactions, dynamics, feedbacks, mutualism, symbiosis, multi-scale, education, community engagement, integration.

Project Website: <https://symbiosis.illinois.edu/>

Participants: <https://symbiosis.illinois.edu/team>

Institute Objectives and Goals:

Our goal is to establish a framework for how the phenotypic variation generated by the mobility of nested symbionts influences the adaptability of traits and the strength and stability of symbiotic interactions by linking molecular mechanisms to organismal outcomes. Symbiotic interactions are keystone in all natural and managed ecosystems, so this is a critical missing link in our understanding of biology and for predicting organismal responses to climate change. GEMS activities are highly integrative but emphasize several themes:

Theme 1: Symbiosis dynamics and discovery

Theme 2: Rules of engagement

Theme 3: Symbioses as engines of rapid adaptation – eco-evolutionary feedbacks

Theme 4: Integrated Education

Theme 5: Outreach and Community Engagement

Theme 6: STEM Equity and Inclusion

Integrating across Biology:

GEMS is integrating biology by funding novel collaborations and co-mentored trainees working across fields toward understanding multi-scale symbiosis – from viruses, plasmids and other mobile genetic elements, the microbes they infect, through the eukaryotic hosts and biogeochemical processes they control. These complex microbial symbioses are ideal for reintegrating molecular and organismal biology because the phenotypes critical to evolutionary and ecological processes in symbiosis are inherently molecular/cellular. Our model promotes ongoing projects on core model systems, while expanding to include perspectives in parallel symbiotic systems, to arrive at a synthetic cross-system and cross-scale understanding of symbiosis. The trainee-led annual retreat, weekly seminars by internal and external speakers, unique GEMS courses, and multi-faceted education and outreach work help to integrate research occurring across subdisciplines and focal systems into a cohesive framework.

Education, Training & Outreach:

- Formal courses, including a seminar series and paper discussions, train students across institutions and disciplines
- Graduate courses in DEI identify areas to improve STEM mentoring and training
- Training on mentoring, authorship, leadership, and more during sponsored workshops and Institute meetings
- Trainee-led development and piloting of curriculum materials related to GEMS science in local middle and high schools
- Cena y Ciencias community engagement program led by Spanish speaking trainees in collaboration with IL SACNAS and Extension reaches families each month
- Monthly programming and week-long summer camp organized by GEMS trainees and faculty in partnership with the local park district and a local not-for-profit (X-Time)
- Science CORPS, a distributed REU program, offered research opportunities to 24 community college students in IL and IN

Broadening Participation Outcomes:

- We aim to flatten the academic hierarchy and push for a more inclusive climate in biology by including trainees and faculty at all levels in Institute-wide feedback and decision-making sessions.
- We encourage trainee-led proposals for research funds and education activities.
- We offer semester-long seminars on DEI and special workshops on inclusive mentoring, power, authorship, etc.
- Cena y Ciencias allows us to engage local communities with monthly science activities in Spanish.
- Our distributed REU program (Science CORPS) provides research experiences to community college students who might otherwise not be able to engage in research.
- Our traditional REU program offers 10 weeks of research on campus to additional community college students.
- Trainees are integrated into curriculum development to learn best practices that employ active and student-centered learning techniques to train the next generation of inclusive educators.

Significant Research Results:

The GEMS Institute currently funds 23 interrelated projects involving more than 18 faculty and 50 trainees focused on symbiosis and reintegrating biology. Below we highlight some of the synthetic themes that emerge from our cross-disciplinary and cross-system studies of multi-scale symbiosis:

- The outcomes of well-studied host-microbe symbioses depend on complex interactions with less-known biotic forces (including viruses, fungi, phage defense systems, and microbial communities) and abiotic forces (drought, light availability, exogenous chemicals).
- The evolution of mobile genetic elements in host-associated microbes has major impacts on host growth and resilience, but also scales up to community and ecosystem levels – influencing competition, inter-guild species interactions, and nutrient cycling.
- Rapid evolution of mobile genetic elements and microbes helps to explain how genetic diversity is generated and maintained across diverse organismal systems.
- Quantifying the population dynamics of plasmids and other MGEs in natural populations requires novel and integrative methodology that combine phylogenomics with population genomics and modeling, and this integration is critical for predicting symbiotic outcomes that control natural and managed ecosystems.
- Experimental evolution of microbial symbionts is a powerful tool to reveal the important drivers of rapid evolution in host-microbe symbiosis as well as their underlying genetic mechanisms.

Project Management:

- GEMS employs a distributed leadership model, with regular executive committee meetings to discuss institute priorities and management, approaches, education, and outreach.
- GEMS funds a combination of novel and ongoing projects related to multiscale symbiosis, education, and outreach.
- Weekly seminars foster collaboration in ongoing research.
- All-Institute meetings and an annual retreat feature GEMS updates and group discussions on new ways to integrate.
- Subgroup meetings help trainees address shared questions across disciplines.
- The evaluation team performs surveys of GEMS activities and courses, including education and outreach efforts, and created a climate survey.

Future plans: We will continue to support ongoing research on multiscale symbiosis while encouraging interdisciplinarity and cross-system synthesis work that builds on GEMS findings:

- We will build on the exciting finding that mobile genetic elements drive substantial genomic diversity of microbial symbionts, lending flexibility to host-symbiont responses to stress and environmental change.
- We will continue to prioritize trainee-focused research, courses, and activities.
- We will continue to leverage expertise from across GEMS labs to promote cross-disciplinary understanding and reunify biology.
- We will build on our successful initiatives to further integrate research, education, and outreach.
- We will continue to disseminate GEMS findings through presentations, publications, and educational materials.

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

Alan Collins & Rachel Whitaker. 2023. CRISPR Comparison Toolkit: Rapid Identification, Visualization, and Analysis of CRISPR Array Diversity - <http://doi.org/10.1089/crispr.2022.0080>

Kevin Ricks & Anthony Yannarell. 2023. Soil moisture incidentally selects for microbes that facilitate locally adaptive plant response. - <https://doi.org/10.1098/rspb.2023.0469>

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Laura Suttentfield, Zoi Rapti, Jayadevi Chandrashekar, Amelia Steinlein, Juan Cristobal Vera, Ted Kim, Rachel Whitaker. BioRxiv 2023. Phage-mediated resolution of genetic conflict alters the evolutionary trajectory of *Pseudomonas aeruginosa* lysogens. - <https://www.biorxiv.org/content/10.1101/2023.10.24.563318v1>

Emily Terrill Sondag, Tara Stewart Merrill, Jenny Drnevich, Jessica Holmes, Eva Fischer, Carla Cáceres, Lynette Strickland. 2023. Differential gene expression in response to fungal pathogen exposure in the aquatic invertebrate, *Daphnia dentifera*. - <https://doi.org/10.1002/ece3.10354>

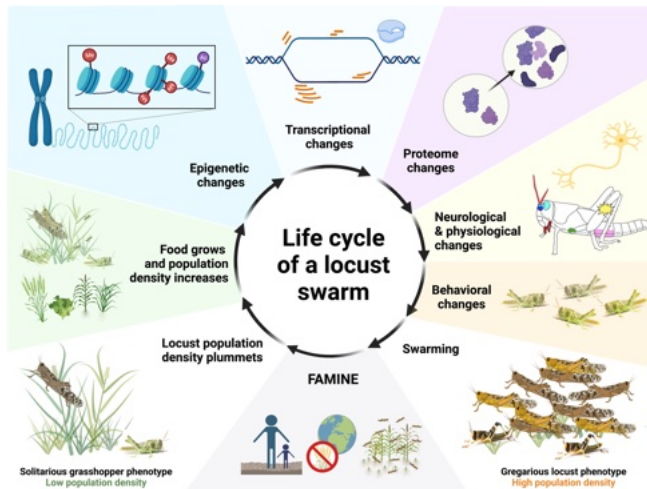
Chris Robinson, Adam Dolezal, Irene Newton. 2023. Host species and geography impact bee-associated RNA virus communities with evidence for isolation-by-distance in viral populations. - <https://doi.org/10.1101/2023.07.16.549238>

James Kosmopoulos, Rebecca Batstone-Doyle, Katy Heath. 2023. Co-inoculation with novel nodule-inhabiting bacteria reduces the benefits of legume-rhizobium symbiosis. - <https://doi.org/10.1101/2023.11.15.567292>

Lilian Caesar, Danny Rice, Alison McAfee, Robyn Underwood, David Tarpy, Leonard Foster, Irene Newton. 2023. Metagenomic analysis of the honey bee queen microbiome reveals low bacterial diversity and Caudoviricetes phages. - <https://doi.org/10.1101/2023.08.29.555332>

Behavioral Plasticity Research Institute (BPRI)

Gabbiani, Fabrizio · 2021795 · Baylor College of Medicine · gabbiani@bcm.edu



Schematic illustration of a locust swarm life cycle of and its environmental impacts.

Elevator Speech: The BPRI investigates locust phase change through an interdisciplinary approach. This work aims to elucidate how locust swarm formation originates and will help mitigate the agricultural consequences of locust swarming, thus improving the well-being of farming communities world-wide.

Keywords: Locust phase polyphenism, phenotypic plasticity, swarming, *Schistocerca gregaria*

Project Website: <https://behavioralplasticity.org/>

Participants: <https://behavioralplasticity.org/index.php/people/>



Institute Objectives and Goals:

- To advance and transform the study of phenotypic plasticity as a cross-institutional and cross-disciplinary Biology Integration Institute.
- The BPRI seeks to become a leader in training the next generation of integrative biologists who can communicate and collaborate across disciplinary boundaries.
- The BPRI aims to leverage its scientific breadth and expertise to address critical needs in locust-affected communities, thereby translating basic research into meaningful societal impacts.

Integrating across Biology

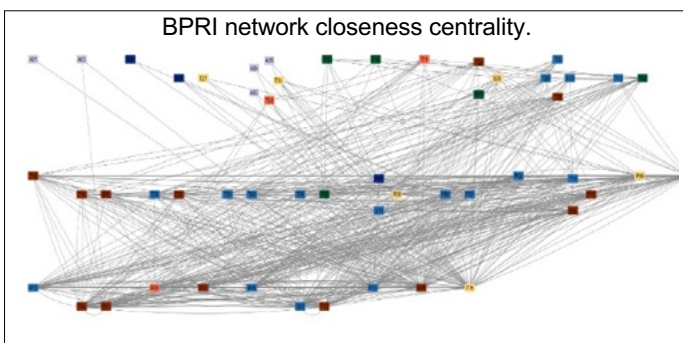
- Integrative project 1: comparative genomics and transcriptomics across *Schistocerca* species.
- Integrative project 2: integrated 'eco-evo-mecho' synthesis review.
- Organized and hosted a two-days BPRI-wide research conference in Houston, Texas.
- Regular research committee meetings to integrate research across labs.
- BPRI-wide crash courses to bring trainees up-to-speed with different research subdisciplines.
- BPRI-wide lab meetings to discuss data and recent results.
- BPRI-wide cross-species genome annotation sessions.

Education, Training & Outreach:

- Students organized the annual research meeting, including the selection, invitation, and introduction of speakers. A total of 56 attendees participated, including 12 non-BPRI members.
- Held a professional development session on scientific writing.
- Held a multi-day BPRI-wide gene annotation jamboree. Collectively annotated 84 genes across six species.
- Held nine cohort trainee meetings.
- Developed seven new crash courses.
- Recruited one cohort of undergraduate students for research training and held monthly meetings with them.
- Created the first of three video documentaries on locust phase change and the BPRI.
- Held two stakeholder meetings with international speakers implicated in locust management and research.
- Maintained social media presence, through regular posts at YouTube, Instagram, and X (Twitter).
- Moderated regular debates and scientific exchanges on the HopperLink platform.

Broadening Participation Outcomes:

- Invited one keynote Diversity, Equity, and Inclusion (DEI) speaker to present and discuss inclusive mentorship.
- Invited faculty from Prairie View A&M, an HCBU, to the research conference and held meetings to discuss potential collaborations. Wrote a grant to support these activities.
- Held an annual climate survey to monitor individual experiences, inform future Diversity, Equity, and Inclusion activities, and assess the impact of past activities.



DEI talk at the 2023 BPRI symposium.

Significant Research Results:

- Analyzed genome structure across six *Schistocerca* species, mapped locust-specific orthologous gene groups, identified many gene duplication events, analyzed gene selection signatures. Extensive collinearity found throughout the *Schistocerca* lineage; ~1,000 gene duplication events found; gene selection signatures found for 64 orthogroups of genes.
- Bulk ATAC-sequencing in *Schistocerca gregaria* identified a change in active regulatory regions from the solitary to gregarious phase.
- Bulk tissue RNA-sequencing analysis in solitary and gregarious phase across three *Schistocerca* locust species identified tens of shared genes differentially expressed between phases.
- Weighted correlation analysis (WGCNA) identified gene modules important for behavioral phenotype differences between solitary and gregarious animals.
- Carried out RNAi experiments to explore the role of various genes in locust phase polyphenism; the second hyperpolarization-activated, cyclic nucleotide gated (HCN2) neural ion channel gene and one heat shock protein (HSP) gene were successfully downregulated.
- Described differences in the nutritional requirements of locust marching bands in the lab and the field.
- Investigated differences in the role of diet and group living on immune responses in the lab and field.
- Investigated the role of gut microbiomes in diets and marching behavior of locust bands.
- Found different macronutrient consumption strategies between phases of *Schistocerca gregaria* in the lab.
- Discovered key differences in collective movement behavior between swarming and non-swarming species.
- Developed a Raman spectrometry phase assay using locust blood that can identify species and phase.
- Investigated maternal effects on locust phase maintenance using female accessory glands transcriptomics.
- Developed two genetic intervention strategies to generate transgenic grasshoppers using CRISPR/Cas9.
- Built a single-cell transcriptomic atlas of the optic lobe of *Schistocerca gregaria* in solitary and gregarious phases and of the optic lobe of *Schistocerca americana*.
- Carried out single-cell transcriptomics of an identified collision detecting neuron in the visual system of *Schistocerca gregaria* and *Schistocerca americana*, confirmed that specific genes determine the physiological properties of the neuron and identified at least five differentially expressed genes across phases.
- Examined how serotonin, a neuromodulator implicated in phase change, modulates appetitive behavior and neural encoding of odorants in *Schistocerca americana*.
- Characterized the modulation of flight behavior by locust phase state.
- Identified strong difference in escape behaviors between isolated and crowded *Schistocerca gregaria*; isolated animals are less prone to initiate escape behaviors.

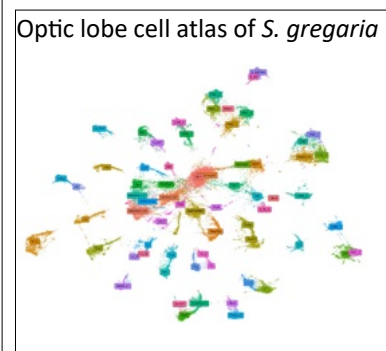
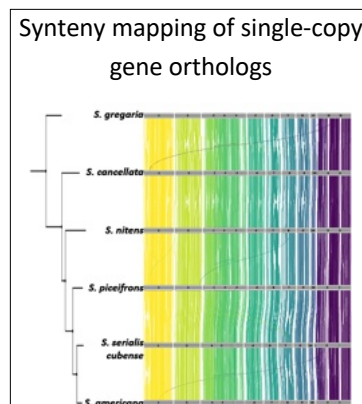
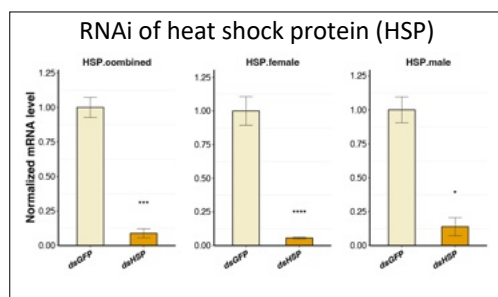
Project Management:

- Monitored communication across the BPRI.
- Held several townhall meetings to improve communication between the BPRI leadership and individual labs.
- Trainees updated their Individual Development Plans (IDPs) and discussed them with the BPRI education coordinator and their mentors to keep expectations in tune.
- Identified post-Covid-19 decreased participation of trainees to BPRI-wide events and addressed the issue through consultation with trainees, education and executive committees as well as NSF.

Future plans:

- Complete the characterization of *Schistocerca* genomes and analyze the associated time-resolved transcriptomics data.
- Pursue further physiological and behavioral characterization of phase change across species.
- Expand comparisons between field and lab work.
- Produce the two remaining videos belonging to the BPRI and locust phase change series.
- Pursue the educational goals promoting BPRI-wide interdisciplinary training and integration.

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:





ASCEND—Advancing Spectral biology in Changing ENvironments to understand Diversity—

The ASCEND BII uses spectral biology, global change studies, and predictive models to understand the causes and consequences of plant diversity in changing environments. We study how variation at one biological scale interacts with environmental change to give rise to emergent properties at the next biological scale. We model these processes that influence biodiversity from organisms to the tree of life in ecological communities and across the biosphere.

Keywords: plant diversity, global change, spectral biology, remote sensing, plant function, community assembly, tree of life, ecological and evolutionary process models

Project Website: www.spectralbiology.org

Participants: <https://www.spectralbiology.org/team>, Co-PIs: Philip Townsend, Peter Reich, Amy Trowbridge, Dudu Meireles. Managing Director: Brett Fredericksen

Institute Objectives and Goals:

ASCEND seeks to investigate the causes and consequences of plant biodiversity across scales in a rapidly changing world—from genes and molecules within cells and tissues to communities, ecosystems, landscapes and the biosphere. In **Theme 1** we examine the mechanistic basis for spectral and functional variation within species, scaling from the variation in genes, transcriptomes, and metabolites to leaves, canopies, and individuals exposed to contrasting environments. **Theme 2** examines the genetic, structural, and biochemical bases for spectral variation within species to illuminate the mechanistic basis for variation among species and the evolutionary processes across the tree of life. **Theme 3** assesses how taxa, sampled across the tree of life, interact locally, leading to the assembly and dynamics of communities at multiple spatial scales, under current and future environmental conditions. **Theme 4** examines the consequences of biodiversity for ecosystem functioning and its response to global change. In **Theme 5** we seek to improve parameterization of tissue-to ecosystem-scale properties at various spatial scales and advance land surface models that incorporate plant functional diversity.

Integrating across Biology

Integration across biological scales is required to address fundamental questions that remain poorly understood including: 1) why and how life's diversity matters for biosphere function and dynamics critical to maintaining Earth's life support systems and 2) how and why variation at the scales of genes and molecules within cells and tissues influences processes at all other scales. We use spectral reflectance signals and other traits across scales as part of our effort to understand how variation in molecules and tissues influence whole plant processes that have community, ecosystem and biosphere consequences. Projects include: **Consequences of disease dynamics for plant function and community assembly** focusing on oak wilt fungal disease impacts on plant photosynthesis, chlorophyll fluorescence, photoprotective pigments and water content through time. Local species interactions and their interplay with disease have consequences for continental scale carbon sequestration. **Integrating and upscaling instantaneous carbon flux responses to forest warming** in the B4WarmED project leading to the discovery that divergent carbon acquisition responses of species appear to drive differences in their growth responses to combined warming and rainfall manipulation, and that carbon acquisition and growth responses appear to regulate survival. **The Wisconsin Aspen study** examines over 400 aspen genotypes and their chemical composition to understand trade-offs among investments in resource allocation including herbivore defense and above- and belowground growth in the context of interactions with the herbivore *Lymantria dispar* (spongy moth). Using bioinformatics tools like genome-wide association, we are uncovering which genes are associated with different spectral bands in three populations of switchgrass and determining if these genetic associations are preserved across different common gardens.

Education, Training & Outreach:

Training by ASCEND falls in several core venues. First, the annual **Winter Symposium** promotes interactions among ASCEND team members at different career stages and provides opportunities to present ongoing ASCEND research. Second, our week-long **Summer Training Workshops** provide opportunities for eager learners from ASCEND and beyond (41 registrants in 2023) to learn about important topics and tools within ASCEND. Sessions included training in bioinformatics, plant physiology, spectroscopy (field, lab, and airborne), professional development, and image processing. In 2023, we held the workshop at the Cedar Creek Ecosystem Science Reserve for hands-on practice with measurement techniques. Third, the **ASCEND weekly virtual meetings** promote regular interactions among core members across multiple institutions and serve to recruit new members into the community by inviting external speakers to present their research regarding spectral biology. New this year are training workshops during some of our weekly meetings to supplement opportunities in our winter symposia and summer training workshops. **Mentoring** is a major emphasis of the Science Team for undergraduates, graduate students and postdocs in a highly collaborative environment on activities within and across the major thematic areas. **Teaching:** the ASCEND team incorporated ongoing research into undergraduate and graduate courses in *Biodiversity Science* and *Plant Physiological Ecology* at UMN.

Outreach. ASCEND has engaged the public through **Spotlight Science exhibitions at the Bell Museum** which hosted ~300 attendees. Here, ASCEND members lead workstations on spectral biology targeted at middle schoolers and families. Additionally, ASCEND early career researchers helped develop the curriculum for the **Global Change Summer Camp** hosted by the Bell Museum and College of Biological Sciences. This camp hosted 31 middle schoolers as they learned about biodiversity and climate change. ASCEND co-developed two **MinuteEarth educational Youtube videos**; one on spectral biology "Apparently tree FINGERPRINTS are a thing" that explains spectral signatures in plants and other life forms and their importance in biodiversity monitoring and disease detection (>87K views), and another on "The Number of Tree Species on Earth" in both English (>180K views) and Portuguese (>54K views). We continue to engage with members of the **Wisconsin Tribal Conservation Advisory Council (WTCAC)** and the Menominee and Stockbridge-Munsee nations in both hands-on trainings and applications to detect pests and pathogens and their impacts on biodiversity and ecosystem function on tribal lands. ASCEND members continue to work with these groups on the establishment of flux towers in two reservations to assist in the monitoring of the forest on tribal lands.



The ASCEND team hosted and participated in two sessions at the Ecological Society of America meeting in Portland in 2023. A special feature in *Ecology* on spectral biology across scales has been initiated.

Significant Research Results:

Our major efforts have focused on projects within and across the major thematic areas, each of which spans two biological scales.

Theme 1. We have conducted experiments to assess whole plant and spectral responses to drought and pest/pathogen exposure in a suite of experiments by exploring traits connecting genetic variation and environment, as well as GxE interactions. We are looking at intra-species variation amongst genotypes of to determine the underlying genetic associations with variance in spectral data using genome-wide associations and we are using quantitative genetics to determine the heritability of different spectral bands. *To understand and detect disease progression across scales*, we conducted a seedling experiment inoculating oak trees with oak wilt and subject to drought conditions to understand plant physiological responses to the disease and have developed physiological models from spectral signatures and drone imagery (Sapes et al. 2024).

Theme 2. We proposed using branches of the tree of life for conservation that will facilitate remote detection, especially for plants (Pinto-Ledezma et al. 2023). We have been developing models predicting structural and chemical traits from fresh, ground and pressed leaf spectra (Kothari et al. 2022) and airborne spectroscopy to understand seasonal variation in plant function (Chlus and Townsend 2023) and evolutionary processes in major plant radiations. *To understand pest-pathogen interactions by integrating plant physiology, plant chemistry and remote sensing across scales*, we developed models to map oak-wilt probabilities across Minnesota and Wisconsin using Sentinel2 satellite data trained with high resolution aerial imagery (NAIP) and UAV data to provide tools for forest management (US NPS, USFS and DNR) (Guzmán et al. 2023).

Theme 3. We are examining spectral and physiological responses to experimental CO₂, diversity, N, warming and rainfall regimes by measuring physiology, phenology, spectral, chemical and/or abundance signatures in different contrasting factorial conditions in the B4WarmED (Stefanski et al 2023), BioCON, TeRaCON, IDENT and FAB experiments in Minnesota to understand effects on plant communities. *To link above and belowground processes in diversity*, we are exploring aboveground-belowground functional relationships in these experiments, contributing to broad syntheses of impacts of global change and plant diversity on soil microbial communities. **Theme 4.** We continue to examine the interactive effects of elevated CO₂ and N on rates of C cycling and N mineralization in grassland plots with different species composition and diversity in the BioCON experiment at CCSR. We also explored how soil enzymes might be a useful tool in such initiatives. **Theme 5.** Through the sTRAITS project, we are evaluating current global trait maps to assess how trait databases are assimilated and upscaled in current models. We have developed a global synthesis product of global trait maps by evaluating current maps of plant traits across latitudinal gradients to understand and better account for the primary drivers (environment, plant functional type) of trait variation at leaf-to-global scales (Dechant et al. 2023).

Broadening Participation Outcomes:

We developed a public engagement exhibit on **Spectral Biology** at the **Bell Museum of Natural History** through the museums Spotlight Science program where young learners could measure the reflectance spectra of plants and learn about biodiversity. We have developed a collaboration with the **Wisconsin Tribal Conservation Advisory Council (WTCAC)**, especially the Stockbridge-Munsee and Menominee nations, to prototype methods for using spectral data to identify species whose loss from the environment will negatively impact biodiversity and associated ecosystem functions. An element of this work is also to identify resistant species within taxa to enable current and future management of threatened species. At the 2023 Ecological Society of American Annual Meeting, ASCEND members hosted and participated in two special sessions regarding spectral biology bringing together early career scientists from a range of perspectives and backgrounds (photo left). The Global Change Summer camp emphasized underrepresented middle school and high school students.

Project Management:

Our weekly meetings, Winter Symposium, and Summer Training Workshop continue to facilitate team interaction, research, training and mentorship activities. We are focused on monitoring diversity and inclusivity as well as peer to peer interactions via annual evaluation surveys and social network analysis. Early career researchers (ECRs) remain a major focus and continue to be featured in blog posts and at ASCEND seminars. We have advanced our data management system to make code and data available for our publications on our website to facilitate the reproducibility of our research.

Future plans:

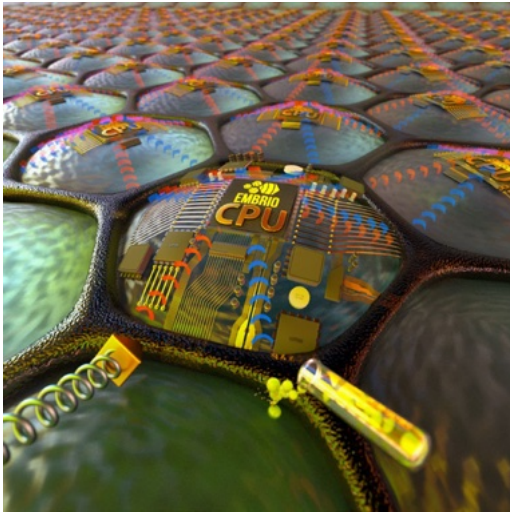
The ASCEND team has initiated a special feature in *Ecology* on spectral biology across scales inviting manuscript submissions from early career scientists within the broader ASCEND community and beyond. We will continue all five themes, advancing bridging projects to integrate themes across scales. These working groups include: i) investigating how light acts as a resource, stressor and cue for plants and serves to connect across biological scales from gene expression (Theme 1) to ecosystem productivity (Theme 4). ii) harnessing phylogenetic variation in Rubisco to inform carboxylation rates and nitrogen use efficiencies across lineages and plant functional groups in global Earth System Models. iii) advancing understanding of evolutionary processes in adaptive radiations using spectral information. We are excited to begin working with the Inter-BII RCN focused on making a common toolkit for integrative sciences amongst the BIIIs. ASCEND members have helped represent early career researchers in this endeavor and plan to help offer shared training opportunities for the wider ECR community

Key Publications:

- Cavender-Bares, J., F. D. Schneider, M. J. Santos, A. Armstrong, A. Carnaval, K. M. Dahlin, L. Fatoyinbo, G. C. Hurtt, D. Schimel, P. A. Townsend, S. L. Ustin, Z. Wang, and A. M. Wilson. 2022. Integrating remote sensing with ecology and evolution to advance biodiversity conservation. *Nature Ecology & Evolution* 6, 506-519
- Chlus, A., Townsend, P.A. 2023. Characterizing seasonal variation in foliar biochemistry with airborne imaging spectroscopy. *Remote Sensing of Environment* 275, 113023.
- Czyż E.A., Schmid B., Hueni A., Eppinga M.B., Schuman M.C., et al.. 2023. Genetic constraints on temporal variation of airborne reflectance spectra and their uncertainties over a temperate forest. *Remote Sensing of Environment* 284, 113338
- Dechant, B., Kattge, J., Pavlick, R.,... Townsend, P. 2023. Intercomparison of global foliar trait maps reveals fundamental differences and limitations of upscaling approaches. *EarthArXiv*
- Guzmán J.A., Pinto-Ledezma J.N., Frantz D., Townsend P.A., Juzwik J., Cavender-Bares J. 2023. Mapping oak wilt disease using phenological observations from space. *Remote Sensing of Environment* 298, 113794
- Pinto-Ledezma J.N., Diaz S., Halpern B., Khoury C., Cavender-Bares J. 2023. No branch left behind: tracking terrestrial biodiversity from a phylogenetic completeness perspective. *Frontiers in Ecology and the Environment* doi:10.1002/fee.2696
- Stefanski A, R Bermudez, KM Sendall, RA Montgomery, PB Reich. 2023. Stomatal behavior moderates water cost of CO₂ acquisition for 21 boreal and temperate species under experimental climate change. *Plant Cell Environ* 46, 3102-3119

The Emergent Mechanisms in Biology of Robustness Integration and Organization (EMBRIO) Institute

Umulis, David - 2120200 - Purdue University - dumulis.purdue.edu



Cells signal mechanical or chemical attack for defense and cell repair

Elevator Speech:

NSF funded the new **EMBRIOInstitute** at **LifeAtPurdue** to crack the code for cellular defense. The 5-year project partners **IndianaUniv, Morehouse, NotreDame, Penn,** and **UPRM** to yield new insights on cell survival and tissue repair

Keywords: chemical stimuli, mechanical stimuli, multimodal signals, biological systems, intracellular changes

Project Website: www.purdue.edu/research/embrio/

Participants: www.purdue.edu/research/embrio/

Institute Objectives and Goals:

EMBRIO will determine how living systems integrate “orthogonal” signals such as chemical and mechanical stimuli to develop responsive phenotypes that coordinate cell and tissue structures for survival and function. Quantitative imaging and simulation will bridge diverse biological systems and through this unification, address a Rules of Life question—How are multimodal signals integrated across scales to coordinate the robust cell biological and morphogenetic responses needed to survive?

Integrating across Biology:

The Core Thrust of the EMBRIO institute has a unifying pipeline to integrate biological processes across scale. At each length scale, both mechanical and chemical cues will be used to modify the behavior within each of the systems establishing the initial and boundary conditions for input into our simulations. Mechanical and chemical responses will be measured using AFM and high-resolution imaging to provide spatiotemporally resolved deformations and calcium (and other second messenger) signaling behaviors. These stimulus-response behaviors will inform our multiscale and integrative modeling, identifying preserved mechano-chemical signaling pathways and permitting translation across systems.

Education, Training & Outreach:

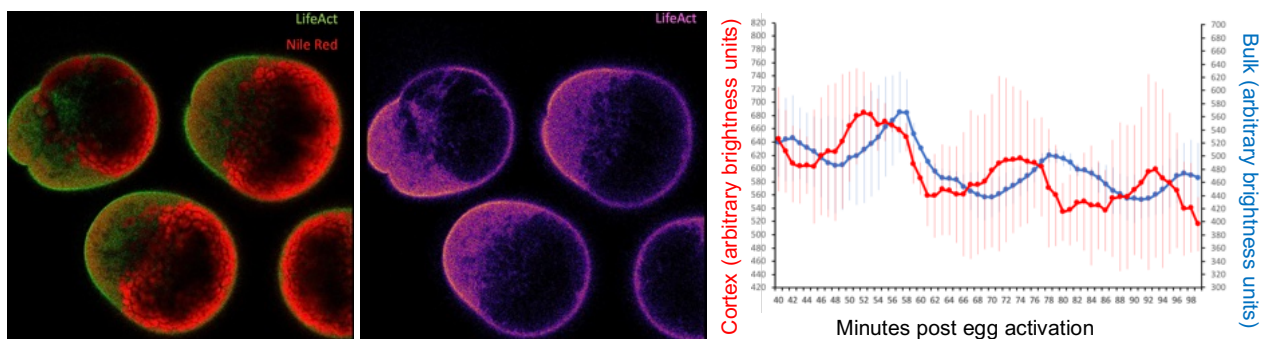
By bridging research and education via design-based approaches, EMBRIO is developing knowledge about evidence-based practices that promote integrative understandings of biological systems; developing computational apprenticeship curricular modules following principles of the Knowledge Integration framework among graduate and undergraduate students; and establishing a knowledge dissemination infrastructure to expand the use of integrative biology approaches in the broader life sciences research community.

Broadening Participation Outcomes:

EMBRIO aims to deliver a diverse workforce capable of advancing the understanding of biological systems by integrating: 1) multimodal experimental research; 2) computational apprenticeship curricular modules to promote working knowledge of signal integration in biological processes; 3) an MSI Affiliate Institution Program; 4) workshops on teaching integrative biology approaches along with visiting graduate students, postdocs, and scientists; and 5) a Virtual Community of Practice.

Significant Research Results:

Our **Core Thrust** developed new simulations for the experimental systems and geometries in Thrusts 1-3 and developed AI acceleration techniques for carrying out massive optimization and cross-species optimizations. **Thrust 1** defined the modeling and experimental space around Ca^{2+} regulation of actin filament polymerization and nucleation mechanisms. In one cellular system, CaMKII is predicted to directly impact on actin assembly or disassembly through interactions with F- and G-actin. In the other cellular system, preliminary inhibitor experiments appear to rule out a significant role for the major actin filament nucleator, the Arp2/3 complex. For **Thrust 2** during plant defense, the role of actin filament nucleation in maintaining the homeostatic cortical array was demonstrated and a bacterial effector that targets cytoskeletal remodeling during defense identified. The Ca^{2+} waves that ramify through plant tissues were found to be distinct depending for MAMP elicitation versus mechanical stimulation. Experiments in *Drosophila* demonstrated the importance of DmPIEZO in cell proliferation regulation as well as control of cellular tension/contraction. Genetic suppression of PIEZO provides evidence that it plays a key role in encoding Ca^{2+} signatures and generation of Ca^{2+} waves. Significant results for **Thrust 3** in live imaging of actin dynamics throughout epiboly progression in zebrafish, documenting the changing actin dynamics in an actin band and an actin ring, along with cell shape changes and cell division in the EVL, which will inform the mathematical simulations of embryo morphogenesis. In the zebrafish tail fin, we observed two waves of calcium transients after various wounding methods. We further identified that reactive oxygen species relax the wound to allow wound closure and tissue regrowth. For **Thrust 4** EMBRIO Institute trainee workshop evaluations thus far reveal the trainings have: 1) met participants expectations, 2) achieved its learning objectives, 3) provided valuable knowledge and skills that could be applied to research projects, and 4) over 550 undergraduates engaged in computational modeling in disciplinary courses, displaying increased confidence and high proficiency in computational practices. Findings and lessons learned have led to a specialized onboarding 1 credit course, “Computational Understanding of Biological Systems and Data”.



Live zebrafish embryos at 1- to 2-cell stage visualizing LifeAct-GFP marking Actin (green left, magenta middle) and Nile Red marking the yolk globules (left). Cellular cortical actomyosin contractions (where Actin is high) lead to segregation of cytoplasm from the yolk to the cells. Quantitation of LifeAct-GFP at cell cortex versus bulk levels in cytoplasm over ~60 min (n=3 embryos, bars are standard deviation)

Project Management:

EMBRIO adapts the Collective Impact framework for processes and principles of highly effective team management and knowledge integration. CIM structures the organization and management of the Institute, its partners, and activities to ensure that all efforts and activities are aligned to common goals. CIM provides a systemic approach to guide and measure impacts and emphasizes relationships between organizational entities and objectives.

Future Plans: Establish full data acquisition through image analysis and simulation pipeline, including new light sheet microscopy instrumentation investment by Purdue advancing our Thrust projects. We have regular institute meetings focused on the biology integration aspects to share resources, calcium sensors, imaging methods and techniques, and other reagents and expertise. We are actively recruiting institute participants and engaging with them through trainings and activities. Broadening participation plans include further developing our URE summer program and expanding our DEI activity. We'll continue to provide all trainees with opportunities for increasing their capacity for leadership and research.

BII: Regional OneHealth Aerobiome Discovery Network (BROADN)

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Attendees of CSU's first Drone Show gather around to watch how BROADN researchers use drones to sample air up to 400 meters above ground.

Elevator Speech: BROADN explores the fascinating world of airborne microbes and their potential impacts. We develop and employ state-of-the-art technology and innovative research methodologies to advance understanding of how airborne microorganisms are released to the atmosphere, how they are transported, and how they influence atmospheric processes, local and distant ecosystems, and human, animal, and plant health. We strive to apply this knowledge toward an understanding of how the aerobiome will respond to a changing climate and other stressors, and the potential environmental impacts of those changes.

Keywords: Bioaerosols, aerobiology, ecology, microbiology, pathology, aerobiome, soil microbiome, phyllosphere, rhizosphere, atmospheric science, aerosol science, aerosol sampling technologies, OneHealth

Project Website: <https://broadn.colostate.edu/>

Participants: <https://broadn.colostate.edu/our-team/>

Institute Objectives and Goals:

BROADN seeks to address the overarching question: "What is the structure and function of the aerobiome, and how does it interact with terrestrial ecosystems?"

BROADN aims to characterize the microbial components of the air, the drivers that shape the evolving composition of the aerobiome, and how this coupled system responds to environmental changes. Our primary research goals are to (1) establish international standards for aerobiome sampling and analysis, (2) develop a modelling framework for predicting aerobiome dynamics, and (3) develop mechanistic models of changes in the metabolic functions between source and aerobiome.

Integrating across Biology:

BROADN seeks to develop mechanistic understanding of the drivers that connect soil, plant, and air microbiomes. Expertise in soil and plant ecology and in microbiome science is needed to understand the dynamics of the populations that serve as potential sources of bioaerosols, and how community compositions in these reservoirs respond to environmental drivers. Because a fundamental issue in environmental sampling is obtaining representative samples under ultra-low-biomass conditions, and because we are sampling particulate matter and not gases, expertise in aerosol science and technology is needed to advance the ability to quantitatively detect airborne microbes and retain their integrity during sampling. Expertise in atmospheric science provides perspective for treating the dynamical atmosphere as the medium for bioaerosol transport and dispersion. Finally, understanding of microbes and their physiology is required for developing hypotheses and interpreting data about microbes identified in the air. Joint field and lab studies bring these various elements together to build mutual understanding of how each contributes to BROADN goals. Training of personnel, especially graduate students, is also aimed at integrating these diverse disciplines.

We have created an Aerobiome Network Discussion group that meets virtually monthly to hear seminars delivered by experts within and beyond the immediate BROADN team. This group, which has expanded to 80 members from 11 institutions, features a broad range of seminar topics, from indoor air contaminants to diurnal variability in fungal spore emissions.

Education, Training & Outreach:

Graduate Education: The first cohort of 4 BROADN Ph.D. students (all from different departments) participated in the first offering of our *Aerobiome Foundations* course, co-taught by 12 BROADN faculty. Feedback from the first cohort of students was positive. Many of our faculty also tuned in to various modules outside of their expertise.

Undergraduate Training:

- Partnered with United in STEM to host 5 undergraduate BIPOC students in BROADN labs. All of these students presented their work in MURALS, a CSU event celebrating multicultural undergraduate research and arts.
- Sponsored a Mechanical Engineering Senior Design project to design a high-volume aerosol sampler. This project evolved into a follow-on project for a new BROADN graduate student.
- Launched our first REU program in summer 2023, hosting 6 undergraduate researchers in various BROADN labs.

Outreach: Numerous events included the *YES!fest* through the High Plains Library District, the Air Quality themed "2nd Saturday at Spur" (Denver, Colorado), and the Little Shop of Physics Science Celebration (at CSU-FC). We engaged with over 5,000 people at these 3 events alone.

Broadening Participation Outcomes:

BROADN participation in outreach events for K-12 and community members is developing strong communication platforms and connections with under-served and under-represented communities. Our emerging partnership with the CSU Spur campus in downtown Denver will facilitate these interactions, as Spur is establishing long term associations with local schools and the adjacent community.

Partnerships with regional institutions (CSU-Pueblo, a Hispanic-serving institution with ~50% minority student enrollment; and Doane University, primarily rural first-generation students) aim to recruit diverse undergraduate and MS students into PhD training programs within the BROADN network.

Through CSU-FC United in STEM, we have recruited first-year undergraduate students of color into paid research positions in BROADN labs. We will assess whether and where these students, and our REU participants, attend graduate school. Recruiting efforts have been bolstered through engagement with CSU-FC student clubs and the Alliance for Minority Participation.

Significant Research Results:

Field studies at the NEON Central Plains Experimental Range grassland site: We have completed three campaigns at this site (spring 2022, fall 2022, and spring 2023), collecting air, soil, and plant samples during continuous measurements of bioaerosol and meteorological parameters. Accomplishments to date include:

- Springtime atmospheric concentrations of ice nucleating particles responded to precipitation events, with the strongest response from those active at warmer temperatures, which were identified as likely to be biological in origin. Emissions correlated with intensity of precipitation.
- Continuous online aerosol observations identified diurnal cycles in fluorescent particles (FP), a proxy for biological particles. In fall 2022, nocturnal enrichments in FP classes and size distributions suggested the presence of airborne bacteria, fungi and pollen, including whole cells, spores and fragments. These FP data are being juxtaposed with genomic sequencing data to better understand identity, distribution, and abundance patterns of the aerobiome.
- The air microbiota in Fall 2022 was diverse, and distinct from the soil and plant microbiota. Air, soil, and plant microbial networks were correlated with environmental variables.
- In our Spring 2023 campaign, we completed our first 6-week collection of 12-hour (day/night) sample collections, at the top and bottom of the NEON tower, in addition to equivalent samples at the ground level at the nearby Semi-Arid Grasslands Research Center and corresponding plant and soil samples. Genomic sequencing data (bacteria and fungi) are nearing completion. This, our most complete dataset to date, will enable multiple investigations including a first assessment of vertical fluxes of bioaerosols.

Pilot studies in the CSU greenhouse: We are exploring whether plant pathogens within a greenhouse aerobiome can be resolved in space and time, using high volume aerosol collectors and modern genetic methods to determine environmental emission patterns.

- Air exchange rates, mixing regimes and ventilation patterns in operating greenhouses were characterized.
- Non-pathogenic, live microbial tracers (live bacterial and fungal spores) were aerosolized in known particle size distributions to determine detection limits.

Low-biomass-sampling technologies and strategies development:

- Development of high-volume-filter sampling protocols, and initial assessment of DNA loss as a function of sampling duration; prototype high-volume sampler (student design project) and estimates of size-dependent capture efficiencies.
- Development of analysis pipeline and initial optimization of extraction and amplification protocols applied to ultra-low-biomass air samples.

Project Management:

BROADN's Science Council, expanded to include our three recently-appointed Goal Leaders, conducts short- and long-term planning and makes decisions on project support. During year 2, the Science Council reformulated BROADN's overarching Research Goals to guide selection of experimental projects and to promote integrative research. We have accordingly restructured our strategic planning and budgeting to align resources with multi-investigator scientific projects that specifically address one of the science goals.

BROADN staff and senior personnel meet weekly to discuss budget, education, outreach, and evaluation. At monthly All-Hands meetings, results of ongoing projects and programmatic news and updates are shared. Pilot results, protocols, and a reference library are shared with the entire team using a Slack workspace. Team Science sessions are organized quarterly.

Annual assessment activities use objective data collected for our various activities as well as participant survey data. Feedback from the assessment team and from our Scientific Advisory Board informs our annual planning.

Future plans:

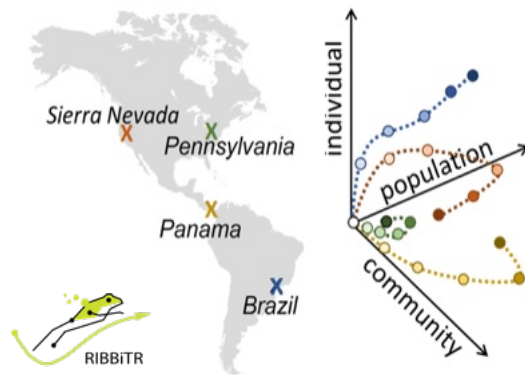
- Hold the 3rd annual BROADN summer symposium in July 2024 to review achievements to date in research, education and outreach, and to assess our progress toward goals and in addressing 2023 Advisory Board recommendations.
- Complete analyses of field data, and plan additional campaigns at NEON sites (all Goals).
- Continue work on developing standards for air sampling in different ecosystems and contexts and investigate methods for high-fidelity collection and preservation of airborne DNA and RNA (Goal 1).
- Continue development of approaches for determination of bioaerosol fluxes (Goal 2).
- Characterize and scrutinize aerobiome isolates for specific traits, which allow survival in the atmosphere (Goal 3).
- Second offering of *Aerobiome Fundamentals*.
- Continue and expand public outreach events to communities that are underserved by STEM programming.

BROADN Year 2 Education and Outreach



Uncovering Mechanisms of Amphibian Resilience to Global Change

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Locations of RIBBITR's 4 study systems and a cross-scale conceptualization of our resilience framework

Elevator Speech: The Resilience Institute Bridging Biology Training and Research (RIBBITR) is taking a team science approach to uncover mechanisms of resilience to global change and train a new generation of integrative biologists. Our focus is on amphibian resilience to the fungal disease chytridiomycosis and other interacting stressors, but alongside that we are developing a resilience framework that can be used across systems responding to a variety of global change stressors.

Keywords: Resilience, Amphibians, Emerging Infectious Diseases, Chytridiomycosis, Global Change

Project Website: www.ribbitr.com

Participants: <https://ribbitr.com/people/>

Institute Objectives and Goals:

We are developing a framework to track resilience across scales, stressors, and systems, and will apply it to a case study involving a fungal disease (chytridiomycosis) and other global change stressors linked to global amphibian declines. Building on past research in four complementary study systems, we aim to answer: (1) How does the history of disturbance differ across systems? (2) How have changes at different levels of biological organization shaped overall system responses? (3) What are the mechanisms contributing to resilience and are they shared across systems? (4) How is resilience modulated by multiple interacting stressors?

Integrating across Biology:

We are leveraging rich histories of research in four regions of the Americas (Eastern and Western US, Panama, and Brazil) where amphibians have begun to show robustness and recovery following disease-induced declines, to develop the amphibian-*Bd* system as a powerful case study for understanding biological resilience. By integrating insights from a wide range of disciplines (from molecular biology and genetics to physiology, ecology, evolution, data science, and modeling), our collaborative team is working to standardize data collection, curation, and analyses, and enabling the robust interpretation of patterns, processes, and mechanisms needed to advance our understanding of resilience.

Education, Training & Outreach:

Our training and outreach activities are reaching high school, undergraduate, graduate, and postdoctoral scholars from across the country. We are focusing on authentic biology research experiences that (1) foster cross-disciplinary understanding, (2) serve large numbers of students with a focus on underrepresented groups, and (3) promote persistence in STEM. During the first two years, key training activities included Zoom "RIBBITR 101", professional development, and open science seminars, in-person training workshops, and the design, implementation, and assessment of new CURE courses at many of our member institutions.

Broadening Participation Outcomes:

Our training and outreach activities aim to promote diversity in STEM by addressing the distinct needs of students at different points of training (high school to postdoctoral) and from diverse backgrounds. Key activities have included summer research experiences for both high school students and undergraduates, and Course-based Undergraduate Research Experiences (CUREs). Each activity is incorporating best practices in STEM teaching/learning and building on established mechanisms to increase participation of underrepresented groups. We have developed assessment tools and are measuring the impact of our activities on knowledge transfer across biological disciplines, belonging, and persistence in STEM.

Significant Research Results:

We have developed and standardized protocols for data collection in the lab and in the field. These protocols have now been used successfully for multiple field seasons across the very different conditions in Pennsylvania, the Sierra Nevadas, Panama, and Brazil to collect analogous data about individuals, populations, and communities of amphibians. We are beginning modeling efforts and experiments aimed at identifying mechanisms of resilience in each system.

We have developed a PostgreSQL database that centralizes all historical and new datasets collected by the RIBBiTR team at its four study sites. The entire dataset adheres to open science principles as it was built through reproducible scripts. At present it is open to use by all RIBBiTR-associates later become publicly available. A web app has been developed to make the database accessible to those less familiar with SQL.

Exome capture data from recovering populations of the *Rana muscosa/sierrae* complex in California allowed us to identify specific gene variants and genomic regions associated with population recovery despite ongoing pressure from *Batrachochytrium dendrobatidis* (Bd), the fungus that causes chytridiomycosis. A manuscript describing this work is under review.

Supplementing traditional visual surveys with automatic acoustic monitoring and environmental DNA (eDNA) techniques is showing promise for detecting changes in the size and status of rare amphibian populations. For example, the critically endangered Panamanian frog has recently been detected using both eDNA and acoustics at sites where we had not seen it with our eyes for several years. Acoustic recordings using hydrophones also helped us to better characterize the breeding ecology of *R. sierrae*, an endangered species which calls only underwater. Manuscripts on these findings have either been published or are under review.

A new CRISPR-based method we developed is now enabling real-time, in the field detection of Bd on amphibians and in water samples. This method, which requires no specialized equipment and requires only human body heat, can give accurate results in approximately 1 hour. This technique was recently published in *Methods in Ecology and Evolution* (DOI: 10.1111/2041-210X.14236).

Project Management: We have a 3-person executive committee and a 4-person external advisory board. We recruited an evaluator, project manager, data manager, and several postdoctoral scholars to our team in year 1. We used a 'team science' approach to develop documents that detail our code of conduct, collaborators' roles, and policies for authorship, data sharing and open science, and resource allocation. We bring in new team members each year using a team-developed project proposal form and our 'pilot and exploratory projects' (PEPs) mechanism. Our project management plan was built around team science and so far, it has quite well for us.

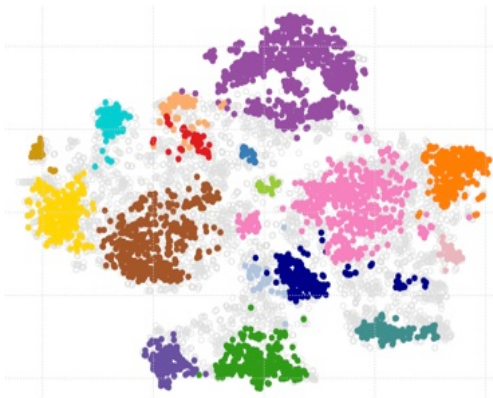
Future plans: In this (our third) year we will continue field work at our 4 study sites, conduct field experiments to test for mechanisms of resilience, continue development of a resilience framework and apply it to our amphibian disease case study. We will also further efforts we began at the SICB 2024 meeting to develop a network of researchers studying resilience to global change. We will hold our final training workshop for graduate students and postdocs and continue training undergraduates and graduate students through authentic research experiences. We will work toward publication of our CURE work and its associated assessment data.

Selected Recent Publications:

- Hoenig, B.D., *et al.* (2023) FINDeM: A CRISPR-based, molecular method for rapid, inexpensive and field-deployable organism detection. *Methods in Ecology and Evolution* 14: 3055-3067. [10.1111/2041-210X.14236](https://doi.org/10.1111/2041-210X.14236)
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- Rollins-Smith, L.A. (2023) The importance of antimicrobial peptides (AMPs) in amphibian skin defense. *Developmental & Comparative Immunology* 142: 104657. [10.1016/j.dci.2023.104657](https://doi.org/10.1016/j.dci.2023.104657)
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- Verble, R.M., *et al.* (2023) Beyond a vision for the future: tangible steps to engage diverse participants in inclusive field experiences. *Integrative & Comparative Biology* 63: 59-65. <https://doi.org/10.1093/icb/icad063>
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BII: Mechanisms of Cellular Evolution

LYNCH, Michael · DBI-2119963, 2021-2026 · Arizona State University · mlynch11@asu.edu



Subcellular spatial proteome of *Paramecium tetraurelia*. Each colored dot represents one of the over 4500 proteins predicted to a specific cellular localization.

Elevator Speech: Our goal is to decipher the general rules by which evolution proceeds at the cellular level in different lineages of organisms, engaging in research and educational activities to help establish a formal field of evolutionary cell biology.

Keywords: ATP synthase; bioenergetics; cellular ultrastructure; eukaryotes; evolutionary theory; experimental evolution; population genetics; prokaryotes; ribosomes; scaling laws.

Project Website: <http://cellularevolution.asu.edu>

Participants: M. Lynch, W. Frasnich, K. Geiler-Samerotte, K. Hu, J. Wideman, F. Ali, L. Brettner, B. Jimenez-Marin, D. Jirsova, M. Lin, B. Trickovic, S. Yanigasaw

Institute Objectives and Goals:

- 1) To connect evolutionary biology to the ultimate roots of phenotypic diversification, the cell, and in doing so, help establish a new field of evolutionary cell biology.
- 2) To perform research to determine how the evolution of a wide variety of cellular features is governed by internal cellular constraints, the laws of biophysics and bioenergetics, and the population-genetic environment.
- 3) To establish educational resources and train next-generation leaders to serve as a founding cohort for this new field.

Integrating across Biology:

To help reveal the Rules of Life at the cellular level, and yield a mechanistic explanation of them from first principles requires the integration of evolutionary theory with observations on the phylogenetic diversity of molecular and cellular features down to the ultrastructural level.

To establish connections between genotypes and phenotypes and an explanatory theory for them, principles from bioenergetics and biophysics are being incorporated.

The BII starts with four cross-linked research projects:

- 1) phylogenetic survey of cellular traits and their costs of synthesis, operation, and maintenance; 2) comparative analysis of the architectural diversity of two of life's key molecular complexes - ATP synthase and ribosomes; 3) development of evolutionary theory to explain cell-level variation and how cellular features scale across the Tree of Life; 4) performance of long-term laboratory experiments to help connect theory and observation.

Taken together, these projects bring together faculty from the life sciences, physics, chemistry, mathematics, and computer science.

Education, Training & Outreach:

Building a cohesive local community via a natural and purposefully constructed interdisciplinary environment for engaging undergraduates, graduate students, and post-doctoral associates from multiple departments. This centers on three primary activities: 1) a journal club designed to integrate different areas of empirical and theoretical research, which includes outside visitors; 2) shared lab meetings to support research ideas and integration; and 3) professional development workshops focused on topics important to support academic and professional success in the sciences.

Building national / international connections through the provision of materials for a course in evolutionary cell biology, open-access databases, semester-long exchange programs, and an annual symposium with focal topics defined by the global community.

Serving as a platform for training postdoctoral fellows, graduate students, and undergraduates in the emerging field of evolutionary cell biology.

Broadening Participation Outcomes:

Capitalizing on the substantial diversity (minorities to military veterans) within the Greater Phoenix area, we are providing opportunities and retention mechanisms for underserved students. This includes a community college internship program, where students from underserved minorities across the Maricopa Community College District can engage with research activities under the tutelage of PIs, graduate students, and postdoctoral associates during each summer term and into the academic year. This internship program creates pathways for students to pursue higher education in the biological sciences. In addition, our efforts include the following: the recruitment of diverse graduate students and postdoctoral associates; a research exchange program with collaborating laboratories around the world; and an annual symposium and workshops focused on fostering a diverse community of scholars in evolutionary cell biology.

Significant Research Results:

1. Phylogenetic census of cellular traits. Uses comparative genomics, intracellular spatial proteomics, ultra-microscopy, and bioenergetic analyses to provide a phylogenetic overview of cellular features and the relative costs of constructing and operating them. Characterizes cellular environments by: 1) constructing a gene-content database across the Tree of Life to pinpoint the phylogenetic locations of gains / losses of key gene functions; 2) connecting genomic data to subcellular localization by using Localization of Organelle Proteins by Isotopic Tagging (LOPIT) to localize proteins to unique organelles and molecular machines; 3) surveying cellular-investment portfolios by using light-sheet microscopy, cryo-EM, and FIB-SEM to quantify internal membrane structures, surface areas, and numbers/sizes of organelles and major complexes (e.g., ribosomes and ATP synthases). Key findings so far include the discoveries of new structural forms of ATP synthase (the engine of ATP production) and new subcellular localization of structural and functional proteins,

2. Evolutionary theory for cellular traits. Draws from empirical observations to build quantitative theory for the mechanisms by which cell-biological features evolve, i.e., how the paths open to evolutionary exploitation depend on the population-genetic environment. This work exploits the exceptional level of molecular understanding of cell biology to move evolutionary theory beyond abstract mathematical formalisms to more biologically realistic constructs: genotype to phenotype, establishing a formal framework for understanding how the limits to cellular diversification are dictated by the range of population-genetic environments across the Tree of Life. Key developments are the establishment of theory for how mean phenotypes of traits under constant selection pressures deviate across lineages with different population sizes, and how genes encoded in nuclear and organelle genomes coevolve, as well as the establishment of computational infrastructure for evaluating such complex issues by parallel computing.

3. Origins of structural diversity in molecular machines. Takes a structural-biology approach to explore how cellular complexes with essential and highly conserved functions are nonetheless free to diverge evolutionarily, e.g., ATP synthase and ribosomes, respectively, the universal hubs of energy and protein production. These projects will provide the first comprehensive evaluation of the degree to which alterations in the population-genetic environment can passively lead to changes in complexity and performance, serving as an empirical entrée into the plausible, but untested, hypothesis of constructive neutral evolution, while tying together projects 1 and 2. Key progress so far involves the transplant of ATP synthase from one organism to another, followed by monitoring the downstream evolutionary changes in molecular performance, and the use of cryo-EM to determine ribosome structure in various eukaryotic lineages. Varying the size of the c-ring in ATP synthase changes the number of protons required per ATP synthesized; we have constructed a yeast strain with a smaller animal-like ATP synthase and are in the process of characterizing this complex using biophysical and biochemical approaches.

4. Mechanistic determinants of cell size and growth rate. Capitalizes and expands upon established long-term evolution experiments with microbes to evaluate the genomic changes that arise in response to selection on cell size and growth rate over gradients of nutrient, temperature, and population-genetic conditions. This project is particularly focused on understanding why prokaryotes and eukaryotes have opposite scaling patterns of growth rate vs. cell size, and why the pattern of evolutionary scaling in prokaryotes coaligns with the universal physiological response to nutrient availability, whereas that in eukaryotes coaligns with the universal response to temperature. At both the phylogenetic and physiological levels, a battery of methodologies (transcriptomics, lipidomics, proteomics, metabolomics) are being employed to elucidate the underlying determinants of these scaling features. In addition, a bar-coding is being applied to laboratory evolution experiments to determine the fitness effects of thousands of de novo mutations. To study how yeast's ribosomal RNA content scales with its growth rate, we have optimized a massively multiplexable single-cell RNA sequencing technology for yeast. One major goal of our work is to find cases where the commonly observed relationship between cell growth, ribosomal content, and cell size is broken, in hopes of gaining insight into the mechanisms that create the laws in the first place. Using our yeast-optimized method, we have shown that the scaling law between cell growth and ribosomal content does not apply to yeast cells that are slowing down growth rate as they consume all available nutrients, and we also see large cell-to-cell variation in ribosomal content for cells growing at the same rate.

Project Management: The overall management strategy involves three levels of oversight: 1) an executive committee, consisting of the PI/coPIs and an ad-hoc member; 2) internal and external advisory committees, consisting of scientists from diverse backgrounds and geographic locations; and 3) a performance-evaluation team administered by ASU. The entire program of educational and outreach events is overseen by a full-time administrator / manager. We have monthly executive committee meetings focused on a fine-scaled management, have engaged with the performance evaluation team on our diverse menu of programs consistently, have engaged with our internal advisory committee, and are scheduled to meet with our external advisory committee in November 2022.

Future plans: New projects have been initiated to help understand the evolution of the structure and mechanical efficiency of the diverse molecular motors deployed in bacterial locomotion, and to help reveal the mechanisms underlying the evolution of multicellularity using the *Volvocales* as a model system (where species range from unicellular to composites of 1024 cells).

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

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- Stern B, Elliot S, and Wideman JG. (2023). An account of conserved functions and how biologists use them to integrate cell and evolutionary biology. *Biology & Philosophy*. 38(5):1-23. doi.org/10.1007/s10539-023-09933-x.
- Sinha SD and Wideman JG. (2023). The persistent homology of mitochondrial ATP synthases. *iScience*. 26: 106700

BII: Host-Virus Evolutionary Dynamics Institute – Annual Progress Update

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BII: Host-Virus Evolutionary Dynamics Institute

Why are there no universal laws in virology comparable to Newton's Laws (Physics) and the Ideal Gas Law (Chemistry)?

The Host-Virus Evolutionary Dynamics Institute (HVEDI) is a project focused on establishing mathematically characterizable relationships in virus-host interactions within and between virus systems across domains of life (Bacteria, Archaea, and Eukarya). Three core virus systems (CVS) are under investigation, one in each domain of life as well as comparator systems with the goal of elucidating fundamental properties of virus systems that may be developed into Universal Laws in Virology.

Keywords: roseolavirus, fusellovirus, siphovirus, cyanophage, potyvirus

Website: <http://ceballoslaboratory.com/services/>

BII: HVEDI Objectives and Goals:

There are ten (10) principal objectives for BII HVEDI:

- (1) Pursue research on core virus systems (CVS);
- (2) Pursue research on comparator systems (COM);
- (3) Characterize *within* systems relationships in CVS and COMs (e.g., genetic substrates underlying physiological observations) to develop models;
- (4) Determine *between* systems relationships among the CVS and determine if emerging mathematical models are generalizable to the COMs;
- (5) Standardize physiological, molecular biology, bioinformatics and modeling workflows across systems to support aforementioned objectives;
- (6) Train junior scientists and cross-train faculty in methods beyond their current areas of expertise;
- (7) Build capacity at smaller institutions and MSIs;
- (8) Develop new courses for network-wide delivery;
- (9) Do K12 and community outreach to increase awareness of importance of virology to society;
- (10) Assess and evaluate all aspects of the project.

Integrating across Biology

The HVEDI BII is integrating the latest techniques in sequencing (e.g., NPS), bioinformatics workflows, hyperspectrometry, differential network modeling, biogeochemistry (e.g., C:N:P elemental analyses), neuroscience (e.g., MEA systems), crop sciences (e.g., potato-potyvirus systems), and other areas of biological sciences to pursue project objectives.

Different HVEDI principals with different areas of expertise are meeting to cross-train and integrate methods from their respective fields of study to address questions that are inaccessible without an integrated approach. For example, Dr. Zhang (coPI) has developed novel methods in differential network modeling that allows the HVEDI team to elucidate potential relationships between categorical variables and continuous variables derived from wet lab experimentation.

Education, Training & Outreach:

The education, training, and outreach component has resulted in the training of multiple graduate and undergraduate students on methods in virology and virus ecology (e.g., environment sampling, experimental infection assays, molecular biology, bioinformatics pipelines, and modeling virus-host system dynamics). This included two qPCR workshops and sampling trips. HVEDI faculty are cross-training in areas that are outside of their respective areas of expertise. One new course "Methods in Virology and Virus Ecology" was delivered during Spring Semester 2023 with more than 120 students from 5 different countries and 8 institutions. Professional development training (e.g., science writing) was delivered to HVEDI student participants. Multiple K12 and community outreach events were hosted including a phage genome hack-a-thon. More than 200 students from EPSCoR jurisdictions including Arkansas and Puerto Rico were served, many from historically marginalized ethnic/racial and economic groups.

Broadening Participation Outcomes:

HVEDI principals, which includes faculty from historically underrepresented racial/ethnic groups, have been cross trained in areas outside of their focused research areas. One such scholar has achieved promotion and tenure since the onset of the BII award. Multiple graduate students from underrepresented groups (~6 of 8) have progressed in their graduate programs. Several (~12) undergraduates and dozens of K12 students from historically underserved racial/ethnic and economic groups have been served.

Two MSIs (i.e., UAPB and Interamerican University) have new research infrastructure (i.e., virology labs) at their home institutions resulting from HVEDI capacity building efforts. These spaces have been equipped with qPCR thermocyclers, electron microscopes, BSL2 TC cabinets, and more.

Significant Research Results:

With regards to the core virus systems (CVS), one paper was published on the impacts of different species of human herpesvirus-6 (HHV-6A vs. HHV-6B) on distinct neuron types (i.e., neurotransmitter phenotypes). Another paper is in preparation tying the findings of this paper back to potential mechanisms of particular neurological disorders (e.g., epileptogenesis). The major finding of this work demonstrated that both HHV-6A and HHV-6B appears to infect glutamatergic and dopaminergic cell types but neither appears to infect GABAergic cells in differentiated human neural stem cell cultures. There are also differences in host immune responses in HHV-6A versus HHV-6B infection as evidenced by distinct cytokine responses.

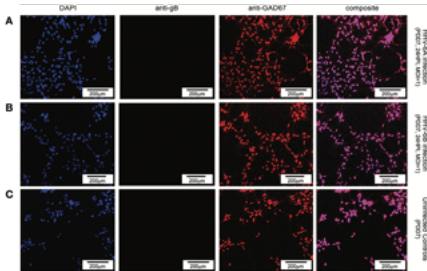


Figure 1. GABAergic cells from differentiated neuronal neural stem cells do not exhibit signs of HHV-6A or HHV-6B infection in fluorescent studies.

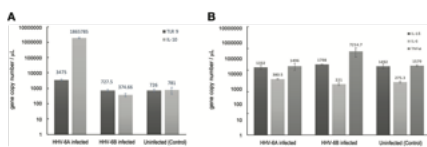


Figure 2. Cytokine activation profiles differ between HHV-6A vs. HHV-6B infected differentiated neural stem cells.

With regards to CVS, two papers are published with two more in preparation on Gordoniaphage. The major findings in the published works were the characterization and sequencing of genomes for three novel siphonviruses of *Gordonia terrae*: Chop, DelRio, GrandSlam. Directed-evolution studies are underway to determine how genomes change in siphoviruses over the course of multiple infection cycles in *Gordonia sp.*

Project Management:

HVEDI is a multi-institutional collaborative with affiliate institutions with diverse profiles (R1, R2, PUI, MSI) and geographic distribution across the United States and its territories (i.e., Puerto Rico). Given the diversity of institution types project management is challenging. HVEDI implemented the use of SLACK as a solution to provide “real time” information to BII partners. The PI (Ceballos) transferred to University of California Merced. Thus, a sub-award was issued to UCM, which added a partner institution. Administrative challenges between the PIs and research accounting (e.g., timely invoicing) has been an issue. There have been significant delays in bricks-and-mortar lab development at UAPB and Interamerican University. The latter is now functioning. The tight-knit collaboration between participating faculty has been critical in overcoming institutional challenges.

Additional Illustrations:

HVEDI research seeks to study three core virus systems and comparator systems. Both *within* and *between* systems characterization will lead to Rules of Life that underlie virus-host interaction dynamics (Schematic 1).

With regards to CVS, two papers are published with three more in preparation. For the fusellovirus system. Major findings in the published works are that a Sulfolobus Spindle-shaped Virus 9 (SSV9) appears to be lytic, whereas all previously described SSVs are reported to be non-lytic. We also developed relative virulence index, I_{sc} , which considers not only area-under-the-curve (AUC) but also $N_{asymptote}$ (similar to “carrying capacity”) in comparing relative detriment to host cultures in experimental infection assays. Four HVEDI affiliate labs are engaged in the fusellovirus CVS research sub-project.

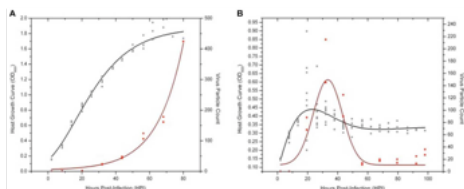


Figure 3. Whereas SSV infection exhibits a non-lytic replication profile in hosts of the Family Sulfolobaceae, SSV9 exhibits a lytic replication profile.

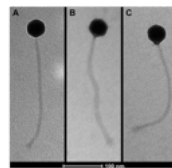


Figure 5. Gordoniaphage: Chop, DelRio, GrandSlam.

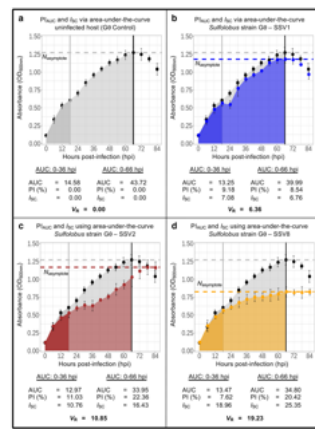
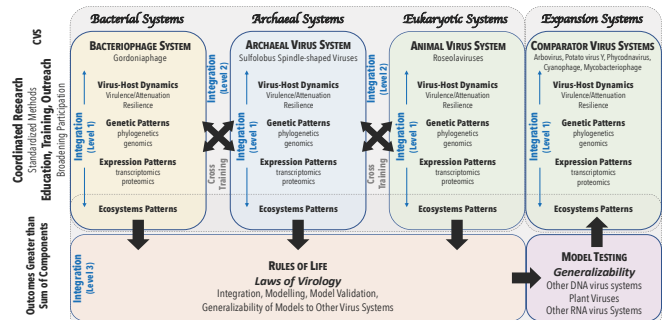


Figure 4. The Stacy-Ceballos index of relative virulence, I_{sc} , is a more robust measure of relative virulence because it takes into account more features of virus-host interactions to determine detriment to host.

Future plans:

In this third funding year, HVEDI continues to develop the CVS and mathematically characterize within system dynamics. We will also start the between systems modeling phase. This includes hiring our third postdoc. We will continue to develop comparator systems including orthomyxovirus, phycodnavirus, potyvirus, cyanophage, and other systems. We are behind on capacity building at University of Arkansas at Pine Bluff. We have recuperated our timeline for capacity building at Interamerican University. Otherwise, the HVEDI team is generally on schedule with research objectives, training goals, and outreach activities.



Schematic 1 – CVS, Comparators, Rules of Life, and Eco-Evolutionary Integration.

New Roots for Restoration Biology Integration Institute (NRR-BII)

Miller, Allison · 2120153 · Danforth Plant Science Center · amiller@danforthcenter.org



Figure 1: Successful day taking soil cores at the Danforth Plant Science Center Field Research Site near St. Louis, MO.

Elevator Speech:

How do long-lived plants coordinate growth over time, and how does this influence surrounding plant communities and soil? New Roots for Restoration Biology Integration Institute advances fundamental understanding of perennial plant biology, both above- and below-ground, in context (in the field). We aim to use plant traits to guide restoration efforts and in breeding perennial crops for more sustainable agricultural systems. @NewRoots_BII

Keywords: Perennial plants, Restoration ecology, Agro-ecology, microbial ecology; Asteraceae (7 species); Fabaceae (10 species); Juglandaceae (1 species); Poaceae (9 species).

Project Website: <http://www.newrootsforrestoration.org>

Participants: The current (January 2024) roster for NRR-BII includes 97 people:

<http://www.newrootsforrestoration.org/team.html>

Institute Objectives and Goals:

The New Roots for Restoration Institute focuses on the overarching theme of **how plant organismal systems (plant roots and shoots) relate to one another (1), and how those relationships influence and are influenced by plant communities (2) and the soil ecosystem (3).**

Goal 1: Scientific advancement in understanding how plant traits influence and are influenced by plant communities and the soil ecosystem.

Goal 2: Integration of scientific disciplines (plant organismal biology, population & community ecology) and research contexts (natural & agricultural ecosystems).

Goal 3: Establishment of an exceptional institute culture fostering collaboration, respect, & diversity in communication, conflict resolution, recruitment, training and retention.

Goal 4: Broadening Participation by welcoming, respecting, and supporting individuals of diverse ethnicities, recognizing and removing barriers to success, and celebrating diverse cultures.

Goal 5: Preparation of the next generation of diverse scientists who will lead an integrated approach to restoration of degraded lands in natural and agricultural ecosystems.

Goal 6: Translation of scientific advances and engagement beyond the Institute.

Integrating across Biology

NRR-BII engages researchers from different biological disciplines (plant organismal biology, population & community ecology, soil ecosystem), research contexts (natural systems, agricultural systems), and organizations (nonprofit research institutes, private and land-grant universities, and botanical gardens). We are carrying out 10 core research projects (Fig. 3) and 11 recently developed emerging projects. Six expertise cores apply technologies developed for contemporary agriculture (e.g., above-ground phenotyping; below-ground phenotyping), microbial ecology and soil science to support projects. Cores are using Institute generated data to advance analytical methods. Through in-person annual meetings, virtual annual meetings, mini-grants programs, and a multi-site REU program, we are training scientists to work across disciplines.

Education, Training & Outreach:

To increase diversity and inclusion in science, and to promote growth and persistence in science careers, our education, training, and outreach activities focus on diversifying, educating, and training Institute participants. In the first two years we

- trained 12 high school students, 47 undergraduate students and 20 graduate students, and 7 post-docs.
- recruited members of historically excluded groups at most career stages/position types within the Institute.
- developed an Institute Code of Conduct, Onboarding Manual, and offered institute-wide DEI training workshops and seminars.
- launched an Institute-wide, distributed REU network where REU interns mentored high school students, and graduate students mentored undergraduate interns. All Institute members participated in mentoring training. REU participants from across participating institutions met virtually on a regular basis to discuss research ideas.
- Established a Youtube channel of seminars.

Broadening Participation Outcomes:

- 1) We increased the % of individuals from historically excluded groups within within NRR-BII from 26% to 44%.
- 2) We recruited high school and research experiences for undergraduate (REU) students to NRR-BII from K-16 education institutions and STEM entities with majority racialized minority students.
- 3) We expanded cultural competence of institute members through a workshop "Trauma-informed outreach, education, and mentoring."
- 4) We maintain a supportive and inclusive culture that nurtures, retains, and advances members of underrepresented groups within the Institute, and ultimately beyond. There are multiple examples of this. We held a panel on "Career advancement and salary negotiation in the biological sciences."
- 5) We institute policies and structures that ensure equitable recognition, appreciation, and compensation for all members. This includes an authorship policy, frequent discussions of contributions and credit, and a weekly newsletter part of which features the work of different Institute members.

Significant Research Results:

Research Goal 1: How do root and shoot traits covary?

- Project 1.1: Assess the extent of root and shoot covariation of perennial species in a field environment across multiple years. Field data collection for eight species completed, soil cores, excavated whole plants for root phenotyping. Sample processing underway.
- Project 1.2 Identify genetic contribution to root and shoot covariation. Planted mapping populations of two perennial, herbaceous species, *Trifolium ambiguum* and *Silphium integrifolium*. Above-ground phenotypic data were collected by hand and with drones, minirhizotron tubes were installed, root imaging took place weekly in 2023; and genetic data are being generated.
- Project 1.3 Understand what proportion of covariation in root and shoot traits is explained by variation among genotypes and populations. Data collection is complete, analyses are underway.

Research Goal 2: Does above- and belowground trait variation predict, and respond to, plant community composition?

- Project 2.1: Assess to what extent above and below ground phenotypic variation predicts coexistence, diversity, and community productivity. Above-, below ground data collection, microbial sampling underway. Wang et al. 2023. Dilution of specialist pathogens drives productivity benefits from diversity in plant mixtures. *Nature Communications*. <https://doi.org/10.1038/s41467-023-44253-4>.
- Project 2.2: Explain how intraspecific variation in above and below ground traits modulates interspecific interactions, biodiversity-ecosystem function relationships. See 1.3 above; baseline soil measurements, plots established, data collection underway.
- Project 2.3: Understand relative production and root and shoot trait variation in monocultures vs. polycultures of perennial herbaceous species. Foundational study in an agricultural setting: experiments now in the ground at seven sites in four states. Above-ground phenotypic data (e.g., flowering time, height, biomass) taken at all sites; soil coring for root phenotyping and soil analyses taken at three sites in 2023. Minirhizotron tubes installed in StL.

Research Goal 3: Do soil and the soil microbiome mediate root/shoot variation and covariation and population/species level interactions?

- Project 3.1: Assess how soil type influences root and shoot variation and covariation (see 1.3). Soil data being processed.
- Project 3.2 Improve ability to predict microbiome composition (and eventually, function) based on plant genotype and/or phenotype. Microbiome samples from Project 1.1 collected and in process; 24 *Tripsacum dactyloides* clones planted in sets of five in Lawrence, Kansas and Gray Summit, MO. Phenotyping, soil sampling, and microbiome sampling will happen in 2024.
- Project 3.3: Explain to what extent soil or root microbiomes, including taxa sensitive to plant community diversity, impact host above- and below-ground traits. 14 native species from project 2.1 were inoculated with one of three treatments. Through engagement with the root phenotyping expertise core, root phenotypes were taken for these 14 species in Kansas.
- Project 3.4: Understand how monocultures and polycultures of perennial crops impact soil abiotic properties and soil community structure. Soil samples were being collected for half of the seven experiments from project 2.3 above.

Project Management:

Director: Allison Miller; Leadership Team: Allison, Kay Havens, Ivan Baxter. Executive Team: Jim Bever (Univ. Kansas), Kris Callis-Duehl (Danforth Center), Alicia Foxx (Chicago Botanic Garden), Kay Havens (Chicago Botanic Garden), Ranjith Udawatta (Univ. Missouri), Ivan Baxter (Danforth Center), Laura van der Pol (The Land Institute), Ruth Kaggwa (Danforth Center), and Eric von Wettberg (Univ. Vermont).

Evaluation Team: Becky Bart, Ben England, Bryan Foster.

External Advisory Committee: Bala Chaudhary, Jennifer Clark, Argelia Lorence, Samniqueka Halsey, Gordon Uno.

Future plans:

- New approaches for in-field phenotyping: Armed with data from multiple projects and growing knowledge of perennial systems, expertise cores are developing fast, cheap ways to quantify above- and below-ground trait variation in the field.
- Synthesis: For projects that are farther along, we are working on models that relate plant traits and community composition to the soil ecosphere.
- Expansion of New Roots projects: 10 core research projects described above have inspired an additional 11 “emerging” projects, collaborations between researchers at different institutions/disciplines. At least three have developed into submitted external proposals. This will continue.

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:



Figure 2 (top left): New Roots for Restoration BII held our second in-person meeting June 2023 at the Chicago Botanic Garden. We welcomed 60+ in-person participants and 20+ virtual participants from the Chicago Botanic Garden, Danforth Center, The Land Institute, Saint Louis University, University of Kansas, University of Missouri, and University of Vermont. The two-day event included project talks, DEI and mentoring training and, field tours.

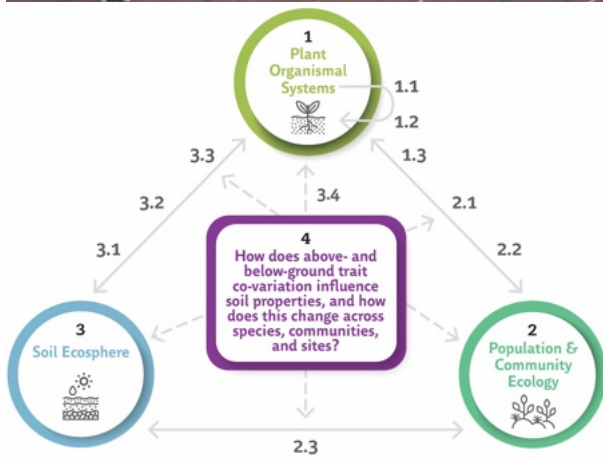


Figure 3 (bottom right): 10 Core research projects currently underway. Each project connects two or more of the three primary biological disciplines represented within New Roots for Restoration.

Figure 4 (right): Intern at the University of Kansas extracting soil hyphae from project 2.3 in prep for project 3.3.

Figure 4 (bottom left): Soil from 2.3 plots was collected and sent to KU to begin the soil feedback experiment. This experiment asks how soil communities of monocultures vs. polycultures influence crop root/shoot traits.





INSITE utilizes three symbiotic systems (leafhopper, squid, anemone) to address how bacteria and animals cope with climate change.

Elevator Speech: [UC Merced, Michigan State University, and Resilient Oceans are joining forces to expand the fundamental knowledge of symbioses and inform immediate and long-term conservation strategies in the face of climate change through INSITE: The Institute for Symbiotic Interactions, Teaching, and Education.

Keywords: *Euprymna*, *Aiptasia*, *Macrosteles*, Climate Change, Symbiosis, Multiscale Models, Experimental Evolution

Project Website: <https://bii-insite.org/>

Participants: <https://bii-insite.org/team/>

Institute Objectives and Goals:

The **specific goals** of INSITE are to (i.) guide the expansion and generalization of model systems for use in predicting response and acclimatization to environmental change; (ii.) train the next generation of researchers to think integratively across disciplines and systems; and (iii.) educate K-12 students and the public about the importance of symbiosis in maintaining biodiversity in the face of climate crises. To accomplish these goals, we have selected a set of three emergent model systems that permit us to integrate empirical and theoretical evidence in order to understand how climate change will affect symbiotic systems from the molecular to phenotypic levels, across ecological and evolutionary timeframes, and from laboratory to the natural environment.

Integrating across Biology

BII-INSITE will establish a framework for how researchers in the field can evaluate and understand the impact of climate change broadly on symbiotic species and provide critical information to guide environmental management plans and shape policies at the local, national, and international scale. Our training and education plan extends this goal to train new generations of scientists that will propel novel scientific discovery along with collaborative efforts with conservation managers to strategize plans for preventing substantial biodiversity loss due to dysbiosis. Such complex issues require diverse perspectives and team membership that collectively are greater than the individual research projects. The highly integrative information we will provide is crucial to fully understand the impact of climate change on symbiotic species, their resilience, and ultimate extinction risk. We have held weekly team meetings for each theme, integrating multiple members of INSITE in the design and implementation of the proposed projects that span multiple disciplines.

Education, Training & Outreach:

One of INSITE's main goals is to understand the resilience of microbial symbiotic systems to climate change and subsequently expand this knowledge through our interdisciplinary training and educational activities. INSITE will harness the expertise of our team to mentor our students throughout their graduate experience, with the goal that they will be better equipped to contribute to scientific enterprises within and/or outside academia (e.g., NGOs, industry, governmental agencies). This first year we have funded 5 currently enrolled doctoral students, recruited 4 new doctoral students (F23) and 3 postdoctoral scholars, trained 23 members of our team in science communication through the Alan Alda Science communication program, developed IDPs for all PD and PhD scholars. We also developed and ran our graduate COOGRE (Cooperative-based Graduate Research Experience course), which included 15 UCM and 1 MSU doctoral students (8 of whom were INSITE scholars), teaching them the value of interdisciplinary team science.

Broadening Participation Outcomes:

Our vision, ideas, and objectives that underlie the establishment of INSITE are entwined to benefit all aspects of the Institute: research, education, training, and outreach. INSITE will provide an open environment to freely exchange ideas, promote research training, develop leadership, and promote science communication to prepare a future generation of "symbio-visionaries" to deepen our understanding of how important symbioses are in maintaining biodiversity. Our trainees will gain the necessary cross-disciplinary skills to develop a cohesive and inclusive network that, when combined, tackles difficult problems associated with climate change. INSITE is committed to increasing EDI in STEM and will create a community both designed to recruit and retain people from diverse and underrepresented backgrounds in science. This first year INSITE connected with community members through various outreach activities (Bobcat Day, CSU Stanislaus Science Day, Coffee with Radio Bio, and attending various tabling events that totaled >9000 community members. INSITE also held our first summer undergraduate mentees (6) from various HSI/MSI institutions training them in symbiosis research. INSITE also hosted a weekly symbiosis journal club where UCM and MSU faculty, graduate and undergraduates could participate in thoughtful discussions on various symbiosis topics (open to all students interested in symbiosis).

Significant Research Results:

Year 1

Experimental evolution of *Vibrio fischeri* to various temperatures (18-32°) is demonstrating fitness costs (loss of luminescence and biofilm production) at higher temperatures (PI Nishiguchi, grad Thieme).

Different evolutionary environments contribute to the molecular evolution and subsequent gene loss in two co-occurring symbiont genomes (*Nasuia* and *Sulcia*) in *Nesophrosyne* leafhoppers (coPI Bennett).

Examining temperature stress on growth and reproduction in *Nesophrosyne* leafhoppers (coPI Bennett, PD Kwak)

CRISPR is presently being attempted successfully in *Euprymna* embryos (coPI Heath-Heckman).

Exploring eDNA for use in predicting bobtail squid populations over a geographical/temperature gradient (coPI Heath-Heckman, grad Nishida)

Particular protein kinases that are conserved broadly across different eukaryotes act as acute temperature sensors and may be subject to temperature shifts in host regulated symbioses (SP Thompson, grad Garcia-Michel).

Mathematical modeling team is developing symbiotic models for temperature adaptation on 3 model symbiotic systems (SP Rutter, PD Williams).

Modeling biotic pressures on symbiont fitness outside the host (PD Williams, grad Cheam).

Project Management:

Progress:

- Holding monthly meetings for entire team.
- Hired all 3 staff (PM, OC, DM).
- Democratic decision making has been easy.
- Weekly theme led meetings for research projects.
- Acquisition of space in proximity with one another.

Challenges:

- Loss of webmaster (sudden death).
- Let go first staff person (OC).
- Acquisition of equipment for projects.
- Budget (PD and PhD increase in salaries after UC strike).

Future plans:

- Continue research theme experiments (Themes 1, 3)
- Initiate field work in Australia and Hawaii (Theme 2)
- Establish server for long term data storage.
- Recruit next cohort of new graduate students.
- Implement grad training plans in spring 2024.
- Organize outreach activities and coordinate with outreach director at UC Merced and MSU.
- Develop K-12 activities to initiate at Summer STEM Bobcat Academy (Cal Teach).
- Develop relationships with conservation managers.
- Reach out to independent private groups interested in INSITE and create relationships with long term stakeholders/investors.

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

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BII: Life Without Water: Protecting Macromolecules, Cells, and Organisms During Desiccation and Rehydration Across Kingdoms of Life

Rhee, Seung · 2213983 · Michigan State University · rheeseu6@msu.edu



Water and Life Interface Institute (WALII) logo

Elevator Speech: The Water and Life Interface Institute (WALII) was established to study how life has adapted to survive with little or no water. Our multidisciplinary approach examines this phenomenon from the molecular to the whole organism to ecological and evolutionary scales across multiple kingdoms of life.

Keywords: anhydrobiosis, desiccation, solid state biology, vitrification, rehydration, intrinsically disordered proteins, evolutionary dynamics

Project Website: <https://www.walii.science/>

Participants: <https://www.walii.science/team.html>

Institute Objectives and Goals:

The Water and Life Interface Institute (WALII) studies how life interacts with water from the molecular to the organismal and evolutionary scales across plants, fungi, and animals. Our long-term goals are to train the next generation of innovators in all sectors of our society while working to understand how organisms tolerate desiccation; invent new technologies, frameworks, and concepts to study life without water (anhydrobiosis); and engineer macromolecules, cells, and organisms that survive desiccation.

Integrating across Biology

WALII has four research themes to address different aspects of anhydrobiosis: 1) Physical and cellular properties of anhydrobiosis; 2) Physiological recovery from desiccation; 3) Engineering resilience to anhydrobiosis; and 4) Evolutionary dynamics of desiccation tolerance. These four themes are interrelated. The findings of each theme combine to create a comprehensive picture of the molecular and organismal mechanisms behind anhydrobiosis.

For example, Theme 1 takes biomolecules identified in Theme 4 or designed in Theme 3 and characterizes how they affect the ability of organisms to survive desiccation. This is done using a newly developed sequencing-based assay that assesses desiccation protection in hundreds of candidate sequences simultaneously. This information will then be integrated into Theme 2 to determine how these changes to physicochemical properties slow or halt life processes and allow for metabolic recovery upon rehydration.

Education, Training & Outreach:

In the last 1.5 years, we launched several training and outreach programs. We started a monthly seminar series for members to present their research, a paired mentorship program for WALII trainees, and a seed grant award to support cross-lab collaborations within WALII. We also held our first Technical Workshop where WALII researchers presented unique techniques that they use in their research and launched a Travel Award program to support team members to travel and learn techniques in other WALII labs.

WALII hosted its first summer undergraduate internship program. Seven undergraduates were mentored in five WALII labs. In addition to research, interns participated in a weekly seminar series where WALII faculty presented their path to science and research, a virtual career panel featuring careers both in and out of academia, and a paired mentorship program. Interns and WALII researchers also had the opportunity to present their research at the virtual WALII Symposium.

WALII members also developed two outreach initiatives to K-12 and the public. We established protocols for Seed Burial Experiments and Tardigrade Hunting. Participants from Wyoming and California submitted samples to the Tardigrade Hunting project through summer camp collaborations with the University of Wyoming INBRE Program/STEAM camps and the City of San Francisco Recreation and Parks Department.

Broadening Participation Outcomes:

WALII's aim is to create an inclusive community of researchers, from all career stages, that supports the educational, professional, and career development goals of its members. Our initial demographic survey revealed that WALII is composed of a diverse group of researchers with **over 65% of WALII members identifying with one or more underrepresented groups in STEM.**

We also hosted booths at the Society for the Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS) National Diversity in STEM (NDiSTEM) conference and the Annual Biomedical Research Conference for Minority Students (ABRCMS) where we promoted open positions at WALII and our undergraduate internship opportunities to hundreds of students from underrepresented groups.

Significant Research Results:

We made great progress across the four themes in our first 1.5 years. Work in Theme 1 has focused on correlating material properties of desiccating biological matter, developing new methodologies for the study of anhydrobiosis, and developing new methods for studying desiccation at sub-cellular resolutions. In Project 1.1 we have examined the biophysical properties of dry systems ranging from molecules to cells, and even whole organisms, to identify what physical properties of dry biological material correlate with survival/protection in the desiccated state. A major take away from these studies is that individual protectants provide protection through distinct physical means, but that cells and whole organisms use a combination of protectants and thus mechanisms to enhance survival in the dry state. Additionally, an overarching goal in these efforts was the creation of new, standardized methodologies that would enhance our ability to both study anhydrobiotic systems in an interdisciplinary, quantitative, and integrative way and break grounds in our understanding of how biology evolved desiccation survival mechanisms from the molecular to the organism level. As part of these efforts, we have developed new protocols for preparation of neat lysates using cryomilling that let us assess the inherent ability of proteins to survive desiccation. We've developed protocols to use multiplexed mass spectrometry to quantify the ability of hundreds of proteins to survive rehydration in a single experiment. Initial results from these experiments point to an inherent ability of some monomeric metabolic enzymes to survive desiccation by optimizing their surface area chemistry. Project 1.2 has focused on the development of protocols for analyzing cell structures, which is summarized below in Theme 2.

Work in Theme 2 has focused on developing model systems that quantitatively express partial or full desiccation tolerance upon full (2.1) or partial (2.2) rehydration, and to seek genetic and metabolic milestones that mark progress toward recovery. In 2.1, maturing *Arabidopsis* seeds (i.e. 13 days after flowering) do not survive cytoplasmic glass formation (see Theme 1) unless dried within the silique (i.e. slow drying). We developed stable transgenic *Arabidopsis* lines expressing fluorescent markers for dry seeds (red fluorescence) and for rehydrating seeds (yellow fluorescence) to first segregate seeds at different levels of rehydration and recovery and then use these seeds for transcriptomics and proteomics. RNAseq shows that gene expression is qualitatively similar but increasingly delayed in dying seeds. We are exploring non-reversible deformation of organelles and real time oxygen consumption to distinguish between healthy and damaged cells. Additionally, a system to track proteome wide changes upon cycles of desiccation and rehydration has been developed using the yeast GFP-fusion collection which constitutes 75% of the yeast proteome. This study will provide the opportunity to assay the physiological expression level and subcellular localization of 4,156 proteins upon repeated cycles of desiccation and rehydration. A pilot study has revealed localization changes of various proteins upon desiccation/rehydration; examining the complete collection will allow us to test how the proteome is rewired under desiccation/rehydration and assess whether it constitutes an adaptive response priming the cell for recovery.

Work in Theme 3 has focused on the development on novel computational methods for the rational design of disordered peptides (3.1), testing the relationship between helicity and desiccation protection (3.1), and developing a novel fluorescence-based osmosensor for *in vivo* assessment of osmotic state (3.2). In pursuit of these goals, we have developed a general-purpose tool for the rational design of intrinsically disordered regions (Holehouse 2023), and – using this tool – tested a library of short, disordered peptide sequences in a yeast-based desiccation assay. In parallel, we have rationally redesigned disordered regions to orthogonally vary sequence chemistry and helicity to assess how helicity impacts protection in an *in vitro* desiccation protection assay (manuscript in press at Protein Science). Finally, we have made strong progress on developing our intracellular osmosensor, including a slew of new designs, proximity labeling to demonstrate *bona fide* orthogonality to yeast proteins, and fitness assays to confirm the sensor does not impact fitness under basal or stressed conditions.

Work in Theme 4 has focused on integrating multi-scale datasets across diverse desiccation tolerant lineages to understand how this complex trait evolved, test if similar mechanisms enable survival of anhydrobiosis across the tree of life, and synthesize and integrate knowledge for new hypothesis generation. We have developed analytical frameworks to compare genes, genomes, expression dynamics, and regulatory elements to identify common features in different desiccation tolerant lineages. Using these comparative frameworks, we have identified a common set of genes that are recruited for desiccation tolerance across grasses, supporting the convergent evolution of this trait in plants (Marks 2023). We have developed diversity panels to survey intraspecific variation and local adaptation in resurrection grasses. Our data provide intriguing evidence that desiccation tolerance may be mediated by changes in ploidy and highlight the significance of polyploidy as a potential driver of local adaptation. These complex interactions illustrate how evolutionary processes associated with genome duplication might shape a plant's ability to thrive under abiotic stress. We have constructed knowledge graphs to catalog and synthesize the literature on desiccation tolerance to integrate findings from plants, animals, and microbes, and generate new hypotheses to test in the other themes.

Project Management:

A WALII All-Hands Google Drive and Slack Workspace have been established to allow document sharing and facilitate communications between WALII members. The Scientific Advisory Board (SAB) was established, and we held our first annual in person retreat in May 2023 to build the WALII community and get feedback from the SAB. Our code of conduct, strategic plan, governance plan, and authorship agreement were developed and disseminated to all WALII members.

Future plans:

Next year, we will use the standardized methods of dehydration and rehydration and characterize the process across species and identify key regulators. The regulators will be tested across scales from *in vitro* molecular to *in vivo* and evolutionary scales. We also plan to increase research integration by launching our travel grant program to strengthen WALII research and integration. We plan to hire 3 new postdoctoral fellows and host our 2nd annual internship program. Additionally, we will also host our 2nd in-person retreat, 2nd virtual Symposium, and host a virtual Town Hall to solicit feedback from WALII members to improve our training and education programs.

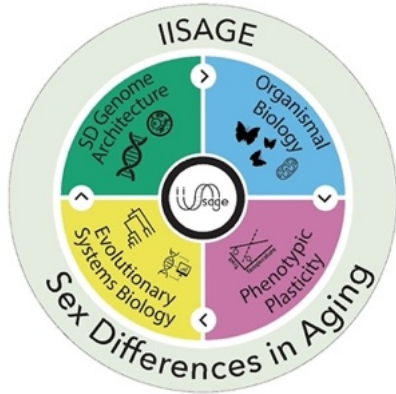
Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

Holehouse, A., Emenecker, R., Guadalupe, K., Shamoan, N. & Sukenik, S. (2023) Sequence-ensemble-function relationships for disordered proteins in live cells. Research Square preprint. <https://doi.org/10.21203/rs.3.rs-3501110/v1>

Marks, R.A., Van Der Pas, L., Schuster, J., & VanBuren, R. (2023) Convergent evolution of desiccation tolerance in grasses. bioRxiv preprint. doi: <https://doi.org/10.1101/2023.11.29.569285>

Integration Initiative: Sex, Aging, Genomics, and Evolution (IISAGE)

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IISAGE (Integration Initiative: Sex, Aging, Genomics & Evolution) will promote integrative and inclusive research and training to reveal the mechanisms and evolution of sex differences in aging.

Elevator Speech:

In humans, females live longer than males. Sex differences in aging are common in animals, but they are not universal, and it is not always females that live longer. IISAGE uses a comparative approach to identify the molecular mechanisms that lead to sex differences in aging and understand how these differences evolved. Integrated with IISAGE research are diverse training and outreach programs designed to increase participation in STEM.

Keywords: sex-specific aging, genomics, epigenetics, life history, senescence, lifespan, physiology

Project Website: www.iisage.org

Participants: <https://www.iisage.org/team/>

Institute Objectives and Goals:

1. Determine how (1) genome architecture, (2) organismal biology, and (3) phenotypic plasticity underpin sex-specific aging, and whether there are general mechanistic rules.
2. Sample broadly across amniotes, fish, moths, and flies - including diverse and model-genetic species - to test for macroevolution of causes of sex-specific aging.
3. Combine phylogenetic comparative methods with machine learning algorithms to develop a data-ready workforce.
4. Facilitate citizen scientists to collect relevant data on additional species that may be endangered or subjects of captive breeding.
5. Empower diverse trainees to fully participate in all aspects of this BII.

Integrating across Biology

The IISAGE collaboration to investigate sex-differences incorporates several different biological disciplines, including molecular and cellular biology, genetics/genomics, evolutionary biology, physiology, and computational biology. Working in parallel across diverse animal taxa, IISAGE labs will collect genome-scale data on gene expression and epigenetic state in both sexes for young and old animals. We will similarly assay DNA-repair efficiency and mitochondrial function. The taxa studied represent natural variation in sex-chromosome complement and genetic architecture in a broad phylogenetic context. For several species, experimental manipulations or natural variation across populations will be used to investigate the impact of altered genome architecture and environmental impacts. Thus, we will use phylogenetic methods in conjunction with machine learning inferences of the genomic and physiological data to distill the major drivers of sex-specific aging.

Education, Training & Outreach:

IISAGE runs a variety of education, training, and outreach programs that support career success of diverse IISAGE members, engage the public, and provide training opportunities for junior scientists.

Specifically we have implemented the following programs:

1. IISAGE Leadership Academy – annual program to provide professional skills training for trainees (25 trainees in 2023).
2. Interdisciplinary seminar series to provide cross training in diverse fields to expose students to ecology, molecular biology, computer science and evolutionary biology (bi-weekly in 2023).
3. Interdisciplinary workshops to provide skills training (two workshops scheduled for spring 2024)
4. Lab visits program – four students participated in IISAGE lab exchanges in 2023.
5. REU program – annual program focused on students belonging to groups traditionally underrepresented in STEM (10 students in 2023).
6. Community science project focused on geckos and aquarium fish initiated ([link to website](#)).
7. Established collaborations with colleagues in the wider scientific community to obtain samples from additional species, coordinate data collection, and encourage trainee interactions.

Broadening Participation Outcomes:

Integrated with its research activities, IISAGE provides education and training aimed at recruitment and retention of diverse trainees into STEM. Outreach activities are integral to IISAGE's mission to increase diversity in STEM while focusing on integrating scientific fields and will impact and engage pet hobbyists, K-12 students, and museum visitors. To achieve these goals we have set up the following programs:

1. To increase the number of trainees from historically underrepresented groups, we engage with the Leadership Alliance, SACNAS, HBCUs, and LatinX serving institutions.
2. To increase the persistence of diverse trainees in STEM we employ near-peer mentoring for all trainees through monthly trainee meetings and trainee-led activities.
3. To reach a broad audience who would not otherwise be engaged in research, we have established the SNAP community science program.

Significant Research Results:

During the first 15 months of funding, IISAGE has achieved the following scientific milestones:

1. Mitochondrial genomes and sex-specific aging - we have data collected from eight species regarding the DNA sequence changes observed in old versus young animals of both sexes. Data analysis is on-going.
2. DNA Methylome and sex-specific aging - we have data collected from several species of bats and reptiles to investigate the changes in DNA methylation between young and old animals of both sexes. Data analysis is on-going.
3. Transcriptome studies and aging – we have data collected from flies and mice to investigate transcriptome changes in old versus young animals of both sexes. Samples from additional species are being processed currently.
4. Experiments manipulating heterochromatin and dosage compensation in *Drosophila* have been started, with sample collection currently on-going.
5. Field collections of several species have been completed, with samples stored as experimental methods are being optimized in non-model species.

Project Management:

Recruitment of a program manager and various trainees was slower than anticipated in year 1. By the beginning of year 2, all trainee positions have been filled and a full-time program manager is in place. All outreach and training programs have been piloted in year 1, and SOPs have been developed. We continue weekly PI calls and a seminar series. Focus in year 2 is on moving the experiments forward in a timely fashion while continuing the training and outreach activities.

Future plans:

1. Continue data collection in species with established protocols and protocol optimization with additional species.
2. Finalize IISAGE database for data tracking and management.
3. Continue established outreach and training programs.
4. Deploy museum kiosk at its first location.
5. Improve outreach to fish and reptile hobbyists to increase engagement in

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

Riddle NC, Biga PR, Bronikowski AM, Walters JR, Wilkinson GS, IISAGE Consortium. Comparative analysis of animal lifespan (2023) *Geroscience* 2023 Oct 27, doi: 10.1007/s11357-023-00984-2.

Bronikowski AM, Meisel RP, Biga PR, Walters JR, Mank JE, Larschan E, Wilkinson GS, Valenzuela N, Conard AM, de Magalhães JP, Duan J(E), Elias AE, Gamble T, Graze RM, Gribble KE, Kreiling JA, and **Riddle NC**. Sex-specific aging in animals: Perspective and future directions (2022) *Aging Cell* 21, e13542, <https://doi.org/10.1111/accel.13542>.

Viral Emergence Research Initiative (Verena)

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Institute members explore DC during an in-person interdisciplinary team science workshop.

Elevator Speech:

The Verena Institute works to understand viral emergence using open data, machine learning, and the science of the host-virus network. Our mission is to provide the evidence base and scientific support for pandemic prevention, all while training the next generation of experts in emerging infectious diseases.

Keywords: viruses, bats, mosquitoes, pandemics, ecoimmunology, viral evolution, network science, climate change

Project Website: <http://viralemergence.org>

Participants: <http://viralemergence.org/team>

Institute Objectives and Goals:

Our goals are to

1. Develop a global One Health platform for open data and computational resources that supports basic science, biosecurity, and conservation.
2. Advance the science of the host-virus network through collaborative and multi-scale biological research, with a blend of computational, field, and laboratory approaches, and a focus on how mechanisms at the molecular and cellular scale determine global dynamics of viral ecology, evolution, and emergence.
3. Train scientists at all career stages in the science of the host-virus network and the science of prediction, as well as core skills in data fluency and boundary spanning, creating the next generation of researchers familiar with our team's unique approach.

Integrating across Biology

Our team has been working since 2019 to develop a unique approach to biology integration. Global viral diversity, biogeography, and even dynamics of emergence in human populations are all emergent properties of microscopic processes; by identifying the genetic, biochemical, and structural basis of compatibility, and the ecological dynamics of opportunities for within- and cross-species transmission, we believe that the most important problems in virology can be explained—and predicted—using machine learning.

Our Institute's work applies this approach to four biological scales (virology, ecology, evolution, and global change), with a particular focus on decoding multi-omic data to understand the heritable basis of immunity in both vertebrates and invertebrates. In our Institute program, we use bats and mosquitoes as model organisms – and key case studies with relevance to human health – with an integrative project that uses bat reservoirs of flaviviruses to tie the systems together.

Education, Training & Outreach:

The Lighthouse Scholars interdisciplinary Ph.D. program is our flagship educational program, and serves a cohort of 8 students across 5 universities, who are training together in a series of six Integration Workshops on different team “ologies.” In 2024, cross-team “mini-rotations” provide a new opportunity for integration and skill development. The Fellows-in-Residence program provides external grad students and postdocs with support for short-term, high-risk collaborations. The Lighthouse Learning Community provides professional development and networking opportunities to students and fellows.

Our research has been cited in the 2023 Economic Report of the President and in the Intergovernmental Panel on Climate Change's Sixth Assessment Report, and has been covered on *PBS News Hour* and in *The New York Times* and *The Atlantic*. In 2022, CarbonBrief reported that one of these studies had broken the all-time record for press coverage and social media discussion of a scientific study on climate change.

Broadening Participation Outcomes:

Our goals for broadening participation are to (1) create a diverse, inclusive, and welcoming environment for team science where participants feel safe, respected, and protected; (2) dismantle specific barriers to inclusion for minority and underrepresented groups in science, particularly by providing new opportunities to support and professional development; (3) flatten hierarchies and achieve equity and respect in our day-to-day interactions; and (4) apply our work to the betterment of society, including global justice in areas including health, scientific research, and the environment. Our goals reflect the broader priorities we feel should exist for scientific institutions, as well as an understanding of specific barriers to participation and cultural issues that exist (and that we have experienced) in emerging virus research and adjacent fields like computational biology. We bring these goals to our research (e.g., the Fellows-in-Residence program), training (e.g., professional development workshops with trainees on team), outreach (e.g., participation in the Skype a Scientist program), and governance (e.g., developing our Team Charter).

Significant Research Results:

Open data ecosystem. Data synthesis: We maintain the largest open access database of the vertebrate-virus network (VIRION; *mBio*); the largest open access database of bat coronavirus surveillance data ever compiled (1996-2016; nearly 90,000 samples tested, covering more than 1 in every 4 bat species from 15 families); and several smaller datasets. We are nearing completion of an open access database of mosquito vector competence experiments (COMET), with 70,000 measurements recorded. **Data stewardship:** In 2023, we launched the Pathogen Harmonized Observatory (Pharos: pharos.viralemergence.org), a global platform for sharing wildlife disease surveillance data, with 6,000+ records entered so far. **Data rescue:** We maintain an R package ('insectDisease') that provides continuous database to the Ecological Database of the World's Insect Pathogens.

Biology of bats and their viruses. Field: We have collected tens of thousands of samples from wild bats for our comparative immunology study. Samples have been contributed both by members of the BII program and a sizable network of external collaborators, and so far, will include contributions from at least twelve countries (Australia, Belize, Bulgaria, Costa Rica, Ecuador, Japan, Kenya, Mexico, Oman, Spain, Uganda, and the United States). Proteomic and transcriptomic analysis of samples is underway. **Lab:** We have set up cell lines from four bat species (four cell lines from *Rousettus aegyptiacus*, two from *Artibeus jamaicensis* and *Carollia perspicillata*, and one from *Hypsignathus monstrosus*), and completed a first round of comparative experiments with Zika virus. Multiple projects are using machine learning models to guide viral discovery from bat tissues in museum collections. **Modeling and data analysis:** Major findings so far include: bat evolutionary history explains hotspots of coronavirus diversification and can even be a proxy for spillover risk; alpha- and betacoronavirus may have divergent patterns of tissue tropism in bats, with implications for optimal sampling; coinfections among virulent bat viruses are significantly more common than expected; that 40% of bats use man-made structures for roosting, especially small, insectivorous bats in temperate habitats, creating opportunities for zoonotic spillover.

Biology of arboviruses and their vectors. Lab: We have developed a method for testing evolutionary bottlenecks within the mosquito body using barcoded viruses, which was piloted on West Nile virus, and is now being applied to yellow fever virus; preliminary results suggest that at higher temperatures, the live attenuated YFV-17D vaccine strain may gain the ability to disseminate from the mosquito midgut. Newer work is exploring differences in temperature-driven viral evolution among four strains of *Aedes aegypti* mosquitoes. **Modeling and data analysis:** Preliminary work is underway analyzing genomic and experimental drivers of variation in vector competence (using the COMET dataset), and developing a machine learning model of the mammal-mosquito-flavivirus network informed by mosquito innate immune genes, which will be used to design future experiments.

Explaining and predicting disease emergence. Genome-to-global virome prediction: Genome composition bias and host range can be used to efficiently identify mammalian viruses with zoonotic potential, leading to the identification of several pox-, bunya-, flavi-, and paramyxoviruses that may already be in early stages of "viral chatter." Orthopoxviruses use a unique mechanism (host adaptation through gains and losses of accessory genes) that can be used to predict host range; hotspots of orthopoxvirus reservoirs coincide with low cross-immunity from historical smallpox vaccination. **Drivers of disease emergence:** Across ~60,000 outbreak records from around the world, the strongest predictor is human-nature interfaces—but the effects of anthropogenic change (e.g., deforestation) vary more by disease; wildlife hunting has a more limited role than historically believed. Climate change has created thousands of novel opportunities for cross-species viral transmission, especially with and among bats, due to their potential for rapid range shifts. Ongoing projects are exploring how climate change may have contributed to the Covid-19 pandemic or the risk of an H5N1 avian influenza pandemic.

Project Management:

Our team is administered by the Executive Committee (including a rotating trainee representative) and overseen by a Science-Policy Advisory Board. In 2023, we recruited a program manager, and formalized a 30-page Team Charter that includes a code of conduct, collaboration guidelines, communications and biosafety policies, and governance structures that allow our team to continue growing with new investigators. Our team continues to use digital platforms like Slack, GitHub, and Google Drive to coordinate across institutions and make the most of remote work. In 2024, we are continuing to map team objectives for evaluation based on our experiences in year 1 and the Design phase.

Future plans:

In summer 2024, the primary institution of the project will shift from Georgetown to Yale, bringing new opportunities and more institutional support. In addition to navigating that transition, our team's goals are to: (1) hire a program evaluator; (2) begin new activities related to DEI, focusing on areas like global inclusion; (3) develop a plan for sustainable cyberinfrastructure; and (4) ramp up analysis of the extensive data we have collected in the field and lab. Team programming will also include: the virology Integration Workshop (virtual); a mini-rotation research development workshop (in-person); and monthly seminars.

Additional Text, Relevant Illustrations, Citations List or Other Items of Choice:

Selected publications: Data proliferation, reconciliation, and synthesis in viral ecology (*BioScience*, 2021); The science of the host-virus network (*Nature Microbiology*, 2021); Optimizing predictive models to prioritize viral discovery in zoonotic reservoirs (*The Lancet Microbe*, 2022); The Global Virome in One Network (VIRION): an atlas of vertebrate-virus associations (*mBio*, 2022); Climate change increases cross-species viral transmission risk (*Nature*, 2022); Urban-adapted mammal species have more known pathogens (*Nature Ecology & Evolution*, 2023); Network embedding unveils the hidden interactions in the mammalian virome (*Patterns*, 2023); Coronavirus sampling and surveillance in bats from 1996-2019: a systematic review and meta-analysis (*Nature Microbiology*, 2023); The coevolutionary mosaic of bat betacoronavirus emergence risk (*Virus Evolution*, 2024). All of our team's publications are available without a paywall at <https://www.viralemergence.org/work>.

Some of our favorite coverage in the popular press: *The Atlantic* - We Created the 'Pandemicene' (April 2022); *The New York Times* - Which Animal Viruses Could Infect People? Computers Are Racing to Find Out (May 2022); *This Week in Virology* podcast ep. 896: Memory B cells, the way we were (May 2022); *Nature* - Could an algorithm predict the next pandemic? (October 2022); *PBS News Hour* - Is climate change accelerating the risk of disease spreading from animals to humans? (March 2023).

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M System Map

wmata.com
 Information: 202-637-7000 | TTY: 202-962-2033
 Metro Transit Police: 202-962-2121 | Text: MYMTPD (696873)

- ### Legend
- **RD** Rod Line • Glenmont / Shady Grove
 - **OR** Orange Line • New Carrollton / Vienna
 - **BL** Blue Line • Franconia-Springfield / Downtown Largo
 - **GR** Green Line • Branch Ave / Greenbelt
 - **YL** Yellow Line • Huntington / Mt Vernon Sq
 - **SV** Silver Line • Ashburn / Downtown Largo

Station Features

- Parking
- Hospital
- Airport

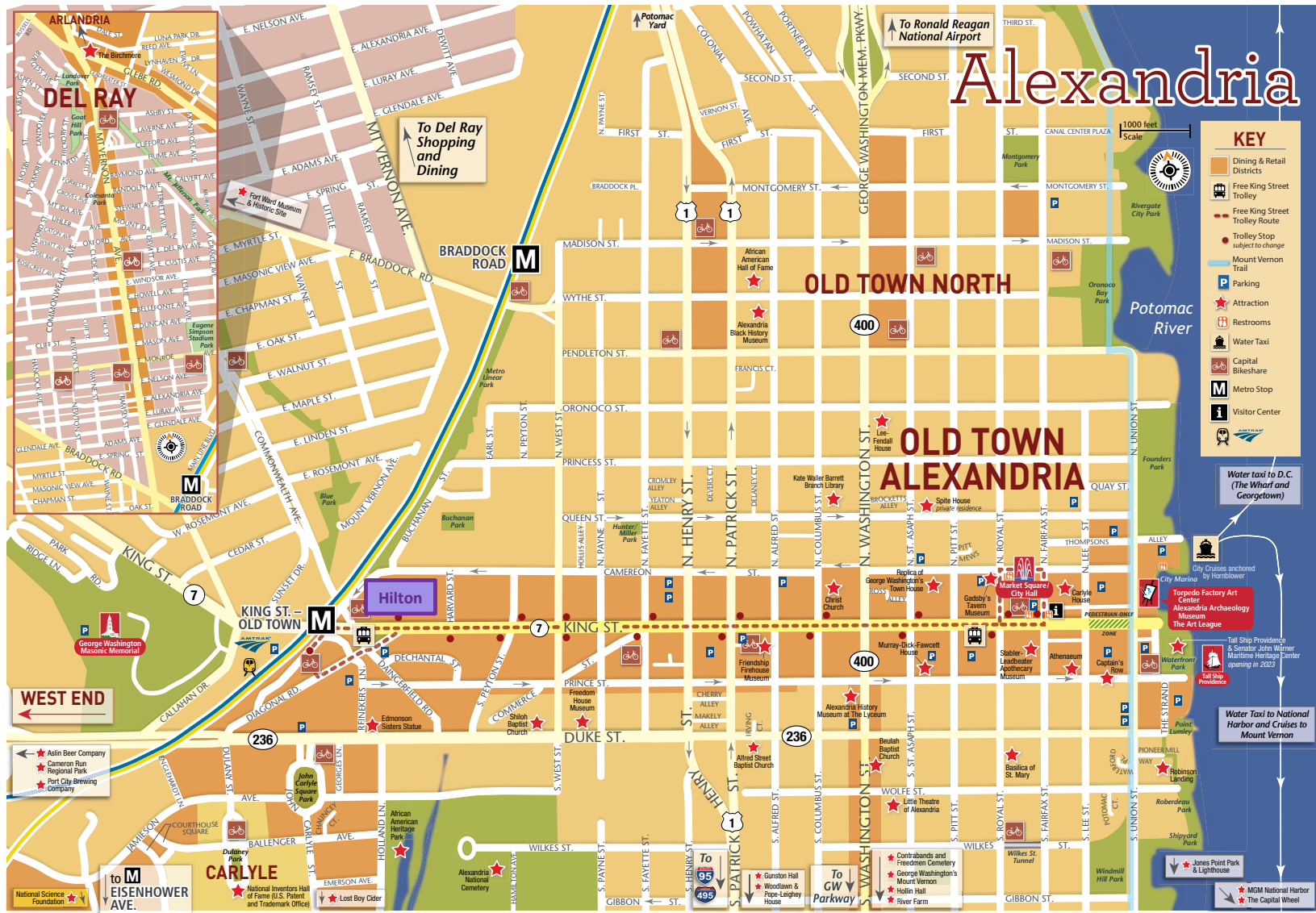
Connecting Rail Systems



NSF Headquarters:
 2415 Eisenhower Ave

Metro is accessible.





Alexandria

- KEY**
- Dining & Retail Districts
 - Free King Street Trolley
 - Free King Street Trolley Route
 - Trolley Stop subject to change
 - Mount Vernon Trail
 - Parking
 - Attraction
 - Restrooms
 - Water Taxi
 - Capital Bikeshare
 - Metro Stop
 - Visitor Center

Water taxi to D.C. (The Wharf and Georgetown)

Tail Ship Providence & Senator John Warner Maritime Heritage Center opening in 2023

Water Taxi to National Harbor and Cruises to Mount Vernon

DEL RAY

To Del Ray Shopping and Dining

OLD TOWN NORTH

OLD TOWN ALEXANDRIA

WEST END

- Asin Beer Company
- Cameron Run Regional Park
- Port City Brewing Company

to **M** EISENHOWER AVE.

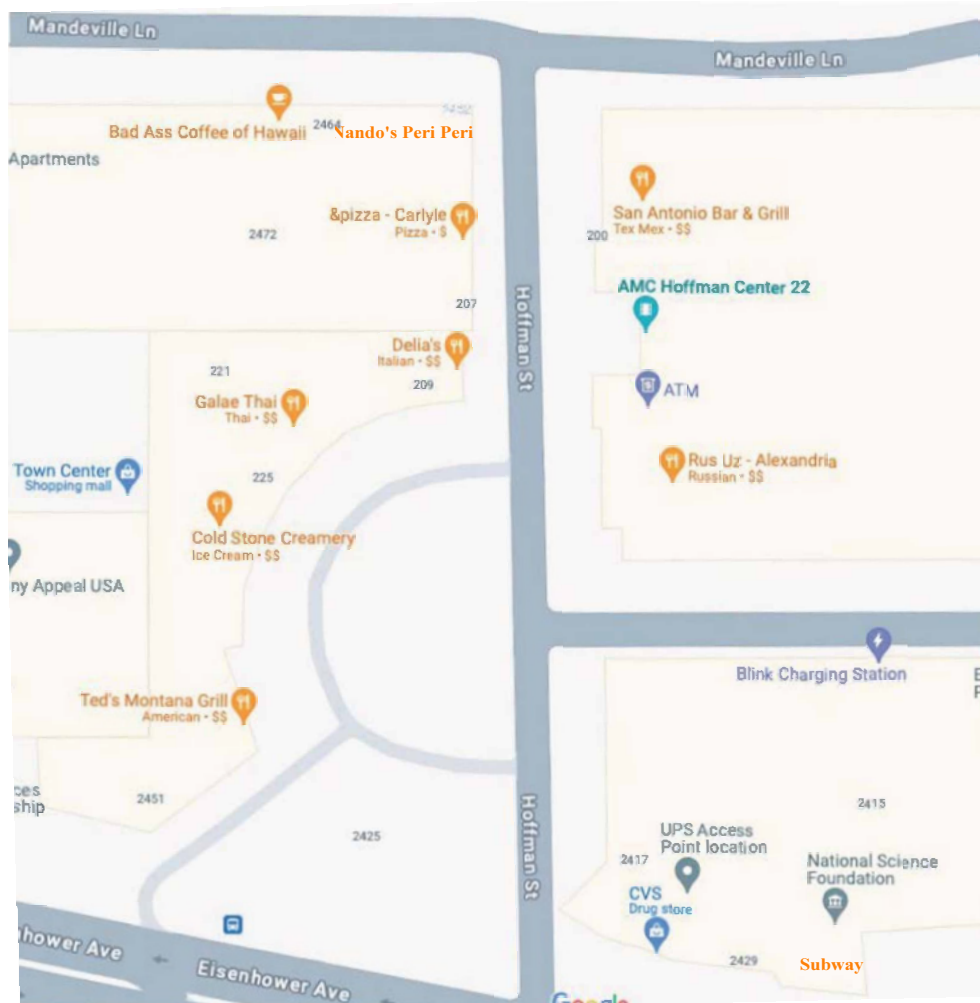
CARLYLE
National Inventors Hall of Fame (U.S. Patent and Trademark Office)

To **GW** Parkway

To **GW** Parkway

to **M** National Harbor

Restaurants for Lunch Near the NSF Building



1. Delia's Mediterranean Grill & Brick Oven Pizza: <https://www.deliasbrickovenpizza.com/menus/>
2. Galae Thai: <https://galaethai.com/>
3. Ted's Montana Grill: <https://www.tedsmontanagrill.com/menu.html> (slow service)
4. &pizza: <https://andpizza.com/menu/>
5. Nando's Peri Peri: <https://www.nandosperiperi.com/find/alexandria/>
6. Rus Uz: <https://rusuz.com/> (closed on Mondays)
7. San Antonio Bar & Grill: closed for lunch.
8. Subway

For lunch, we suggest smaller groups rather than larger groups for faster service.