

*The Seventh Annual*  
Ecology, Evolution, & Behavior  
**Research Symposium**



**ECOLOGY  
EVOLUTION  
BEHAVIOR**

**MICHIGAN STATE  
UNIVERSITY**

May 1, 2023  
Michigan State University  
Henry Center for Executive Development  
3535 Forest Rd, Lansing, MI 48910

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Collins, <a href="#"><u>poster</u></a>	Lorena, <a href="#"><u>poster</u></a>	Williams, <a href="#"><u>lightning</u></a>
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Davis, <a href="#"><u>talk</u></a>	Mead, <a href="#"><u>poster</u></a>	Young, <a href="#"><u>talk</u></a>
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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**

Kayla Davis, Co-Chair

Moriah Young, Co-Chair

Sam Ayebare

Cynthia Fiser

Devin Lake

Wendy Leuenberger

Caitlin Mack

## Welcome from the EEB Director

Welcome to the seventh annual Michigan State University Ecology, Evolution, and Behavior (EEB) Research Symposium! EEB serves as the intellectual home of our >200 core members and 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. 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 Kayla Davis and Moriah Young: Sam Ayebare, Cynthia Fiser, Devin Lake, Wendy Leuenberger, and Caitlin Mack, 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. A special thank you to Kay Holekamp, EEB's previous director, for having the brilliance to initiate the symposium seven years ago.

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, Engineering.

Thank you for attending the EEB symposium!

Sincerely,

A handwritten signature in black ink, which appears to read "Elise Zipkin". The signature is fluid and cursive.

Elise Zipkin, EEB Director



## **Twitter and 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:  
#MSUEEB2023

# Keynote Speaker

Dr. Mason Fidino

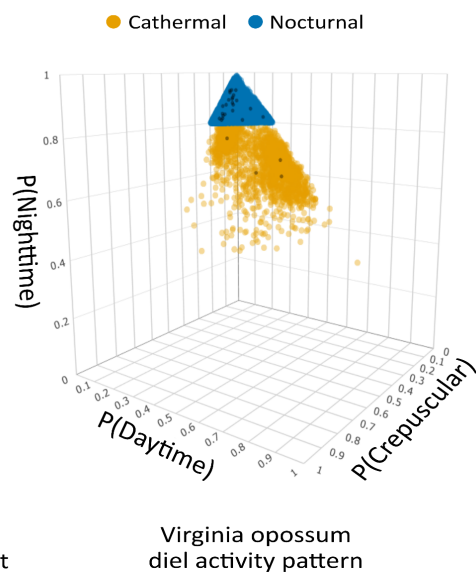
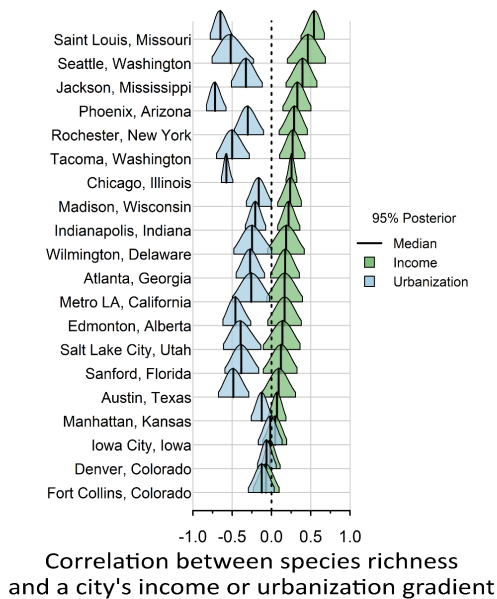
Urban Wildlife Institute

Lincoln Park Zoo

<https://masonfidino.com/>



Disentangling spatiotemporal variation in mammalian responses to urbanization and daily activity patterns through a global camera trap study



 **LINCOLN PARK ZOO.**  
FOR WILDLIFE. FOR ALL.



## **Awards**

The following awards will be presented:

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

Best lightning talk (1st)

Best poster (1st, 2nd)

Art in Science Prize

## **Thank you to our judges:**

Chris Blackwood

Keyana Blake

Sophie Buysse

Andrew Eagar

Cynthia Fiser

Asia Hightower

Minako Izutsu

Ben Kline

Devin Lake

Wendy Leuenberger

Andrea Morrow

Ashwini Ramesh

Shinhan Shiu

Olivia Smith

Nicole Wonderlin

Daniel Trego

Jacqui Carroll

Sue Nichols

# 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	<b>Welcome &amp; Opening Remarks</b> <i>Elise Zipkin, EEB director</i> <i>Kayla Davis</i>	Auditorium
9:00-10:00	<b>Keynote Address</b> <i>Mason Fidino, Urban Wildlife Institute at the Lincoln Park Zoo</i>	Auditorium
10:00-10:10	Break	
10:10-11:10	<b>Session I Oral Presentations</b> (Moderator: Cynthia Fiser) 10:10- Nicole Wonderlin (ENT) 10:25- Robin Waterman (PLB) 10:40- Wendy Leuenberger (IBIO) 10:55- Meaghan Clark (IBIO)	Auditorium
11:10-11:20	Break	
11:20-12:00	<b>Session II Oral and Lightning Presentations</b> (Moderator: Sam Ayebare) 11:20- Kayla Davis (IBIO) 11:35- Samuel Ayebare (IBIO) 11:50- Peter Williams (IBIO) 11:55- Ashwini Ramesh (IBIO, MMG)	Auditorium
12:00-1:00	Lunch	Atrium
1:00-2:20	<b>Session III Oral and Lightning Presentations</b> (Moderator: Caitlin Mack) 1:00- Ben Kline (IBIO) 1:15- Miranda Wade (IBIO) 1:30- Olivia Fitch (IBIO) 1:45- Sara Hugentobler (IBIO) 2:00- Alyssa Saunders (IBIO) 2:05- Andrew Eagar (PLB) 2:10- Kevin Liu (CSE) 2:15- Minako Izutsu (MMG)	Auditorium

<b>2:20-3:20</b>	<b>Poster Session/Mingling/Break</b>  Hazel Anderson (IBIO), Shreya Balla (PLB), Keyana Blake (PSL & BEACON), Sophie Buysse (PLB & KBS), Erin Collins (IBIO), Kara Dobson (IBIO & KBS), Asia Hightower (PLB & IMPACTS), Brooke Jeffery (IBIO), Caitlin Mack (IBIO), Louise Mead (IBIO & BEACON), Andrea Morrow (IBIO), Jamily Lorena Ramos de Lima (IBIO), Alyssa Saunders & Ben Kline (IBIO), Abby Sulesky-Grieb (MMG, Plant Resilience Institute, PBHS), Blackwood Lab (PLB & PSM), Shiu Lab (PLB, CMSE, BEACON)	Atrium
<b>3:20-4:05</b>	<b>Session IV Oral Presentations</b> <b>(Moderator: Devin Lake)</b>  3:20- Moriah Young (IBIO) 3:35- Emily Conway (PLB) 3:50- Riley Pizza (PLB)	Auditorium
<b>4:05-4:50</b>	<b>EEB Community Engagement</b> <b>(Moderator: Wendy Leuenberger)</b>  4:05- Olivia Smith 4:20- Cinnamon Mittan 4:25- Ashwini Ramesh 4:30- Brooke Jeffery 4:35- Q & A	Auditorium
<b>4:50-5:00</b>	<b>Closing Remarks, Awards</b>  Devin Lake, Cynthia Fiser, and Moriah Young EEB Research Symposium Planning Committee	
<b>5:00-6:30</b>	<b>Happy Hour!!</b>	Four Seasons Lounge

# EEB Research Symposium Detailed Schedule

8:00-8:45	<b><u>Registration and Breakfast</u></b>	Entrance Lobby
	Please arrive at the Henry Center in advance in order to check in and pick up your name tag. Refreshments will be provided.	
8:45-9:00	<b><u>Welcome &amp; Opening Remarks</u></b>	
	<i>Elise Zipkin, EEB director</i>	
	<i>Kayla Davis</i>	
9:00-10:00	<b><u>Keynote Address</u></b>	
	<b>Disentangling spatiotemporal variation in mammalian responses to urbanization and daily activity patterns through a global camera trap study</b>	
	<i>Mason Fidino, Urban Wildlife Institute, Lincoln Park Zoo</i>	
	<i>Urban Wildlife Information Network</i>	
10:00-10:10	<b>Break</b>	
10:10-11:10	<b><u>Session I Oral Presentations</u></b>	
	(Moderator: Cynthia Fiser)	
	<b>Distinct diurnal and nocturnal flower visitor communities provide pollination services in urban gardens</b>	<a href="#">abstract</a>
	Nicole Wonderlin, Graduate student Department of Entomology	
	<b>Testing adaptive hypotheses for selection on anther position traits through slow-motion videos of pollinators</b>	<a href="#">abstract</a>
	Robin Waterman, Graduate student Department of Plant Biology, Kellogg Biological Station	
	<b>Estimating long-term species and community trends of butterflies in the Midwestern United States</b>	<a href="#">abstract</a>
	Wendy Leuenberger, Graduate student Department of Integrative Biology	
	<b>Secret lives of snakes: Pedigree-based insights into demography and inbreeding in the threatened eastern massasauga rattlesnake</b>	<a href="#">abstract</a>
	Meaghan Clark, Graduate student Department of Integrative Biology, Kellogg Biological Station	
11:10-11:20	<b>Break</b>	

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11:20-12:00

**Session II Oral and Lightning Presentations**

(Moderator: Sam Ayebare)

**Breeding season management is unlikely to improve population viability of a data-deficient migratory species in decline**

[abstract](#)

Kayla Davis, Graduate student  
Department of Integrative Biology

**Co-existence mechanisms in a diverse tropical bird community**

[abstract](#)

Sam Ayebare, Graduate student  
Department of Integrative Biology

**Characterizing the role of interannual environmental variability in structuring the life histories of global ecological communities**

[abstract](#)

Peter Williams, Postdoc  
Department of Integrative Biology

**Rules of infection: Disentangling within-host assembly patterns**

[abstract](#)

Ashwini Ramesh, Postdoc  
Department of Integrative Biology and Microbiology and Molecular Genetics

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**Lunch**

12:00-1:00

Please join us in the Henry Center atrium for lunch.

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1:00-2:20

**Session III Oral and Lightning Presentations**

(Moderator: Caitlin Mack)

**Genomic variation of brook trout (*Salvelinus fontinalis*) along the Minnesota shoreline of Lake Superior: Implications for identifying source populations of coaster brook trout**

[abstract](#)

Benjamin Kline, Graduate student  
Department of Integrative Biology

**Of microplastics and minnows: quantifying the molecular effects of lifelong microplastics exposure on fathead minnows (*Pimephales promelas*)**

[abstract](#)

Miranda Wade, Graduate student  
Department of Integrative Biology

**A Tale of Two Tails: The role of hox genes in vertebrate caudal region evolution**

[abstract](#)

Olivia Fitch, Graduate student  
Department of Integrative Biology, BEACON

**Chinook salmon (*Oncorhynchus tshawytscha*) Life History  
Diversity in the Yuba River of California**

Sara Hugentobler, Graduate student  
Department of Integrative Biology

[abstract](#)

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**From efish to zfish: How a large deletion in *CFAP221* affects  
sperm flagella phenotype**

Alyssa Saunders, Graduate student  
Department of Integrative Biology

[abstract](#)

**How Mycorrhizas Mediate Plant-Soil Feedback: Hypothesized  
Mechanisms & Available Evidence**

Andrew Eagar, Postdoc  
Department of Plant Biology

[abstract](#)

**Overview of Liu Lab Research**

Kevin Liu, Faculty  
Department of Computer Science and Engineering, BEACON,  
BMS/GGS

[abstract](#)

**Periodic population bottlenecks influence the rate of adaptation  
and distribution of fitness effects of fixed mutations**

Minako Isutzu, Postdoc  
Department of Microbiology and Molecular Genetics, BEACON

[abstract](#)

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2:20-3:20

**Poster Session/Mingling/Break**

**Please join us in the atrium for refreshments and poster  
presentations.**

**Poster 1     Investigating plant-frugivore taxonomic and functional diversity  
relationships in the Tropical Andes**

Hazel Anderson, Graduate student  
Department of Integrative Biology

[abstract](#)

**Community     MSU Science Festival BioBlitz: 3 Years of Nature Engagement**

Engagement  
Poster 2     Hazel Anderson, Graduate student  
Department of Integrative Biology

[abstract](#)

**Poster 3     Gene flow from crops increases invasive potential in a  
drought-tolerant non-native plant**

Shreya Balla, Undergraduate student  
Department of Plant Biology

[abstract](#)

**Poster 4     Digging into the dark: Belowground mechanisms in species  
coexistence and ecosystem processes**

Chris Blackwood, Faculty  
Department of Plant Biology, Plant, Soil and Microbial Sciences

[abstract](#)



Poster 5	<b>Comparative gene expression analysis of duplicated glutamate receptor genes in the brains of zebrafish and spotted gar</b> Keyana Blake, Undergraduate student Department of Physiology, BEACON	<a href="#">abstract</a>
Poster 6	<b>The impact of modelling connections between reasoning and results on scientific literacy in an introductory biology lab</b> Sophie Buysse, Graduate student Department of Plant Biology, Kellogg Biological Station	<a href="#">abstract</a>
Poster 7	<b>Genetic monitoring of steelhead in the Klickitat River to estimate productivity, straying, and migration timing</b> Erin Collins, Postdoc Department of Integrative Biology	<a href="#">abstract</a>
Poster 8	<b>Warming and drought effects on volatile emissions of <i>Solidago canadensis</i></b> Kara Dobson, Graduate student Department of Integrative Biology, Kellogg Biological Station	<a href="#">abstract</a>
Poster 9	<b>Using <i>Capsella bursa-pastoris</i> to investigate leaf shape variation</b> Asia Hightower, Graduate student Department of Plant Biology, IMPACTS	<a href="#">abstract</a>
Poster 10	<b>Cis-regulatory Evolution in Enteric Nervous System Development</b> Brooke Jeffery, Graduate student Department of Integrative Biology	<a href="#">abstract</a>
Poster 11	<b>Trends in reproductive management of captive African painted dogs (<i>Lycaon pictus</i>) over time</b> Caitlin Mack, Graduate student Department of Integrative Biology	<a href="#">abstract</a>
Poster 12	<b>Testing a Collaborative CURE Model Using a Large-scale Salamander Research Network</b> Louise Mead, Faculty Department of Integrative Biology, BEACON	<a href="#">abstract</a>
Poster 13	<b>Diurnal and nocturnal rodents invest differently in visual and olfactory brain structures</b> Andrea Morrow, Graduate student Department of Integrative Biology	<a href="#">abstract</a>
Poster 14	<b>Evolution of the vertebrate central nervous system by whole genome duplication</b> Jamily Lorena Ramos de Lima, Graduate student	<a href="#">abstract</a>

Department of Integrative Biology

Community  
Engagement  
Poster 15

**Biology on Tap: Putting the “pub” in public science outreach**

[abstract](#)

Alyssa Saunders and Benjamin Kline, Graduate students

Department of Integrative Biology

Poster 16

**Enhancing biological understanding using AI**

[abstract](#)

Shinhan Shiu, Faculty

Department of Plant Biology, Computational Math, Science, &  
Engineering, BEACON

Poster 17

**Drought and Nutrient Excess Influence the Membership and  
Transmission of the Microbiome of Common Bean, *Phaseolus  
vulgaris* L.**

[abstract](#)

Abby Sulesky-Grieb, Graduate student

Department of Microbiology and Molecular Genetics, Plant  
Resilience Institute, PBHS

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3:20-4:05

**Session IV Oral Presentations**

(Moderator: Devin Lake)

**Soil bacterial community responses to multiple climate  
stressors in an early successional plant community**

[abstract](#)

Moriah Young, Graduate student

Department of Integrative Biology, Kellogg Biological Station

**Local site conditions, not landscape context, influence restored  
plant communities within urban contexts**

[abstract](#)

Emily Conway, Graduate student

Department of Plant Biology

**Seed mix design does not affect restored tallgrass prairie  
community structure compared to edge effects and  
plant-consumer interactions**

[abstract](#)

Riley Pizza, Graduate student

Department of Plant Biology

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4:05-4:50

**EEB Community Engagement session**

(Moderator: Wendy Leuenberger)

**Peer review perpetuates barriers for historically excluded  
groups**

[abstract](#)

Olivia Smith, Postdoc

Department of Integrative Biology, Center for Global Change and  
Earth Observations

**Introduction to Field Biology: A summer workshop for MSU  
undergrads at KBS**

Cinnamon Mittan, Postdoc  
Department of Integrative Biology

**Presidential Postdoc Community Engagement**

Ashwini Ramesh, Postdoc  
Department of Integrative Biology and Microbiology and Molecular  
Genetics

**Graduate Student Accessibility and Support Network: MSU's  
first organization for all chronically-ill, disabled, and  
neurodivergent grad students**

[abstract](#)

Brooke Jeffery, Graduate student  
Department of Integrative Biology

**4:50-5:00**

**Closing Remarks & Awards**

Devin Lake, Cynthia Fiser, and Moriah Young  
EEB Research Symposium Planning Committee

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**5:00-6:30**

**Happy Hour!!**

**Please join us in the Four Seasons Lounge for happy hour**

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# Henry Center Map

3535 Forest Rd, Lansing, MI

(517) 353-4350

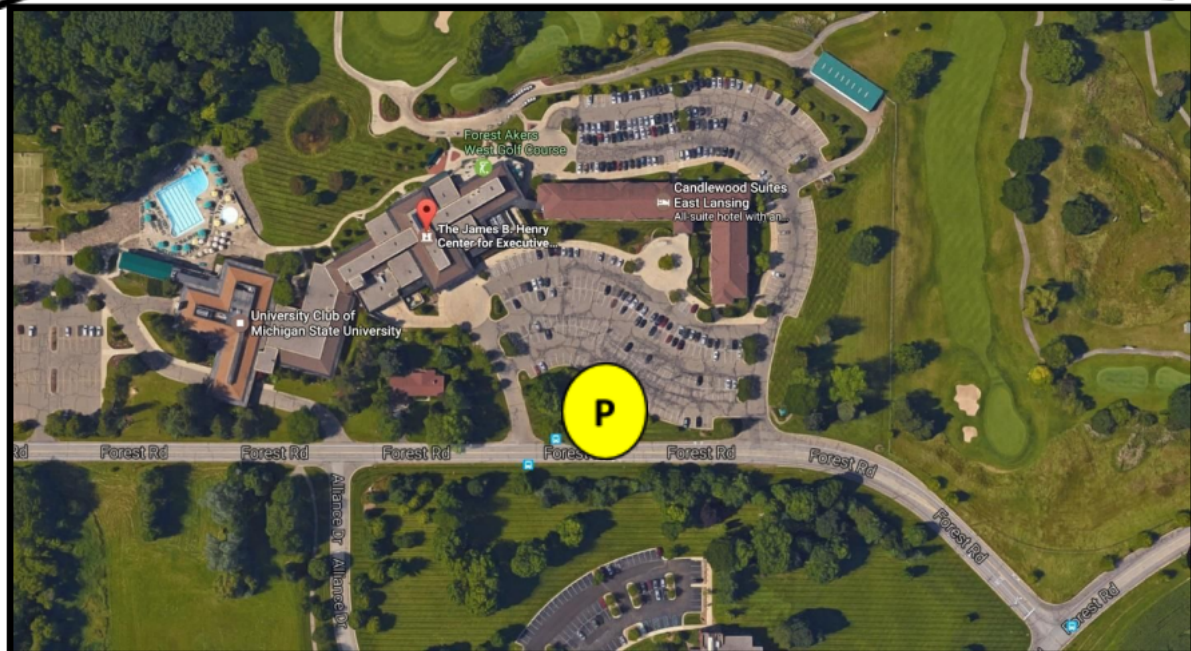


## Directions:

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**

Mixed greens, cucumbers, tomatoes, banana peppers, chopped eggs, sunflower seeds, diced ham, cottage cheese.

Dressings: ranch, balsamic vinaigrette, cilantro vinaigrette

## **Breads & Spreads**

Taco salad

Hummus, pita bread, tortilla chips, jalapeno cheddar bread

Butter, olive oil, balsamic vinegar

## **Hot Buffet**

Chicken fajitas with onion and peppers

Taco meat with hard shell tacos

Fiesta corn with peppers and cilantro

Jalapeno poppers

Spanish rice with black beans

Flour tortillas, lettuce tomatoes, shredded cheese, sour cream, salsa, guacamole, jalapenos

## **Desserts & Beverages**

Lemon torte

Tiramisu

Regular coffee, decaf, tea service

## **Abstracts**

Alphabetical by presenting author's last name.

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### **MSU Science Festival BioBlitz: 3 Years of Nature Engagement**

**Hazel J. Anderson**

Integrative Biology

The MSU Science Festival is an annual month-long celebration of STEAM with events in April on MSU's campus and throughout the state of Michigan. After the online pivot for the 2020 Festival, a BioBlitz was introduced in 2021 as a featured event type to engage people online and explore the natural world around them. A BioBlitz is a community science-led tally of living things in a defined area. iNaturalist is a commonly used tool for BioBlitzes with over 100,000,000 observations made by over 2,500,000 observers. Observations uploaded to iNaturalist are shared with data repositories such as the Global Biodiversity Information Facility to help enable biodiversity science research. For the inaugural BioBlitz in April 2021, the MSU Science Festival partnered with 6 organizations across Michigan (nature centers, parks, and natural areas) and 119 observers contributed 858 observations of 382 species identified by 313 people. In 2022, the BioBlitz expanded to 13 partner organizations and 118 observers submitted 1,089 observations of 414 species identified by 118 people. Participants were able to visit partner organization locations and any nature near them to make observations. In 2023, the BioBlitz has grown to 20 partner locations and we expect the number of observations to increase as well with several partners hosting BioBlitz exploration events during our Statewide Earth Day Celebration on April 22nd. The intended impact of these events is to encourage people to explore and expand their knowledge about nature while contributing data to science.

### **Investigating plant-frugivore taxonomic and functional diversity relationships in the Tropical Andes**

**Hazel J. Anderson**, Beth E. Gerstner, and Phoebe L. Zarnetske

Integrative Biology

Quantifying spatial patterns of biodiversity plays a critical role in determining conservation priorities and ecosystem function and clarifying the underlying processes of community assembly, species-area relationships, and environmental filtering. There is a growing body of literature that recognizes the need to move past solely focusing on taxonomic diversity (TD) to quantify biodiversity and has emphasized the advantages of

using traits to determine functional diversity (FD), which reflects the roles species play in their communities and ecosystems. Yet there is a lack of knowledge about how taxonomic and functional diversity covaries across spatial scales, and between taxonomic groups that depend on each other. Plant-frugivore communities are an ideal focal group for filling these gaps due to their sufficient trait and occurrence data, and the consumptive and seed dispersal interactions between plants and their frugivorous (fruit-eating) birds and mammals species. Here we focus on the Tropical Andes, a biodiversity hotspot, and quantify scale-dependent relationships of TD and FD for plants and frugivores. We expect that areas with high fruiting plant TD and FD will be most positively correlated with areas with high frugivore TD and FD due to their interdependence. Preliminary results in Ecuador show both high plant TD and frugivore TD in forested areas, and a peak in plant TD in mid-elevation areas. The results of this study will contribute to existing knowledge of how TD and FD covary across spatial scales, and will further our ability to prioritize conservation areas that maintain biotic interactions and maximize biodiversity across multiple dimensions.

## **Co-existence mechanisms in a diverse tropical bird community**

**Samuel Ayebare**, Jeffrey W. Doser, Andrew Plumptre, Isaiah Owionji, Hamlet Mugabe and Elise F. Zipkin

### **Integrative Biology**

Niche theory predicts that ecologically similar species can co-exist through multidimensional niche partitioning. However, due to the challenges of accounting for both abiotic and biotic processes in ecological niche modelling, the underlying mechanisms that facilitate co-existence among competing species are poorly understood. In this study, we evaluated potential mechanisms underlying the co-existence of ecologically similar bird species in a biodiversity rich trans-boundary montane forest in east-central Africa by computing niche overlap indices along an environmental elevation gradient, diet, forest strata, activity patterns, and within-habitat segregation across horizontal space. We found strong support for abiotic environmental habitat niche partitioning, with 55% of species pairs having separate elevational niches. For the remaining species pairs that exhibited similar elevational niches, we found that within-habitat segregation across horizontal space and vertical foraging forest strata provided the most likely mechanisms of species co-existence. Co-existence of ecologically similar species within a highly diverse montane forest was determined primarily by abiotic factors (e.g., environmental elevational gradient) that characterize the Grinnellian niche and secondarily by biotic factors (e.g., vertical, and horizontal segregation within habitats) that describe the Eltonian niche. Thus, characterizing distinct niches for ecologically similar species requires accounting for multiple potential niche axes of community structuring.

## **Gene flow from crops increases invasive potential in a drought-tolerant non-native plant**

**Shreya Balla, Acer VanWallendael**

Plant Biology

Domesticated, non-native species do not typically pose a threat to native habitats, since they are usually poor competitors in the wild. However, when wild populations of the same species colonize nearby, gene flow between populations can result in novel genotypes with higher invasive potential. Proso millet (*Panicum miliaceum*) is a grain crop native to Asia, and has both weedy and domesticated populations in North America. It is typically a selfing species, but outcrossing occurs rarely through wind pollination. Previous research showed that plants in the wild share genetic material with both domesticated and weedy populations, so may represent historical or recent successful crosses between the populations. We measured growth and reproductive traits from 'parent' and potential 'hybrid' individuals to determine if gene flow has resulted in phenotypic variation that might contribute to invasiveness in this species. We found substantial variation in phenotypes representing a spectrum across weedy and domesticated traits, particularly in regions where weedy and domesticated plants occur in large numbers. These results indicate that at least some of the plants we examined descended from crosses with domesticated populations. While proso millet is not currently a problematic invasive species, an increase in genetic and phenotypic diversity could allow the species to invade new habitats and pose a greater threat to native populations.

## **Digging into the dark: Belowground mechanisms in species coexistence and ecosystem processes**

**Chris Blackwood**

Plant Biology, Plant, Soil and Microbial Sciences

Our lab examines ecology and evolution of plants and microbes. We focus on interactions between organisms belowground, and between organisms and soil particles. Current projects are focused on 1. coexistence of closely related plant species, and 2. cascading effects of tree root traits on pathogen populations and soil carbon.



## **Comparative gene expression analysis of duplicated glutamate receptor genes in the brains of zebrafish and spotted gar**

**Keyana Blake**, Jamily Lorena Ramos De Lima, Julia Ganz, and Ingo Braasch

Department of Physiology

Genome duplication is an important factor in the evolution of organisms. It is hypothesized that genome duplication causes the evolution of higher cognitive functions and emerging complex brain structures in vertebrates. The teleost fish zebrafish (*Danio rerio*), an important biomedical model species, went through an ancestral teleost genome duplication (TGD). Over evolutionary time, ~80% of teleost gene duplicates have been lost (non-functionalization), and the remaining single gene serves the primary function. In contrast, metabotropic glutamate receptor (grm) genes have a particularly high rate of 70% retained duplicates from the TGD. Grms regulate synaptic transmission and memory, so it is essential to understand how grm evolved. Generally, retained gene duplicates are thought to evolve by neo-functionalization (gain of new functions) and/or sub-functionalization (distribution of ancestral functions among duplicates). To characterize grm gene evolution before and after the TGD, we analyze grm gene expression in spotted gar (*Lepisosteus oculatus*), an 'unduplicated', non-teleost fish outgroup that diverged before the TGD. Gar thus can be used as a proxy to the pre-TGD condition to identify the functionalization in teleosts like zebrafish. Using RNA in-situ hybridization on brain sections, we aim to identify the gene expression of grm duplicates in zebrafish and compare to the single grm genes in spotted gar to make inferences about the type of functionalization of grm gene duplicates in teleost. Our results will not only identify the expression patterns of grm genes in two important biomedical models but broaden our understanding of genome duplication and its evolutionary potential.

## **The impact of modelling connections between reasoning and results on scientific literacy in an introductory biology lab**

**Sophie Buysse** and Mike Wiser

Plant Biology

Science literacy is an important skill needed to navigate society. Students use science literacy skills to apply scientific knowledge both inside and outside the classroom, including interpreting popular media and communicating with their peers. As such, increasing science literacy is often a goal of introductory biology classes. However, college students who have taken general education science courses have a similar level of science literacy as the general public. One important aspect of science literacy is understanding the application of science and particularly the relationship between science and society. This includes

understanding the scientific and societal context for experiment results, which students often struggle to understand in introductory biology courses. I used a modelling framework to address this gap in scientific literacy. Models are good instructional tools because they focus on connections and can integrate concepts across disciplines. By using a box and arrow model, students will physically connect their experiment results with the application in both science and society, including in their own lives. This exercise aims to build skills in students to understand the context of classroom science, the application of science, and the connection between science and society. We implemented a box and arrow modelling activity in an introductory biology laboratory to assess if modelling experiment rationale, outcomes, and importance for society increased student's ability to accurately articulate the relevance of their experiment results and their science literacy skills. We hypothesize that our activity will stimulate students to think more critically about the context of their experiment.

## **Secret lives of snakes: Pedigree-based insights into demography and inbreeding in the threatened eastern massasauga rattlesnake**

**Meaghan I. Clark**, Gideon S. Bradburd, Eric T. Hileman, Jennifer A. Moore, and Sarah W. Fitzpatrick

### **Integrative Biology**

Small and fragmented populations are at high risk of extirpation. The loss of genetic diversity associated with strong genetic drift in small populations can lead to inbreeding depression. The eastern massasauga rattlesnake (*Sistrurus catenatus*) is federally threatened and has experienced significant habitat fragmentation over the past 200 years. We leverage long-term monitoring of two populations of *S. catenatus* in Michigan to learn about their population history, present status, and potential future. Using SNPs generated via RAD-sequencing of 1000+ individuals, we reconstruct multi-generational wild pedigrees for each population to both learn about inter-generational dynamics within populations and measure individual reproductive output as an estimate of fitness. We combine pedigree information with genetic estimates of inbreeding to test for inbreeding depression in each population. Using whole genome sequencing, we examine historical demography in *S. catenatus* to improve our understanding of the threats that face this species.

## **Genetic monitoring of steelhead in the Klickitat River to estimate productivity, straying, and migration timing.**

**Erin E. Collins**, Jon E. Hess, Shawn Bechtol, Nico Romero, Shawn R. Narum, and Joseph S. Zendt

### **Integrative Biology**

Salmonids with complex life history variation present challenges for conservation management, but genetic approaches alongside fisheries monitoring can address questions regarding viability of natural populations. We genotyped adult ( $n=3,108$ ) and juvenile ( $n=2,624$ ) samples of anadromous *Oncorhynchus mykiss* that were collected in the Klickitat River, WA, USA at traps in the lower drainage to examine tributary level productivity, straying from outside sources and variation in adult migration timing. Genetic assignment of steelhead from this system indicated that the majority were produced within or near tributaries of the middle Klickitat River (juvenile mean = 72.8%; adult mean = 87.3%). Analyses with parentage-based tagging identified that most hatchery-origin adults assigned to the Skamania Hatchery (80.8%) as expected since this has been the release stock for decades within the Klickitat River drainage. Hatchery-origin adults were also identified from programs operating outside the Klickitat River, which were primarily strays from Snake River hatcheries. Most natural-origin steelhead assigned to the Klickitat River, but there were also natural-origin fish identified as strays from other regions of the Columbia River (22.3% of natural returns). We also examined genes known to be associated with migration timing in adult steelhead collected at the trap and observed a strong relationship between migration date and alleles for early and late migration, but individual outliers were detected across seasons. Our results indicate that genetic variation of steelhead in the Klickitat River has been influenced by hatchery programs as well as natural-origin straying from other sub-basins, but genetic diversity remains high throughout the sub-basin, and both early and late migration alleles are maintained. The genetic diversity present in Klickitat River steelhead may enable this Endangered Species Act listed (threatened) species to better adapt to stochastic environmental conditions compared to less diverse populations.

## **Local site conditions, not landscape context, influence restored plant communities within urban contexts**

**Emily E. Conway** and Lars Brudvig

### **Plant Biology**

There is an increasing need to restore urban ecosystems, which face habitat loss and degradation at higher rates than non-urban ecosystems in addition to supporting novel species assemblages, modified environmental conditions, and altered landscape contexts. However, most studies testing the consequences of ecological restoration have been conducted in non-urban areas. Thus, it's unclear if we can extend current knowledge and

tools from restoration ecology to urban systems. We lack understanding of fundamental questions, like: how do local and landscape factors structure variation in restoration outcomes in urban settings? To identify these factors, we surveyed 30 urban prairie restoration plantings across southern Michigan. We collected plant community and site condition data (e.g., soil attributes) and we quantified landscape context as the percentage of urban land surrounding each site. Variation in plant community composition was related primarily to site-level factors, such as soil compaction, texture, and water holding capacity. Non-prairie species responded primarily to the age of the plantings; there was a decrease in both richness ( $p < 0.05$ ) and abundance ( $p < 0.05$ ) of non-prairie species with age. Several predictors of prairie species richness and abundance were approaching significance; sites with warmer winters and summers supported lower richness of prairie species ( $p < 0.08$ ) and older sites supported greater prairie species abundance ( $p < 0.1$ ). Surprisingly, the surrounding landscape structure wasn't an important driver of urban plant community composition. Together these findings illustrate the importance of abiotic site conditions, not landscape context, for shaping plant community composition.

## **Breeding season management is unlikely to improve population viability of a data-deficient migratory species in decline**

**Kayla L. Davis**, Sarah P. Saunders, Stephanie Beilke, Erin Rowan Ford, Jennifer Fuller, Ava Landgraf, Elise F. Zipkin

Integrative Biology

A major challenge in conservation is developing effective approaches to mitigate population declines in the face of ongoing environmental change. For migratory species, it is often more feasible to implement management during periods of stationarity, like the breeding season, when populations are less mobile. However, such management strategies are only successful if the demographic rates targeted (e.g., reproductive rates) contribute substantively to population growth. Thus, evaluation of population growth rate sensitivity to variation in demographic parameters is needed to determine the most effective conservation strategies. This is especially true for small and declining populations that require targeted and urgent action to mitigate declines under current and future environmental change. Here, we used a coupled integrated population model-Bayesian population viability analysis (IPM-BPVA) to estimate demographic rates and population viability within the context of climatic and management-related changes for a data-deficient, declining population of black terns in the Upper Midwestern United States. We found that current conservation efforts during the breeding season are unlikely to reverse the declines observed within the last decade (from an average of 307 breeding pairs in 2013 to 53 in 2022). Rather, interventions aimed at increasing adult survival are projected to reduce local extinction probability by 30–46% compared to no additional management or management targeting other rates, depending on the climate scenario. Our results highlight the importance of enhancing

management efforts for migratory species during migration and nonbreeding periods, which constitute a much larger, and generally riskier, proportion of the annual cycle compared to the breeding season.

## **Warming and drought effects on volatile emissions of *Solidago canadensis***

**Kara Dobson** and Phoebe Zarnetske

Integrative Biology

Volatile organic compounds (VOCs) are secondary metabolites emitted by all plant species in unique, species-specific blends. VOCs are crucial forms of communication for plant communities and aid in plant defense. A species' VOC mixture is not static, however, and is known to change in response to stressful events. Currently, there is a lack of knowledge on how abiotic climate change stressors affect chemical emissions for many plant species in their natural communities. To address this knowledge gap, we collected VOC emissions from Canada goldenrod (*Solidago canadensis*) within five climate treatments of the Rainfall Exclusion eXperiment (REX) at the Kellogg Biological Station Long Term Ecological Research site (KBS LTER): warming, drought, warming + drought, irrigated control, and ambient control. These treatments were applied to the plants in situ using open-top chambers to mimic climate warming and rainout shelters to cause drought. After three weeks of drought and five months of warming, the composition of plant VOCs in the warming + drought and drought treatments differed significantly from the composition of plant VOCs in the warming and ambient treatments. We found little effect of any climate treatment on the abundance of VOCs. To further these results, we plan to investigate which VOCs are leading these compositional differences and hope to identify their role in plant defense. As plant VOCs play an important role in plant fitness, experiments that investigate these stress-induced shifts in plant emissions are crucial in our efforts to predict and plan for climate change effects on plant communities.

## **How Mycorrhizas Mediate Plant-Soil Feedback: Hypothesized Mechanisms & Available Evidence**

**Andrew Eagar**, Kurt A. Smemo, Rich P. Phillips, and Chris B. Blackwood

Plant Biology

Plant-soil feedback, a phenomenon where plants alter their soil environment in ways

that either hinder or bolster growth and reproductive success, shapes plant community composition and ecosystem function. These complex interactions are primarily driven by soil-borne pathogens and mutualists, resulting in net-negative feedback for most plants. However, most plant-soil feedback studies have been conducted with plant species from a single mutualism type (arbuscular mycorrhizas), limiting our understanding of plant-soil feedback in many ecosystems. Recent work in systems comprised of both arbuscular and ectomycorrhizal plant species has revealed that ectomycorrhizal plants promote positive feedback instead of negative, leading to new hypotheses in this field. In this brief presentation, I will discuss these new ideas, provide supporting evidence, and discuss future directions in this exciting research area.

## **A Tale of Two Tails: The role of hox genes in vertebrate caudal region evolution**

**Olivia E. Fitch**

Integrative Biology

Teleost fishes make up almost half of extant vertebrate species. The evolutionary success of teleosts has been attributed to the emergence of the homocercal configuration of their caudal skeleton. Considered a synapomorphy and key innovation of the teleost clade, homocercality, i.e., superficial caudal dorso-ventral (DV) symmetry, enables more sophisticated modes of swimming compared to the more ancestral heterocercal condition, i.e., DV asymmetry as seen outside of teleosts. The genetic-developmental mechanisms underlying the hetero-to-homocercal transition (HTHT) in teleost ancestry have yet to be uncovered. Metscher & Ahlberg (2001) proposed that the symmetry of the teleost caudal fin resulted from a homeotic duplication of the caudal fin. I hypothesize that the genetic mechanism underlying this proposed homeotic duplication is a hox gene duplication following the ancestral teleost whole-genome duplication (TGD). To test this hypothesis, I compare caudal development in the homocercal teleost zebrafish (*Danio rerio*) to the heterocercal spotted gar (*Lepisosteus oculatus*), which represents the closest living outgroup to teleosts. To this end, we use comparative genomics, developmental studies, gene expression analyses, and chromatin profiling to identify candidate hox genes and regulatory elements for caudal region development that may underlie the HTHT and contribute to our understanding of vertebrate caudal region evolution and development. This study is supported by the NSF EDGE program and the NSF BEACON Center for Evolution in Action.

## **Using *Capsella bursa-pastoris* to investigate leaf shape variation**

**Asia Hightower, Emily Josephs, Dan Chitwood, and Alan Prather**

### **Plant Biology**

Anyone who grows houseplants knows that leaves are a great indicator of plant health; For crop breeders, leaves are important for herbicide/pesticide resistance strategies; and for food scientists, leaves are important sources and avenues for nutrient rich diets and famine relief strategies. From the average person to plant biologists, there are two key features of leaves that are always in consideration whether explicitly or implicitly: what do leaves look like (leaf morphology) and how has their shape/color/size changed over time (leaf evolution). Underlying and uniting both key features is the process of leaf development. There have been many studies done in model systems like *Arabidopsis thaliana*, *Zea mays*, and *Cucumis sativus* that have contributed to our current understanding of many of the major genes/pathways in the leaf development process, leaf morphology, and leaf evolution separately. There is significantly less understanding of how those major gene/pathways interact together with other cytogenetic and ecological factors to shape leaf morphology over time; especially in non-model polyploid species like the tetraploid *Capsella bursa-pastoris* (CBP). To address this gap in knowledge, we are using a novel approach to studying the intersection of leaf morphology, development, and evolution. This approach includes modeling leaf morphology through herbaria specimens of CBP across the United States over a 100-year timespan using morphometric techniques. Historical studies of CBP leaf shape used discrete groups of leaf shape types determined through phenotyping. Through morphometric and dimension reduction techniques, we have found more robust continuous variables that can explain differences in lobing. Through analysis of changes in lobing over time and by climate region, we have found variation to be sustained throughout the continental U.S. and different by climate region, in accordance with paleo-lobing patterns. Interestingly, we've found lobing to be more affected by climate changes over each accessions growing season, indicating a plastic response in leaf shape. These interesting results will aid us in understanding how CBP has been such a successful invasive species in the U.S. and how responses to climate change can potentially and indirectly affect fitness and establishment for an invasive species.

## **Chinook salmon (*Oncorhynchus tshawytscha*) Life History Diversity in the Yuba River of California**

**Sara Hugentobler, Mariah Meek**

### **Integrative Biology**

Chinook salmon (*Oncorhynchus tshawytscha*) display incredible life history diversity, which underpins their ability to adapt to environmental change. To protect this diversity, we must be able to identify it. In the Yuba River in California, there is a concerted effort to understand and protect federally listed Chinook populations. Unfortunately, we lack a complete understanding of this life history diversity. Of particular importance is understanding the timing and abundance of returning adult spring and fall run. Previous work has shown that there is likely a bimodal pulse of spring run followed by one pulse of Fall run. Newly described genomic variation in the GREB1L to ROCK1 region of the genome (hereafter

referred to as GREB1L) is tightly linked with run timing in Chinook and linking it with passage timing in the Yuba River will verify the distributions of spring and fall run across the migration window. Migration timing data from acoustic tags and fin clips was collected in 2010 and 2011. Using 16 loci from the GREB1L region, we assigned Chinook to either homozygous early, homozygous late, or heterozygous and compared that with DPD passage results. We found that GREB1L genotypes are present in the system, and the homozygous early genotype is associated with both pulses of early DPD passage while the homozygous late genotype is associated with later DPD passage. This knowledge will aid the agencies in determining the passage timing of spring and fall run in the Yuba River so they can make informed decisions about management.

## **Periodic population bottlenecks influence the rate of adaptation and distribution of fitness effects of fixed mutations**

**Minako Izutsu, Devin M. Lake, Misty Thomas, Joseph L. Graves, Jr., and Richard E. Lenski**

### **Microbiology and Molecular Genetics**

Population bottlenecks are common in nature and impact the rate of adaptation. On the one hand, each bottleneck reduces the genetic variation that fuels adaptation in evolving populations. On the other hand, in a resource-limited environment, a small founding population can undergo more generations and produce more descendants than a large one, which allows surviving beneficial mutations to spread more quickly. We investigate the impact of bottlenecks on the dynamics of adaptation in experimental populations of *Escherichia coli*. We propagated 48 populations under 4 dilution regimes (2-, 8-, 100-, and 1000-fold), all reaching the same final population size, for 150 days. A theoretical model predicts that fitness gains should be maximized with 8-fold dilutions. However, we observed earlier and greater fitness gains in the populations subjected to 100- and 1000-fold dilutions than in those that evolved in the 8-fold regime. We then sequenced the whole genomes of 48 evolved clones at two time points and found that the clones evolved in the 100-fold dilution regime have fewer mutations than those evolved in the 1000-fold regime, although the former had higher mean fitness than the latter. Our results imply that mutations that fixed in the 100-fold dilution regime provided larger benefits than those that fixed in the 1000-fold regime. We also found high parallelism at the gene level, both within and between treatments. We address the failure of the theoretical model using computer simulations, and we discuss the effects of population bottlenecks on adaptive evolution.



## **Graduate Student Accessibility and Support Network: MSU's first organization for all chronically-ill, disabled, and neurodivergent grad students**

**Brooke E. Jeffery**

Integrative Biology

There are disabled scientists at all levels—university presidents, department chairs, research and teaching faculty, and graduate and undergraduate trainees. So why is disability excluded from STEM academic/research culture? Brooke Jeffery, President of the Graduate Student Accessibility and Support Network (GSASN), will discuss disability presence in STEM nationally and at MSU, the barriers to disability inclusion in the academic/research space, and MSU's first university-wide student organization for all chronically-ill, disabled, and neurodivergent graduate students. By ensuring disabled graduate students have access to the health care, emotional support, and institutional backing they need to complete their graduate program(s) and by generating academic, professional development, and outreach opportunities for this population of students, GSASN is advancing disability inclusion in academia and beyond.

## ***Cis*-regulatory Evolution in Enteric Nervous System Development**

**Brooke Jeffery**, Ann Davidson, Emmaline Kepp, Andrew Thompson, Ingo Braasch, and Julia Ganz

Integrative Biology

A key innovation of the vertebrate lineage is the neural crest cell population. During embryogenesis, neural crest cells migrate and differentiate into diverse cell types, such as craniofacial bone & cartilage, pigment cells, and the peripheral nervous system, including the enteric nervous system (ENS). The ENS is the largest, most complex division of the peripheral nervous system and is essential for gut development and function. While key genes for ENS formation have been identified, the fundamental *cis*-regulatory interactions that direct ENS development remain largely elusive. Uncovering the regulatory basis of ENS development is particularly important for understanding Hirschsprung disease (HSCR), an intestinal motility disorder characterized by absence of enteric neurons in the terminal part of the gut. HSCR has been associated with mutations in putative enhancers modulating the expression of regulators of ENS development. Moreover, HSCR-related putative enhancers did not show overt sequence conservation across vertebrates in previous studies. Using Assay for Transposase-Accessible Chromatin with sequencing (ATAC-seq), we have identified novel putative *cis*-regulatory elements governing ENS development in zebrafish (*Danio rerio*), which we are currently functionally testing. Additionally, our *in silico* comparative analyses of genomes spanning vertebrate clades has revealed conservation of putative *cis*-regulatory elements in distantly related species otherwise undetectable through

direct sequence alignments. By detecting hidden homology of *cis*-regulatory elements, we can distinguish the most important regulatory sequences—transcription factor binding sites—driving ENS development and expand the number of species in which we can model regulatory variants implicated in human disease *in vivo*.

## **Genomic variation of brook trout (*Salvelinus fontinalis*) along the Minnesota shoreline of Lake Superior: Implications for identifying source populations of coaster brook trout**

**Benjamin Kline**, Nadya Mamoozadeh, Cory Goldsworthy, Nick Peterson, Loren Miller, Mariah Meek

### **Integrative Biology**

Brook trout (*Salvelinus fontinalis*) are one of only two native charr to inhabit the Lake Superior basin, and are a species of immense ecological, social, and cultural value. Lake Superior harbors a unique life history type of brook trout, known as the coaster brook trout, which is a lake-inhabiting form of brook trout endemic to this region. Despite the innate importance of this life history form, there is limited knowledge of population-level relationships of coaster brook trout in the Lake Superior basin. As such, we developed a study to examine genetic connectivity and source-sink dynamics among brook trout populations in an effort to better characterize relationships between resident and coastal brook trout in Lake Superior. We will analyze genomic data for over 1,600 brook trout from 22 rivers along the Minnesota shoreline of Lake Superior, in addition to a subset of individuals collected from Lake Superior. Samples collected from riverine locations represent reaches above and below natural waterfalls that inhibit upstream movement, allowing us to investigate potential relationships between above- and below-barrier populations. Additionally, we will analyze genomic data for domestic brook trout representing the most commonly stocked hatchery strains to explore whether domestic introgression is occurring in wild populations. Finally, we will estimate effective population size ( $N_e$ ) of brook trout populations above and below barriers to infer genetic population health and conservation status. Results from this study will help to inform conservation and management of coaster life history in the Lake Superior Basin.

## **Estimating long-term species and community trends of butterflies in the Midwestern United States**

**Wendy Leuenberger**, Jeff Doser, Nick Haddad, Leslie Ries, Wayne Thogmartin, Elise Zipkin

### **Integrative Biology**

Insects play critical functional roles in ecosystems and recent work indicates that many insect species are declining. However, determining population and community trends is

challenging as data on insects are limited and rates of decline are difficult to measure, especially over long time periods and broad spatial extents. Butterflies are commonly surveyed by volunteer programs, as these species are charismatic, widespread, and easily identified, especially within the Midwestern United States. Our objective is to evaluate butterfly species and community dynamics across the Midwestern region for the last 20+ years by leveraging five long-running citizen science programs (IL, OH, IA, and MI structured monitoring surveys, and North American Butterfly Association counts) to estimate annual summer butterfly abundance indices. To accomplish this objective, we are developing integrated community models to characterize weekly species abundance indices at the county-level through the summer. The model will link parameters of individual butterfly species through a community-level distribution, which are then jointly estimated through a unified, integrated analysis of the available data sources. Our approach will provide estimates of both species-level dynamics (abundance, distribution) and community metrics (richness, composition), delivering guidance on which species and communities of butterflies are declining and if any traits (e.g., migratory status, voltinism, host plant breadth) are associated with these declines. Our findings can help inform species status assessments and other management decisions aimed at mitigating insect losses.

## **Overview of Liu Lab Research**

**Kevin J. Liu**

Computer Science and Engineering

The Liu lab creates new computational methodologies for efficient and accurate comparative genomic analyses – especially in the context of complex evolutionary scenarios – and then connects the resulting insights to phenotype and function. This lightning talk will provide an overview about our research as well as selected research highlights.

## **Trends in reproductive management of captive African painted dogs (*Lycaon pictus*) over time**

**Caitlin Mack**

Integrative Biology

African painted dogs (*Lycaon pictus*) have been in human care for several decades. Difficulties those caring for them have faced include high pup mortality in litters, as well as needing to provide for and manage their complex social needs. Painted dogs live in packs, with one dominant breeding pair per pack. During the time painted dogs have been kept in zoos, the zoo field has experienced shifts in the culture and emphasis on animal welfare. Through examining historical and modern records, papers, and care standards, this poster will map the development of painted dog reproductive management over their time in human

care, looking for similarities and differences, as well as how certain standards, such as artificial dens, developed over time. The painted dog can be complicated to manage in a captive setting, but recent work and breeding success highlights how far their care and management have come. It is important to examine how the zoo field has developed and evolved in their husbandry and management of species over time. Doing this can demonstrate how things changed as knowledge and ideas changed, as well as indicating areas that could still be improved or may need further research.

## **Testing a Collaborative CURE Model Using a Large-scale Salamander Research Network**

**Louise Mead**, Alexa Warwick, Tracy Melvin, Kristine Grayson, Caitlin Fisher-Reid, Raisa Hernández Pacheco, Tanya Matlaga, Sean Sterrett, Jill Fleming, Chris Sutherland, David Miller, and Evan Grant

### **Integrative Biology**

Course-based Undergraduate Research Experiences (CUREs) engage students in the practice of science and can enhance undergraduate education by including a large number of students in authentic research. We developed a CURE framework that integrates students into an intellectually diverse and established research network. Our course-based research modules leverage the Salamander Population Adaptation Research Collaboration network (SPARCnet), founded in 2013 by researchers at Pennsylvania State University and USGS Northeast Amphibian and Research Monitoring Initiative. Network research questions examine individual and population level responses of *Plethodon cinereus* to environmental variation and changes expected under human disturbance. Applying the same cover-board plot study design and sampling methods, participants mark salamanders, and thus have long-term spatial-capture-recapture data and basic population demographic data. Our modules engage students in collecting and analyzing field data from a wide geographic range, emphasizing ecology and evolutionary processes, while simultaneously helping students understand both the collaborative nature of science and the quantitative skills required for working with large data sets. We implemented modules in a variety of undergraduate biology courses engaging students in original and publishable data collection, leading to analysis and interpretation of large, multi-year data sets. We paired classrooms during the research experience to develop cross-institution student collaborations. We measured student self-efficacy, science identity, and quantitative and scientific literacy in classrooms using our modules, comparing paired and unpaired implementations. The results of the project will advance knowledge of how this pedagogical approach impacts student outcomes using a cross-institution collaborative CURE framework.

## **Diurnal and nocturnal rodents invest differently in visual and olfactory brain structures**

**Andrea Morrow**, Laura Smale, Barbara Lundrigan

### **Integrative Biology**

Over the course of mammalian evolution, transitions from one daily activity pattern to another (e.g., nocturnality to diurnality) have occurred many times. These transitions are accompanied by changes in the animals' sensory world, as far more photic cues are available during the day than at night. Diurnal animals may capitalize on information carried by these cues if they have a sensory brain capable of extracting it. Nocturnal species are exposed to minimal light, which may have led to selection for adaptations that increase their ability to obtain information carried in other kinds of cues, such as olfactory ones. Here, we test the hypothesis that diurnal species invest more in visual processing, and less in olfactory processing, compared to nocturnal species. Using a phylogenetic framework, we compare the relative sizes of one olfactory brain structure (the olfactory bulb) and two visual brain structures (lateral geniculate nucleus and superior colliculus) of 13 rodent species (5 diurnal; 8 nocturnal). Animals were euthanized and brains removed and frozen. Olfactory bulbs were removed and weighed, and the remaining brain was weighed, sectioned, and stained. Photomicrographs of the stained tissue were taken, and volumes of the two visual regions estimated in Stereo Investigator. Using ANCOVAs to examine the effect of activity patterns on the relative sizes of each brain region, we found that diurnal species had larger visual regions and smaller olfactory regions, compared to nocturnal species, suggesting a tradeoff in investment between visual and olfactory regions of the brain.

## **Seed mix design does not effect restored tallgrass prairie community structure compared to edge effects and plant-consumer interactions.**

**Riley B. Pizza**, Nash Turley, and Lars Brudvig

### **Plant Biology**

The decisions land managers make, especially regarding seed mixes, can influence whether restoration efforts form target native plant communities. Changing the number of species in a seed mix (interspecific diversity), or the number of seed sources of each species (intraspecific diversity) can impact plant community composition by modifying the abundance of ecologically important dominant species. However, aspects of seed mix design are rarely tested, especially at large spatial scales. Moreover, other factors known to influence plant communities including proximity to the edge and consumer pressure may play a larger role in shaping these communities than seed mix design. Thus, I aim to understand the impacts of (1) seed mix inter- and intraspecific diversity, (2) fences that exclude consumers, and (3) edge effects on restored prairie communities. To address these questions, we conducted a prairie restoration experiment at Kellogg Biological station where interspecific and

intraspecific seed mix diversity, distance from the edge, and consumer access were manipulated. We found that there was no effect of seeded intraspecific diversity on species diversity or composition, whereas sowing high interspecific diversity increased species richness by two species/m<sup>2</sup>. Additionally, one common non-sown community dominant (*Elymus repens*, a weedy exotic graminoid) was affected by our seed mix treatments: areas with higher inter- or intraspecific diversity had less *Elymus repens*, indicating reduced invasibility. Finally, excluding consumers and sowing near habitat edges reduced sown richness. Together, these results indicate that edge proximity and consumer pressure shape community structure, whereas seed mix composition may be more influential at controlling individual nuisance species abundances.

## **Rules of infection: Disentangling within-host assembly patterns**

**Ashwini Ramesh, Nina Wale, Christopher Klausmeier**

Integrative Biology, Microbiology and Molecular Genetics

Why do parasites exhibit a wide dynamical range within their hosts? For instance, why do some hosts get sick (infected) but not others? Why do some hosts get more sick than others? Such divergent infection outcomes ought to stem from niche interactions, i.e., with the resources that parasites steal from hosts and the immune cells that kill them. Yet, despite two decades of empirical focus on infection dynamics, we lack a mechanistic framework of within-host infection dynamics that could outline those divergent infection outcomes. To fill that need, we build on a niche framework to illustrate general principles of within-host infection via joint exploitative and immune mediated apparent competition along resource gradients. Hosts and parasites alike require multiple resources, and their disease dynamics shift considerably with multiple resources like in *Daphnia* infected by a castrating bacterium (*P. ramosa*). Using theory, we show how with sufficient trade-offs increasing the phosphorus (P) to carbon (C) supply ratio to host shifts outcomes of infection from clearance (no growth) to sustained infection (i.e. successful invasion and persistence within the host) to dampened infection dynamics. Then, we outline future experiments to test how complex within-host interaction with nutrient supply gradients governs infection outcomes and life-history traits. Together, this mechanistic framework offers new perspectives to better tackle within-host infection dynamics through an ecological lens.

## **Evolution of the vertebrate central nervous system by whole genome duplication**

**Jamilly Lorena, Keyana Blake, Julia Ganz, 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.

## **From efish to zfish: How a large deletion in *CFAP221* affects sperm flagella phenotype**

**Alyssa N. Saunders**

Integrative Biology

Electric fish are most well-known for their electric abilities, but the African electric fish family, Mormyroidea, possesses another interesting feature: sperm that lack flagella. Aflagellate sperm have evolved several times within invertebrate lineages, but mormyroids are the only known case of aflagellate sperm evolving within vertebrates. Mormyroids have a large deletion in Cilia- and Flagella-Associated Protein 221 (*CFAP221*), a gene associated with cilia/flagella formation, in a region that is conserved among other vertebrates. Mutations in *CFAP221* in humans and mice lead to several detrimental phenotypes including infertile aflagellate sperm. Could the gene deletion in mormyroids be the cause of their sperm flagella loss? In order to test this hypothesis, I have created a mutant line of zebrafish with a precise deletion mimicking the one found in mormyroids and examined their sperm.

## **Biology on Tap: Putting the “pub” in public science outreach**

**Ben C. Kline and Alyssa N. Saunders**

Integrative Biology

Biology on Tap is a fun and informal biology talk series that is open to the public and held at bars and pubs in the Greater Lansing area. After a pause during the coronavirus pandemic, this event series was revitalized by a group of EEB graduate students in Fall 2022. Talks are held during the first Thursday of every month and feature MSU-based speakers from a variety of biological disciplines and career stages. This project serves as a great example of the benefit of bringing science outreach to unconventional spaces and gives speakers the opportunity to present their work in new ways.

## **Enhancing biological understanding using AI**

**Shinhan Shiu, Brianna Brown, Huan Chen, Kenia Segura Aba, Thilanka Ranaweera, Eleanore Siler, and Melissa Lehti-Shiu**

Plant Biology, Comp Math Sci & Engr

Biological data has accumulated at a rapid pace due to, in a large part, advances in technologies for their collection. Novel insights, including in evolutionary biology, can be revealed through integrating these data even when they were not collected for the intended purposes. However, integrating biological datasets poses serious challenges because of their sizes, heterogeneity, modalities, and quality differences. We will present a few case studies addressing genetic and molecular evolutionary questions by integrating heterogeneous dataset using machine learning and other artificial intelligence-based approaches. Our goal is to demonstrate their utilities, limitations, and highlight future directions.

## **Peer review perpetuates barriers for historically excluded groups**

**Olivia Smith, Kayla Davis, Riley Pizza, Robin Waterman, Kara Dobson, Brianna Foster, Julie Jarvey, Leonard Jones, Wendy Leuenberger, Nan Nourn, Emily Conway, Cynthia Fiser, Zoe Hansen, Ani Hristova, Caitlin Mack, Alyssa Saunders, Olivia Utley, Moriah Young & Courtney Davis**

Integrative Biology

Peer review is central to the scientific process and scientists' career advancement, but bias at various stages of the review process disadvantages some authors. Here we use peer review data from 312,740 biological sciences manuscripts across 31 studies to (1) examine evidence for differential peer review outcomes based on author demographics, (2) evaluate the efficacy of solutions to reduce bias and (3) describe the current landscape of peer review policies for 541 ecology and evolution journals. We found notably worse review outcomes (for



example, lower overall acceptance rates) for authors whose institutional affiliations were in Asia, for authors whose country's primary language is not English and in countries with relatively low Human Development Indices. We found few data evaluating efficacy of interventions outside of reducing gender bias through double-blind review or diversifying reviewer/editorial boards. Despite evidence for review outcome gaps based on author demographics, few journals currently implement policies intended to mitigate bias (for example, 15.9% of journals practised double-blind review and 2.03% had reviewer guidelines that mentioned social justice issues). The lack of demographic equity signals an urgent need to better understand and implement evidence-based bias mitigation strategies.

## **Drought and Nutrient Excess Influence the Membership and Transmission of the Microbiome of Common Bean, *Phaseolus vulgaris* L.**

**Abby Sulesky-Grieb, Marie Simonin, Matthieu Barret and Ashley Shade**  
Microbiology and Molecular Genetics

The plant microbiome plays an important role in plant health, including benefits such as water and nutrient assimilation and plant growth promotion, and is comprised of multiple compartments, including the rhizosphere, rhizoplane, phyllosphere, and endosphere of internal tissues such as roots and seeds. It has been demonstrated that plant microbiome members can be vertically transmitted to subsequent generations through the endophytic seed microbiome, but little is known about the role and importance of these microbes. Our research aims to understand the inheritance of the microbiome of common bean (*Phaseolus vulgaris* L.) via the seed, and how this microbiome is impacted by drought and excess nutrient conditions. We conducted a multi-generational experiment in controlled growth chamber conditions where plants grown from a starting Gen0 seed pool received a control, drought, or high nutrient condition for two generations. The Gen1 and Gen2 rhizosphere, root and seed microbiome and plant health were analyzed to assess impacts of treatment. We found 8 taxa that were consistent in each microbiome compartment across all generations and detected significant impacts of Gen1 parental plant treatment on the resulting microbiome in Gen2. Reduced impact of stress treatment on plant growth in Gen2 also suggests potential influence of the previous generation's exposure. We expect these results to increase understanding of key microbiome members responsive to altered environmental conditions, and their persisting impact on the plant microbiome. Ultimately, this work will provide insights into potential agricultural management techniques to increase plant health and resilience under changing climate conditions.

## **Of microplastics and minnows: quantifying the molecular effects of lifelong microplastics exposure on fathead minnows (*Pimephales promelas*)**

**Miranda Wade, Kennedy Bucci, Chelsea Rochman, Mariah Meek**

### **Integrative Biology**

Microplastics are an important, pervasive pollutant, with mixed impacts on organisms across ecosystems. There is a need to increase our understanding of the molecular response to microplastics as species are increasingly living their entire lives in the presence of plastic pollution. To this end, we performed an experiment using liver tissue from fathead minnows (*Pimephales promelas*) living in different microplastic treatments. We tested two microplastic concentrations, reflecting both current and predicted future conditions, of both pristine plastic and environmental plastic gathered from Lake Ontario. We used directional mRNA sequencing to determine differential gene expression in single genes and across gene modules among the treatments. We addressed the following questions: 1) is there a consistent, measurable effect of microplastics exposure and 2) if there are changes in gene expression attributed to the microplastics, do these differ across either concentration or source? Our findings indicate that there is an effect of microplastics, although the effect is stronger in female minnows. Additionally, there is evidence of metabolic and liver changes in the fish exposed to microplastics compared to the controls. Many of the differentially expressed genes are known to interact with bisphenol A (BPA), a chemical associated with plastic. As fathead minnows are an important toxicological model species, our hope is that the results of this study will have implications across aquatics species and ecosystems. Additionally, this increases our knowledge of the molecular response of species to anthropogenic pollution with the goal of informing environmental policy decisions regarding microplastic pollution.

## **Testing adaptive hypotheses for selection on anther position traits through slow-motion videos of pollinators**

**Robin Waterman, Sally Song, Nicholas Bhandari, and Jeffrey Conner**

### **Plant Biology**

Interactions with pollinators are an important driver of floral trait evolution in plants that rely on animal-mediated pollination for reproductive success. While many studies have found evidence for selection on certain floral traits, these measures provide little insight into the adaptive function of the traits. The present study uses observational data to test functional hypotheses in a system for which selection on floral traits has been well-characterized. In wild radish (*Raphanus raphanistrum*), the anther position traits anther exertion (long filament – corolla tube lengths) and anther separation (long – short filament lengths) are of interest because of the high correlations among and strong evidence for correlational selection on

their component traits. It has been hypothesized that the mechanism by which these traits affect fitness is altering how well pollinator bodies, particularly sweat bees, make contact with the anthers. We tested this hypothesis using slow-motion videos of pollinators visiting wild radish plants. We quantified the extent of contact between both short and long anthers and three sections of pollinators' bodies, then measured anther position on the visited flowers. During this talk I'll present some preliminary results from this project.

## **Characterizing the role of interannual environmental variability in structuring the life histories of global ecological communities**

Jeff Doser, Kelly Kaspar, Lala Kounta, Adriana Uscanga, Casey Youngflesh, and **Peter Williams**

Integrative Biology, Institute for Biodiversity, Ecology, Evolution, and Macrosystems

Climate change increases interannual climate variability, leading to more extreme climate events. To know how species will respond to more variable climates, we first need to understand how species have evolved to deal with variability. Life history theory predicts that environmental variability should influence species longevity, but this has not been tested. Our research synthesizes several global datasets to characterize the role of environmental variability in shaping communities of birds and mammals. Our project brings together a team of postdoctoral researchers with diverse research backgrounds, funded by the Institute for Biodiversity, Ecology, Evolution, and Macrosystems (IBEEM) at MSU.

## **Distinct diurnal and nocturnal flower visitor communities provide pollination services in urban gardens**

**Nicole E. Wonderlin**

Entomology

Urban gardens are thought to be a key tool for mitigating biodiversity and plant-pollinator interaction loss due to their ubiquity in urban landscapes and the variety of resources they provide. To date, most pollination research in these habitats has focused on diurnal pollination, omitting a potentially important group of pollinators. To assess the diversity and pollination activity of both diurnal and nocturnal pollinators in urban gardens, I monitored all plant visitors to a focal inflorescence for 24-hour cycles and calculated the frequency and duration of visitation. I also measured the contribution of day and night communities to pollination and plant fecundity using a pollinator exclusion experiment. Plants open to only diurnal pollination tended to produce more seeds, while plants open to only nocturnal pollinators produced larger seeds, signaling a potential tradeoff between seed production and size among visitor communities. On average, diurnal plant visitors tended to have higher

visitation frequencies, but nocturnal visitors had significantly longer visit durations. Distinctly different arthropod communities engaged in daytime versus nighttime floral visitations. Differences in plant visitation and dynamic impacts on plant fecundity indicate that diurnal and nocturnal communities play unique roles in urban spaces.

## **Soil bacterial community responses to multiple climate stressors in an early successional plant community**

**Moriah Young, Sarah Evans, and Phoebe Zarnetske**

### **Integrative Biology**

Soil microbes play a central role in ecosystem processes, thus understanding how they respond to climate change is crucial to our ability to predict ecosystem processes in a changing world. Additionally, studies looking at the effects of multiple climate stressors occurring simultaneously on soil microbes are lacking. To address these knowledge gaps, we used an integrative approach that combines field experimentation with metagenomic amplicon sequencing to quantify how multiple climate change stressors affect soil microbes.

We ran a fully factorial experiment at Kellogg Biological Station's Long Term Ecological Research site with the following treatments across 6 replicate plots: open-top chambers to mimic year-round warming; rainout shelters to mimic a 6-week drought; and insecticide to reduce insect herbivory. Soil samples were taken in summer 2021 at four different times: pre-drought, peak-drought, post-drought, and recovery. In order to characterize the soil bacterial community structure across samples, DNA was extracted to sequence 16S V4 gene amplicons.

Preliminary results reveal that there were no strong differences in soil microbial community composition among treatments or time of sampling. This multi-year study began in 2021 and will continue through 2023 to further elucidate the short and longer-term responses of microbes to warming and drought. This research will ultimately advance understanding and prediction of soil microbial community responses to multiple climate stressors over time, while accounting for multi-year legacy effects of drought, warming, and reduced herbivory.