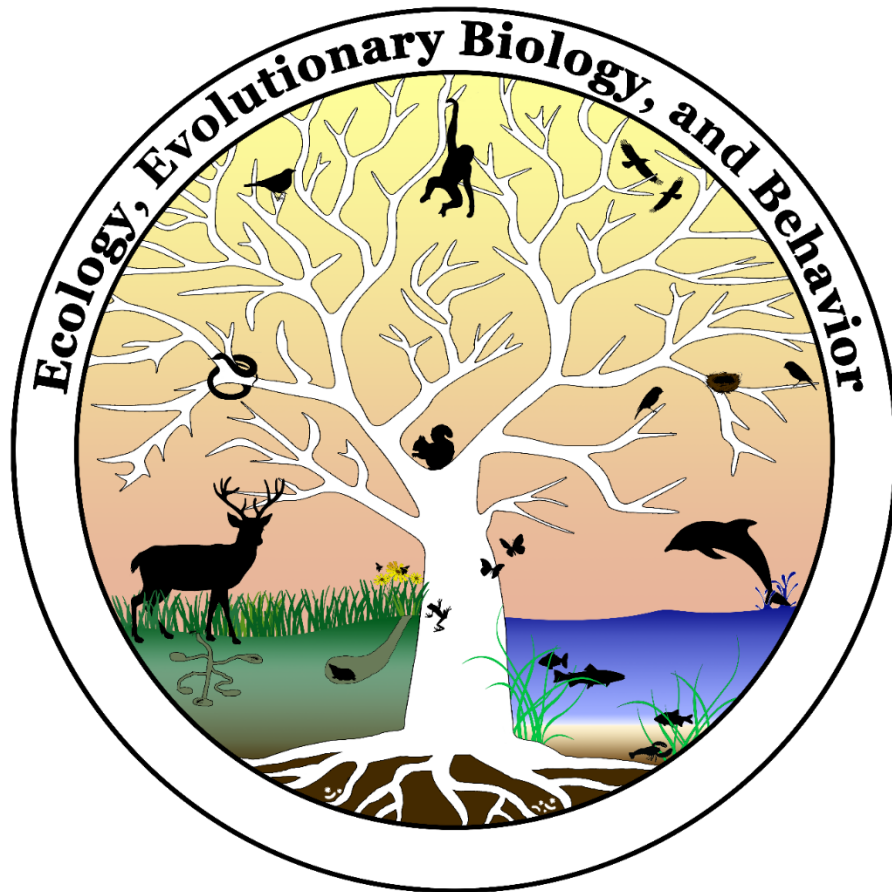


The Third Annual
Ecology, Evolutionary Biology, & Behavior
Research Symposium



April 29, 2019
Michigan State University
Henry Center for Executive Development
3535 Forest Rd, Lansing, MI 48910

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[#MSUEEBB2019](#)

This event made possible by:

Ecology, Evolutionary Biology, & Behavior (EEBB) Program

Kay Holekamp, EEBB Director

Barbara Bloemers, EEBB Grad Group (EGG) Advisor

EEBB Research Symposium Planning Committee

[Connie Rojas](#), Co-Chair

[Miranda Wade](#), Co-Chair

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[Isabela Borges](#)

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And the Sponsors on the next page!



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Thank you for your generous sponsorship!

Welcome from the EEBB Director

Welcome to the third annual EEBB Research Symposium! Today's presentations will be made by graduate students, post-docs and faculty in EEBB. I suspect the poster and platform presentations you see today will impress you with the quality and breadth of research being conducted by members of the EEBB community. The inspiration for this symposium grew out of discussions at the EEBB Retreat in December 2015, where our graduate students argued for an annual meeting at which they could learn about the research being conducted in EEBB labs other than their own. The CNS dean's office now includes sufficient funds in EEBB's annual budget to allow us to hold this symposium regularly, so we are grateful to current dean Phil Duxbury for continuing that tradition. We also thank COGS and our other sponsors for their contributions. The massive amount of work needed to make this symposium possible was done by the members of the EEBB Graduate Student Organization, EGG (EEBB Graduate Group) currently led by Christopher Warneke. In addition, special thanks are owed to EGG members Connie Rojas, Miranda Wade, Ani Hristova, Caitlin Mack, Isabela Borges, and Dan Turner for their impressive efforts on behalf of this Symposium. Finally, as always, EEBB secretary Barbara Bloemers has been heroic in her efforts to help EGG members organize this Symposium.



We will be looking for feedback after today's event to help us improve future symposia ([feedback form](#)).

Thank you for attending this symposium, and for your continued support of the EEBB program. You all make me very proud to be part of EEBB at MSU!

Sincerely,

A handwritten signature in black ink, which appears to read "Kay Holekamp".

Kay Holekamp, EEBB Director

Code of Conduct

EEBB Research Symposium

The EEBB Research Symposium is open to all members of the Michigan State University community, and is for sharing work in Ecology, Evolutionary Biology, and Behavior.

Expected Behavior

Treat all Research Symposium attendees and presenters with respect, realizing that the diversity of the attendees means there are a diversity of views.

Critique ideas, not people.

Refrain from discriminatory or harassing behavior/speech, towards attendees or anyone else on the premises.

Respect the rules and policies of Michigan State University and the Henry Center (the symposium venue).

Unacceptable Behavior

Harassment, discriminatory behavior, or intimidation are considered unacceptable in any form.

Remember that behavior that may be acceptable to one person may not be acceptable to another, so use discretion to ensure that respect is communicated. Harassment, even that intended in a joking manner, is still harassment and is considered unacceptable behavior.

Abuse of any sort (physical, verbal, or otherwise) is considered unacceptable behavior.

Behavior that endangers the health or safety of oneself or others is considered unacceptable.

Disruption of any of the sessions of activities at the Research Symposium is not allowed.

Retaliation against symposium participants that report unacceptable behavior is not allowed.

The use or distribution of illegal drugs is unacceptable, as is non-compliance with state and MSU alcohol-related laws and policies.

Reporting Information

Anyone witnessing or experiencing behavior that constitutes a threat to public safety should contact law enforcement (by calling 911).

To report incidents of harassment, particularly of sexual harassment or relationship violence, contact MSU's Office of Institutional Equity (OIE). OIE can be reached at 517 353 3922 or at their website oie.msu.edu. You may file reports with them anonymously or not, depending on your choice and the situation. It may also be necessary to notify the MSU Police, which can be reached at their non-emergency number of 517 355 2221.

All MSU Employees, which will include the majority of attendees, classify as Mandatory Reporters, and are required to report incidents of relationship violence or sexual misconduct to OIE and the MSU Police. If you, as a Mandatory Reporter, are confused about what you need to report, you can contact OIE for guidance, through the methods listed above.

Consequences

Anyone requested to stop any unacceptable behavior is expected to immediately comply.

Consequences of any behavior that is reported to OIE and/or the MSU Police will be in line with MSU policy, and will be handled by those two organizations.

This code of conduct was based on those of the Ecological Society of America Meetings Code of Conduct and the KBS Code of Conduct. These are available at these links:

<https://www.esa.org/esa/meetings/esa-meetings-code-of-conduct/>

http://www.kbs.msu.edu/wp-content/uploads/2018/03/KBS-Code-of-Conduct_FINALsignature.pdf

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 about their work, it is considered allowed.

If you are choosing to tweet, feel free to use the hashtag: [#MSUEEBB2019](#)

Keynote Speaker

Dr. Elizabeth Tibbetts

Department of Ecology and Evolutionary Biology

University of Michigan

<https://sites.lsa.umich.edu/tibbetts-lab/>

Communication systems and social behavior coevolve to shape the way animals look, think, and act. We study how the coevolution of social behavior and communication influences animal morphology, physiology, neurobiology, and behavior. A lot of our work focuses on *Polistes* paper wasps, especially *Polistes dominulus*, which have visual signals of fighting ability and *Polistes fuscatus*, which have visual signals used for individual recognition.



Awards

The following awards will be presented:

Best oral presentation

Best lightning talk

Best poster

Thank you to our judges (click their name to see their website!):

[Andrea Bierema](#)

[Janette Boughman](#)

[Ingo Braasch](#)

[Nate Emery](#)

[Eben Gering](#)

[Tom Getty](#)

[Andrea Glassmire](#)

[John Guittar](#)

[Nadya Mamoozadeh](#)

[Mariah Meek](#)

[Gary Roloff](#)

[Laura Smale](#)

[Chao Song](#)

[Acer VanWallendael](#)

[Will Wetzel](#)

EEBB Research Symposium Schedule Overview

↗ denotes lightning talk

Time	Event	Location
8-8:45am	Registration & Breakfast	Entry Hall
8:45-9:00am	Welcome & Opening Remarks <i>Kay Holekamp (IBIO), EEBB Director</i> <i>Christopher Warneke (PLB), EEBB Grad Group President</i>	A169
9:00-10:00am	KEYNOTE ADDRESS (Moderator: Isabela Borges) <i>Dr. Elizabeth Tibbetts, University of Michigan</i>	A169
10-10:15am	Coffee Break	
10:15-11:00am	SESSION I (Moderator: Miranda Wade) <i>10:15 Courtney Larson (ENT)</i> <i>10:30 Alan Bowsher (MMG)</i> <i>10:45 Robert Logan (IBIO)</i>	A169
11-11:15am	Coffee Break	
11:15am-12:15pm	SESSION II (Moderator: Dan Turner) <i>11:15 Gideon Bradburd (IBIO) ↗</i> <i>11:20 Erin Zylstra (IBIO) ↗</i> <i>11:25 Rufus Isaacs (ENT) ↗</i> <i>11:30 Kayla Davis (IBIO)</i> <i>11:45 Tracy Montgomery (IBIO)</i> <i>12:00 John Guittar (MMG)</i>	A169
12:15-1:15pm	Lunch	Atrium
1:15-2:15pm	SESSION III (Moderator: Ani Hristova) <i>1:15 Nadya Mamoozadeh (IBIO) ↗</i> <i>1:20 Nate Emery (PLB) ↗</i> <i>1:25 Emily Josephs (PLB) ↗</i> <i>1:30 Zoe Hansen (MMG)</i> <i>1:45 Lili Johnson-Ulrich (IBIO)</i>	A169

	<i>2:00 Alexander Lalejini (CSE)</i>	
2:15-3:30pm	POSTER SESSION & Break	Atrium
3:30-4:30pm	SESSION IV (<i>Moderator: Connie Rojas</i>)	A169
	<i>3:30 Eben Gering (IBIO) ✕</i>	
	<i>3:35 Kevin Liu (CSE) ✕</i>	
	<i>3:40 Andrea Glassmire (ENT) ✕</i>	
	<i>3:45 Andrew Thompson (IBIO)</i>	
	<i>4:00 Kevin McCormick (IBIO)</i>	
	<i>4:15 Acer VanWallendael (PLB)</i>	
4:30-5:00pm	Closing Remarks & Awards	A169
	<i>EEBB Research Symposium Planning Committee</i>	
<i>Directly following closing remarks</i>	Reception	Beggar's Banquet in East Lansing

EEBB Research Symposium

Detailed Schedule:

8:00am	<u>REGISTRATION & BREAKFAST</u>	Entry Hall
	Please arrive at the Henry Center in advance in order to check in and pick up your name tag. Refreshments will be provided.	
8:45am	<u>WELCOME & OPENING REMARKS</u> <i>Kay Holekamp (IBIO), EEBB Director</i> <i>Christopher Warneke (PLB), EEBB Grad Group President</i>	
9:00am	<u>KEYNOTE ADDRESS</u> "What wasps can teach us about cognition, developmental plasticity, and communication" Dr. Elizabeth Tibbetts <i>Department of Ecology and Evolutionary Biology</i> <i>University of Michigan</i>	
10:00am	<u>COFFEE BREAK</u> (15 minutes)	
10:15am	<u>SESSION I</u> <i>Oral Presentations</i>	
10:15am	Decadal differences in leaf litter decomposition in Augusta Creek, an MSU experimental field site <i>Courtney Larson, Graduate student</i> <i>Department of Entomology</i>	Abstract
10:30am	Locally-adapted <i>Mimulus</i> ecotypes differentially impact rhizosphere communities in an environment-dependent manner <i>Alan Bowsher, Post-doctoral fellow</i> <i>Department of Microbiology and Molecular Genetics</i>	Abstract
10:45am	The effects of non-rainfall moisture on fungal communities and standing grass litter decomposition in a hyperarid desert <i>Robert Logan, Graduate student</i> <i>Department of Integrative Biology, KBS</i>	Abstract
11:00am	<u>COFFEE BREAK</u> (15 minutes)	

11:15am

SESSION II

Lightning Talks & Oral Presentations

11:15am

PopGen in Space

LIGHTNING TALK ✂

Gideon Bradburd, *Faculty*

Department of Integrative Biology

[Abstract](#)

11:20am

Integrating data from across the annual migratory cycle to understand population dynamics of the eastern monarch butterfly

LIGHTNING TALK ✂

Erin Zylstra, *Post-doctoral fellow*

Department of Integrative Biology

[Abstract](#)

11:25am

Monitoring the status and trends of wild bee populations

LIGHTNING TALK ✂

Rufus Isaacs, *Faculty*

Department of Entomology

[Abstract](#)

11:30am

Optimizing aerial seabird survey design: pitfalls and progress

Kayla Davis, *Graduate student*

Department of Integrative Biology

[Abstract](#)

11:45am

Individual participation in cooperative mobbing behavior

Tracy Montgomery, *Graduate student*

Department of Integrative Biology

[Abstract](#)

12:00pm

An ecological framework for understanding and preventing pathogen expansion in the gut microbiome

John Guittar, *Post-doctoral fellow*

Department of Microbiology and Molecular Genetics, KBS

[Abstract](#)

12:15pm

LUNCH (1 hour)

Please join us in the Henry Center atrium for lunch.

Atrium

[Menu](#)

1:15pm

SESSION III

Lightning Talks & Oral Presentations

1:15pm	<p>Improving wildlife conservation by integrating genomic, environmental, and ecological information LIGHTNING TALK ✂ Nadya Mamoozadeh, <i>Post-doctoral fellow</i> <i>Department of Integrative Biology</i></p>	Abstract
1:20pm	<p>Flowering phenology predicts plant flammability LIGHTNING TALK ✂ Nate Emery, <i>Post-doctoral fellow</i> <i>Department of Plant Biology</i></p>	Abstract
1:25pm	<p>Detecting adaptive divergence in complex traits LIGHTNING TALK ✂ Emily Josephs, <i>Faculty</i> <i>Department of Plant Biology</i></p>	Abstract
1:30pm	<p>A metagenomic perspective of the human gut resistome response to pathogen invasion Zoe Hansen, <i>Graduate student</i> <i>Department of Microbiology and Molecular Genetics</i></p>	Abstract
1:45pm	<p>Innovation and fitness in wild spotted hyenas Lily Johnson-Ulrich, <i>Graduate student</i> <i>Department of Integrative Biology, BEACON</i></p>	Abstract
2:00pm	<p>Evolving signal-driven digital organisms with SignalGP Alexander Lalejini, <i>Graduate student</i> <i>Department of Computer Science and Engineering, BEACON</i></p>	Abstract

2:15pm	<u>POSTER SESSION</u> & BREAK	Atrium
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Please join us in the atrium for refreshments and poster presentations.

Poster 1	<p>Consequences of diversity on microbial responses to exometabolite-mediated interactions in a synthetic microbial community John Chodkowski, <i>Graduate student</i> <i>Department of Microbiology and Molecular Genetics</i></p>	Abstract
----------	--	--------------------------

- Poster 2 **Do nest boxes increase American kestrel (*Falco sparverius*) occupancy in western Michigan blueberries?** [Abstract](#)
Melissa Hannay, *Graduate student*
Department of Integrative Biology
- Poster 3 **Public Support for Salmon and Trout Conservation** [Abstract](#)
Sara Hugentobler, *Graduate student*
Department of Integrative Biology, KBS, ESPP
- Poster 4 **Choice of biofuel crop creates a tradeoff for pollinator conservation and yield** [Abstract](#)
Lindsey Kemmerling, *Graduate student*
Department of Integrative Biology, KBS
- Poster 5 **Genetic control of a plant-mite mutualism** [Abstract](#)
Erika LaPlante, *Graduate student*
Department of Plant Biology
- Poster 6 **Parental social behavior of the African painted dog** [Abstract](#)
Caitlin Mack, *Graduate student*
Department of Integrative Biology
- Poster 7 **The Meek Lab: conservation in a changing world**
Mariah Meek, *Faculty*
Department of Integrative Biology
- Poster 8 **Olfactory bulb size and daily activity patterns in rodents** [Abstract](#)
Andrea Morrow, *Graduate student*
Department of Integrative Biology
- Poster 9 **The role of drift in electric signal variation among the mormyrid fish *Paramormyrops kingsleyae*** [Abstract](#)
Sophie Picq, *Post-doctoral fellow*
Department of Integrative Biology, BEACON
- Poster 10 **Sensory mechanisms for localizing spermatophores in the axolotl (*Ambystoma mexicanum*), an aquatic salamander** [Abstract](#)
Taylor Rupp, *Graduate student*
Department of Integrative Biology

- Poster 11 **Do lichens follow the Biotic Interactions Hypothesis? Testing partner specificity along a latitudinal gradient** [Abstract](#)
Klara Scharnagl, *Graduate student*
Department of Plant Biology
- Poster 12 **Seasonal patterns of diversity, assembly, and host-specificity in core microbiota of perennial biofuel crops** [Abstract](#)
Jackson Sorensen, *Graduate student*
Department of Microbiology and Molecular Genetics
- Poster 13 **Under ongoing climate change in Michigan, growth of some sugar maple populations may increase and in others decrease** [Abstract](#)
Scott Warner, *Graduate student*
Department of Plant Biology
- Poster 14 **The Wetzel Lab: Studying the ecology of plants and insects in a variable world**
Will Wetzel, *Faculty*
Department of Entomology, KBS
-

3:30pm

SESSION IV

Lightning Talks & Oral Presentations

- 3:30pm **A farewell to Lansing: How art, outreach, and conservation partnerships can enhance a post-doc's journey** [Abstract](#)
LIGHTNING TALK ✂
Eben Gering, *Post-doctoral fellow*
Department of Integrative Biology, BEACON, KBS
- 3:35pm **Fast and accurate statistical introgression mapping using large-scale genomic sequence datasets** [Abstract](#)
LIGHTNING TALK ✂
Kevin Liu, *Faculty*
Department of Computer Science and Engineering, BEACON, Quantitative Biology
- 3:40pm **Disentangling the dimensions of phytochemical diversity: alpha and beta diversity within and across classes of plant chemicals differ in their consequences for a generalist herbivore** [Abstract](#)
LIGHTNING TALK ✂

Andrea Glassmire, *Post-doctoral fellow*
Department of Entomology, KBS

3:45pm

Genomic mechanisms of developmental delay and environmentally-cued hatching in annual killifish

[Abstract](#)

Andrew Thompson, *Post-doctoral fellow*
Department of Integrative Biology, BEACON

4:00pm

Submissiveness personality traits in spotted hyenas (*Crocuta crocuta*)

[Abstract](#)

Kevin McCormick, *Graduate student*
Department of Integrative Biology, BEACON

4:15pm

Geographic dependence of fungus resistance genetic architecture in locally adapted switchgrass

[Abstract](#)

Acer VanWallendael, *Post-doctoral fellow*
Department of Plant Biology, PRI, GLBRC

4:30pm

CLOSING REMARKS & AWARDS

EEBB Research Symposium Planning Committee

5:00pm

RECEPTION

Beggar's Banquet in East Lansing

Henry Center for Executive Development

3535 Forest Rd, Lansing, MI

(517) 353-4350

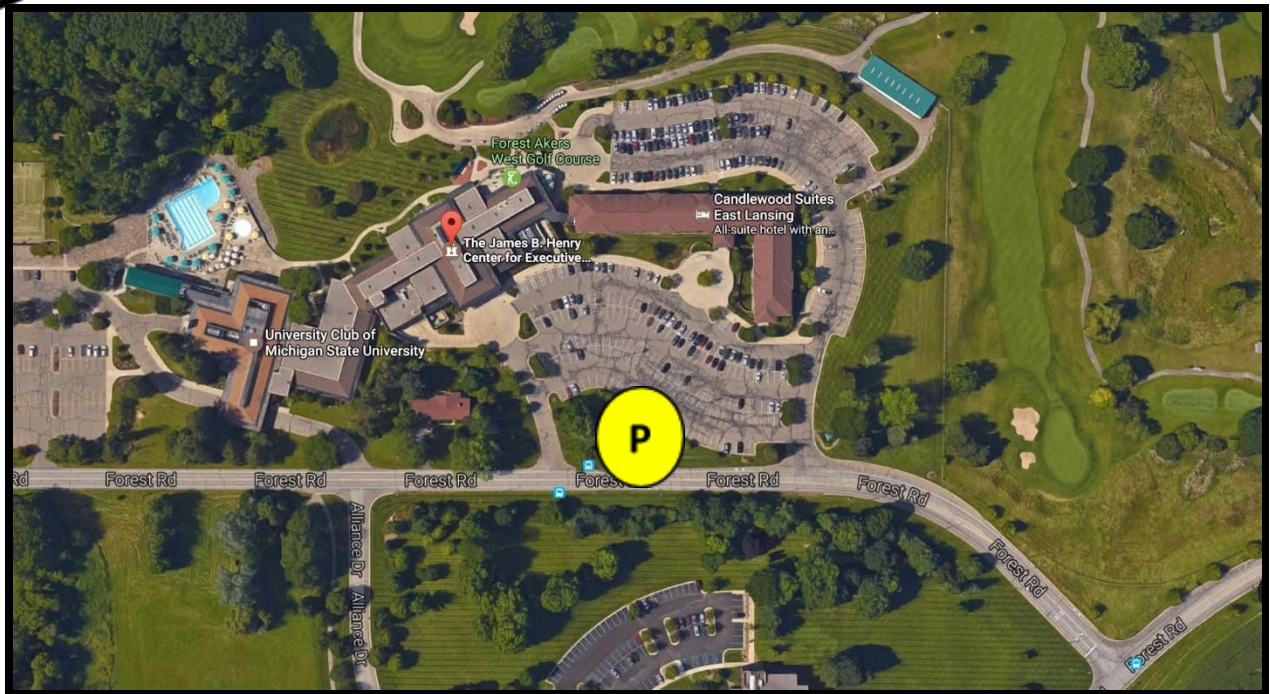


Directions:

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:

MENU

Make-Your-Own Salad Bar: Spinach Salad

Baby Spinach, Sliced Mushrooms
Sliced Cucumber, Dried Cherries, Diced Turkey
Pecans, Tomatoes, Shredded Cheese, Cottage Cheese

G Dressings: Ranch, Raspberry Vinaigrette, Poppy Seed Vinaigrette

Composed Salads

Greek Chopped Salad over Romaine Lettuce **G V**
Bowtie Pasta Salad with Asparagus and Mushrooms
and Creamy Basil Dressing **V**

Breads & Spreads

Artisan French Baguette, Wheat Pita Bread
Extra Virgin Olive Oil, Butter

Roasted Garlic Hummus **G D V**

Chicken Salad **G D**

Hot Buffet

Cream of Asparagus & Boursin Cheese Soup **V**

Grilled Chicken Thighs with Red Cabbage,

Bok Choy, and Mango Relish **G D**

Baked Salmon with Corn & Black Bean Relish and

Roasted Pepper Beurre Blanc **G**

Whole Grain Penne Pasta with Smoked Vegetables,

Marinara Sauce, Fresh-Grated Parmesan Cheese **V**

Fresh Green Beans

Herb-Roasted New Potatoes **G V**

Desserts & Beverages

Salted Caramel Cheesecake

Tiramisu

Regular Coffee, Decaf, and Tea Service

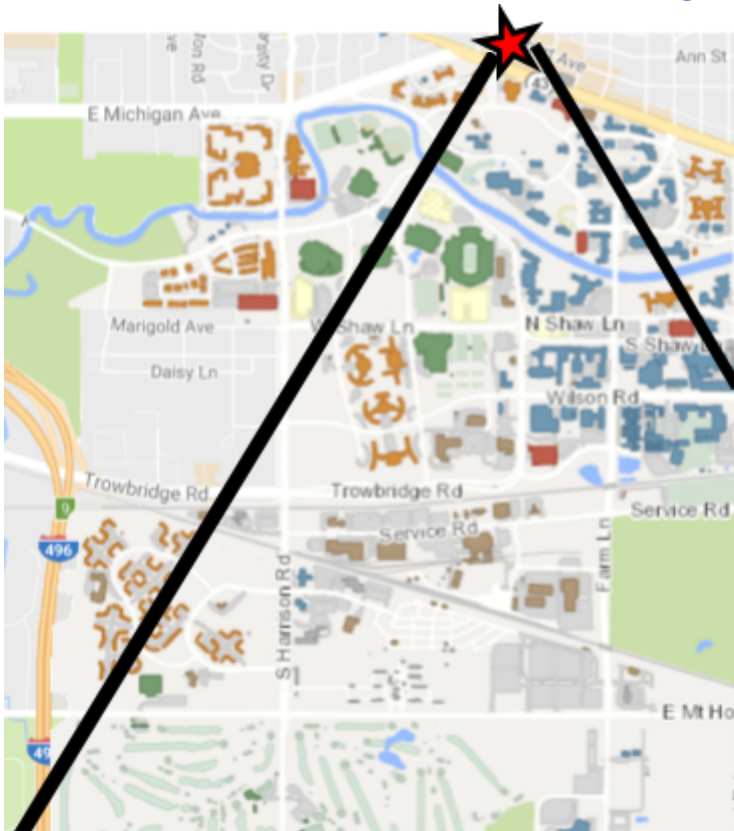
Symbol Key:

G Gluten Free **D** Dairy Free **V** Vegetarian

Beggar's Banquet

[218 Abbot Road, East Lansing, MI](#)

(517) 351-4540



Directions:

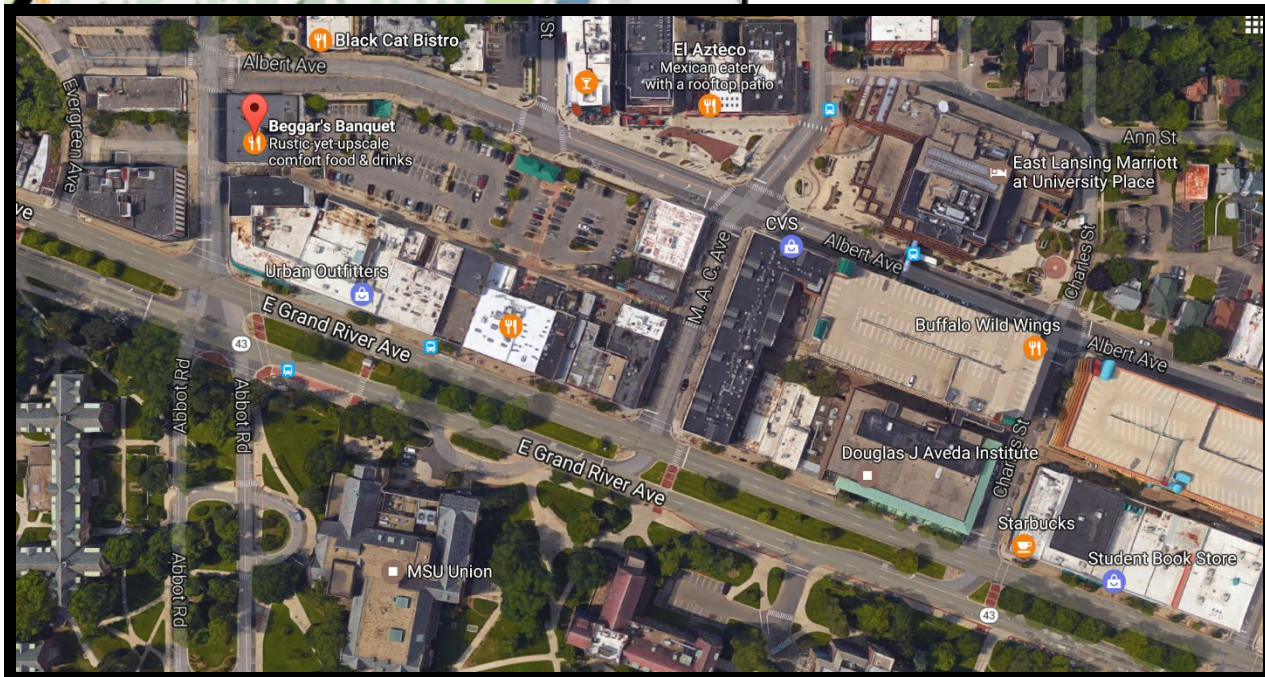
From the Henry Center, travel east on Forest Rd. toward Harrison Rd. Turn left on Harrison Rd, right on Michigan Ave, left on Abbot Rd. Beggar's Banquet is on the first block and will be on your right.

Parking:

The usual parking lot next to Beggar's is temporarily closed. The Grove St. Garage (behind Hopcat) is nearby, but charges by the hour. The campus Grand River Ramp (Ramp #6) is \$1.50/hour, and is free after 6pm. Other options are indicated on the map.

Hors d'oeuvres will be provided, compliments of EEBB. Cash bar.

Monday hours: 10am-1am



Abstracts

Alphabetical by presenting author's last name.
All authors at Michigan State University unless otherwise stated.

Locally-adapted *Mimulus* ecotypes differentially impact rhizosphere communities in an environment-dependent manner

Alan W. Bowsher, Patrick J. Kearns, Damian Popovic, David B. Lowry, Ashley Shade

Microbiology and Molecular Genetics

Plant roots and soil microbes have extensive interactions that influence plant productivity, health, and resistance to stress. Although there is mounting evidence that plant species and even genotypes can differentially alter the structure of soil microbial communities, environmental conditions can potentially outweigh plant genetic effects. In this study, we used a reciprocal transplant experiment to understand the contributions of both the environment and the host plant to rhizosphere microbiome composition of locally-adapted ecotypes of *Mimulus guttatus* Fisch. ex DC (see monkeyflower). Two genotypes of a coastal ecotype and two genotypes of an inland ecotype were planted at both coastal and inland sites. After four months of growth, we collected rhizosphere and bulk soil and assessed microbial community composition by 16S rRNA gene sequencing. We found that each ecotype exhibited some of the same compositional shifts in microbial communities (relative to bulk soil) in both 'home' and 'away' environments. This was despite the major differences in abiotic (salt content, moisture, and nutrient availability) and biotic (native microbial community composition) conditions between the two sites. We also found that, while some impacts on rhizosphere composition were shared by both ecotypes, other effects were specific to each ecotype, indicating genetic divergence in factors that shape rhizosphere communities, such as root exudate composition. Nevertheless, differences between the ecotypes were environment-dependent, indicating that environmental factors can outweigh genetic factors in shaping the *M. guttatus* microbiome in the field sites examined here. Overall, our findings demonstrate that wild plants strongly impact the structure of soil microbial communities, yet also highlight the complex interplay between host identity and host environment in regulating those communities.

PopGen in Space

Gideon Bradburd

Integrative Biology

Genetic variation within species is often structured by geography. Much of the theory, methods, and data applied to the study of the spatial distribution of genetic variation has relied on the approximating assumption that organisms are well described as discrete demes embedded within some geographic context. Many species violate this assumption, but the

complexities of the alternative -organisms living, dispersing, reproducing, and dying somewhere in space -- have been difficult to capture in a theoretical or statistical model.

However, recent advances in theory, alongside the advent of genomic datasets of ever-increasing size and geographic scope and methods for analyzing them, are facilitating a revolution in the study of organisms in continuous space. Here, I present some ongoing work in the Bradburd lab on new statistical methods in population genetics.

Consequences of diversity on microbial responses to exometabolite-mediated interactions in a synthetic microbial community

John Chodkowski & Dr. Ashley Shade

Microbiology and Molecular Genetics

Interactions among microbial populations are expected to have consequences for microbial community function, but it is challenging to observe microbial interactions in the environment.

Exometabolites are one method of microbial interaction via excreted chemical signals, and they can be used to cue or inhibit neighboring populations. We developed a synthetic microbial community approach using a transwell system. In this system, discrete member populations are physically separated but share a media reservoir of community goods, including resources and exometabolites. Our system allows for the investigation of microbial interactions facilitated by exometabolites. Here, we used the transwell system to ask how diversity (number of members) and time over stationary growth influence community exometabolites and member gene transcription. Community members included *Burkholderia thailandensis*, *Chromobacterium violaceum*, and *Pseudomonas syringae*. These common environmental bacterial strains were chosen because of their established genomic resources and exometabolite production, and reports of interactions among them. We quantified and compared the dynamics of exometabolite production and transcriptional responses across 7 community conditions- monoculture (3), pairwise (3), full (1). We found that *B. thailandensis* had a strong influence on its neighbors' transcriptional responses and hypothesized that competitive strategies, like antimicrobial production, were responsible. Indeed, *B. thailandensis* had the greatest number of up-regulated biosynthetic gene clusters in pair and full community conditions. Interspecies co-expression networks revealed that *B. thailandensis* was enriched for up-regulated antibiotics, and metabolic analysis confirmed the production of some of these antibiotics. To explore how increased diversity may result in non-additive and potentially unexpected community outcomes, we also report unique transcriptional and exometabolite outcomes observed only in the full community. We expect that this work will contribute to building a systems-level understanding of the impacts of microbial interactions for community outcomes.

Optimizing aerial seabird survey design: pitfalls and progress

Kayla Davis, Matt Farr, Randy Wilson, Emily Silverman, Allison Sussman, Jim Lyons, Elise Zipkin
Integrative Biology

Characterizing seabird species' composition, distribution, and abundance is necessary for assessing the impacts of changing environmental conditions and for guiding management practices. However, estimating seabird trends is particularly challenging because it can be difficult to locate and count flocks in the vast marine environment. The typical study design consists of aerial surveys in which observers count individuals within flocks and attempt to identify seabird species from planes moving at 150–200 km/h at an altitude of 50–100 m.

Inherent to this study design are issues not considered explicitly in subsequent analyses including imperfect observer detection, flock size estimation error, species misidentification, and constraints of the survey unit. We investigate these issues and the potential for biasing estimates with a case study examining seabirds in the Gulf of Mexico. As part of the ongoing Gulf of Mexico Marine Assessment Program for Protected Species (GoMMAPPS), seabird data are collected during aerial surveys with a double observer protocol. This protocol allowed us to compare records of species identification and flock detection and estimation from two, independent observers. We evaluated the extent and magnitude of observation errors and the potential for proliferation into subsequent analyses. Our results indicated that observers detect birds relatively consistently. However, important inconsistencies exist in flock counts (especially for flock sizes greater than 100 individuals) and species-level identification (particularly in mixed flocks). We propose suggestions for handling these issues, including modeling species groups instead of individual species and using an ordinal modeling approach to address potential discrepancies in flock sizes.

Flowering phenology predicts plant flammability

Nathan Emery, Keely Roth, Alex Pivovarovff

Plant Biology

Changes in plant phenology provide vital information on climatic shifts, species interactions, and ecological processes. By quantifying plant phenology, we reveal patterns of how plants are integrating environmental conditions and we use this information to inform conservation, policy, and management. In wildfire-prone regions of the world and especially California, a critical ecological process and management issue is wildfire disturbance. To gauge wildfire risk in these regions, scientists and managers monitor live fuel moisture (LFM), a proxy for plant flammability. We investigated the relationship between plant phenology and live fuel moisture for the widespread shrub species *Adenostoma fasciculatum* from two counties in Southern California over 6 years and analyzed the data in the context of LFM thresholds of wildfire risk. We found a strong correlation between reproductive phenology and LFM for *A. fasciculatum* ($p < 0.001$, adjusted $r^2 = 0.63$). This robust relationship between reproductive phenology and LFM is a prime example of phenological patterns providing insight into ecological processes. We also correlated reproductive phenology from the National Phenology Network with nearby live fuel moisture measurements from the National Fuel Moisture Database and found a similar relationship that spans the state of California. With simple observations of reproductive phenology, on-the-ground measurements allow for rapid assessment of plant flammability with the potential for large spatial coverage. This study reveals how observations of plant phenology can inform us about ecological processes and potentially contribute to management decisions.

A Farewell to Lansing: how art, outreach, and conservation partnerships can enhance a postdoc's journey.

Eben Gering

Integrative Biology, BEACON, Kellogg Biological Station

The futures of science and conservation depend on public enthusiasm for research and 'enlightened' environmental policy. To combat anti-science rhetoric and declining STEM education, scientists are avidly exploring 1) approaches to research and conservation that engage a broader range of citizens, 2) effective (e.g. multidisciplinary) forms of science outreach and communication. Here, I will present diverse examples of collaboration between IBIO members, other disciplines, and Lansing-area artists. I will also reflect on the scientific, societal, and personal value of this type of work. In addition to showcasing past projects, I hope the talk will inspire further connectivity between IBIO and our wonderful (and wonderfully-talented) local community.

Disentangling the dimensions of phytochemical diversity: alpha and beta diversity within and across classes of plant chemicals differ in their consequences for a generalist herbivore

Andrea E. Glassmire, Luke N. Zehr, and William C. Wetzel

Entomology, Kellogg Biological Station

Plant chemical diversity is known to be an important functional trait in regulating herbivorous insects. The specific dimensions of chemical diversity, however, have been examined through a single dimension of diversity, either the average (alpha) or the turnover (beta) in chemical diversity between plants, and thus the underlying mechanism of chemical diversity is lacking. Our objective was to examine the degree to which intraspecific phytochemical trait diversity influences herbivore performance. We hypothesized that chemical beta-diversity—differences in phenotypes among plants in a patch—would make it difficult for moths to select a quality host, causing decreased oviposition on preferred host plants. We tested this hypothesis using an emerging model system for understanding how plant chemical diversity contributes to female oviposition preference in tomato host plants. We partitioned the different classes of compounds (e.g. acyl sugars and terpenes) into measures of chemical dissimilarity in comparison to a focal tomato cultivar using a set of tomato genotypes created by introgressing cultivated tomato with a wild relative (*Solanum pennellii*). Using wind tunnel experiments, we manipulated tomato plants containing low (e.g. chemically similar) or high beta (e.g. chemically dissimilar) chemical diversity to examine whether the oviposition preference of females of the tomato hornworm, *Manduca sexta*, changes depending on the neighboring plant. We found that moths took longer to approach their first plant when neighbors were chemically dissimilar. Moths had a higher tendency to switch between plants if they were more chemically dissimilar. Finally, moths had a higher preference for one tomato plant variety if they were chemically different. These results suggest that chemical diversity among plants within a patch makes host selection more difficult.

An ecological framework for understanding and preventing pathogen expansion in the gut microbiome

John Guittar, Thomas Koffel, Chris Klausmeier, Ashley Shade, Elena Litchman
Microbiology and Molecular Genetics, Kellogg Biological Station

The human gut microbiome provides critical functions for human health, including the digestion of otherwise indigestible substrates and protection against pathogen expansion. Healthy gut conditions are maintained in part through positive feedback loops which involve both the host and anaerobic mutualists that persist in the anoxic gut environment. However, opportunistic pathogens exploit similar positive feedback systems in the gut to enable exponential expansion and chronic infection. While the molecular mechanisms of infection for many enteric pathogen systems have been studied and described in detail, there has been little work drawing them together to identify commonalities, and to explore ways in which ecological principles could inform alternative treatments alongside more traditional targeted mechanism-specific treatments. In my talk, I will introduce an ecological framework and mathematically explicit model aimed to understand, predict, and develop general strategies to prevent pathogen expansion in the gut. To conclude, I will use a customized version of the model to shed light on why taxa from the Bacterial family Enterobacteriaceae often bloom in the gut after broad-spectrum antibiotic treatments.

Do nest boxes increase American kestrel (*Falco sparverius*) occupancy in western Michigan blueberries?

Melissa Hannay, Olivia Utley, Sarah Groendyk, Catherine Lindell
Department of Integrative Biology

Populations of the American Kestrel (*Falco sparverius*; hereafter, kestrel) have been declining in North America for the last several decades. Along with being a conservation concern, this trend is also concerning for certain agricultural operations. The kestrel diet contains organisms that are potential pests to fruit growers, such as insects, small mammals, and frugivorous birds; kestrels can provide valuable ecosystem services in the form of pest control. The cause for declining kestrel populations remains unknown. Kestrels are secondary cavity nesters; as with other such species, cavities could be a limiting resource. To investigate if providing nest boxes could increase kestrel occupancy, we installed 34 nest boxes in or near blueberry growing operations along two 8-mile transects in western Michigan in 2015 and 2016. These transects were broken into approximately 1.5 km long sites. We surveyed these transects from 2015 to 2018, recording kestrel absence or presence along each site. We additionally surveyed two 8-mile transects that had no boxes installed. We constructed a multi-year dynamic occupancy model to investigate the effect of nest boxes on kestrel occupancy, along with factors that could influence kestrel detection. We predict that sites with nest boxes installed will show higher kestrel occupancy than sites without, as boxes could provide a resource that is potentially limited in western Michigan.

A Metagenomic Perspective of the Human Gut Resistome Response to Pathogen Invasion

Zoe Hansen, Brian Nohomovich, Wonhee Cha, and Shannon Manning.

Microbiology and Molecular Genetics

Introduction: Bacterial foodborne pathogens are the most common culprit of diarrheal diseases. Since pathogens are not normal contributors to the gut microbial community, these microbes are interesting candidates for drivers of ecological change. Recent research has shown that introduction of enteric pathogens significantly alters the gut microbial community composition and can cause reduction in microbial diversity while also increasing rates of gene transfer. Additionally, the ubiquitous nature of antibiotic resistance, when considered in conjunction with these greater gene transfer frequencies, raises significant concerns of its prevalence and spread. The impact of infection upon the human gut 'resistome' (the swath of antibiotic resistance genes (ARGs)) has yet to be fully explored, especially from an ecological perspectives. Here, we investigate how the resistome of the human gut is altered by pathogen invasion using metagenomics approaches and analyses.

Methods: In this study, explore the resistome present in two distinct groups of gut microbial communities: patients infected with *Campylobacter*, an enteric pathogen (Cases, $n = 26$), and healthy family members (Controls, $n = 39$). To assess resistome composition, high throughput shotgun sequencing was performed via Illumina Hi-Seq on DNA extracted from fecal samples of all individuals. Using metagenomics data, we investigated the composition of the gut resistomes of infected and healthy patients.

Results: The data represented here were collected from preliminary metagenomics analysis.

Our analysis shows that 415 unique ARGs were identified from a cumulative total of 173,611,981 paired end reads from the entire cohort. These unique genes correspond to 41 distinct resistance mechanisms, and 18 different antibiotic drug classes. The median number of unique ARGs is much higher in Cases vs. Controls (100 vs. 30, respectively; $p < 0.0001$), indicating that resistance gene diversity is increased in patients with enteric infections. Additionally, the types of resistance observed in Cases is different than that of Controls; the most relatively abundant ARGs in the Cases are of the Multi-Drug Resistant class (13.7% of all genes), while the most abundant ARGs in Controls are of the class Tetracyclines (25.4% of all genes), a finding that raises concern about the impact pathogen infection may have on harboring multi-drug resistant microbes.

Conclusion: This study suggests that pathogen invasion in the human gut can result in alterations of resistome composition. Specifically, the observed increase in multi-drug resistance in infected patients raises concerns about the persistence and spread of multi-drug resistant microorganisms. Further studies will aim to characterize the alternative roles of ARGs as well as associated mobile genetic elements (MGEs), as this may provide more insight into patterns of transmission within gut microbial communities.

Public Support for Salmon and Trout Conservation

Sara Hugentobler and Mariah Meek

Department of Integrative Biology, KBS, ESPP

In order to garner support conservation Chinook Salmon populations, it's critical to understand the public stance on conservation action, specifically as it relates to this species and other closely related species. Using targeted questions, we surveyed approximately 1000 individuals and evaluated their stance on Salmon and Trout conservation relative to the individual's demographic groups. Most demographic groups appeared to be inaccurate predictors of conservation attitude, and in general, most respondents indicated overall support for Salmon and Trout conservation. This is possibly due to the nature of these populations, being that they are popular game fish as well as economically important in some states. This public support indicates that more protections would be supported by the general public, and therefore be more effective.

Monitoring the status and trends of wild bee populations

Rufus Isaacs, Kelsey Graham, Tom Wood, and Jason Gibbs

Entomology

Wild bees provide valuable ecosystem services to crops and natural habitats, and their status is of great interest to farmers and other land managers. However, to determine the status of these insects there must be accurate historical and contemporary data on the distribution and abundance of bees. Through collaborations with private landowners, fruit and field crop farmers, and the museums at the University of Michigan and MSU, we are documenting the identity, abundance, and trends in wild bee populations as well setting a foundation for future comparisons. The overall trends for bee abundance and species richness are negative in most settings, with particular bee species declining much more than others. However, some species are expanding their range and their abundance. Examination of pollen sources is ongoing from historical collection material as well as on newly trapped bees to explore the role of changing diets in bee population changes.

Innovation and fitness in wild spotted hyenas

Lily Johnson-Ulrich, Sarah Benson-Amram, Kay Holekamp

Integrative Biology, BEACON

Cognitive ability varies considerably within species, and it is widely assumed that this variation must have large fitness consequences. However, direct evidence for a link between cognition and fitness remains rare. Previous research examined innovation in wild spotted hyenas confronting a novel puzzle box baited with meat and found that variation in innovation in spotted hyenas was unrelated to age, sex, or social rank. Here, we used the same dataset from wild spotted hyenas to investigate potential links between innovation and fitness. We found that innovative hyenas had lower offspring survivorship than did non-innovators, but greater annual cub production (ACP), measured as the average number of cubs born per year. We hypothesized that greater ACP might compensate for lower offspring survival. To test this idea, we also measured annual cub survivorship (ACS), calculated as the average number of

cubs born per year that also survived to at least 1 year of age. Here, there was no significant difference between innovators and non-innovators, suggesting that higher ACP does compensate for lower offspring survival, at least to one year of age. While the effect of innovation on lifetime fitness is unclear, these results suggest that innovation might be linked to different reproductive strategies.

Detecting adaptive divergence in complex traits.

Emily B Josephs

Plant Biology

Characterizing the genetic basis of adaptation is a longstanding goal of evolutionary biology. Adaptation in quantitative traits likely often occurs through subtle shifts in allele frequencies at many loci, a process called polygenic adaptation. Even though many traits have a polygenic basis, conventional methods lack power for detecting polygenic adaptation. In this talk, I describe strategies for detecting polygenic adaptation and applications to plant phenotypes. Ultimately, these methods can be applied to multiple domesticated and wild species to give us a broader picture of the specific traits that contribute to adaptation and the overall importance of polygenic adaptation in shaping trait variation.

Choice of biofuel crop creates a tradeoff for pollinator conservation and yield

Lindsey Kemmerling and Sean Griffin

Department of Integrative Biology, KBS

In order to prevent the loss of biodiversity, adapt to climate change, and sustainably support a growing population, biodiversity must be incorporated into working landscapes. One agricultural product, biofuel, is most often obtained from annual monocultures such as corn.

As an alternative, perennial biofuel crops have the potential to both produce energy and conserve biodiversity, but this depends largely on the crop chosen and the land used for planting. Working in an experiment with four native, perennial, biofuel crop varieties -switchgrass, native grasses, successional restoration, and actively restored prairie- we tested the effect of crop type on crop yield and the abundance and diversity of pollinators, a group of significant conservation interest. We asked two questions: 1) How does biofuel crop management affect pollinator communities? 2) What are the tradeoffs between crop yield and pollinator conservation? We found that crop types differed strongly in pollinator abundance

($\chi^2=62.8$, $p=1.5E-13$), pollinator richness ($\chi^2=114.7$, $p=2.2E-16$), and crop yield ($\chi^2=87.4$, $p=2.2E-16$). Successional restoration, with higher floral abundance, had higher abundance and richness of pollinators than all other crops, with native grasses having the lowest. Switchgrass and prairie treatments were intermediate in these responses. However, native grasses and restored prairie had the highest biofuel yield. Based on our results, we suggest the planting of restored prairie as a biofuel crop to maximize both conservation value for pollinators and crop yield. Understanding these tradeoffs can inform land management decisions for designing resilient working landscapes that both support biodiversity and yield goods and services.

The Vascular Flora of Baker Woodlot, Michigan State
University Campus: A comparison after 40 years
Matthew Kolp, Matthew T. Chansler, Garrett E. Crow, and L. Alan Prather
Plant Biology, Kellogg Biological Station
MSU Herbarium Poster.

Evolving Signal-driven Digital Organisms with SignalGP

Alexander Lalejini and Charles Ofria

Computer Science and Engineering, BEACON

Together, carefully designed laboratory experiments, mathematically rigorous simulations, and studies of natural evolutionary dynamics in digital organisms are beginning to yield insight into the evolution of complex traits and behaviors. Digital organisms balance the speed and transparency of simulations with the open-ended realism of laboratory experimental systems. Here, we present Signal-driven Genetic Programs (SignalGP), a new class of digital organism that emphasizes dynamic interactions among organisms and between organisms and their environment. SignalGP allows digital methods to realize a broader and richer spectrum of evolutionary dynamics that more closely rivals that of biological evolution.

In digital evolution, self-replicating computer programs (digital organisms) mutate, compete, and evolve *in silico*. Digital evolution systems enable perfect data tracking, and modern compute power allows experimenters to observe many generations of evolution at tractable time-scales (thousands of generations in minutes as opposed to months or years). In laboratory settings, the types of biological organisms we choose to work with can influence our repertoire of experimental possibilities; the same is true in digital evolution. Different types of digital organisms have different genetic program representations that impose different sensory interfaces and mechanisms for processing sensory information.

SignalGP is a genetic program representation that allows digital organisms to dynamically react to signals from the environment or other agents. In traditional digital evolution systems (e.g., *Avida*), genetic programs are expressed procedurally: actions are performed one at a time in a single chain of execution and must explicitly check for new sensory information. These traditional digital organisms must generate explicit queries in order to identify (and react to) any changes in their environment. In SignalGP, program expression is signal-driven: genetic programs are segmented, and each segment can be independently expressed in response to a signal. For example, if a SignalGP organism senses a nearby predator, any evolved predator-response code in the organism is automatically expressed (in parallel with existing expression patterns). The mechanism by which signals specify and trigger segments of code is inspired by transduction of chemical signals in natural cells. The specific signals used and the actions taken in response to those signals remain under the purview of evolution. We have verified the functionality of SignalGP digital organisms, demonstrating their ability to evolve solutions to a variety of computational problems that require frequent organism-organism or organism-environment interactions, such as phenotypic plasticity in a changing environment and distributed consensus. Our next steps are to investigate a range of challenging questions in evolutionary biology, focused primarily on watershed events such as group formation, division of labor, or the evolution of complex regulatory networks. We are developing open-source research software for this work with web-based interfaces to

encourage the scrutiny, replication, reuse, and extension of our methods within the scientific community.

Genetic control of a plant-mite mutualism

Erika R. LaPlante & Marjorie G. Weber

Department of Plant Biology

Many plants defend themselves by providing rewards like food and shelter to arthropod predators in return for protection against herbivores and pathogens, facilitating defense through tri-trophic interactions. Though these indirect defense traits are well recognized ecologically, little is known about their underlying genomic drivers. Here, I investigate the genomic underpinnings of indirect defense using a particularly under-explored but ecologically wide-spread system: mutualisms between grape plants (*Vitis vinifera*) and “bodyguard” mites that eat plant pests. In these mutualisms, *Vitis* plants have suites of morphological traits that attract beneficial mites to plant leaves (e.g. mite domatia and deep vein axils). Together, these traits mediate mutualistic interactions between plants and mite bodyguards: mites thrive in the hospitable environment provided on the leaf surface, and in turn eat pests (herbivores and pathogenic microbes) off of the plant leaves. Here, I investigate the genetic underpinnings of the expression of morphological traits that attract beneficial mites, on cultivars of domesticated grape, *Vitis vinifera*. I use a Genome Wide Association study approach that combines phenotypic data from 402 distinct cultivars of grape collected from USDA-ARS maintained plots and genotypic data from a pre-existing gkSNP dataset from these same plants, generated by Dr. Sean Myles. Results revealed few SNPs of large effect that are correlated with the mite-defense morphological traits (e.g. expression of domatia). By studying the underlying genetics involved in domatia formation, this study provides an excellent opportunity to link genotype to ecologically- and agriculturally-relevant plant phenotypes.

Decadal differences in leaf litter decomposition at Augusta Creek, an MSU experimental field site

Courtney E. Larson and M. Eric Benbow

Entomology

Augusta Creek, a stream in MSU's W. K. Kellogg Experimental Forest, has hosted field studies that revolutionized stream ecology and changed the way riverine systems were viewed. Descriptive studies on leaf litter decomposition in the 1970's served as formative evidence for the River Continuum Concept. Yet, these studies were limited by their time. Genomic technologies were not developed for microbial community assessment and riparian invaders were not yet a concern. Several invasions, including Common Buckthorn and Emerald Ash Borer, reshaped riparian conditions and leaf litter inputs of Augusta Creek; therefore, it serves as an ideal site to revisit the hypotheses tested forty years ago, updated to address colonizing microbes and invasion dynamics. The aim was to determine how leaf taxa (invasive vs. native) alters leaf litter decomposition rates as well as the macroinvertebrate and microbial communities. Preliminary analysis determined faster decomposition and different microbial colonizers in the invasive leaf litter. We also compare these findings to those of Petersen and

Cummins (1974), who found different processing rates and colonization among leaf taxa. This experiment continues the legacy of leaf litter decomposition research at Augusta Creek, informing larger fields of invasive species and microbial ecology.

Fast and accurate statistical introgression mapping using large-scale genomic sequence datasets

Qiqige Wuyun and **Kevin J. Liu**

Computer Science and Engineering, BEACON, Quantitative Biology

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.

The effects of non-rainfall moisture on fungal communities and standing grass litter decomposition in a hyperarid desert

Robert Logan, Kathryn Jacobson, Peter Jacobson, Sarah Evans

Integrative Biology, Kellogg Biological Station

Although drylands represent over 40% of the Earth’s land surface, we still lack a strong understanding of what controls carbon cycling in these systems. Decomposition of aboveground standing litter is an important, though often ignored, component of C cycling in drylands and recent work has begun to highlight the central role that non-rainfall moisture (NRM; fog, dew, and high humidity) can play in this process. However, we still know relatively little about how decomposers themselves respond to different moisture regimes and how this may affect overall decomposition rates. We examined the fungal communities on standing grass litter at two sites in the hyperarid Namib Desert (an NRM-dominated zone and a rain-dominated zone) to see how local moisture regimes influence decomposers. While fungal communities differ between the sites, we found a core fungal taxa that dominates litter at both locations. Mass loss rates on sterile litter were 380% higher in the NRM zone than in the rain zone, highlighting the importance of NRM for fungal decomposition, especially in a rain-sparse system. Finally, reciprocally transplanting litter revealed that while all litter decomposed faster in the NRM-zone, communities from the NRM-dominated zone seemed more sensitive to changing moisture regimes than did those originating in the rain zone. Understanding how moisture regimes shape litter-associated microbial communities in drylands can help us make

more informed predictions of how C-cycling processes in these systems may change under future climate conditions.

Parental social behavior of the African painted dog

Caitlin Mack

Department of Integrative Biology

When social species of animals are kept in captivity, it can be difficult to replicate their natural social dynamics. This is true of the African painted dog (*Lycaon pictus*), an endangered canid native to sub-Saharan Africa. The Association of Zoos and Aquariums (AZA) has a Species Survival Plan, a collaborative breeding and transfer plan, for this species. Understanding the best methods to create social dynamics and integrate animals into a pack is essential for the successful breeding and rearing of pups. Painted dogs have a high pup mortality rate and it can be difficult to create a cohesive pack. The research described here aims to study how the presence of pups and yearlings affects the social behavior of adults in captive packs of African painted dog (*Lycaon pictus*). The primary research question is whether the presence of young results in a higher frequency and duration of affiliative social behaviors by the adult members of the pack. To study this, the behavior of painted dog packs at four different AZA-accredited zoos are being observed three times over the course of one year. While studies have been done on the social behavior of painted dogs in the wild and in captivity, there has not been much previous work done specifically on the effect of pups on the adults dogs. The conclusions from this study can provide insight into how to increase pack cohesion and help increase reproductive success in captivity.

Improving wildlife conservation by integrating genomic, environmental, and ecological information

Nadya R. Mamoozadeh and Mariah H. Meek

Integrative Biology

For many species of conservation concern, spatiotemporal patterns of neutral and adaptive genetic variation and the environmental and ecological factors influencing this variation are poorly understood. These knowledge gaps compromise the ability of conservation and management plans to protect genetic variation important for the short-and long-term persistence of imperiled populations. Here, we use brook trout (*Salvelinus fontinalis*) in the Lake Superior basin as a system in which to evaluate the following questions: 1) how is neutral and adaptive genomic variation distributed across local and regional landscapes, 2) what environmental and ecological variables most strongly influence neutral and adaptive genetic diversity, and 3) how have historical management practices influenced contemporary patterns of genomic variation. Addressing these questions will provide valuable information to improve conservation and management efforts for brook trout, including identification of populations most in need of management intervention and prioritization of environmental features for habitat restoration. More broadly, results from this work will offer valuable insights into environmental and ecological variables most strongly influencing neutral and adaptive genomic diversity in salmonid fishes, many of which support valuable commercial or

recreational fisheries but are increasingly threatened by habitat loss and a changing global climate.

Submissiveness Personality Traits in Spotted Hyenas (*Crocuta crocuta*)

S. Kevin McCormick and Kay E. Holekamp
Integrative Biology, BEACON

Animal personality refers to traits that vary across individuals, but are consistent within individuals across time and context. A common animal personality trait quantified in social animals is aggressiveness. An individual's submissiveness is typically assumed to be negatively correlated with its aggressiveness, such that more aggressive individuals are less submissive and vice versa. This may be true during agonistic interactions, but an individual's submissiveness, particularly when observed in contexts other than aggressive interactions, may represent a trait that is independent of aggressiveness. Here, we used repeated measures of critical incident sampling of spotted hyenas within a clan that has been observed for over 30 years. Prior research on this group yielded evidence that intensity of aggressive acts is consistent within individuals across time and context. Utilizing similar methods, we determined that the intensity of submissive behavior also varies consistently across time and contexts within individuals exhibiting unsolicited appeasement. Interestingly, submissiveness is neither positively nor negatively correlated with aggressiveness scores within individuals.

The Meek Lab: Conservation in a changing world

Mariah Meek
Integrative Biology
Lab poster.

Individual participation in cooperative mobbing behavior

Tracy M Montgomery, Kenna DS Lehmann, Kay E Holekamp
Integrative Biology

Understanding the physiological and social factors that mediate cooperative behavior among animals is central to the study of social evolution. Spotted hyenas frequently cooperate to mob lions, approaching as a tightknit group while vocalizing loudly in an attempt to drive the lions away from a carcass or den. This cooperation occurs despite low average relatedness within groups and hierarchical rank relationships that determine priority of resource access. Mobbing behavior increases the chances of hyenas gaining control of a carcass, which may increase the fitness of participating hyenas. However, mobbing behavior is also risky, as lions are the leading cause of mortality in most hyena populations; even approaching lions in a group, individuals risk injury or death while mobbing. Identifying specific individuals who participate in mobbing, and the traits that predict this participation, is vital to understanding this collective behavior. We assessed participation with respect to demographic, social, and hormonal traits of individuals who participate more or less frequently in several hundred mobs

observed in Kenya from 1988 to 2017. Preliminary results indicate that female hyenas that are neither pregnant nor lactating are likeliest to participate in mobbing, perhaps because harm to them would not result in death of dependent offspring.

Olfactory bulb size and daily activity patterns in rodents

Andrea Morrow, Laura Smale, and Barbara L. Lundrigan

Department of Integrative Biology

Olfaction is an essential sense modality by which animals gain information about their surroundings through chemical stimuli; it can aid in finding food, interacting with conspecifics, evading predators, and more. In contrast to vision, olfaction does not depend on light cues. For species with a daily activity pattern (i.e., temporal niche) that is restricted to the hours of darkness (i.e., strictly nocturnal), when photic cues are minimal, we expect olfactory capabilities to be especially well developed. In this study, we aim to test this hypothesis by looking at the variation in olfactory bulb (OB) size, relative to brain size, among rodent species occupying a range of temporal niches. The OBs receive direct input from the olfactory nerves, and their sizes can be used as a proxy for investment in olfactory function. Our sample includes 14 species, representing 3 families of extant rodents. Each species is categorized as nocturnal, diurnal, or both (active during the day and night, i.e. cathemeral, crepuscular, or arrhythmic) based on behavioral data from field studies. Preliminary observations suggest a positive relationship between olfactory bulb size (relative to brain size) and nocturnal behavior. However, there is considerable variation that is not explained by temporal niche, including evidence for phylogenetic constraints. This research was supported by BEACON: An NSF Center for the Study of Evolution in Action.

The role of drift in electric signal variation among the mormyrid fish *Paramormyrops kingsleyae*

Sophie Picq, Sperling J, Cheng C, Carlson B, Hopkins C, Gallant J

Department of Integrative Biology, BEACON

Communication signals are highly diverse traits. This diversity is usually assumed to be shaped by selective forces, whereas the null hypothesis of divergence through drift is often not considered. In Gabon, the weakly electric fish *Paramormyrops kingsleyae* is widely distributed in multiple independent drainage systems, which provide a natural evolutionary laboratory for the study of genetic and signal divergence in separate populations. We quantified geographic variation in the electric signals of 327 fish from nine localities, and compared it to the neutral genetic variation estimated from microsatellite markers in the same individuals, to test whether drift may be driving divergence of their signals. We found that signal distances were not correlated with genetic distances, suggesting that signal divergence in *P. kingsleyae* cannot be explained by drift alone. Secondly, utilizing a behavioral assay, we found that *P. kingsleyae* individuals can discriminate between different signal waveforms. We suggest that these signals play a role in intraspecific communication such as mate choice and are likely shaped by selective forces. We plan to investigate the roles of sexual and natural selection in driving signal divergence in this species during our upcoming field trip to Gabon this summer.

Sensory mechanisms for localizing spermatophores in the axolotl (*Ambystoma mexicanum*), an aquatic salamander

Taylor Rupp, Heather Eisthen

Department of Integrative Biology

Salamanders transfer sperm externally using a gelatinous capsule of sperm called a spermatophore. Sperm transfer between axolotls is initiated when the female starts to follow the male. The male deposits a spermatophore then continues to walk forward with the female close behind. The female then picks up the spermatophore with her cloaca, fertilizing her eggs internally. How does the female determine the location of the spermatophore? We predict that female axolotls rely on two sources of cues: visual, tactile, and chemical cues from spermatophores, and tactile feedback from males. We collected spermatophores from courting axolotls and then introduced a spermatophore into an aquarium containing a different female. Female axolotls exposed to spermatophores exhibited longer, more frequent bouts of a courtship behavior called tail fanning than did control females not exposed to spermatophores. This result suggests that spermatophores provide sensory cues important for courtship in female axolotls. Males are another potential source of cues. A male occasionally provides a female with tactile feedback while she is following him by displacing her with his tail, hindlimbs, or cloaca. This physical contact may serve to correct the female's trajectory and properly align her cloaca with the spermatophore. We found that in cases where this tactile feedback occurs, females were more likely to acquire spermatophores. These experiments help elucidate the sensory mechanisms that female salamanders use during spermatophore localization. More broadly, this research provides insight into the evolution of external sperm transfer in salamanders and the diversification of mating strategies amongst amphibians.

Do lichens follow the Biotic Interactions Hypothesis? Testing partner specificity along a latitudinal gradient

Klara Scharnagl & Alan Prather

Plant Biology, BEACON, Kellogg Biological Station

As a component of my dissertation work, I am testing the biotic interactions hypothesis in lichens by sequencing both the fungal and algal partners of multiple individuals of certain lichen species. Lichens were collected from seven different field sites along a latitudinal gradient. Lichen species were chosen based upon their geographical location and range (tropical, extra-tropical, or spanning both) and the number of individuals collected per species. At least ten individuals were needed for a species to be included. I extracted DNA using the Sigma REExtract'n'Amp kit, and fungal ITS, algal ITS, and algal rcbL regions were amplified and sequenced. Preliminary sequence clean-up, alignment, and NCBI BLAST searches were conducted using UGENE, and downstream analyses were conducted in the 'ape' package in R. While this work is ongoing, we hypothesize a more generalist pattern of association (multiple algal partners for a given lichenized fungal species) in extra-tropical regions, and a more specialist pattern of association (more one-to-one algal-fungal partnerships) in tropical regions. In the future I will be investigating whether there is a phylogenetic signal or an

environmental signal in the lichen symbiosis by sequencing both the fungal and algal partners of multiple species across three lichen families along a latitudinal gradient from 11S to 60N in the Americas. The role of symbioses in driving patterns of biodiversity across environmental gradients has not been extensively explored, yet this may be one of the more important biotic interactions driving these patterns.

Seasonal patterns of diversity, assembly, and host-specificity in core microbiota of perennial biofuel crops

KL Grady, **JW Sorensen**, N Stopnisek, J Guittar, A Shade

Department of Microbiology and Molecular Genetics

The aerial surface of plants, known as the phyllosphere, makes up a large portion of the terrestrial microbial environment (an estimated 10⁸ km² globally). Phyllosphere microbes can influence ecosystem services by moderating biogeochemical fluxes of greenhouse gasses.

They also can benefit their hosts by improving plant stress tolerance or promoting the production of plant growth hormones. However, we have limited information about the composition, dynamics and functions of bioenergy crop phyllosphere microbiota. Here, we characterize the diversity and assembly of microbial communities present in the phyllosphere and nearby soil of two perennial cellulosic feedstocks for biofuel - switchgrass (*Panicum virgatum*) and miscanthus (*Miscanthus x giganteus*) over the course of the 2016 and 2017 growing seasons at the Great Lakes Bioenergy Research Center's Biofuel Cropping System Experiment (Kellogg Biological Station, Hickory Corners, MI). We sampled both nitrogen-fertilized and unfertilized sub-plots to assess the effect of N-fertilization on phyllosphere community structure and function. We used 16S rRNA gene sequencing to assess microbiome diversity and structure. We found that community membership of the phyllosphere was distinct from that of soils, but that soils, and particularly the rare biosphere, served as a reservoir for >90% of taxa found on leaves. The phyllosphere harbored relatively simple communities of less than 150 taxa per time point, and had a core microbiome (comprised of taxa that are both persistent and abundant) which included several Proteobacteria lineages. There were directional changes in the phyllosphere communities over the growing season, suggesting that these consortia were fit for life on the leaf surface rather than transient and randomly assembling from the air or soil. Miscanthus and switchgrass phyllosphere communities became more differentiated mid-season and converged again towards senescence, indicating an influence of host. There was no strong influence of fertilization on the phyllosphere structure. Understanding the dynamics of community assembly, structure, and function of phyllosphere microbiota is a first step toward managing these communities to benefit their hosts. In the case of bioenergy crops, we interrogate these communities for functions that may improve crop productivity or wellness, or enable efficient cellulose degradation from plant material.

Genomic mechanisms of developmental delay and environmentally-cued hatching in annual killifish

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Integrative Biology, BEACON

Annual killifishes are emerging biomedical models due to their unique embryonic dormant stages and their rapid senescence. Consequently, they are being used to study development, metabolism, cell proliferation, stress tolerance, and aging in vertebrates. They inhabit seasonal pools that desiccate, resulting in the death of the adult population. Unique adaptations including specialized egg structures, desiccation resistance, and up to three ontogenetic diapause stages slowing developmental and metabolic rates enable the embryonic population to survive annual dry seasons. When the habitat floods, annual killifish terminate their third and final diapause (DIII), hatch, and begin a new lifecycle. Here we explore the genomics of embryonic DIII in annual killifishes, the only vertebrate diapause known to occur after completion of organogenesis. We use scanning electron microscopy, comparative transcriptomics, phylogenetic methods and model rates of gene evolution to investigate the genetics of killifish annualism, diapause, and environmentally-cued hatching. We discover hundreds of candidate genes involved in diapause and delayed hatching in three killifish species: the Rio pearlfish, the striped panchax, and the Venezuelan lyretail. Specifically, we find 10 differentially expressed killifish transcripts with homologs also differentially expressed in the same direction during dormancy in other animals. These 10 transcripts illustrate the conserved roles of these homologs during delayed development in metazoans from insects to killifish to mammals. Additionally, tight linkage of diapause and hatching with the expression of a complex family of hatching enzymes leads us to analyze regulatory mechanisms associated with environmentally-cued hatching in comparison to other aquatic vertebrates. Lastly, we show that diapause has up to 7 origins in killifishes and detect over 160 genes that with increased rates of molecular evolution in annual compared to non-annual killifishes. Our integrative framework combining development, genomics, evolution, and ecology provides important insights into the mechanisms of diapause and the diversity of vertebrate hatching strategies as well as candidate genes associated with arrested development, metabolic depression, and stress tolerance in vertebrates in the face of changing environments.

Geographic dependence of fungus resistance genetic architecture in locally adapted switchgrass

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Plant Biology, PRI, GLBRC

Pathogens play an important role in the evolution of plant populations, but the genetic mechanisms of resistance to pathogens are rarely studied outside traditional crop systems. This study uses locally adapted ecotypes of the emerging biofuel crop switchgrass (*Panicum virgatum*) to examine the temporal and spatial variation in the genetic architecture of resistance to a fungal pathogen, switchgrass leaf rust (*Puccinia novopanici*). To identify loci underlying variation in pathogen resistance in switchgrass, we planted clones of an outcrossed mapping population at eight locations in the United States from southern Texas to central Michigan. We measured rust progression at these sites for three years, then mapped quantitative trait loci (QTLs) using function-valued transformations of rust progression curves.

We mapped fifty-one total QTLs over the three-year period that varied in presence and strength. We discovered two loci that were consistently associated with resistance across multiple sites and years. These two focal QTLs were almost exclusively present in northern sites, raising questions about the geographic range of resistance. Since we found that there is no difference in rust species composition between the north and south, it is possible that the difference in genetic architecture is due to rust strain differences. The beneficial alleles at the focal loci confer a 33% decrease in rust, and a 26% increase in biomass, indicating that these loci have high adaptive importance for switchgrass. Our results show an important role for a fungal pathogen in the local adaptation of switchgrass and illustrate the environmental dependence of the genetic architecture of plant disease resistance.

Under ongoing climate change in Michigan, growth of some sugar maple populations may increase and in others decrease

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Climate change is already affecting tree growth, and its effects are expected to intensify. Warming is expected to hinder growth by increasing respiration and drought stress, but, in regions where precipitation will increase along with temperature, the negative effects of warming may be ameliorated or even surpassed by the positive effects of increased precipitation. Further, while summer warming is expected to be almost universally detrimental, fall and spring warming could be beneficial in extending the growing season provided that late-fall growth does not interfere with pre-winter hardening or that early cambial activation in the spring does not make trees vulnerable to late-spring frosts. With so many variables under consideration, and because species will respond differently across their distribution, it is necessary to mathematically model the relationship between growth and climate in multiple populations to understand how a suite of changing climate variables will together affect growth. We took tree cores from four populations of sugar maple (*Acer saccharum*) across two degrees of latitude from the southern to northern Lower Peninsula. We used all-subsets multiple regression to select the most important climate variables with which to model the relationship between tree-ring widths and climate. Into these models we inputted projections of climate through the rest of this century, spanning relatively benign to severe climate-change scenarios, to project future growth. We found that future growth will be specific to location and not necessarily predictable according to latitude. At our most southerly site (latitude 42.36), growth is expected to decrease by 13.9% under the most benign to 33.1% under the most severe climate change scenario. At the next-most southerly site (42.62), not far from the first, growth is expected to increase by between 5.9 and 11.2%. At the second-most northerly site (44.12), growth is expected to decrease by 5.3–10.5% and, at the most northerly (44.12), to have anywhere from no significant change to an 11.1% increase. Our results underscore the importance of studying many populations throughout a species range to identify potentially climate-change-resilient populations whose seed could be used to populate areas without resilient populations.

The Wetzel Lab: Studying the ecology of plants & insects in a variable world

Will Wetzel

Entomology, Kellogg Biological Station

Lab poster.

Integrating data from across the annual migratory cycle to understand population dynamics of the eastern monarch butterfly

Erin R. Zylstra

Integrative Biology

Monarch butterflies (*Danaus plexippus*) in eastern North America are well known for their multi-generational, long-distance migrations between wintering locations in Mexico and breeding locations in the northern U.S. and southern Canada. The overwintering population has severely declined since surveys began in 1993. Numerous factors have been identified as potential causes of this decline, the most prominent of which is the loss of milkweed hostplants in the summer breeding grounds due to increased rates of herbicide application.

Other factors include loss of overwintering habitat due to logging, severe winter storms, declines in nectar resources along fall migration routes, introduction of non-native plants, and changes in temperature and precipitation in the spring and summer. Although it is likely that several of these factors influence population dynamics, understanding their relative importance is critical to designing effective conservation and management strategies. We combined data on monarch abundance throughout their annual cycle and modeled changes in population size as a function of environmental and anthropogenic factors in a Bayesian, hierarchical framework. To do this, we modeled monarch counts from multiple, volunteer based monitoring programs in the summer breeding grounds as a function of land use, spring and summer climate, and size of the monarch population at the end of the winter when individuals begin leaving overwintering sites. We then modeled population size in 19 wintering colonies just after the butterflies arrive as a function of forest cover, colony location, fall climate and nectar availability, and our model-based index of population size the preceding summer. Unlike previous analyses based on data from a single monitoring program, preliminary results indicate a relatively strong link between butterfly abundance in summer and size of overwintering colonies. Results also suggest that population dynamics are governed by multiple factors operating in different seasons and at different spatial scales. Our study highlights the importance of modeling population dynamics of migratory species throughout the annual cycle and will allow us to predict how management actions that target a particular threat or life stage are likely to affect future population dynamics of monarchs in eastern North America.