The Ninth Annual

Ecology, Evolution, & Behavior

Research Symposium

ECOLOGY
EVOLUTION
BEHAVIOR

MICHIGAN STATE
UNIVERSITY

May 6, 2025
Michigan State University
Henry Center for Executive Development
3535 Forest Rd, Lansing, MI 48910

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This event made possible by:

Ecology, Evolution, and Behavior (EEB) Program
Elise Zipkin, EEB Director
Barbara Bloemers, EEB Grad Group (EGG) Advisor

EEB Research Symposium Planning Committee
Devin Lake, Co-Chair
Katrina Culbertson, Co-Chair
Esther Wong
Trip Hash

Welcome from the EEB Director

Welcome to the ninth annual Michigan State University Ecology, Evolution, and Behavior (EEB) Research Symposium! EEB serves as the intellectual home of our >200 core members. It is a place to be inspired, challenged, and surprised. Today's presentations by EEB's graduate students, postdocs, and faculty showcase the quality and breadth of research being conducted by our MSU community. The symposium, like other EEB events, are particularly important now, a time of uncertainty. I hope that each of you have a chance to connect with old friends and new colleagues during this all-day, interactive event.

Huge thank you to the EEB Graduate Group (EGG) and particularly to the symposium committee, co-chaired by Devin Lake and Katrina Culbertson, with members Esther Wong and Trip Hash, for their extraordinary work organizing this impressive event. As always, EEB secretary Barbara Bloemers has been heroic in her efforts to help EGG members organize this symposium. EEB's vibrant program is only possible through the hard work and service of our dedicated students, postdocs, and faculty.

The EEB program is funded through generous support from the Provost, the VP for Research and Innovation, the Graduate School, and the colleges of Natural Science, Agriculture and Natural Resources, and Engineering.

Thank you for attending the EEB symposium!

Elise Zipkin

Elise Zipkin, EEB Director

Social Media Policy

The twitter and social media policy is an opt-out policy. Unless the presenter of the poster or oral presentation states that you are not allowed to tweet/post about their work, it is considered allowed. If you are choosing to tweet, feel free to use the hashtag: #MSUEEB2025

Keynote Speaker

Dr. Francisco Dini-Andreote
Assistant Professor of Phytobiomes
Pennsylvania State University
https://dalab.psu.edu/

The Ecology of Suppressive Soils

We are excited to announce Dr. Francisco Dini-Andreonte as the keynote speaker for the 9th annual EEB Research Symposium! He studies the ecological and evolutionary processes that create and maintain microbial diversity. Fitting at the intersection of ecology and microbiology, Dr. Dini-Andreonte seeks to understand the implications of microbial diversity for ecosystem functioning.

Awards

The following awards will be presented:

Best oral presentation (1st, 2nd, 3rd)

Best poster (1st, 2nd)

Art in Science Prizes (Professional Judges Winner, 1st, 2nd Popular Choice)

Thank you to our judges:

Victor Aguiar de Souza Penha, Abby Beilan, Chris Blackwood, Stephanie Bristow, Sophie Buysse, Alexandra Castillo-Ruiz, Brittany Coppinger, Andrew Cortese, DeShae Dillard, Emily Dolson, Leah Dunlap, Andrew Eagar, Summer Eckhardt, Seyed Ali Eshtehardian, Cynthia Fiser, Olivia Fitch, Kadeem Gilbert, Lezhi Hao, Trip Hash, Chia Hsieh, Brooke Jeffery, Benjamen Kline, Chris Kozakiewicz, Devin Lake, Wendy Leuenberger, Sylvie Martin-Eberhardt, Jim Moran, Riley Pizza, Alanna Post, Bruna Rodrigues do Amaral, Alyssa Saunders, Alisha Shah, Olivia Smith, Lauren Sulivan, Carol Waldmann Rosenbaum, Alexa Warwick, Geoffrey Williams, Phoebe Zarnetske, Zehua Zhou

EEB Research Symposium Schedule Overview

(All events at the Henry Center)

Time	Event	Location
8:00 - 8:45	**Registration and Breakfast**	Entrance Lobby/Atrium
8:45 - 9:00	**Welcome & Opening Remarks** *Elise Zipkin, EEB director*	Auditorium
9:00 - 10:00	**Keynote Address** *Dr. Francisco Dini-Andreonte, Pennsylvania State University*	Auditorium
10:00 - 10:10	**Break**	
10:10 - 11:05	**Session I: Oral Presentations** **(Moderator: Katrina Culbertson)** 10:10 - Princess Abu (PLB) 10:25 - Seyed Ali Eshtehardian (CSE) 10:40 - Andrew Cortese (PSM) 10:55 - Emily Dolson (CSE) 11:00 - Victor Aguiar de Souza (IBIO)	Auditorium
11:05 - 11:15	**Break**	
11:15 - 12:00	**Session II: Oral Presentations** **(Moderator: Esther Wong)** 11:15 - Brittany Coppinger (IBIO) 11:30 - Santiago Rodriguez Castro (IBIO) 11:45 - DeShae Dillard (ENT)	Auditorium
12:00 - 1:00	**Lunch**	Atrium
1:00 - 1:25	**Community Engagement Session** **Journal Article Accessibility** *Led By: Olivia Smith*	Auditorium
1:25 - 1:35	**EEB Announcements and Art in Science Award** *Jamily Lorena Ramos de Lima and Jonah Branding*	Auditorium
1:35 - 1:40	**Break**	
1:40 - 2:40	**Poster Session/Mingling/Break** **Session 1 (1:40 - 2:10)** Chris Kozajiewicz (IBIO & KBS), Emily Bardwell (IBIO), Kadeem Gilbert (PLB, KBS, PRI), Karli Boer (IBIO), Josefa Corpuz (PLB), Narda Trivino (FOR), Kelly Waters (ENT), Michelle Volk (FW), Samantha Wescott (IBIO), Alexa Warwick (FW), Anna Weller (IBIO & MMG)	Atrium

	Session 2 (2:10 - 2:40) Olivia Fitch (IBIO), Lezhi Hao (IBIO), Mujahid Ali Shah (IBIO), Zahid Hasan Chowdhury (PSM), Alanna Post (GEO), Abigail Lipeprt (FW & MMG), Svea Hall (PLB), Zehua Zhou (IBIO), Isabella Rinaldi (IBIO & NEURO), Jamily Lorena Ramos de Lima (IBIO), Trey Ursillo (IBIO), Abby Beilman (EES)	Atrium
2:40 - 2:45	**Break**	
2:45 - 3:50	**Session III: Oral Presentations** **(Moderator: Devin Lake)** 2:45 - Rachel Drobnak (PSM & KBS) 3:00 - Lais Petri (PLB & IBEEM) 3:15 - Bruna Rodrigues do Amaral (IBIO) 3:30 - Ingo Braasch (IBIO & GGS) 3:35 - Alexandra Castillo-Ruiz (PSY & NEURO) 3:40 - Grace Smith-Vidaurre (IBIO & CMSE) 3:45 - Ashwini Ramesh (IBIO & IBEEM)	Auditorium
3:50 - 4:00	**Break**	
4:00 - 4:45	**Session IV: Oral Presentations** **(Moderator: Trip Hash)** 4:00 - Sophie Buysse (PLB & KBS) 4:15 - Sara Moledor (PLB) 4:20 - Andrew Eagar (PLB) 4:25 - Special Event with Elise Zipkin	Auditorium
4:45 - 5:00	**Awards** *Devin Lake & Katrina Culbertson*	Auditorium
5:00 - 6:30	**Happy Hour!**	Four Seasons Lounge

EEB Research Symposium Detailed Schedule

8:00-8:45	**Registration and Breakfast** Please arrive at the Henry Center in advance in order to check in and pick up your name tag. Refreshments will be provided.	Entrance Lobby
8:45-9:00	**Welcome & Opening Remarks** *Elise Zipkin, EEB director*	
9:00-10:00	**Keynote Address** **The Ecology of Suppressive Soils: Innovations for Sustainable Agriculture** *Dr. Francisco Dini-Andreote* *Assistant Professor of Phytobiomes at Penn State*	
10:00-10:10	**Break**	
10:10-11:05	**Session I: Oral Presentations** **(Moderator: Katrina Culbertson)**	
	Does the soil environment for seed stratification and early establishment affect spatial segregation of closely related plant species? Princess Abu, Graduate student Department of Plant Biology	abstract
	Sufficient information is sufficient for the evolution of cooperation Seyed Ali Eshtehardian, Graduate student Computer Science and Engineering	abstract
	The non-host with the most? Arbuscular mycorrhizal trees enhance diversity of ectomycorrhizal fungi in mixed temperate forests Andrew Cortese, Postdoc Department of Plant, Soil, and Microbial Sciences	abstract
	Research in the Evolutionary Control of Digital Ecologies Lab Emily Dolson, Faculty Computer Science and Engineering	abstract
	Housing vacancies shape patterns of bird disease in an urbanized landscape Victor Aguiar de Souza Penha, Postdoc Department of Integrative Biology	abstract

11:05 - 11:15	**Break**	
11:15 - 12:00	**Session II: Oral Presentations** **(Moderator: Esther Wong)**	
	Detecting complex information encoding in vocal signals: applying traditional bioacoustics analyses to synthetic vocalizations Brittany Coppinger, Postdoc Department of Integrative Biology	abstract
	Seeing Heat in Motion: How Pythons Track Prey Using Infrared Sensing Santiago Rodriguez Castro, Graduate Student Department of Integrative Biology	abstract
	Mapping the Mess of Diptera Ecology DeShae Dillard, Graduate Student Department of Entomology	abstract
12:00 - 1:00	**Lunch**	
1:00 - 1:25	**Community Engagement Session** **Journal Article Accessibility** Olivia Smith, Faculty Department of Horticulture	abstract
1:25 - 1:35	**EEB Announcements**	
	EEB Art in Science Award Announcement Jamily Lorena Ramos de Lima	
	EGG Positions Announcement Jonah Branding	
1:35 - 1:40	**Break**	
1:40 - 2:40	**Poster Session / Mingling** **Presenters will be available at odd numbered posters from 1:40 - 2:10pm, and at even numbered posters from 2:10 - 2:40pm**	
Poster 1	**Uncovering the ecology of wildlife diseases through genomics** Chris Kozakiewicz, Faculty Department of Integrative Biology	abstract
Poster 2	**Expression of posterior hox genes in the holostean fish spotted gar: implications for the hetero-to-homocercal caudal transition and vertebrate appendage evolution** Olivia Fitch, Graduate Student Department of Integrative Biology	abstract
Poster 3	**Assessing the genomic impacts of stocking on lake trout**	abstract

(*Salvelinus namaycush*) recovery in Lake Superior
Emily Bardwell, Graduate Student
Department of Integrative Biology

Poster 4 **Evolution of carotenoid-consistent integumentary colors in early diverged avian lineages** abstract
Lezhi Hao, Graduate Student
Department of Integrative Biology

Poster 5 **The Gilbert Lab: Studying symbiotic interactions in plants, and the traits that mediate them** abstract
Kadeem Gilbert, Faculty
Department of Plant Biology, Kellogg Biological Station

Poster 6 **Targeted ablation and regeneration of enteric nervous system neurons in zebrafish** abstract
Mujahid Ali Shah, Postdoc
Department of Integrative Biology

Poster 7 **Underground Economics: Soil Nitrogen Availability as a Control on the Plant-AMF Mutualism** abstract
Karli Boer, Graduate Student
Department of Integrative Biology

Poster 8 **Should plant-soil feedback be considered in the selection of crop rotation sequences** abstract
Zahid Hasan Chowdhurry, Graduate Student
Department of Plant, Soil and Microbial Sciences

Poster 9 **Soil Pathogens' Impact on the Germination of Prairie Plants** abstract
Josefa Corpuz, Graduate Student
Department of Plant Biology

Poster 10 **Forest recovery dynamics after the Gatlinburg wildfires in Tennessee, USA** abstract
Alanna Post, Graduate Student
Department of Geography

Poster 11 **The role of soil bacterial communities in the plant soil feedback effects on oak regeneration under red pine** abstract
Narda Trivino, Graduate Student
Department of Forestry

Poster 12 **Examining relationships between lake sampling efforts and community demographics** abstract
Abigail Lippert, Undergraduate Student
Department of Fisheries and Wildlife, Department of Microbiology, Genetics, and Immunology

Poster 13 **Seasonal microbial succession in beetles and soil during carrion decomposition** abstract
Kelly Waters, Graduate Student
Department of Entomology

Poster 14 **Correlation Between Shifts in Lobelia Species' Floral Morphology and Hybridization Risk Due to Sympatry** abstract
Svea Hall, Staff
Department of Plant Biology

Poster 15 **Evaluating the abilities of different sequencing technologies to characterize mixed-strain *Borrelia burgdorferi* infections to assess changes in temporal and spatial strain diversity** abstract
Michelle Volk, Graduate Student
Department of Fisheries and Wildlife

Poster 16 **Tracing fin evolution in T-box family genes** abstract
Zehua Zhou, Graduate Student
Department of Integrative Biology

Poster 17 **Acquisition of neurotoxin-producing bacteria by new hosts** abstract
Samantha Westcott, Graduate Student
Department of Integrative Biology

Poster 18 **Characterization of Enteric Nervous System Development in Spotted Gar (*Lepisosteus oculatus*)** abstract
Isabella Rinaldi, Undergraduate Student
Department of Integrative Biology, Department of Neuroscience

Poster 19 **Warwick Lab Poster** abstract
Alexa Warwick, Faculty
Department of Fisheries and Wildlife

Poster 20 **Evolution and diversification of duplicated genes after a genome duplication in the fish brain** abstract
Jamily Lorena Ramos de Lima, Graduate Student
Department of Integrative Biology

Poster 21 **Evolvability of Antibiotic Resistance** abstract
Anna Weller, Undergraduate Student
Department of Integrative Biology, Department of Microbiology, Genetics, and Immunology

Poster 22 **Assessing the effect of the urban fabric on avian species richness using community-science data** abstract
Trey Ursillo, Graduate Student
Department of Integrative Biology

Poster 23 **The Role of Shifts in Seasonality on Aquatic Carbon Cycling: A Comparative Study of Land Surface Phenology Datasets in Select U.S. Ecoregions** abstract

Abby Beilman, Graduate Student
Department of Earth and Environmental Sciences

Poster 24 **Into the weeds: a 2-year transplant of agricultural weeds** abstract

Robin Waterman, Graduate Student
Department of Plant Biology, Kellogg Biological Station

2:40 - 2:45 **Break**

2:45 - 3:45 **Session III: Oral Presentations**

(Moderator: Devin Lake)

On-farm assessment of prairie strip soil health across Michigan abstract

Rachel Drobnak, Graduate Student
Department of Plant, Soil and Microbial Sciences; Kellogg Biological Station

Antecedent climate effects on grassland productivity under disturbance and fertilization abstract

Laís Petri, Postdoc
Department of Plant Biology, IBEEM

Protecting birds in protected areas: a multi-scale analysis of landscape context and species occurrence abstract

Bruna Rodrigues do Amaral, Graduate Student
Department of Integrative Biology

I’m a Fish, You’re a Fish - That’s Terrific! On the Quest for our Fishy Ancestors abstract

Ingo Braasch, Faculty
Department of Integrative Biology, Genetics and Genome Sciences Program

Neurolabs going wild: studying the effects on a natural microbiota on brain and behavior development abstract

Alexandra Castillo-Ruiz, Faculty
Department of Psychology, Neuroscience Program

Animal vocal communication and data science research in the BIRDS Lab abstract

Grace Smith-Vidaurre, Faculty

Department of Integrative Biology; Department of Computational Mathematics, Science, and Engineering

Global quantification of plant species competitive ability along resource gradients abstract

Ashwini Ramesh, Postdoc

Department of Integrative Biology

3:45 - 4:00 **Break**

4:00 - 4:45

Session IV: Oral Presentations

(Moderator: Trip Hash)

Consistent selection across environments in two populations of *A. thaliana* abstract

Sophie Buysse, Graduate Student
Department of Plant Biology; Kellogg Biological Station

Root versus Fungi: How trees invest in growth may be determined by their mycorrhizal association abstract

Sara Moledor, Graduate Student
Department of Plant Biology

(A few of) the 2025 IBEEM fellows present: How do mycorrhizal trait-by-environment interactions shape density-dependent demographic processes in hardwood forests? abstract

Andrew Eagar, Postdoc
Department of Plant Biology

Special Event with EEB Director Elise Zipkin

4:45 - 5:00

Closing Remarks & Awards

Devin Lake and Katrina Culbertson
EEB Research Symposium Planning Committee

5:00 - 6:30 **Happy Hour!**
Please join us in the Four Seasons Lounge for happy hour

Henry Center Map

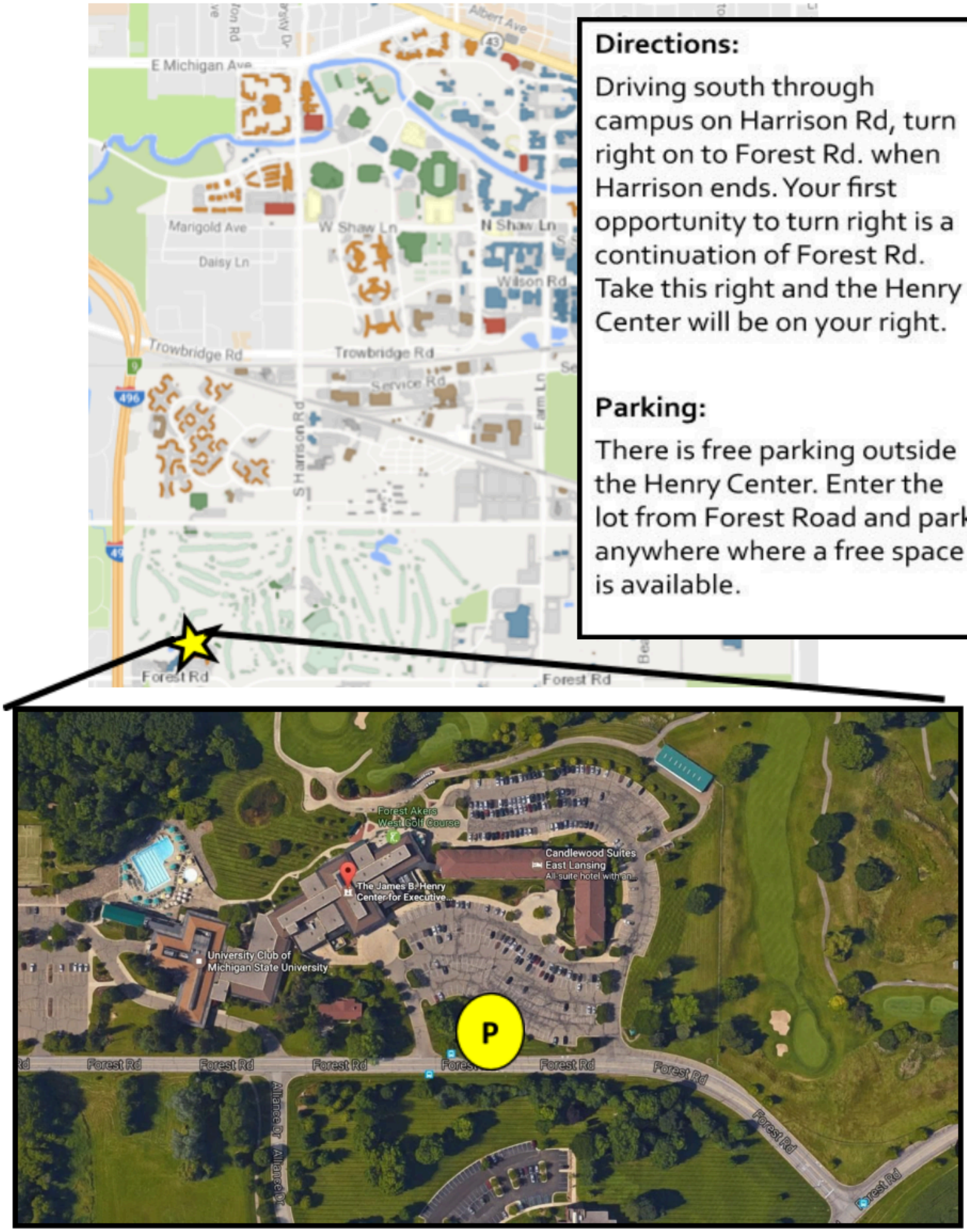
3535 Forest Rd, Lansing, MI (517) 353-4350

Directions:

Driving south through campus on Harrison Rd, turn right on to Forest Rd. when Harrison ends. Your first opportunity to turn right is a continuation of Forest Rd. Take this right and the Henry Center will be on your right.

Parking:

There is free parking outside the Henry Center. Enter the lot from Forest Road and park anywhere where a free space is available.



Henry Center Lunch Menu

Garden Salad Bar

Romaine, Iceberg, Tomatoes, Cucumber, Garbanzo Beans, Sunflower Seeds, Cottage Cheese (D), Bacon, Feta Cheese (D), Banana Peppers

Dressings: Greek Dressing, Ranch (E, D, Soy), Raspberry Vinaigrette, Olive Oil, Balsamic Vinegar

Breads & Spreads

Greek Salad

Hummus (Soy), Pita Bread (W, D), Mini Rolls, Butter

Hot Buffet

Grilled Chicken Thighs Shawarma

Baked Cod with Oregano, Tomato, Olives, Olive Oil

Spanakopita (W, D)

Mediterranean Rice (W)
Baked Squash Medley with Peppers, Onion, Green Beans, Olive Oil, and Herbs

Tzatziki Sauce (D), Tahini Sauce, Sesame Seeds

Desserts & Beverages

Baklava (W, D, Nuts)

Lemon Leche Cake (E, D, Soy, W)

Regular coffee, decaf, tea service

Allergen Guide: W - Wheat, E - Eggs, D - Dairy

Abstracts

Alphabetical by the presenting author's last name.

Does the soil environment for seed stratification and early establishment affect spatial segregation of closely related plant species?

Princess H. Abu, Chris B. Blackwood, and Andrea L. Case

Plant Biology

Shared ancestry of closely related plant species should increase niche similarity. When closely related species are spatially segregated at any scale, it begs investigation of the mechanisms responsible. Lobelia cardinalis and Lobelia siphilitica (Campanulaceae) are closely related North American wetland species with similar habits and overlapping geographical ranges. They are often found in shared habitats, but typically spatially segregated on a local scale—sometimes as little as ~10m apart. We hypothesized that seeds of coexisting L. cardinalis and L. siphilitica disperse into each other's habitat even when they co-occur on a small scale (<50 meters), but that species-specific soil conditioning constitutes an ecological filter that inhibits the germination and establishment of heterospecifics, maintaining spatial segregation. We specifically predicted that soil from heterospecific patches would inhibit germination compared to conspecific soil.

We conducted a seed germination study that separated the effects of conspecific and heterospecific soil conditioning during cold-stratification and seedling recruitment. First, we cold-stratified seeds of both species in soil-free conditions as well as in conspecific-conditioned and heterospecific-conditioned field soil collected from 8 natural population sites. We then planted seeds from each stratification treatment onto potting soil as well as conspecific-conditioned and heterospecific-conditioned field soil. Germination was recorded over 10 weeks and statistical analyses were done to assess the effects of stratification environment, recruitment environment, and their interaction on germination success. Heterospecific seeds emerged from natural seed banks sampled beneath both species, indicating that seeds do disperse between patches. In the experiment, seeds of both species germinated best when stratified soil-free and planted in potting soil. Conditioned field soil reduced seed germination of both species, but was especially strong in L. siphilitica and more pronounced during cold-stratification. However, contrary to our predictions, seeds of L. siphilitica germinated better when stratified in L. cardinalis-conditioned soil than it did when in soil conditioned by conspecifics. We conclude that seed–soil interactions may not be a major factor inhibiting the recruitment and establishment of heterospecific seeds post-dispersal, and that negative plant–soil feedback strongly affects germination in these species. Consistent spatial segregation at local scales may be maintained by factors later in the life cycle.

Housing vacancies shape patterns of bird disease in an urbanized landscape

Victor Aguiar de Souza Penha, Kevin McGraw, and Mathieu Giraudeau

Integrative Biology

Wildlife health is shaped by many environmental factors, including anthropogenic activities (e.g. pollution, habitat alteration). Urban influences may also include direct or indirect human social constructs, including racial or economic inequities that shape how urban areas are developed or occupied. The Great Recession of 2007-2009 had a major impact on mortgage lending in the USA and led to a massive increase in housing foreclosures and vacancies. This provided a 'natural experiment' to investigate how a dramatic shift in housing occupancy affected health patterns in a widespread backyard-bird species (house finch, Haemorhous mexicanus). We examined several human social and economic predictors (e.g. human population change, median household income, housing density, % vacant households) of disease (a protozoan gut parasite) in house finches from the desert southwestern United States (Phoenix, Arizona) in 2010-2011. We found that birds were less heavily parasitized in areas with more housing vacancies. This result suggests that relaxing human-development/-occupancy constraints on wildlife can provide real-time health and survival benefits to backyard birds.

Assessing the genomic impacts of stocking on lake trout (Salvelinus namaycush) recovery in Lake Superior

Emily Bardwell, Ben Kline, Erin Collins, Nadya Mamoozadeh, and Mariah Meek

Integrative Biology

Lake trout (Salvelinus namaycush), a native keystone species of the Great Lakes, is essential to the region's ecology, economy, and culture. However, the population collapsed in the 1950s, leading to a decline in genetic and phenotypic diversity. Hatchery stocking has supported recovery in Lake Superior, but its genetic impacts remain uncertain. Of particular concern is the potential introgression of splake, a brook trout-lake trout hybrid stocked since the 1970s. While splake are not expected to reproduce naturally, previous studies suggest they may interbreed with wild lake trout, posing a risk to the genetic integrity of these native trout. This study investigates the extent and effects of splake introgression in lake trout across the U.S. portion of Lake Superior using restriction-site associated DNA sequencing (RAD-seq). We will identify whether and where introgression is occurring and assess its impact on genetic health. Additionally, we will analyze our dataset to clarify the genetic influence of stocked domestic lake trout on wild populations. As lake trout face modern environmental challenges, understanding the distribution of genetic diversity will be crucial for effective management. Our findings will inform strategies to protect the species' genetic integrity and ensure the long term viability of Lake Superior's lake trout populations.

The Role of Shifts in Seasonality on Aquatic Carbon Cycling: A Comparative Study of Land Surface Phenology Datasets in Select U.S. Ecoregions

Abby M Beilman and Kelly S Aho
Earth & Environmental Science

Projections indicate that the duration and timing of seasons will shift as climate change progresses. As such, processes mediated by seasonality will likely experience changes as well. Situated within terrestrial landscapes, inland waters represent one key ecosystem impacted by these potential shifts. Prior literature has observed the relationship between seasonal change and generic organic matter cycling in these ecosystems. The more specific relationship of land surface phenology and aquatic carbon cycling, however, is not as consistently examined. Here, we seek to evaluate and compare three remotely sensed land surface phenology datasets: NEON's phenocam, National Phenology Network's phenology indices, and NPP Land Surface Phenology (Land Cover Dynamics) derived from NASA's VIIRS. Specifically, we will examine watershed-scale phenology dynamics around NEON aquatic sites, focusing on one site per major United States ecoregion. Through comparison of these products to each other and to changes in biogeochemical data from the NEON aquatic sites (dissolved carbon dioxide and methane), we seek to determine the most suitable product for understanding phenology-carbon cycling dynamics in the face of a changing climate. This poster examines a subset of these results for relationship validation and product selection. We expect that this study as a whole will elucidate drivers of aquatic carbon cycling at a country-wide scale, and provide insights into what interactions between phenology and climate change mean for the future of freshwater aquatic ecosystems.

Underground Economics: Soil Nitrogen Availability as a Control on the Plant-AMF Mutualism

Karli L. Boer, Sophia R. Burke, and James J. Moran
Integrative Biology

Arbuscular mycorrhizal fungi (AMF) can facilitate enhanced plant nutrient acquisition, leading to increased growth. However, plant response to AMF colonization yields inconsistent results, highlighting critical knowledge gaps in our comprehensive understanding of this symbiosis. These inconsistencies, framed in the parasitism-to-mutualism continuum, underscores the need to identify controls on plant-carbon allocation to AMF and its dependence upon reciprocal AMF nutrient exchange. We undertook a greenhouse experiment with manipulated nitrogen availability and used stable isotope tracers to quantify bidirectional (plant to AMF and AMF to plant) exchange of plant-derived carbon for AMF-harvested soil nitrogen. We hypothesize that under nitrogen deficient conditions, plants will increase carbon allocation to AMF and AMF will in turn increase nitrogen harvest resulting in elevated nitrogen transfer to the plant.

In this greenhouse experiment, winter wheat (var. Jupiter) was grown in split-pots with AMF (Mycobloom ® and soil inoculum), with plant roots confined to one half of each pot whilst AMF retained full pot access. Nitrogen was either supplied on the no-plant side, or on both the plant and no-plant side with a full mixture of all other essential nutrients applied to all half-pots, ensuring nitrogen was the only limiting nutrient. Height data revealed that different treatments confirmed nitrogen limitations in half-pots that received nitrogen-deficient fertilizer. Further, preliminary stable isotope results demonstrate effective AMF-transfer of nitrogen to the host plant. Measurements in progress will quantify the carbon and nitrogen exchange rate for the plant-AMF interaction and even identify plant impacts on the associated prokaryotic community.

I'm a Fish, You're a Fish - That's Terrific! On the Quest for our Fishy Ancestors

Ingo Braasch

Integrative Biology, Genetics and Genome Sciences

In this presentation, I will offer an overview of the research conducted in the MSU FishEvoDevoGeno Lab [http://www.fishevodevogeno.org], which seeks to unravel the evolutionary origins of humans from our fish ancestors. Through the integration of comparative genomics, developmental biology, and functional genetics, our work strives to reconstruct the last common ancestor of bony vertebrates—a fish that lived approximately 450 million years ago. Over the past decade, our analyses of the spotted gar (Lepisosteus oculatus), a “living fossil” fish, have uncovered the genomic and anatomical foundations of key features in vertebrate evolution, including the visual system, limbs, skeleton, teeth, and other body structures. These findings challenge long-standing theories about innovations specific to the tetrapod lineage and reveal the intricate histories of gene families across vertebrate evolution.

Consistent selection across environments in two populations of A. thaliana

Sophia F. Buysse, Jeffrey K. Conner, and Emily B. Josephs

Plant Biology, Kellogg Biological Station

Abiotic environments can be strong selective forces on plant communities. Plant populations have evolved to escape or avoid drought. However, environmental shifts due to climate change may alter selective forces. In this study, I investigate selection on drought-related traits and on plasticity of those traits in two locally adapted populations of A. thaliana in a cool, wet chamber common garden and a hot, dry chamber common garden. A. thaliana from Italy escape drought by flowering earlier and investing less in vegetative growth. In contrast, genotypes from Sweden avoid drought by flowering later and investing more in vegetative growth. We find that despite these different drought strategies, selection in both treatments and both populations is for plants that flower earlier and have more vegetative growth. These results suggest environmental shifts may not shift the optimum flowering time or vegetative investment, and plant populations already well-adapted to their environments may continue to persist through environmental shifts.

Neurolabs going wild: studying the effects of a natural microbiota on brain and behavior development

Alexandra Castillo-Ruiz

Psychology, Neuroscience Program

All mammals evolved in a world teeming with microbes, so it is not surprising that the microbiota (the collection of microorganisms living in/on us) influences many aspects of mammalian physiology. Recently, I demonstrated that effects of the microbiota extend to brain development in standard lab mice. However, the microbiota of these animals is far from ‘natural’ as it has been curated to be pathogen-free and shows less diversity than that of wild mice. Remarkably, colonizing lab mice with a natural (wild) microbiota alters their response to immune challenges in adulthood and may confer a survival advantage. The contributions of a naturally-occurring microbiota to brain and behavior development are unknown. Therefore, research in my newly formed lab will tackle this question by comparing genetically identical mice harboring a wild vs. a lab microbiota. This work represents a novel intersection of multiple disciplines including developmental neuroscience, microbiology, and ecology. In addition, the work will inform the scientific community, beyond neuroscience, of the potential pitfalls inherent in using animal models with curated/sanitized microbes to understand how the “real” world works.

Should plant-soil feedbacks be considered in the selection of crop rotation sequences?

Md Zahid Hasan Chowdhury, Pedro M. Antunes, Teresa Dias, Christopher B. Blackwood, Brook J. Wilke, Christopher W. Fernandez, Catherine Fahey, and Akihiro Koyama

Plant, Soil and Microbial Sciences

Plant-soil feedback (PSF) can be a major driver of plant performance in communities. This ecological mechanism can be used to refine the selection of crop rotation sequences to maximize agricultural yields via nutrient use optimization, pathogen reduction, and enhancement of mutualisms between crops and microbes. Yet, PSF has been rarely considered to determine crop rotation sequences. We conducted a greenhouse experiment using soil collected from an agricultural field in northern Ontario, Canada, to investigate if the biomass of four major crops commonly cultivated in rotation (canola, maize, soybean, and wheat) varied through PSF. We trained soil by growing each of the four crops in a ‘training phase’, and then reciprocally planted the four crops in the trained soils in a ‘feedback phase’.

PSF for each crop was calculated by comparing the total biomass of each crop grown in soils trained by each of the three other crops (i.e., in rotation) against the total biomass in self-trained soil (i.e., monocropping). PSF values varied among the training-feedback crop combinations, ranging from -21% (wheat after maize) to +22% (soybean after maize). These results indicate that assessing PSFs under controlled conditions can serve as a basis for determining the most productive and sustainable crop rotation sequences. We are initiating a new study using the same four crops to test if we can observe similar PSFs when using different soil collected from an agriculture field at the W. K. Kellogg Biological Station (Michigan State University) where the greenhouse results will be validated in the field trial.

Detecting complex information encoding in vocal signals: applying traditional bioacoustics analyses to synthetic vocalizations

Brittany A. Coppinger, Summer G. Eckhardt, Arlena Cross, Raneem Samman, G. Alexandra Juárez, Vanessa Ferdinand, and Grace Smith-Vidaurre
Integrative Biology

Some animals capable of vocal learning can encode group and individual identity information in their vocalizations. Quantifying such identity information can yield new discoveries about the functions of vocal learning for social recognition. However, the accuracy with which bioacoustics tools detect the complex information that animals can encode in vocalizations over more than one social level is difficult to assess with empirical datasets. Synthetic vocalizations are a powerful tool to test the accuracy of bioacoustics analyses for detecting complex vocal information encoding. We generated synthetic vocalizations with group and individual identity information encoded in frequency modulation patterns, or changes in frequency over time that animals are expected to modify via learning. We created character strings to represent frequency modulation, used musical notation to convert strings to frequency values, and built an R package, paRsynth, that interfaces with other packages to produce synthetic vocalizations. We performed experiments to test how well a clustering pipeline that relied on spectrographic cross-correlation, a traditional bioacoustics tool to quantify acoustic similarity, could detect varying amounts of identity information encoded over two social levels, as well as over social conditions expected to influence the uniqueness of identity information. We found that the accuracy of this analytical pipeline for detecting complex information encoding varied with the amounts of information originally encoded, as well as with social conditions that influenced the distinctiveness of vocalizations at each social level. These findings are important for future empirical and computational work on how learned vocal information encoding may facilitate social recognition.

Soil Pathogens' Impact on the Germination of Prairie Plants

Josefa Corpuz and Lauren Sullivan

Plant Biology

Plants' interactions with soil microbial communities can create plant-soil feedbacks (PSFs). These PSFs in turn drive plant community composition. However, little is known about PSFs' effects on seed germination or the community composition of soil microbes during plants' seed stage. Germinating seeds and seedlings are particularly susceptible to fungal seed-borne and soil pathogens. We conducted a multi-factor PSF experiment to test the impact of soils with different pathogen loads on seed germination for eighteen plant species native to Midwestern prairies and two species of agricultural interest. Our results confirm the importance of PSFs during a plant's seed stage. These results are an example of the complex interactions between plants at early life stages and their surrounding microbiota, and could have implications for ecological restoration efforts.

The non-host with the most? Arbuscular mycorrhizal trees enhance diversity of ectomycorrhizal fungi in mixed temperate forests

Andrew M. Cortese, Sara M. Moledor, Andrew E. Eagar, Kurt A. Smemo, Richard P. Phillips, and Chris B. Blackwood

Plant, Soil and Microbial Sciences

Communities of ectomycorrhizal (ECM) plants and fungi are intimately linked, and their diversity is often positively related. Temperate deciduous forests are comprised of a mosaic of ECM trees and arbuscular mycorrhizal (AM) trees, in which ECM-dominated patches often exhibit reduced nitrogen cycling while AM patches exhibit elevated nitrogen cycling rates. Because ECM fungi are both taxonomically and functionally diverse, and exhibit differential abilities to access organic nitrogen, they can be susceptible to elevated levels of mineral nitrogen. The influence of AM trees on ECM fungi in mixed AM-ECM forests has remained unexplored, but in these forests the diversity of ECM fungi may be enhanced by the dominance of ECM trees in patches. In our study, we tested the influence of AM, ECM, and combined AM-ECM tree diversity, as well as ECM dominance and soil characteristics, on the functional and taxonomic diversity of ECM fungi sequenced from soils and tree roots. We used linear mixed-effects models and multivariate tests to identify the drivers of ECM fungal diversity and composition across three mixed AM-ECM forests in the Adirondack Mountains, NY. We found some support for ECM dominance enhancing ECM fungal diversity, but most interestingly found that the diversity of non-host AM trees had a much greater effect on ECM fungal diversity than ECM host tree diversity. We also found negative effects of soil nitrogen on ECM fungal diversity. Our results suggest that non-host interactions are important for structuring ECM fungal communities, but manipulative experiments are needed to determine the mechanisms driving these relationships.

Mapping the Mess of Diptera Ecology

DeShae Dillard, Douglas A. Landis, and Hannah J. Burrack

Entomology

Diptera, among the most abundant and diverse of insect orders, offer the distinct opportunity to serve as a biomonitoring tool for the conservation of ecosystem services in agriculture. However, the limited understanding of Diptera ecology in agricultural systems hinders the effective adoption of this approach. To address this gap, we functionally trait-mapped all 122 Diptera families in North America according to diet for both larval and adult life stages. Diet was categorized by ten feeding guilds: 1) Phytosaprophage, 2) Necrophage, 3) Coprophage, 4) Microbivore, 5) Herbivore, 6) Parasitoid, 7) Predator, 8) Parasite, 9) Nectivore, and 10) Hematophage. Each feeding guild can be further classified under key insect-mediated ecosystem services in agriculture, including decomposition, herbivory, biological control, and pollination. As anticipated, many Diptera exhibit multifunctionality, occupying multiple feeding guilds and contributing to multiple ecosystem services segregated by life stage. For example, Syrphid larvae are generalists that facilitate decomposition, herbivory, and biological control, while adults specialize in pollination. Other Diptera, such as Sciaridae, are larval specialists that function solely in decomposition. Our findings suggest that a functional understanding of Diptera families can inform agricultural management. Sampling conducted in 2023 and 2024 suggests Sciaridae may be influenced by nitrogen cycling, namely nitrogen fixation and fertilizer application. By understanding the ecological role of Diptera in agriculture, we can develop sustainable management practices and enhance agroecosystem resilience through holistic biomonitoring of insect-mediated ecosystem services.

Research in the Evolutionary Control of Digital Ecologies Lab

Emily Dolson

Computer Science and Engineering

In contexts ranging from cancer to evolutionary computation (evolution-inspired machine learning algorithms), steering the course of evolution is important. However, it is also challenging, particularly, when there are also complex ecological interactions among the evolving population(s). My lab works on this problem via a combination of theory, in silico experiments, and collaborations with wet lab biologists. In this talk, I will give a quick overview of our most recent work.

On-farm assessment of prairie strip soil health across Michigan

Rachel Drobnak and Christine Sprunger
Plant, Soil and Microbial Sciences; Kellogg Biological Station

Farmers care about improving soil health by using conservation practices; however, there is a lack of research assessing the effectiveness of conservation practices on soil health across environmental and management conditions, making successful implementation difficult (Irvine et al., 2023). Many experiments on agricultural conservation practices take place under specific soil type or crop management conditions, limiting the usefulness of results. In contrast, on-farm studies are conducted on privately-operated farms, and include a wider set of conditions. On-farm studies include more statistical noise but can provide useful insight for a wider range of farm types. Prairie strips (zones of perennial polyculture vegetation integrated within and around row crop fields) are one of many edge-of-field (EOF) conservation practices (practices which install perennial vegetation adjacent to the cropland) with more field station research than on-farm research. Prairie strips increase plant biodiversity, which has been shown to enhance soil biological activity and soil carbon sequestration (Sprunger et al., 2020; Martin & Sprunger, 2022). Little is known, however, about their impact on soil health outside of experimental site conditions. This study uses prairie strips and perennial buffer strips to answer two questions, (1) How do EOF practices alter soil health on working farms? and (2) Do prairie strips alter soil health differently than other EOF practices? To answer these questions, 8 Michigan farms with EOF practices were soil sampled July 2023. Farms differed in their management and environmental conditions, allowing us to assess how soil health metrics respond to EOF practices.

(A few of) the 2025 IBEEM fellows present: How do mycorrhizal trait-by-environment interactions shape density-dependent demographic processes in hardwood forests?

Andrew C. Eagar, Bailey H. McNichol, Sarah E. Neumann, Christopher B. Blackwood, and Rich K. Kobe
Plant Biology

Conspecific density dependence (CDD), where tree seedling demography is influenced by the proximity of conspecific adults, affects temperate hardwood forest biodiversity and ecosystem function. While generalizing CDD outcomes among trees is challenging due to intrinsic species differences, grouping trees by their mycorrhizal type (arbuscular or ectomycorrhizal) can make trends more apparent. These mutualisms between plant roots and fungi contribute to density-dependent interactions by enhancing nutrient access, defending against pathogens, or supporting seedling establishment. Different mycorrhizas tend to facilitate dichotomous CDD outcomes, with arbuscular mycorrhizas generating negative CDD between seedlings and adults and ectomycorrhizas generating positive CDD. However, in situ studies of CDD in forested ecosystems are rare because of the logistically challenging spatial and temporal scales governing forest demographic processes. For postdocs with limited funding and time, these challenges are especially problematic.

The Institute for Biodiversity, Ecology, Evolution, and Macrosystems (IBEEM) at MSU is helping overcome these challenges in studying forests at broad spatiotemporal scales by funding a collaborative effort between the departments of Forestry, Plant Biology, and Plant, Soil, and Microbial Sciences. Thanks to IBEEM's support, a serendipitous research idea has quickly become reality. Leveraging a 26-year dataset tracking the demographic success of ten Michigan tree species along a forested resource gradient, our IBEEM team is studying CDD in arbuscular and ectomycorrhizal trees in a global change context. Using spatially explicit models at both the species and community level, we will show how mycorrhizas mediate CDD in a generalizable framework for studying temperate forests under global change.

Sufficient information is sufficient for the evolution of cooperation

Seyed Ali Eshtehardian and Chris Adami

Computer Science and Engineering

Whether or not cooperation is an evolvable trait has been the subject of much discussion in evolutionary theory. Evolutionary game theory has suggested that cooperation is selected for if the genotype of a player is correlated with the phenotype of its opponent. This "inclusive fitness theory" has been criticized because it breaks down if fitness effects are non-additive. Here we present a new approach based on communication theory that shows that cooperation is selected for if the information that a player has about the opponent's phenotype exceeds the cost-to-benefit ratio of the game. We present numerical simulations of the iterated Prisoner's Dilemma (iPD) in which a player's strategy can evolve to take into account the opponent's previous move. We validate our theory for different cost/benefit ratios and establish the minimum amount of information that a player must have for cooperation to be beneficial. The new theory generalizes Queller's inclusive fitness rule by replacing covariance/variance by information/entropy, respectively. Because information is a non-additive concept, the theory also escapes the criticisms directed at inclusive fitness theory, and establishes that cooperation fundamentally depends on communication that distinguishes cooperators from defectors.

Expression of posterior hox genes in the holostean fish spotted gar: implications for the hetero-to-homocercal caudal transition and vertebrate appendage evolution

Olivia E. Fitch, Alexandra Stapleton, Rachel Alcorn, Brett L. Racicot, Camilla Peabody, and Ingo Braasch

Integrative Biology

The hetero-to-homocercal caudal fin transition in fish evolution has been of interest to vertebrate anatomists, paleontologists, and functional morphologists for nearly two centuries. Posterior Hox B & C cluster genes have been proposed to play a role in homocercal caudal fin development, but the role that these genes play during heterocercal caudal fin development has yet to be studied. We investigate hox gene expression in the heterocercal spotted gar to gain insight into the ancestral condition. We found that posterior Hox B & C genes express during heterocercal caudal fin development and through crucial comparisons between spotted gar and zebrafish, we propose that hoxc13a has been neo-functionalized for homocercal caudal fin development. Additionally, we identified a modular expression of posterior hox genes throughout the appendages of spotted gar. This study contributes the first comprehensive look at posterior hox gene expression in a heterocercal fish filling in an important evolutionary gap necessary to understand the hetero-to-homocercal transition. Through this work, we have established spotted gar as a model for future functional and genomic studies to understand hox gene regulation in vertebrate appendages.

The Gilbert Lab: Studying symbiotic interactions in plants, and the traits that mediate them

Kadeem J. Gilbert

Plant Biology, Kellogg Biological Station, Plant Resilience Institute

We are ecologists, evolutionary biologists, molecular biologists, and plant ecophysiologists interested in plant biotic interactions, the diversity of plant traits, and how those traits regulate their interactions with other organisms. We are excited by plant symbioses, the biology of carnivorous plants, and physiological traits of leaves that alter microenvironmental conditions, among other things.

Correlation Between Shifts in Lobelia Species' Floral Morphology and Hybridization Risk Due to Sympatry

Svea Hall, Andrea Case, and Chris Blackwood

Plant Biology

In North America, the genus Lobelia includes 24 closely related and morphologically similar species. These species usually have high degrees of overlap in both reproductive seasons and geographic range; often with five or more species at a sympatric field site observed flowering concurrently. Closely related species are not expected to coexist if they are similar enough to hybridize; hybrids are often less fit than their parents, so species that continue to waste reproductive resources with frequent hybridization would likely be less competitive. The fact that these Lobelia species have persisted in sympatry, despite their similarity and lack of geographic and temporal isolation, suggests the existence of another isolating mechanism preventing hybridization. It is possible that sympatric populations of Lobelia species have faced selective pressure to diverge morphologically from their close relatives to avoid cross-pollination and subsequent hybridization. To test this, I investigated the effect of calculated sympatry on 3D floral morphological traits, categorized as true size traits, pollinator attraction-related traits, and pollinator access-related traits. I measured over 50 floral structure- and shape-related morphological traits from almost 300 Lobelia flowers representing over 20 North American species. My results indicated that Lobelia floral size, attraction, and access traits were all always very strongly affected by an increase in the degree of calculated sympatry.

Evolution of carotenoid-consistent integumentary colors in early diverged avian lineages

Lezhi Hao, Kevin J. McGraw, and Victor Aguiar de Souza Penha
Integrative Biology

Carotenoid pigments generate bright colors in the integuments of many birds, with ketocarotenoids giving primarily red and orange colors and xanthophylls giving yellow colors. Because carotenoids cannot be synthesized by birds and exclusively come from diet sources, the ability to metabolize dietary carotenoids into ketocarotenoids is a crucial evolutionary pathway for creating a new repertoire of avian coloration. Compared to modern lineages such as Passeriformes, less is known about the evolution of carotenoid-consistent colors in older clades where bright red, orange, and yellow integuments first occurred in living birds today. In this study we characterize and compare the distribution of xanthophyll- and ketocarotenoid-consistent colors in different parts of the integument (e.g. plumage, bill, facial skin, legs) of all species in the two basal clades on the avian phylogenetic tree (Palaeognathae and Galloanserae) by visually color-scoring photos, scientific illustrations, and text descriptions from Birds of the World, supplemented with pigment analyses using High Performance Liquid Chromatography (HPLC) and reflectance spectroscopy, and known evidence of carotenoid presence from the existing literature. Then we test the following hypotheses in these two ancient lineages: 1) Diverse color mechanisms beyond ketocarotenoids underlie red and orange integumentary colors; 2) Carotenoid coloration of plumage is a rare ancient avian trait that transitioned from carotenoid coloration in bare parts; 3) Ketocarotenoid colors evolved later than xanthophyll colors; and 4) Carotenoid coloration in these lineages is driven by sexual selection. We aim to shed light on how carotenoid-consistent colors in different integuments first evolved in the early evolutionary history of modern bird lineages.

Uncovering the ecology of wildlife diseases through genomics

Christopher P. Kozakiewicz
Integrative Biology, Kellogg Biological Station

Presenting lab poster

Examining relationships between lake sampling efforts and community demographics

Abigail L. Lippert, Kendall Ash, Patrick Hanley, Xinyu Sun, Patricia A. Soranno, and Kendra Spence Cheruvelil
Fisheries and Wildlife, Microbiology and Molecular Genetics

Lakes provide numerous ecosystem services such as drinking water, recreation, natural habitat, climate control, and aesthetic enjoyment. Lakes have been shown to reduce stress and provide physical health benefits such as decreased risk of cardiovascular issues, obesity, and cancer. Previous studies on environmental justice (EJ) have shown that there is unequal distribution, quality, and monitoring of lakes in communities of color. However, there is limited research examining who is sampling lakes in various communities, and how this may be impacted by lake accessibility.

Combining data from the LAGOS-US research platform, USGS, US Census Bureau, and Global Biodiversity Information Facility, we study how community demographics interact with lake accessibility. We developed an open access data module, LAGOS-US HUMAN, which assigns demographic information from the US Census and accessibility metrics (boat launches, bus stops, public trails, and public land) from USGS and USDOT to all 479,950 lakes > 1 ha in the conterminous US. Using hierarchical generalized linear models, we are studying how different demographic makeups of lake communities influence the likelihood of the lake having accessible features. We are also using fish sampling data from the Global Biodiversity Information Facility and sampling organization data from LAGOS-US LIMNO to assess patterns in lake sampling. This can help us understand and address biases in lake sampling patterns that may negatively impact marginalized communities. This research is an important contribution to the conversation of equal access to natural resources in the United S

Roots versus Fungi : How trees invest in growth may be determined by their mycorrhizal association

Sara M Moledor, Andrew Eagar, Kurt Smemo, Elizabeth Huenupi, Oscar Valverde-Barrantes, Richard P Phillips, and Christopher B Blackwood

Plant Biology

Trees may not be mobile but their investment in belowground growth is responsive to soil heterogeneity. Upon encountering a nutrient hotspot, a tree may optimize nutrient capture via root proliferation or by changing root architecture. Alternatively, a tree may invest in mycorrhizal symbionts, the hyphae of which are very adept at accessing physically or chemically out-to-reach nutrients. Similarly, a tree may prioritize investment in roots vs fungi following a physical disturbance (think: tree fall, burrowing mammals). For this study, we aim to detect such functional complementarity– not just at the tree species level - but at the tree community level and we predict that the particular root vs fungal strategy is strongly coordinated with mycorrhizal dominance (arbuscular or ectomycorrhizal).

To do this, we utilize arbuscular- and ectomycorrhizal- dominated plots in three temperate forests in the northeast United States over several years for spatial and temporal resolution. In-growth cores allow us to measure how fungal accumulation, fine root accumulation, and fine root traits respond to nutrient enrichment and disturbance. In soil cores from ECM tree communities, which are typically nutrient-depleted, we predict a strong response to fertilization and disturbance via hyphal proliferation. In cores from AM tree communities, we predict soil nutrient saturation will diminish foraging responses in both roots and hyphae and that recovery post-disturbance will be primarily root-oriented. A tree community's preferential investment in roots vs fungi represents microscale observations that have macroscale consequences, such as forest carbon sequestration and nutrient cycling, and may refine climate change modeling.

Antecedent climate effects on grassland productivity under disturbance and fertilization

Laís Petri, Eric Seabloom, Drew Peltier, and Lauren L. Sullivan
Plant Biology, IBEEM

Past environmental conditions and landscape modifications can shape the present and future dynamics of ecological communities and the functions they provide. Still, there is little understanding of how past events and conditions experienced by grassland communities differentially influence changes in their productivity over time. We addressed this research gap by using long-term plant data of a temperate grassland experiencing a full factorial manipulation of nutrient addition and disturbance at Cedar Creek Ecosystem Science Reserve to ask (1) over what time scales do previously experienced precipitation and temperature influence grassland biomass and litter production, and (2) how these antecedent conditions vary among initial disturbance event and levels of nutrient addition. To address these questions, we built a stochastic antecedent model to estimate both yearly and seasonal effects of past climate data up to two years prior on these experimental grasslands. Our findings reveal that weather conditions in the current year and the preceding year are the most influential on grassland productivity under low nutrient levels. But the timing of antecedent weather effects tends to shift to earlier years (more years in the past) with increasing levels of nitrogen. Lastly, differences in memory length between intact and disturbed plots become more variable at higher nutrient levels. These results indicate that ecosystem productivity and the functions it provides are shaped by past environmental conditions, with lagged effects further altered by anthropogenic disturbances. Effective management strategies will need to account for the diverse time frames over which climate and human activities jointly impact ecosystems.

Forest recovery dynamics after the Gatlinburg wildfires in Tennessee, USA

Alanna J. Post and Kyla Dahlin

Geography

In 2016, several large, mixed-severity wildfires occurred in Tennessee's Great Smoky Mountains National Park (GRSM). Since the fires, managers have noticed that forest recovery has been variable. As such, we aim to examine what drives the differences in forest recovery post-wildfire. In particular, we are interested in the differences and changes in forest structure as these are often related to forest health and productivity. GRSM is host to a National Ecological Observatory Network (NEON) site which collects many different types of data including near-annual airborne lidar. We derived forest structure metrics from the available flights between 2015 and 2022, and quantified the magnitude of change post-recovery using difference metrics (e.g., LAI 2016 - LAI 2015). Topographic data, fire severity maps, and vegetation spectral indices were acquired from NEON's AOP datasets and the National Park Services online GIS database. Pre-fire (2015-16) and post-fire (2016-17) difference metrics were compared to burn severity classes in an ANOVA, and post-fire ΔLAI and ΔPorosity ratio were found to be related to burn severity class. From this, ΔLAI and ΔPorosity ratio were then regressed with a variety of topographic and environmental variables to examine relative importance/impact of these variables on changes in forest structure. Model selection was done using random forest and the best model was tested using Monte Carlo simulation.

Global quantification of plant species competitive ability along resource gradients

Ashwini Ramesh, Lais Petri, Alejandra Martínez Blancas, Amar Tiwari, Pat Bills, Lauren Sullivan, and Phoebe L. Zarnetske

Integrative Biology

The maintenance of species diversity in the face of climate change is critical for ecosystem stability and function. Understanding how species coexistence is governed across resource gradients is fundamental to anticipating and mitigating biodiversity loss. Resource competition plays a central role in this context, influencing species interactions and diversity patterns. Despite its importance, a comprehensive understanding of resource-biodiversity relationships remains elusive. Here, we synthesize how plant species competition shifts across resource gradients in diverse ecosystems worldwide. Our approach integrates food web theory, meta-analysis, data-fitting, and climate mapping to propose unified community assembly rules in a changing world. This effort involved scanning > 3,500 papers and utilizing data from 67 studies to construct a comprehensive database. Our analysis reveals that approximately 56% of species pairs exhibit trade-offs along nutrient gradients, with around 25% increasing or decreasing in competition intensity with nutrient availability. Moreover, our examination of geographical bias in scientific output highlights dominance by the Global North and China, with significant underrepresentation of the Global South. Despite this disparity, we found no evidence of parachute science, ensuring that each study involved at least one author affiliated with the study site, underscoring progress toward more inclusive and equitable science.

Evolution and diversification of duplicated genes after a genome duplication in the fish brain

Jamily Lorena, Grace Urban, Keyana Blake, Julia Ganz, and Ingo Braasch
Integrative Biology

The vertebrate lineage has undergone two whole-genome duplication (WGD) events. Additionally, lineage-specific WGDs are also observed such as in the ancestor of the teleost fishes (Teleost Genome Duplication, TGD). WGD-derived extra copies of DNA have been proposed to be the raw material that can seed evolutionary innovations, adaptations, and diversification, with the teleost fishes being the most diverse group of living vertebrates. Genome-wide, around 80% of the extra gene copies from the TGD have been lost again, i.e. they underwent non-functionalization. However, from the remaining genes that are retained as duplicates, regulatory changes or coding mutations may generate complementary expression patterns and protein functions among the TGD duplicates (sub-functionalization); and/or gene duplicates acquire new expression patterns or protein functions (neo-functionalization). It is noteworthy that genes with functions in development and in the nervous system show particularly high TGD duplicate retention rates. For example, glutamate receptor genes, which play fundamental roles in the development and function of the vertebrate nervous system, have retention rates of over 70% in teleosts. Here, using comparative gene expression studies, we investigate the expression patterns of glutamate receptor genes in the brain of the spotted gar (Lepisosteus oculatus), a ray-finned fish that diverged from teleosts before the TGD. Results are compared to the expression patterns of glutamate receptor TGD duplicates in the zebrafish as an example teleost species. Thereby, we aim to understand how and why so many of these genes were kept in duplicate following the TGD and how their functional divergence may have contributed to teleost nervous system evolution, development, and diversification.

Characterization of Enteric Nervous System Development in Spotted Gar (Lepisosteus oculatus)

Isabella R. Rinaldi, Brooke E. Jeffery, Julia Ganz, and Ingo Braasch
Integrative Biology, Neuroscience

The enteric nervous system (ENS) provides the intrinsic innervation to the gastrointestinal tract. Because of its central role in controlling gut function, identifying the genetic basis of ENS development is important for understanding its role in gastrointestinal diseases. The zebrafish (Danio rerio) model system has been crucial in understanding the genetic basis underlying ENS development, as gene regulatory networks governing developmental processes are often shared across the vertebrate lineage. Recent work has identified the spotted gar (Lepisosteus oculatus), a non-teleost fish, as a bridge between the teleost zebrafish and humans if genetic elements cannot be linked between zebrafish and humans. To use gar as a bridge species, we aimed to characterize ENS development in spotted gar. I first performed whole-mount immunohistochemistry between stages 25 and 34 of gar development using the pan-neuronal markers Elavl and acetylated-α-Tubulin (α-Tub) to determine when ENS neurons differentiate. Elavl and α-Tub were detected in enteric neuronal cell bodies and nerve fibers respectively at stages 32-33 and 33-34 but not at stages 25-30. This suggests that ENS neurons differentiate at the beginning of stage stages 31-32. To identify neuronal subtypes, I am currently performing immunohistochemistry with subtype markers Nitric oxide synthase 1, Serotonin, and Choline Acetyltransferase at stages 33-34. Additionally, I will perform HCR to detect expression of the bnc2 gene. Characterizing ENS development in spotted gar will allow us to establish the gar ENS as a model for human ENS diseases and contribute to a better understanding of the evolution of vertebrate ENS development.

Protecting birds in protected areas: a multi-scale analysis of landscape context and species occurrence

Bruna R. Amaral, Jeff Doser, Aaron Weed, Kate Miller, and Elise Zipkin
Integrative Biology

Protected areas are crucial for conserving biodiversity, providing resources for species and supporting ecosystem services, while reducing human-wildlife conflicts. However, their efficacy in protecting avian populations might be limited by the surrounding landscape. As protected areas exist within a matrix of distinct land-uses, neighboring areas can distinctly affect birds within the protected land. Some National Parks in the Northeastern US, despite having undisturbed and managed forest areas, have experienced declines in avian communities, while others have stable or increasing populations. Hierarchical models fitted within a Bayesian framework provide a flexible and robust approach to investigate scale-dependent community responses to landscape change, considering the land-use inside and outside of parks. Using bird point counts from the Marsh Billings-Rockefeller Historical Park and forest cover satellite data from MRLC, we will develop a multi-species multi-scale removal-sampling model to estimate how forest area affects forest bird community trends at varying spatial scales. We expect most birds to be positively associated with forest area, and that species within the same guild will respond similarly at a similar scale. For example, we expect interior forest obligate birds to be strongly affected by forest cover at smaller scales (park level), while forest generalist might respond at larger spatial extents (regional level). Additionally, our study may reveal how management practices implemented in parks might not be influencing species in the scale where they are most vulnerable. Understanding the role that landscape context plays is crucial to identify at which scale management is more efficient and should be implemented.

Seeing Heat in Motion: How Pythons Track Prey Using Infrared Sensing

Santiago Rodriguez Castro and Heather L. Eisthen
Integrative Biology

Infrared (IR) sensation enables the detection of objects based on the amount of radiant heat they produce. Among vertebrates, three families of snakes independently evolved IR sensitivity: boas, pythons, and crotalines. Snakes use IR sensing primarily in prey capture, although its use in nesting and thermoregulation has also been proposed. Research has shown that the IR system allows snakes to precisely strike warm objects without any other sensory input. Such spatial accuracy is supported by neural circuitry in the midbrain that generates an egocentric map of the IR realm surrounding the animal. However, since IR-emitting prey move, positional information alone may be insufficient to guide behavior. We are using juvenile ball pythons as a model to understand whether and how motion is used by the IR system. Using an electrically controlled heating device mounted on an XYZ robot, we can control moving IR stimuli like those a snake would encounter in a natural hunting scenario to examine responses to different types of motion. These results will allow us to determine some of the capabilities and limitations of the IR system of pythons, as well as to generate hypotheses regarding the function of IR-responsive neurons in the snake brain. This work is the first step in a series of experiments that aim to understand the neural processes underlying the integration of visual and IR information and shed light on the mechanisms that allow the construction of coherent representations of the world when multiple sensory inputs are involved.

Targeted ablation and regeneration of enteric nervous system neurons in zebrafish

Mujahid Ali Shah, Katherine Moran, Helen Rueckert, and Julia Ganz
Integrative Biology

The enteric nervous system (ENS), the largest part of the peripheral nervous system, regulates gut motility, digestion, and inflammatory responses, ensuring gut homeostasis. In vertebrates, the fundamental cell types, molecular processes, and developmental origins of the ENS are conserved between mammals and zebrafish (teleosts), despite some species-specific differences in structure and complexity. ENS dysfunction is linked to gastrointestinal disorders such as Hirschsprung disease (HSCR), which is characterized by the absence of ENS neurons in the distal gut, leading to severe intestinal obstruction. Currently, the only treatment is surgery, which often results in post-surgical complications. Restoring ENS neurons represents a promising therapeutic approach, however previous regeneration studies in mammals using chemical and mechanical ablation have shown slow recovery and incomplete neuronal regeneration. Zebrafish studies using laser ablation targeting only few cells in one gut region demonstrated early neuronal recovery and unintended tissue damage. To address these challenges, we developed a chemical-genetic ablation model in zebrafish using the Gal4/UAS-nitroreductase (NTR) system for targeted ENS neuron ablation. Metronidazole treatment induced spatially and temporally controlled cell death in NTR-expressing neurons, confirmed by morphological alterations, significant neuronal loss, and TUNEL assays. Immunoassays and confocal microscopy revealed complete ENS neuron regeneration by day 9 post ablation. Among the regenerated neurons, nitrergic and cholinergic populations fully recovered, while serotonergic and vipergic neurons showed only partial recovery, indicating subtype-specific differences in regenerative capacity and/or timing. This study establishes a robust model for ENS regeneration, providing a valuable platform for investigating the molecular-cellular mechanisms of ENS regeneration to develop potential therapeutic strategies for ENS diseases in the future.

Journal articles must be made accessible: a collaborative research project by the Accessibility Research Group

Olivia M. Smith, Brooke E. Jeffery, Wendy Leuenberger, Caitlin Mack, Gina Pizzo, Bobicheng Zhang, and Courtney L. Davis
Horticulture

Recent work has illuminated inequities in academic publishing, but little attention has been paid to the inequities disabled scientists face. We reviewed the websites of 541 ecology and evolution journals to examine the extent that they prompt authors to prepare accessible manuscripts. Nearly three-quarters of journals do not encourage authors to consider accessibility when preparing manuscripts. Existing guidelines primarily focus on colorblind-friendly figures, which was mentioned almost twice as much as other recommendations. Our survey signals an urgent need for widespread journal policy reforms. We conclude with recommendations for an iterative process of reform in collaboration with the disability community.

Animal vocal communication and data science research in the BIRDS Lab

Grace Smith-Vidaurre
Integrative Biology; Computational Mathematics, Science, and Engineering

Vocal learning, the social learning of vocalizations, is rare across vertebrate taxa. This cognitive trait appears to have evolved repeatedly and independently across eight mammalian and avian taxa. Several hypotheses for the evolution of vocal learning pose that this trait evolved to facilitate social recognition for social cohesion. However, to make new discoveries about why and how vocal learning evolved across phylogenetically distant vertebrate taxa, we need to overcome challenges associated with testing evolutionary hypotheses about social recognition. We also need more empirical research on the functional diversity of vocal learning and the robustness of this trait to developmental experiences. Research in the Behavior IntegRated with Data Science (BIRDS) Lab integrates empirical experiments with parrots and songbirds together with data science approaches that can lead to new discoveries about why and how vocal learning evolved, and the current functions of vocal learning for social recognition. First, we test longstanding ideas about how vocal learning evolved for social recognition using agent-based models to overcome challenges traditionally associated with empirical work. Additionally, we quantify information encoded in avian vocalizations to test how bioacoustics tools can be used for functional inferences about vocal learning. Finally, we use experimental approaches to test how learned vocalizations are used for social recognition, and how developmental experiences influence vocal information encoding. The BIRDS Lab works at the cutting edge of integrating animal behavior research with computational approaches to study the origins and continued evolution of complex vocal communication.

The role of soil bacterial communities in the plant soil feedback effects on oak regeneration under red pine

Narda J. Triviño Silva, Christopher W. Fernandez, Andrew L. Vander Yacht, and Akihiro Koyama

Forestry

Oaks (Quercus spp.) are an important component of forests in the Lake States region of North America. In the face of the current decline in oak regeneration due to deer herbivory, competition with more shade-tolerant species (e.g., Acer spp.), pests and other pressures, observations suggest that red pine overstories provide ideal conditions for oak regeneration. A potential mechanism for this is plant-soil feedback (PSF) which occurs when plants affect biotic and/or abiotic soil properties that could influence subsequent seedling performance. A 10-week greenhouse experiment was conducted to test 1) if growth of red oak seedlings benefits from red pine soils more than from red oak soils and 2) if red maple, the most prominent competitor against oaks, benefits from oak soils more than red pine soils. At harvest, dry biomass and soil pH were measured and rhizosphere bacterial communities were sequenced. Results showed that the shoot/root ratio of maple seedlings increased by 40% in oak soils compared to red pine soils. Oak total dry weight was higher in oak soils than in pine soils, but only when rhizosphere bacterial evenness was low, which suggests an important role of bacterial community diversity in oak growth. Lastly, we observed a general increase in bacterial evenness as pH increased across soil treatments and plant species. These results indicate that bacterial diversity in soils and soil abiotic factors such as pH could be critical factors that explain the successful regeneration of red oak under red pine.

Assessing the effect of the urban fabric on avian species richness using community-science data

Trey Ursillo and Kevin McGraw

Integrative Biology

Currently, more than half of all humans live in urban areas, representing an increase of 30% since 1950 and expected to increase to 68% by 2050. Rapid urbanization has wide-ranging effects on the natural world, including loss of biodiversity and habitat. Birds in particular have experienced global declines due to urbanization, exhibiting a 29% decrease in abundance (~3 billion individuals) in North America since 1970. Anthropogenic factors, such as artificial landcover and built structures, are the most likely drivers of reduced avian urban biodiversity, rather than non-anthropogenic factors such geography, climate, or topography. These results imply that avian species richness can be improved in urban areas by altering the "urban fabric", commonly defined as the physical structures that make up a city, including buildings, roads, parks, and other open spaces. However, research on the fine-scale, contemporary characteristics of the urban fabric that deter or attract native birds is insufficient. I used broadly available community-science data to investigate how features of the urban fabric influence urban avian species richness in Detroit, MI, a heavily urbanized and spatially heterogeneous city. Preliminary results indicate that built and natural features significantly affect bird species richness across Detroit, implying that avian species richness in cities can be conserved and improved through structural changes to the urban fabric. Future research will involve incorporating multiple cities across the United States, as well as assessing how urban avian species richness varies as a function socioeconomic status across urban subareas.

Evaluating the abilities of different sequencing technologies to characterize mixed-strain Borrelia burgdorferi infections to assess changes in temporal and spatial strain diversity

Michelle Volk and Jean Tsao
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Borrelia burgdorferi (Bb), the bacterial agent of Lyme disease, has a highly polymorphic outer surface protein that is critical for the establishment of infection in vertebrate hosts. This results in genetically distinct strains that vary in virulence and pathogenicity, and diversity within ticks can be affected by the duration of establishment of tick populations as well as host diversity. Assessing the diversity of Bb within ticks and tick populations is complicated by the occurrence of mixed-strain infections, which are common in ticks. To understand the full diversity, we need to evaluate sequencing methods that can distinguish all individual strains within ticks. In this study, we evaluated the abilities of AVITI short-read sequencing and Nanopore long-read sequencing to describe the diversity of strains within mixed-strain samples that we created from cultures, which we strain typed using Sanger sequencing. We also sequenced Bb extracted from nymphal blacklegged ticks collected from sites in Michigan to explore the strain diversity and mixed infections in field-collected ticks with the ultimate goal of comparing strain diversity in endemic vs newly established tick populations across invasion gradients. Results from this research can help inform on disease risk as different strains are associated with varying clinical manifestations and virulence. Thus, there is an epidemiological significance to understand changes in Bb diversity spatially and temporally over the course of in

Warwick Lab poster

Alexa R. Warwick

Fisheries and Wildlife

Presenting lab poster

Into the weeds: a 2-year reciprocal transplant of agricultural weeds

Robin Waterman

Plant Biology, Kellogg Biological Station

Weedy plants invading crop fields face a range of novel selection pressures. While the evolution of herbicide resistance in problematic weeds has been well-studied, changes in other traits that may allow weeds to initially establish in agricultural environments are not well understood. Adaptive phenotypic plasticity and adaptive evolution have previously been proposed as important mechanisms of adaptation for agricultural weeds, but there are few prior experimental tests of these hypotheses. In this presentation I discuss my efforts to address the relative roles of plasticity and evolution using reciprocally transplanted plants of three species of common annual weeds sourced from regionally paired agricultural and non-agricultural environments.

Seasonal microbial succession in beetles and soil during carrion decomposition

Kelly Waters, Anthony Grigsby, Bethany Mikles, Jennifer Pechal, and M. Eric Benbow

Entomology

When carrion decomposes outdoors, decomposition fluid and organic material are introduced into the soil beneath the carcass, thus altering the microbial communities over time. Several families of beetles interact with this soil while feeding on the carcass or fly larvae, altering their internal microbiome. As part of a seasonal decomposition study, beetles and soil samples were collected underneath replicate stillborn swine carcasses throughout decomposition to investigate differences in bacterial community successional change during the spring, summer, and fall seasons of one calendar year. DNA was extracted from all samples and sequenced using 16S amplicon based high-throughput sequencing. The resulting data were assembled, quality-filtered, and analyzed with the QIIME2 software. During each season, the soil communities significantly changed across time points consistent with trajectories that have been previously reported in other studies of carrion and human cadaver decomposition, but the taxa and rate of change were different among seasons. During the beginning stages of decomposition, Firmicutes is reported to be the most dominant bacterial phyla of soil communities but is then replaced by Proteobacteria as decomposition progresses. All soil samples from underneath the carcasses had communities that were also significantly different from control soil samples. Analysis is ongoing to identify the succession of bacteria in beetle internal microbiomes and how this relates to soil community structure during decomposition. These data demonstrate predictable differences in the soil microbial communities at varying time points during decomposition which could allow for future reliable microbiome-based postmortem interval estimate using bacterial communities.

Evolvability of Antibiotic Resistance

Anna Weller, Richard Lenski, Devin Lake, and Zachary Blount
Integrative Biology, Microbiology and Molecular Genetics

The evolution of antibiotic resistance is becoming a major public health issue. Therefore, determining the when and how it occurs would be highly beneficial. Not much research has been done on how the factors of antibiotic resistance—mutation rate, population size, and genetic background—individually and collectively impact resistance potential. The Long-Term Evolution Experiment provides a history of dramatic changes in mutation rate, population size, and novel innovations which may impact resistance potential, thus using a population of E. coli, resistance evolvability can be examined by their subjection to different antibiotic concentrations. Previous work has found that relaxed selection acted on a population from the LTEE. My research found this same result using a different population as well as the mutator phenotype increasing the tempo of relaxed selection

Acquisition of neurotoxin-producing bacteria by newt hosts

Samantha M Westcott, Joshua S Iizuka, Gary M Bucciarelli, Elizabeth A Heath-Heckman, and Heather L Eisthen
Integrative Biology

Newts in the genus Taricha possess a potent neurotoxin, tetrodotoxin (TTX). Decades of research show how newts use TTX as a defensive compound against potential predators, but the mechanisms shaping newt toxicity are poorly understood. Newts have long been thought to make TTX endogenously; however, researchers recently isolated TTX-producing bacteria from the skin of rough-skinned newts (Taricha granulosa), raising questions about how the newt-microbe symbiosis shapes host TTX concentrations. We are investigating how newts acquire these TTX-producing bacteria.

To determine whether Taricha obtain TTX-producing bacteria through horizontal transmission, we are rearing larvae in the presence or absence of an adult conspecific. Under natural conditions, larvae possess TTX as embryos which decreases through metamorphosis. We are comparing TTX concentration with larval skin and gut microbial communities across host developmental stages, from eggs to early juveniles. Additionally, we are studying development of their toxin-storing glands to examine the relationships among gland formation, animal toxin concentration, and microbiome composition. Immature toxin glands first appear during metamorphosis, potentially explaining why larvae lose most of their initial TTX stores during early developmental stages. Increasing glandular volume may increase the newt capacity to accumulate TTX from their microbial symbionts. These data will be the first systematic investigation of bacterial transmission in toxic Taricha newts. By characterizing the mode of transmission, we will be able to further explore mechanisms shaping newt toxicity.

Tracing fin evolution in T-box family genes

Zehua "Tony" Zhou and Ingo Braasch

Integrative Biology

T-box family genes exhibit complex temporal and spatial expression patterns across organs in all jawed vertebrates. Thes transcription factors have shown to be promising of answering if the median fish fins (dorsal, anal, and caudal fin) are related to origin of paired fins (pectoral and pelvic fin) and how paired fins evolved to limbs in the tetrapod lineage. Previous studies have shown that tbx5 and tbx4 are involved in fin patterning where tbx5 is expressed exclusively in the pectoral and tbx4 exclusively in the pelvic fins. Such clearly divided expressions are mirrored in the tetrapod fore- and hind- limbs as well. Additionally, median fins positions of both catshark and lamprey are delineated by tbx18 expression. It has been widely accepted that evolution of paired fins results from co-option of median fins developmental modules; therefore investigating tbx18 from a phylogenetic scope can assist understanding the evolutionary history of fins. In this study we chose the spotted gar (Lepisosteus oculatus) as a reference species due to its ancestral genome and low mutation rate among ray-finned fishes. We examined the sequence similarity of the tbx18 locus of more than 30 vertebrate species that occupy phylogenetic significant positions. Using different sequence alignment algorithms also detecting rearrangements and inversions, we compared sequence similarity with various stringencies to identify conserved non-coding elements (CNEs). CNEs are often gene regulatory elements so that by identifying tbx18-neighboring CNEs preserved across taxa or conserved only among specific lineages, we trace the gene regulatory landscape of tbx18 across vertebrate evolution.