

The Sixth Annual
Ecology, Evolution, & Behavior
Research Symposium



**ECOLOGY
EVOLUTION
BEHAVIOR**

**MICHIGAN STATE
UNIVERSITY**

May 2, 2022

Michigan State University

Henry Center for Executive Development

3535 Forest Rd, Lansing, MI 48910

Table of Contents

Acknowledgements	3
Welcome from the EEB Director	4
Twitter and Social Media Policy	5
Keynote Speaker	6
Awards & Judges	7
Schedule Overview	8
Detailed Schedule	10
Henry Center Map & Lunch Menu	14
Presentation Abstracts	16

Alcorn, poster	Fiser, poster	Malmstrom, lightning
Branding, talk	Fitch, poster	Moreno, talk
Buysse, poster	Fong, talk	Saunders, poster
Clark, talk	Graham, talk	Smith, talk
Dahlin, lightning	Heath-Heckman, lightning	Spagnuolo, talk
Do, poster	Jaynes, talk	Utley, talk
Doser, lightning	Kline, poster	Wuyun, talk
Lowry lab, poster	Liu, lightning	
Saunders, community engagement poster		
Branding, community engagement poster		

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

Wendy Leuenberger, Co-Chair

Jeff Doser, Co-Chair

Asia Hightower

Ani Hristova

Emily Liljestrang

Kota Nakasato

Welcome from the EEB Director

Welcome to the sixth 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 Jeff Doser and Wendy Leuenberger: Asia Hightower, Ani Hristova, Emily Liljestrand, and Kota Nakasato, 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 six 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 cursive script that reads "Elise Zipkin".

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:

#MSUEEB2022

Keynote Speaker

Dr. Simone Des Roches

School of Aquatic and Fishery Sciences

University of Washington

<https://www.simonedr.com/>

The rapid loss of intraspecific variation is an often overlooked biodiversity crisis. Intraspecific variation, which includes the genomic and phenotypic diversity found within species, is threatened by local extinctions, abundance declines, and direct selection by humans. Although ecologists have long acknowledged that variation among species influences the environment, only recently have researchers demonstrated the ecological importance of variation within species. Therefore, loss and changes to intraspecific variation can have substantial consequences for ecosystems and



human society through nature's contributions to people ("NCP," an extension of ecosystem services). My work shows that intraspecific effects are often comparable to, and sometimes stronger than, species effects. I then review the literature demonstrating that intraspecific variation supports the main types of NCP (material, non-material, and regulating) and highlight strategies to conserve and restore this important form of biodiversity. I conclude with a discussion of intraspecific variation in the context of social, ecological, and evolutionary dynamics in urban areas.

Awards

The following awards will be presented:

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

Best faculty lightning talk (1st)

Best poster (1st, 2nd)

Thank you to our judges:

Sam Ayebare

Emily Conway

Kayla Davis

Emily Dolson

Asia Hightower

Rebecca Panko

Gary Roloff

Nina Wale

Nicole Wonderlin

Vote for the best faculty lightning talk [here!](#)

EEB Research Symposium Schedule Overview

(All events at the Henry Center)

Time	Event	Location
8:00-9:00	Registration and Breakfast	Entrance Lobby/Atrium
9:00-9:15	Welcome & Opening Remarks <i>Elise Zipkin, EEB director</i> <i>Jeff Doser</i>	Auditorium
9:15-10:15	Keynote Address <i>Simone Des Roches, University of Washington</i>	Auditorium
10:15-10:35	Break	
10:35-11:35	Session I Oral Presentations (Moderator: Kota Nakasato) 1035- Steven Fong (FW) 10:50- Jonah Branding (PHL) 11:05- Qiqige Wuyun (CSE) 11:20- Matthew Andres Moreno (CSE)	Auditorium
11:35-12:00	Session II Lightning talks (Moderator: Jeff Doser) 11:35- Elizabeth Heath-Heckman (IBIO, MMG) 11:40- Kevin Liu (CSE) 11:45- Carolyn Malmstrom (PLB) 11:50- Kyla Dahlin (GEO) 11:55- Jeff Doser (IBIO)	Auditorium
12:00-1:10	Lunch	Atrium
1:10-2:10	Session III Oral Presentations (Moderator: Ani Hristova) 1:10- Olivia Smith (IBIO) 1:25- Kyle Jaynes (IBIO) 1:40- Olivia Spagnuolo (IBIO) 1:55- Olivia Utley (IBIO)	Auditorium
2:10-2:35	EEB Community Engagement (Moderator: Wendy Leuenberger) 2:10- EEB Collaborative Research Group 2:15- EEB Reading Group	Auditorium

2:20- Q&A Session on EEB Community Engagement

2:35-2:50	Break	
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2:50-3:20	Session IV Oral Presentation (Moderator: Asia Hightower) 2:50- Carolyn Graham (PLB) 3:05- Meaghan Clark (IBIO)	Auditorium
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3:20-4:15	Poster Session/Mingling/Break Rachel Alcorn (IBIO), Jonah Branding (PHL), Sophie Buysse (PLB), Woo Seok Do (IBIO), Cynthia Fiser (ENT), Olivia Fitch (IBIO), Ben Kline (IBIO), Alyssa Saunders (IBIO), Lowry lab (PLB)	Atrium
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4:15-4:30	Closing Remarks, Awards Ani Hristova, Wendy Leuenberger EEB Research Symposium Planning Committee	Auditorium
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4:30-6:00	Happy Hour!!	Four Seasons Lounge
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EEB Research Symposium Detailed Schedule

8:00-9:00	<u>Registration and Breakfast</u>	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.	
9:00-9:15	<u>Welcome & Opening Remarks</u>	
	<i>Elise Zipkin, EEB director</i>	
	<i>Jeff Doser</i>	
9:15-10:15	<u>Keynote Address</u>	
	Conserving diversity within species for ecosystems & people	
	<i>Simone Des Roches, School of Aquatic and Fishery Sciences, University of Washington</i>	
10:15-10:35	Break	
10:35-11:35	<u>Session I Oral Presentations</u> (Moderator: Kota Nakasato)	
	Using genomic techniques to evaluate supplemental control effectiveness on invasive sea lamprey populations in the Great Lakes	abstract
	Steven Fong, Graduate student Department of Fisheries and Wildlife	
	Who Understands Computational Models?	abstract
	Jonah Branding, Graduate student Department of Philosophy	
	Introgression detection and analysis	abstract
	Qiqige Wuyun, Graduate student Department of Computer Science and Engineering	
	Hereditary Stratigraphy: Genome Annotations to Enable Phylogenetic Inference over Distributed Digital Evolution Populations	abstract
	Matthew Andres Moreno, Graduate student Department of Computer Science and Engineering	
11:35-12:00	<u>Session II Lightning talks</u> (Moderator: Jeff Doser)	
	Bobtail Squid as a model for the evolution and development of mutualisms	abstract
	Elizabeth Heath-Heckman, Faculty Department of Integrative Biology, Microbiology and Molecular	

Genetics

Novel algorithms for complex comparative genomic and phylogenomic analyses

[abstract](#)

Kevin Liu, Faculty

Department of Computer Science and Engineering

The power of small: Viruses and plant ecology

[abstract](#)

Carolyn Malmstrom, Faculty

Department of Plant Biology

Introducing MSU's Institute for Biodiversity, Ecology, Evolution, and Macrosystems (IBEEM)

[abstract](#)

Kyla Dahlin, Faculty

Department of Geography, Environment, and Spatial Sciences

Spatial relationships between geodiversity and genetic diversity

[abstract](#)

Jeff Doser, Postdoc

Department of Integrative Biology

Lunch

12:00-1:10

Please join us in the Henry Center atrium for lunch.

1:10-2:10

Session III Oral presentations

(Moderator: Ani Hristova)

Complex landscapes stabilize farm bird communities and their expected ecosystem services

[abstract](#)

Olivia Smith, Postdoc

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

Exploring patterns of persistence in rediscovered Harlequin frogs,

[abstract](#)

Kyle Jaynes, Graduate student

Department of Integrative Biology

Effects of livestock grazing on spatial and temporal niche partitioning of large carnivores

[abstract](#)

Olivia Spagnuolo, Graduate student

Department of Integrative Biology

: The effects of landscape characteristics on pest removal by American Kestrels

[abstract](#)

Olivia Utley, Graduate student

Department of Integrative Biology

2:10-2:35

EEB Community Engagement session

(Moderator: Wendy Leuenberger)

This new session features the first cohort of EEB Postdoctoral

fellows. Olivia Smith and Daniela Palmer will discuss the community engagement component of their fellowship and answer questions about the process.

EEB Collaborative Research Group

Olivia Smith

EEB Reading Group

Daniela Palmer

Q&A Session on EEB Community Engagement

2:35-2:50

Break

2:50-3:20

Session IV Oral Presentations

(Moderator: Asia Hightower)

Multivariate defensive trait evolution across scales in Vitis

Carolyn Graham, Graduate student
Department of Plant Biology

[abstract](#)

Pitfalls and promise in population genetic approaches for detecting demographic declines in long-lived species

Meaghan Clark, Graduate student
Department of Integrative Biology

[abstract](#)

3:20-4:15

Poster Session/Mingling/Break

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

Poster 1

Investigating the role of the T-box gene family in the developmental evolution of fishes using the spotted gar model system

Rachel Alcorn, Staff
Department of Integrative Biology

[abstract](#)

Poster 2

Population Differentiation for Plasticity in *Arabidopsis thaliana*

Sophie Buysse, Graduate student
Department of Plant Biology

[abstract](#)

Poster 3

Hatching enzyme evolution and expression in spotted gar, a model organism for vertebrate evolutionary developmental genomics

Woo Seok Do, Undergraduate Student
Department of Integrative Biology

[abstract](#)

Poster 4

**Fresh out of the Lowry Lab
David Lowry, Faculty
Department of Plant Biology**

[abstract](#)

- Poster 5 **Ground beetle (Coleoptera: Carabidae) communities within KBS LTER prairie strips and surrounding row crop** [abstract](#)
Cynthia Fiser, Graduate student
Department of Entomology
- Poster 6 **Examining adaptive genetic variation in response to thermal stress in brook trout across the native range** [abstract](#)
Ben Kline, Graduate student
Department of Integrative Biology
- Community Engagement Poster 7 **VERITIES: A Scientific Virtue-based Responsible Conduct of Research Initiative** [abstract](#)
Jonah Branding, Graduate student
Department of Philosophy
- Poster 8 **Cilia- and flagella-associated protein 221 C-Terminus Deletion Necessary for Aflagellate Sperm in Mormyrid Weakly Electric Fishes** [abstract](#)
Alyssa Saunders, Graduate student
Department of Integrative Biology
- Community Engagement Poster 9 **Build-a-Fish MSU: An Engaging Activity for K12 Students to Learn About Fish Biodiversity** [abstract](#)
Alyssa Saunders, Graduate student
Department of Integrative Biology
- Poster 10 **A tale of two tails: Developmental evolution of a key innovation in the fish caudal region** [abstract](#)
Olivia Fitch, Graduate student
Department of Integrative Biology
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4:15-4:30

Closing Remarks & Awards

Ani Hristova, Wendy Leuenberger
EEB Research Symposium Planning Committee

4:30-6:00

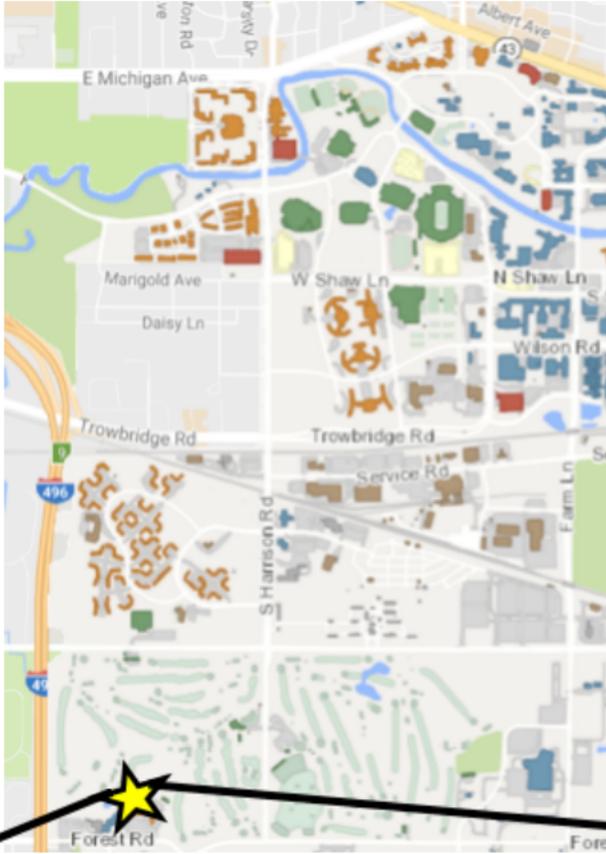
Happy Hour!!

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

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

Bread, butter, olive oil, balsamic vinegar

Hot Buffet

Chicken fajitas with onion, peppers, flour tortillas, cheese, salsa, guacamole

Cheddar and jack cheese enchiladas

Fiesta corn with peppers and cilantro

Spanish rice with black beans

Cheese and vegetable quesadillas

Desserts & Beverages

Lemon meringue pie

Tiramisu

Regular coffee, decaf, tea service

Abstracts

Alphabetical by presenting author's last name.

Investigating the role of the T-box gene family in the developmental evolution of fishes using the spotted gar model system

Rachel C. Alcorn, Keyana Blake, Olivia E. Fitch, Ingo Braasch
Integrative Biology

Ray-finned fishes make up over 50% of living vertebrate species and are diverse in both species number and body plans. We are interested in identifying genetic evolutionary mechanisms underlying morphological diversity of these fishes including the configuration of their different fin types. Of these mechanisms, the T-box (tbx) gene family encodes transcription factors necessary for development of body appendages, organs, and other major structures during vertebrate embryonic development. Paired fins in fishes are regulated by tbx5 and tbx4 in early development of pectoral (anterior) and pelvic (posterior) fins, respectively. Embryonic tail development in fishes is thought to be regulated by tbx6, tbx16, and tbx18, where tbx18 is also involved in dorsal and anal fin positioning. Holostean fishes, gars and bowfin, are the closest living outgroup to the teleost fishes, the largest group of all fishes. Here we use spotted gar (*Lepisosteus oculatus*) with asymmetrical (heterocercal) caudal regions and small, posteriorly located dorsal fins, as comparison to teleosts, with symmetrical (homocercal) caudal regions, and to bowfin, with large dorsal fins spanning most of its back. The objective of this study is to better understand the function of the T-box gene family in development of holostean fishes in comparison to the established zebrafish model. By using RNA in-situ hybridization, spatial and temporal patterning of expression for T-box genes in spotted gar embryos can be analyzed. Findings of this study will enrich current functional understanding of the T-box gene family and their involvement in the evolution of diverse body plans among ray-finned fishes.

VERITIES: A Scientific Virtue-based Responsible Conduct of Research Initiative

Jonah Branding, Eric Berling, Marilyn Amey, Ike Iyioke, Thomas Jeitschko, Chet McLeskey, Jesenia Rosales, Michael O'Rourke, Robert T. Pennock
Philosophy, VERITIES

Ensuring that scientists conduct research responsibly is essential for the advancement of science. Scientific misconduct, ranging from questionable research practices through

intentional dishonesty, can set science back by wasting both the time of the scientific community and the limited funding available to support research. As such, one important aspect of scientific training is focused upon helping scientists to conduct their research responsibly, and many funding agencies now explicitly require this for their supported scientists. Unfortunately, the standard methods of teaching responsible conduct of research are known to be imperfect. Drawing on Pennock's theory of vocational virtue and using O'Rourke's Toolbox model of guided dialogue, we developed an alternative curriculum for training scientists to act responsibly that emphasizes internally derived values rather than externally imposed rules. This approach focuses on the ways that the virtuous characteristics of scientists lead to responsible and exemplary behavior. This scientific virtues-based approach can augment traditional approaches, and we believe that by focusing on the positive roles of virtues, especially through participant-driven discussions, responsible conduct of research training will be more engaging, and thus more influential, than simply completing the tasks required to satisfy traditional certification requirements. We piloted and assessed this approach in the BEACON Center for the Study of Evolution over the last decade. Results have shown that participants greatly prefer this engaging virtues-based model over the traditional methods of RCR training. Under a new NSF grant project (VERITIES), we are now extending it to other units across MSU, including EEB.

Who Understands Computational Models?

Jonah Branding

Philosophy, VERITIES

The rise of computational models in biology and other sciences raises novel issues for the philosopher of science. One such issue is: who can be said to "understand" a computational model--the human researcher, her computer, or some broader hybrid system involving the researcher and her computer? Borrowing from John Searle's classic "Chinese Room" argument, I argue that only human researchers can be said to understand scientific models. This suggests that there are limits to human understanding which will not be overcome by future advancements in computer power.

Population Differentiation for Plasticity in *Arabidopsis thaliana*

Sophia Buysse, Jeffrey Conner, and Emily Josephs

Plant Biology, Kellogg Biological Station

Rapid climate changes are projected to increase environmental stress on populations and impact species persistence. Plasticity is the ability of a genotype to produce different phenotypes in response to different environmental conditions. Adaptively plastic populations are more likely to survive rapid environmental changes through an immediate response to stressors and persist long enough to genetically adapt to new environments. Understanding

plasticity will be important during periods of rapid environmental change and in the increasingly variable climates projected for the coming decades. To investigate population differentiation for plasticity, we grew multiple genotypes from locally adapted *Arabidopsis thaliana* populations native to Rödåsen, Sweden (SW) and Castelnuovo di Porto, Italy (IT) in each of two chamber environments: current and future. Each environment simulated either current or future conditions for near the SW native population. Plants were phenotyped for developmental landmarks, drought response, biomass allocation, and fitness. Plasticity was typically in the same direction in both populations. For example, in the future environment, both SW and IT decrease in specific leaf area. This is likely adaptive as plants grow thicker leaves in drier climates to reduce water loss. However, IT is more plastic than SW for most of the traits we analyzed. This contradicts expectations; because the SW native environment is more variable, we expected SW to be more plastic than IT. Future work will identify if plasticity is adaptive and use recombinant inbred lines to identify quantitative trait loci for plasticity as a first step in identifying genetic mechanisms of plasticity.

Pitfalls and promise in population genetic approaches for detecting demographic declines in long-lived species.

Meaghan I. Clark and Gideon S. Bradburd
Integrative Biology, Kellogg Biological Station

Patterns of genetic diversity and relatedness are shaped by both historical and contemporary demographic events. Detecting recent demographic change is a crucial component of conservation genetics, as many natural populations face declines due to recent habitat alteration and climate change. In species with long lifespans, there is a lag between the start of a decline in population numbers and the resulting decrease in genetic diversity. This lag slows the rate at which diversity is lost, but also makes it difficult to detect recent declines using genomic data. However, the genomes of long-lived individuals can provide a window into the past and can potentially be contrasted with those of younger individuals to learn about recent changes in the population. We use forward-time, individual-based simulations to quantify the genetic patterns associated with recent demographic changes in long-lived species and evaluate how these patterns change between age classes. We compare these results to Wright-Fisher simulations to evaluate how longevity can be both a hindrance and a boon to detecting recent demographic declines from population genomic data.

Introducing MSU's Institute for Biodiversity, Ecology, Evolution, and Macrosystems (IBEEM)

Kyla M. Dahlin, Phoebe L. Zarnetske, Kendra S. Cheruvellil, Gideon S. Bradburd, John D. Robinson, and Elise F. Zipkin

Geography, Environment, and Spatial Sciences, ESPP

MSU's newly funded Institute for Biodiversity, Ecology, Evolution, and Macrosystems (IBEEM) focuses on critical interdisciplinary science questions related to understanding and predicting ecological and evolutionary responses to global changes including climate change and land use change. IBEEM aims to facilitate interactions among MSU's diverse areas of expertise including macrosystems biology, ecology, evolution, machine learning, data mining, statistics, data science, remote sensing, geographical information sciences, water resources, systems integration and modeling, sustainability science, and land-atmosphere interactions. This short presentation will introduce IBEEM to the EEB community and highlight opportunities for engagement in the coming years.

Hatching enzyme evolution and expression in spotted gar, a model organism for vertebrate evolutionary developmental genomics

Woo Seok Do, Ingo Braasch, and Andrew W. Thompson
Integrative Biology,

Hatching is an essential process for every vertebrate. It is a key developmental transition that allows the animal to break out of the egg envelope and become a free-living organism. Aquatic vertebrates such as teleost fishes, use highly derived metalloproteases as hatching enzymes to break down egg envelope proteins. However, the highly complex evolutionary history and developmental characterization of this gene family is lacking in non-teleost fishes such as the spotted gar. Spotted gar is a species of ray-finned fish known as a "living fossil" due to its slow rate of evolution. It is an informative study organism that bridges the gap between fish and other terrestrial vertebrates. The aim of this project is to identify the enzymes that spotted gar uses for hatching and locate the gar hatching gland. Hatching enzyme gene candidates of spotted gar were identified by comparing metalloprotease genes from other vertebrates to the gar genome. An evolutionary tree was generated using metalloprotease genes identified in previous studies as well as several gar sequences that we identified to be members in this gene family. We compared these candidate sequences to patterns of gar gene expression to identify metalloproteases expressed during the gar embryonic pre-hatching stage. We identified several key gar genes closely related to teleost hatching enzymes for spatio-temporal characterization using RNA in situ hybridization on gar embryos to reveal the location of the spotted gar hatching gland.

Spatial relationships between geodiversity and genetic diversity

Jeffrey W. Doser, Rachel H. Toczydlowski, Jasper Van doninck
Integrative Biology, Institute for Biodiversity, Ecology, Evolution, and
Macrosystems

Geodiversity, the variation in Earth's abiotic processes and features, shows clear

spatio-temporal relationships with biodiversity across multiple spatial scales. While these relationships have been explored for taxonomic, functional, and phylogenetic diversity, there is limited understanding of the spatial relationship between biodiversity and intraspecific genetic diversity, or the genetic variation within a species, in large part due to limited availability of spatially-explicit genetic data and the associated computational tools. Areas of high geodiversity may help buffer biodiversity against climate change by harboring more species and their unique functions. In this project, we seek to address questions such as: (1) can geodiversity predict genetic diversity; (2) how does the relationship between geodiversity and genetic diversity vary across similar species; and (3) are these patterns consistent across geographic scales?

Ground beetle (Coleoptera: Carabidae) communities within KBS LTER prairie strips and surrounding row crop

Cynthia Fiser and Douglas Landis
Entomology,

Perennial prairie strips are a conservation strategy aimed at mitigating the detrimental effects of intensive agriculture while promoting biodiversity and encouraging ecosystem services. Ground beetles (Coleoptera: Carabidae) are important generalist predators in agricultural systems that prey on a variety of insect pests and weed seeds. Little is known about how prairie strips in US row crops may alter Carabid abundance, community structure and predation services.

We measured the abundance, richness, and community composition of ground beetles in newly-established prairie strips and the surrounding row crops using pitfall traps. Data were collected over a three year period within the prairie strips and at varying distances into the surrounding row crop. We expected ground beetle abundance and richness to differ 1) over time, as prairie strip vegetation establishes; 2) with crop management history (reduced-input conventional vs. biologically-based); and 3) with distance from the prairie strip.

To date, I have identified 41 ground beetle species, including several abundant generalist predators and weed seed eaters. Total abundance increased from 2019(456) to 2020 (753). Ground beetle community composition differed with crop management history and between two years of the study but did not appear to differ strongly with distance from the prairie strip. This analysis will frame future research questions for the provision of ecosystem services by ground beetles in row crops containing prairie strips.

A tale of two tails: Developmental evolution of a key innovation in the fish caudal region

Olivia E. Fitch, Andrew W. Thompson, Camilla Peabody, Ingo Braasch
Integrative Biology, BEACON

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. The genetic evolutionary mechanisms underlying the hetero-to-homocercal transition (HTHT) in teleost ancestry have yet to be uncovered. We test the hypothesis that differential outgrowth of two caudal structures in fish, 1.) the post-vertebral notochord and associated structures, and 2.) the caudal fin, ultimately resulted in the diversity of caudal morphologies in ray-finned fishes including the HTHT, and may extend to vertebrate caudal diversity more generally. We also test if this differential outgrowth may be controlled by homeotic genes such as Hox cluster genes which are deeply homologous genes that determine animal body axes. To test these hypotheses, we compare caudal development in the homocercal teleost zebrafish with the heterocercal spotted gar, representing the closest living outgroup to teleosts. To this end, we use comparative genomics, morphological studies, gene expression analyses, and chromatin profiling to identify candidate genes and regulatory elements for caudal region development that may underlie the HTHT and contribute to our genomic understanding of vertebrate caudal region evolution and development.

Using genomic techniques to evaluate supplemental control effectiveness on invasive sea lamprey populations in the great lake

Steven Fong, Kim Scribner, Nick Johnson, and John Robinson

Fisheries and Wildlife

Sea lamprey (*Petromyzon marinus*) are invasive in the Great Lakes of North America. Chemical lampricides and barriers have been used to control sea lamprey populations, but recently the addition of sterile male release and pheromones (supplemental controls) have been added to the more traditional control methods. Supplemental controls have been recently tested, but complexities in sea lamprey demographics and life history characteristics have made long-term assessment difficult. With the expansion and affordability of next generation DNA sequencing techniques, we can gather long-term data that previously would have been too labor intensive or impossible to gather. For the first 4-years of this 10 to 12-year project we will document and monitor larval sea lamprey populations under current barrier and chemical lampricide treatment methods. For the subsequent 4 to 6 years, supplemental controls will be deployed and examined using the initial 4-years of collected

data. Assessment will be based on the number of adult sea lamprey contributing to the next generation and if larval populations are compensating for reduced annual recruitment (e.g., experiencing faster growth and/or higher survival). RAD-Seq will be utilized at ~3000 target sequences, containing select single nucleotide polymorphism markers, to perform pedigree reconstructions and close-kin mark-recapture analysis. Estimates will allow managers to evaluate annual number of effective breeding adults and total number of spawning adults that contribute to age-1 cohorts. These data will inform managers on the effect supplemental controls has on efforts to control invasive sea lamprey populations in the Great Lakes.

Multivariate defensive trait evolution across scales in *Vitis*

Carolyn D. K. Graham, and Marjorie G. Weber

Plant Biology

Hypothesized trade-offs and synergisms between traits are fundamental to our understanding of the generation and maintenance of diversity. Evolutionary biologists have thus been long interested in identifying correlations between ecologically relevant traits. However, correlations between traits at the interspecific level may be obscured or even reversed at the intraspecific level, making research across levels of biological organization critical for a full understanding of evolutionary trait correlations. I conducted a multi-scale study of trait correlations focused on a set of ecologically important traits with an extensive body of interactions: plant defenses. I quantified eight defense-related traits (trichomes, specific leaf area, secondary metabolism, CaOx crystals, carbon to nitrogen ratio, leaf thickness, mite domatia, and food bodies) across 20 species of the grape genus *Vitis* to look for interspecific correlations in defense investment indicative of trade-offs or synergisms using phylogenetic comparative methods. I additionally performed the same quantifications across 18 genotypes of the widespread *Vitis* species *V. riparia* to contrast patterns in defense investment at the inter- and intraspecific levels. I then performed a series of no-choice bioassays with a generalist herbivore to determine the overall defensive capacity of each *Vitis* species and genotype. Finally, I used occurrence data and average climate metrics to look for associations between *Vitis* defense traits and latitude, annual temperature, precipitation, temperature seasonality, and precipitation seasonality. Preliminary analysis has revealed few significant correlations between defense traits across nor within *Vitis* species, indicating that at both the interspecific and intraspecific levels, defense traits evolve independently in this clade.

Bobtail Squid as a model for the evolution and development of mutualisms

Elizabeth Heath-Heckman

Integrative Biology, Microbiology and Molecular Genetics

Exploring patterns of persistence in rediscovered Harlequin frogs

Kyle E. Jaynes, Mónica I. Páez-Vacas, David Salazar-Valenzuela, Juan M. Guayasamin, Andrea Terán-Valdez, Fausto R. Siavichay, Luis A. Coloma, and Sarah W. Fitzpatrick

Integrative Biology, Kellogg Biological Station

Amphibians face global declines, and it remains unclear the extent to which species have responded, and through what mechanisms, to persist in the face of emerging diseases and climate change. In recent years, the rediscovery of species considered possibly extinct have sparked public and scientific attention. These are hopeful cases in an otherwise bleak story. Yet, we know little about the population status of these rediscovered species, or the biology underlying their persistence. In this talk, I will highlight the iconic Harlequin frogs (Bufonidae: *Atelopus*) as a system that was devastated by declines but now encompasses numerous rediscoveries in the last two decades. I'll share temporal and spatial patterns of rediscoveries across the genus (105 species) and provide genomic data on six decimated species with varying decline histories in the geographic epicenter of rediscoveries (Ecuador) to explore patterns of genomic diversity in persisting populations.

Examining adaptive genetic variation in response to thermal stress in brook trout across the native range

Benjamin Kline, Mariah Meek, Clint Kraft, Pete McIntyre

Integrative Biology,

Identifying the underlying genetic variation that enables organisms to respond to thermal stress is essential to understanding how freshwater fish will persist in rapidly changing environments. Unlike other organisms, fish are confined to aquatic habitats and are often unable to relocate to more favorable environments if local conditions decline. Aquatic organisms under climate change must either adapt to local conditions or die. Given the accelerated rate of climate change and the direct and measurable effects on native species, it is essential that conservation scientists and managers have the proper tools to monitor populations exposed to extreme and unstable environmental regimes. Using brook trout (*Salvelinus fontinalis*) as a model organism, we are examining the standing genetic variation of populations exposed to a range of thermal conditions across the native species range. Specifically, we are using a genetic panel that targets regions of the genome associated with thermal tolerance to identify population-level variation that may influence the capacity of fish to respond to heat stress. In doing so, we hope to create a tool that enables managers to proactively quantify and assess which populations of brook trout are expected to be buffered from the effects of climate change, and equally importantly, which populations are most at

risk of local extinction.

Novel algorithms for complex comparative genomic and phylogenomic analyses

Kevin J. Liu

Computer Science and Engineering, BEACON, BMS

This lightning talk provides an overview of our lab's recent and ongoing research. Our main focus is developing new computational methodologies for efficient and accurate comparative genomic analyses – especially in the context of complex evolutionary scenarios – and then connecting the resulting insights to phenotype and function. The end goal of our big-data-driven approach is to generate hypotheses that result in new biological and biomedical discoveries.

Fresh out of the Lowry Lab

Daniel Anstett, Nathan Emery, Leslie Kollar, Jason Olsen, Lauren Stanley, Acer VanWallendael, **David Lowry**

Plant Biology, Kellogg Biological Station

The research of the Lowry lab is centered on identifying the genetic and physiological mechanisms of ecological adaptations, understanding how those adaptations contribute to the formation of new species, and developing approaches to translate our knowledge of adaptations into the improvement of crop species. To understand the physiological, developmental, and genetic mechanisms of adaptive divergence between plant populations, the Lowry lab is focused on research in two systems for evolutionary genomics: Monkeyflowers (*Mimulus*), and *Panicum* grasses.

The power of small: Viruses and plant ecology

Carolyn M. Malmstrom

Plant Biology, Center for Microbial Ecology

Viruses are abundant on Earth but in the past have been largely omitted from the study of terrestrial ecology. Now interest in viruses has been awakened by the SARS-CoV-2 pandemic and deep-sequencing discoveries of thousands of novel viruses throughout the biosphere. In this lightning talk, I will highlight why viruses are cool and important for ecology and outline some exciting research directions in plant virus ecology in particular.

Hereditary Stratigraphy: Genome Annotations to Enable Phylogenetic Inference over Distributed Digital Evolution Populations

Matthew Andres Moreno, Emily Dolson, Charles Ofria

Computer Science and Engineering, BEACON

Phylogenies provide direct accounts of the evolutionary trajectories behind evolved artifacts in genetic algorithm and artificial life systems. Phylogenetic analyses can also enable insight into evolutionary and ecological dynamics such as selection pressure and frequency dependent selection. Traditionally, digital evolution systems have recorded data for phylogenetic analyses through perfect tracking where each birth event is recorded in a centralized data structures. This approach, however, does not easily scale to distributed computing environments where evolutionary individuals may migrate between a large number of disjoint processing elements. To provide for phylogenetic analyses in these environments, we propose an approach to enable phylogenies to be inferred via heritable genetic annotations rather than directly tracked. We introduce a “hereditary stratigraphy” algorithm that enables efficient, accurate phylogenetic reconstruction with tunable, explicit trade-offs between annotation memory footprint and reconstruction accuracy. In particular, we demonstrate an approach that enables estimation of the most recent common ancestor between two individuals with fixed relative accuracy irrespective of lineage depth while only requiring logarithmic annotation space complexity with respect to lineage depth. This approach can estimate, for example, MRCA generation of two genomes within 10% relative error with 95% confidence up to a depth of a trillion generations with genome annotations smaller than a kilobyte. We also simulate inference over known lineages, recovering up to 85.70% of the information contained in the original tree using a 64-bit annotation.

Cilia- and flagella-associated protein 221 C-Terminus Deletion Necessary for Aflagellate Sperm in Mormyrid Weakly Electric Fishes

Alyssa N. Saunders, and Jason R. Gallant

Integrative Biology

Mormyrid weakly electric fishes are a family of osteoglossiforms that have aflagellate immotile sperm. Lack of flagella on sperm has been observed in several species of invertebrates, but mormyrids are the only known vertebrate species to have aflagellate sperm. Cilia- and flagella-associated protein 221 (CFAP221) is a eukaryotic gene involved in cilia/flagella formation. When CFAP221 function is disrupted in mice, individuals have symptoms of primary ciliary dyskinesia including aflagellate sperm. Mormyrids have a large deletion in the C-terminus of this gene. Therefore, we hypothesize the large deletion in CFAP221 is necessary for the aflagellate phenotype of mormyrid sperm. To test this hypothesis, we are replicating the CFAP221 deletion of mormyrids in zebrafish (*Danio rerio*) using CRISPR/Cas9 and have begun characterizing the sperm of F0 (crispant) individuals.

We have found a variety of phenotypes in these individuals including samples that completely resemble wild type zebrafish sperm, samples that are a mixture of flagellated and aflagellate sperm, and samples with curled flagella.

Build-a-Fish MSU: An Engaging Activity for K12 Students to Learn About Fish Biodiversity

Olivia E. Fitch, Brooke E. Jeffery, Jamily Lorena, and **Alyssa N. Saunders**

Build-a-Fish MSU is a collaborative project by a group of Integrative Biology graduate students that aims to teach K12 students about the biodiversity of fishes in an engaging format. The presentation was initially developed for MSU Science Festival 2022 and was presented both virtually and in-person to classrooms of local schools. During the presentation, we teach participants about why learning about fish is significant, how the evolution fish morphology is influenced by environmental pressures, and the diversity of fish morphology. We present the fish body in four parts (head, body, tail, and fins) and explain the function of these parts and various forms that they can take. During this portion of the presentation, participants build their own fish either by drawing or using pre-made drawings of fish body parts that they cut out and paste together. We aim to continue presenting this project in the future to continue teaching young scientists about the exciting biodiversity of fishes!

Complex landscapes stabilize farm bird communities and their expected ecosystem services

Olivia M. Smith, Christina M. Kennedy, Alejandra Echeverri, Daniel S. Karp, Christopher E. Latimer, Joseph M. Taylor, Erin E. Wilson-Rankin, Jeb P. Owen, and William E. Snyder

Integrative Biology, Center for Global Change and Earth Observations

Birds play many roles within agroecosystems and are declining, in part from agriculture. Thus, it is imperative to identify how to manage agroecosystems to support birds for multi-functional outcomes. Both the average amounts of services/disservices provided and their temporal stability are important for farm planning. We conducted point-count surveys for four years across 106 locations on 27 diversified farms in Washington and Oregon, USA. We classified birds as ecosystem service/disservice providers using indices spanning supporting, regulating, provisioning, and cultural services/disservices. We then examined service/disservice index pairwise correlations and assessed the relative importance of local, farm, and landscape complexity on the average and temporal stability of avian service/disservice provider indices. Farms that had more conservation-friendly practices generally had higher service provider indices, but farm management did not generally impact disservice provider indices. Disservice provider indices were lower on farms

in complex landscapes. Local vertical vegetation complexity tended to increase the temporal stability of service provider indices but not the disservice provider indices. Greater landscape complexity was generally associated with increased temporal stability of service and disservice provider indices. Our results suggest that farmers can manage their farms to harness ecosystem services from birds through farm diversification. Disservices provided by birds, however, seem to be most negatively impacted by landscape-level complexity. Greater incentives for farmers to increase natural cover at the landscape-scale are likely necessary to achieve multifunctional outcomes for conservation and agriculture.

Effects of livestock grazing on spatial and temporal niche partitioning of large carnivores

Olivia Spagnuolo, Sabrina Salome, Julie Jarvey, Allie Richardson, Rebecca Fisher, and Kay Holekamp
Integrative Biology

The Masai Mara National Reserve (MMNR) has long been ecologically and economically valuable, boasting 25% of Kenya's wildlife, serving as one of only four remaining refugia for East African carnivores, attracting tourists, and providing forage for livestock in times of drought. The number of livestock that grazed illegally within the MMNR has varied greatly over the years, increasing sixfold between 2008 and 2013 alone. In 2013, an average of over 2,200 cattle entered the MMNR daily. Using our historical ecological dataset and our recently developed land cover classification method, we investigated the effects of livestock grazing intensity on activity patterns and space use of apex predators, as well as on spatial and temporal niche partitioning within the carnivore community. Specifically, we quantified the spatiotemporal patterns of species-specific habitat preference and distance from the MMNR boundary for lions (*Panthera leo*) and cheetahs (*Acinonyx jubatus*). This yields valuable and urgently-needed information for wildlife managers in the MMNR and the Mara Conservancies, and may have broad implications for carnivore conservation in multiuse landscapes.

The effects of landscape characteristics on pest removal by American Kestrels

Olivia J. Utley, Sarah A. Groendyk, Melissa B. Hannay, Megan E. Shave, Oliva M. Smith, and Catherine A. Lindell
Integrative Biology

Enhancing pest regulation services by attracting and supporting avian predators in agroecosystems has been proposed as a strategy to increase crop productivity and sustainability. A key component of this strategy is understanding the effects of landscape context and crop type on predator interactions with species that are detrimental, beneficial, or

inconsequential for crops. American Kestrels (kestrels) can be attracted to landscapes using nest boxes to reduce avian pest activity in Michigan fruit crops. However, the effects of landscape characteristics and crop type on pest removal have yet to be examined. We hypothesized that higher proportion of open habitat and more forest edge density would increase pest removal through increased prey accessibility in open habitat and increased prey abundance due to spillover from forest habitat. We used nest box cameras to monitor and categorize prey removal by American Kestrels (kestrels) in Michigan blueberry and cherry crops. We found that prey removal was lower in more open habitats and higher with more forest edge, likely linked to prey abundance. Pesticide use in crops may reduce invertebrate prey abundance in open habitats while forest edge increases spillover of all prey types. Predators, such as kestrels, are likely to have a net beneficial effect on crops because prey species that spillover and remain in crops are likely to be pests. Future work should consider the costs of kestrel removal of beneficial species, such as predatory arthropods, and effects on the amount of crop damage.

Introgression detection and analysis

Qiqige Wuyun and Kevin Liu

Computer Science and Engineering, BEACON

Recent advances in biomolecular sequencing have revealed the important role that interspecific gene flow has played in genome evolution throughout the Tree of Life. Current and future genomic studies will bring large amounts of genomic sequence to bear upon this topic, and scalable computational methodologies are needed to detect and analyze genomic signatures of interspecific introgression in large-scale datasets.

To address the methodological gap, we introduce a new computational framework known as PHiMM (or “fast PhyloNet + Hidden Markov Model”). PHiMM combines inference and learning under a combined model of genetic drift, substitutions, recombination, and gene flow with a coalescent-based approximation technique. We compare the performance of PHiMM against the state of the art using synthetic and empirical genomic sequence data. We find that PHiMM offers better computational runtime and main memory usage by multiple orders of magnitude, while returning comparable inference accuracy.