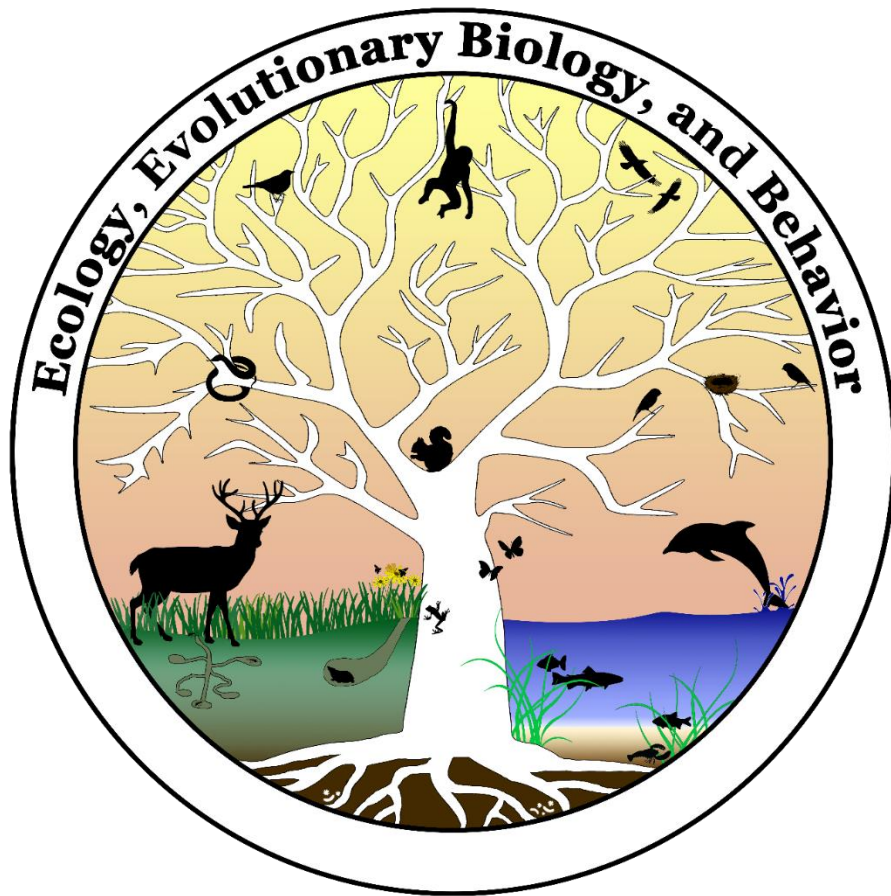


The Second Annual
Ecology, Evolutionary Biology, & Behavior
Research Symposium



April 30, 2018
Michigan State University
Henry Center for Executive Development
3535 Forest Rd, Lansing, MI 48910

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Garrison , poster	Oberosler , poster	Wang , Zinan, talk
Gering , poster	Ortiz Londono , poster	Warner , poster
Guittar , poster	Ou , poster	Wiser , talk
Hugentobler , poster	Pang , talk	Wuyun , poster

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[#MSUEEBB2018](#)

This event made possible by:

Ecology, Evolutionary Biology, & Behavior Program

Kay Holekamp, EEBC Director

Barbara Bloemers, EEBC Grad Group Advisor

EEBC Research Symposium Planning Committee

Courtney Larson, Co-Chair

Ravi Ranjan, Co-Chair

Darren Incorvaia

Julie Jarvey

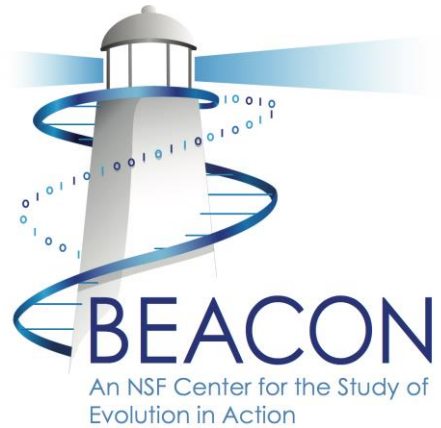
Mauricio Losilla

Caitlin Mack

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And the Sponsors on the next page!



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Thank you!

Welcome from the EEBB Director

Welcome to the second annual EEBB Research Symposium! Today's presentations will be made by graduate students, post-docs and faculty in EEBB. I hope 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. CNS dean Jim Kirkpatrick included sufficient funds in EEBB's budget to allow us to move forward, so we are grateful to him for that. 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 Kenna Lehmann. In addition, special thanks are owed to EGG members Darren Incorvaia, Julie Jarvey, Courtney Larson, Mauricio Losilla, Caitlin Mack, Ravi Ranjan, Taylor Rupp, and Christopher Warneke for their tireless efforts on behalf of this Symposium. Finally, 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,

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. If the recipient of the behavior feels like it is harassment, then it is harassment, regardless of the perpetrator's intent.

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: [#MSUEEBB2018](#)

Keynote Speaker

Dr. Mathew Leibold
Department of Biology, University of Florida
<http://www.leiboldlab.com/>



Dr. Leibold is a pioneer in community and ecosystem ecology, and works to integrate ecological processes to facilitate solving urgent environmental issues. His group had a big role in reviving the concept of the ecological niche as a relationship with two parts: the effects of the environment on the organism, and the response of the organism to the environment. He also played an important role in developing the theory of metacommunities, which are now a driving force in modern ecology. If you would like more information on Dr. Leibold and his group's work, follow the link above.

Awards

The following awards will be presented:

Best oral presentation

Best lightning talk

Best poster

Thank you to our judges:

Andrea Bierema

Lars Brudvig

Henry Chung

Andrew Dennhardt

Sarah Fitzpatrick

Minako Izutsu

Helen McCreery

Abhijna Parigi

Shinhan Shiu

Laura Smale

Wei Wang

Elise Zipkin

Overview EEBB Research Symposium

8:00-8:45am	Meeting Registration	Entry Hall
8:45-9:00am	<p>Welcome</p> <p>A169</p> <p><i>Kay Holekamp (IBIO), EEBB Director</i></p> <p><i>Kenna Lehmann (IBIO), EEBB Grad Group President</i></p>	
9:00-10:00am	<p>Oral Presentations I (<i>moderator Julie Jarvey</i>)</p> <p>A169</p> <p>9:00 <i>Gabriela Quinlan (ENT)</i></p> <p>9:15 <i>Lily Johnson-Ulrich (IBIO)</i></p> <p>9:30 <i>Carina Baskett (PLB)</i></p> <p>9:45 <i>Kyla Dahlin (GEO) LIGHTNING TALK</i></p> <p>9:49 <i>Gary Roloff (FW) LIGHTNING TALK</i></p> <p>9:53 <i>Kevin Liu (CSE) LIGHTNING TALK</i></p>	
10:00-11:00am	Break & Poster Session I (<i>odd-numbered posters</i>)	A138
11:00am-12:00pm	<p>Keynote Address (<i>moderator Ravi Ranjan</i>)</p> <p><i>Dr. Mathew Leibold, University of Florida</i></p>	A169
12:05-1:00pm	Lunch	Atrium
1:00-2:00pm	<p>Oral Presentations II (<i>moderator Courtney Larson</i>)</p> <p>A169</p> <p>1:00 <i>Siobhan Cusack (CMB)</i></p> <p>1:15 <i>Robert Mobley (IBIO)</i></p> <p>1:30 <i>Emily Dolson (CSE)</i></p> <p>1:45 <i>Lars Brudvig (PLB) LIGHTNING TALK</i></p> <p>1:49 <i>Mariana Szucs (ENT) LIGHTNING TALK</i></p> <p>1:53 <i>Ingo Braasch (IBIO) LIGHTNING TALK</i></p>	A169
2:00-3:00pm	Break & Poster Session II (<i>even-numbered posters</i>)	A138
3:00-4:00pm	<p>Oral Presentations III (<i>moderator Darren Incorvaia</i>)</p> <p>A169</p> <p>3:00 <i>Bethany Moore (PLB)</i></p> <p>3:15 <i>Genevieve Pang (FW)</i></p> <p>3:30 <i>Zinan Wang (ENT)</i></p> <p>3:45 <i>Michael Wiser (BEACON)</i></p>	
4:00-4:30pm	<p>Closing Remarks & Awards</p> <p><i>EEBB Research Symposium Planning Committee</i></p>	A169
<i>Directly after the symposium</i>	Reception	Beggar's Banquet in East Lansing

Schedule Detail: EEBB Research Symposium

8:00am **Meeting Registration** **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 **Welcome** **A169**

Kay Holekamp, EEBB Director

Kenna Lehmann, EEBB Grad Group President

9:00am **Oral Presentations I** **A169**

9:00am **How landscape composition affects honey bee colony growth and survival**

*Gabriela Quinlan, Graduate Student,
Entomology*

[abstract](#)

9:15am **Predictors of innovation in spotted hyenas**

*Lily Johnson-Ulrich, Graduate Student,
Integrative Biology*

[abstract](#)

9:30am **Stronger anti-herbivore defense at lower latitudes in a widespread temperate herb**

*Carina Baskett, Graduate Student,
Plant Biology*

[abstract](#)

9:45am **Ecology from space!**
LIGHTNING TALK
Kyla Dahlin, Faculty,
Geography, Environment, & Spatial Sciences [abstract](#)

9:49am **Hogs gone wild: Ecology and behavior of feral swine in Michigan**
LIGHTNING TALK
Gary Roloff, Faculty,
Fisheries and Wildlife [abstract](#)

9:53am **Fast and accurate inference of phylogenetic networks using large-scale genomic sequence data**
LIGHTNING TALK
Kevin Liu, Faculty,
Computer Science and Engineering [abstract](#)

10:00am **Break & Poster Session I** **A138**

Please join us in the breakout room for refreshments and poster presentations.

Poster 1 **Fast and Accurate Introgression Detection using Statistical Phylogenomic Inference**
Qiqige Wuyun, Graduate Student,
Computer Science and Engineering [abstract](#)

Poster 3 **Phytohormones can resuscitate dormant environmental bacteria**
Patrick Kearns, Post-doc,
Microbiology and Molecular Genetics [abstract](#)

- Poster 5 **Mechanisms of Adaptive Evolution**
Viviana Ortiz Londono, Graduate Student,
Plant Soil, and Microbial Sciences [abstract](#)
- Poster 7 **Factors influencing gene family size variation among related species in a plant family**
Peipei Wang, Post-doc,
Plant Biology [abstract](#)
- Poster 9 **The scent of a pathogen: An avian chemosignal predicts host infection status in feral chickens (*Gallus gallus*)**
Eben Gering, Post-doc,
Integrative Biology [abstract](#)
- Poster 11 **Trait-based community assembly and succession across an infant gut metacommunity**
John Guittar, Post-doc
Microbiology and Molecular Genetics [abstract](#)
- Poster 13 **Evaluating the effects of contrasting management regimes on tropical mammal diversity**
Valentina Oberosler, Graduate Student,
Integrative Biology [abstract](#)
- Poster 15 **The effects of solar installations on desert plants**
Miranda Wade, Graduate Student,
Integrative Biology [abstract](#)
- Poster 17 **Microbiome diversity and assembly in the phyllosphere of perennial bioenergy crops**
Jackson Sorenson, Graduate Student,
Microbiology and Molecular Genetics [abstract](#)

Poster 19 **An –omics approach to assess emergent properties within a 3-member synthetic microbial community**
John Chodkowski, Graduate Student
Microbiology and Molecular Genetics [abstract](#)

Poster 21 **Evaluating the role of herbivory and salt spray on the evolution of locally adapted intraspecies ecotypes of Seep Monkeyflower (*Mimulus guttatus*) across a coast-inland moisture gradient**
Damien Popovic, Graduate Student,
Plant Biology [abstract](#)

Poster 23 **The ghost of trees past: how long do plant-soil feedbacks persist to influence current tree seedling dynamics?**
Clarice Esch, Graduate Student,
Forestry [abstract](#)

11:00am **Keynote Address** **A169**
Metacommunity ecology - from v 1.x to 2.0
Dr. Mathew Leibold, University of Florida

12:05pm **Lunch**
Atrium

Please join us in the Henry Center atrium for lunch. [menu](#)

1:00pm **Oral Presentations II**
A169

1:00pm **Modeling degrees of genetic redundancy among
paralogs in *Arabidopsis thaliana***
*Siobhan Cusack, Graduate Student,
Cell and Molecular Biology* [abstract](#)

1:15pm **The Sensory Space of the Threespine Stickleback**
*Robert B. Mobley, Graduate Student,
Integrative Biology* [abstract](#)

1:30pm **Ecological Communities in Evolutionary Computation**
*Emily Dolson, Graduate Student,
Computer Science and Engineering* [abstract](#)

1:45pm **Toward prediction in restoration ecology**
LIGHTNING TALK
*Lars Brudvig, Faculty,
Plant Biology* [abstract](#)

1:49pm **What enables populations to colonize a novel
environment?**
LIGHTNING TALK
*Marianna Szucs, Faculty,
Entomology* [abstract](#)

1:53pm **Odyssey of Strange Fish: Investigating Fish Genomes
and Development to Illuminate Vertebrate Evolution**
LIGHTNING TALK
Ingo Braasch, Faculty,

2:00pm Break & Poster Session II

A138

Please join us in the breakout room for refreshments and poster presentations.

Poster 2 Identity-dependent of Plant Traits in Responding to Grazing

*Maowei Liang, Graduate Student,
Geography, Environment, & Spatial Sciences*

[abstract](#)

Poster 4 Variable impacts of habitat context on monarch butterfly (*Danaus plexippus* L.) oviposition and egg survival

*Andrew Myers, Graduate Student,
Entomology*

[abstract](#)

Poster 6 Benbow Lab: Novel microbiome research for human health, forensics and environmental science

*Joseph Receveur, Graduate Student,
Entomology*

[abstract](#)

Poster 8 LTR_retriever: a highly accurate and sensitive program for identification of LTR retrotransposons

*Shujun Ou, Graduate Student,
Horticulture*

[abstract](#)

Poster 10 Quantifying Impacts of Floodplain Availability on Chinook Salmon (*Oncorhynchus tshawytscha*)

*Sara Hugentobler, Graduate Student,
Integrative Biology*

[abstract](#)

Scott Warner, Graduate Student,
Plant Biology

[abstract](#)

3:00pm **Oral Presentations III**
A169

3:00pm **Predicting specialized metabolism genes using a machine learning approach in *Arabidopsis thaliana***

*Bethany Moore, Graduate Student,
Plant Biology*

[abstract](#)

3:15pm **The relative roles of genetic variance and phenotypic plasticity on *Ixodes scapularis* emergence timing in the eastern United States**

*Genevieve Pang, Graduate Student,
Fisheries and Wildlife*

[abstract](#)

3:30pm **Genetic mechanisms underlying desiccation resistance in desert fruit flies**

*Zinan Wang, Graduate Student,
Entomology*

[abstract](#)

3:45pm **Uncovering student conceptions about randomness**

*Michael Wiser, Post-doc,
BEACON*

[abstract](#)

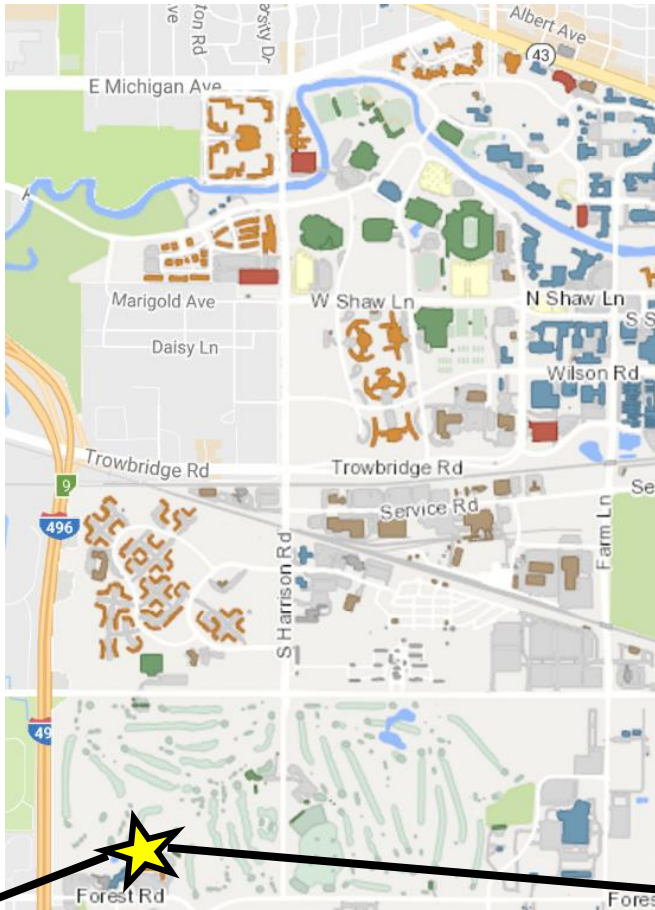
4:00pm **Closing Remarks & Awards** **A169**
EEBB Research Symposium Planning Committee

After Reception [Beggar's Banquet](#), East Lansing

Henry Center for Executive Development

3535 Forest Rd, Lansing, MI

(517) 353-4350

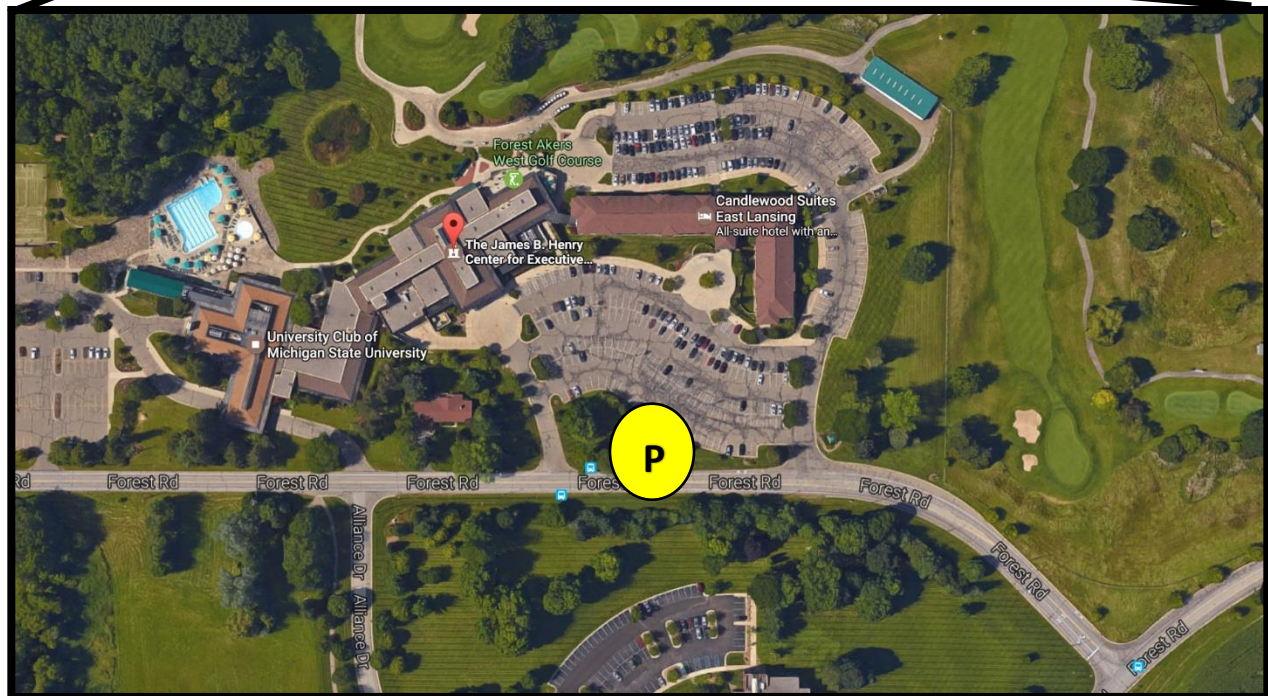


Directions:

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:

Make-Your-Own Salad Bar: Tossed Garden Salad

Mixed Baby Greens, Sliced Cucumbers, Grape Tomatoes,
Banana Peppers, Sunflower Seeds, Chopped Egg,
Shredded Cheese, Diced Ham, Cottage Cheese

G Dressings: Ranch, Balsamic Vinaigrette, Cilantro Vinaigrette

Composed Salads

Mexican Quinoa Salad with Orange-Lime Dressing **G D V**

Taco Salad **G**

Breads & Spreads

Jalapeño Cheddar Bread, Miniature Croissants
Tortilla Chips, Pita Bread
Extra Virgin Olive Oil, Butter

Traditional Hummus **G D V**

Seafood Salad **D**

Carving Station

Carved Roast Flank Steak **D**

Demi-glaze **G D**, Horseradish Cream **G**

Hot Buffet

Southwest Chicken Fajitas with
Grilled Onions & Peppers, Warm Flour Tortillas,
Shredded Cheese, Guacamole, and Salsa

Cheddar & Jack Cheese Enchiladas **V**

Fiesta Corn with Sweet Peppers and Black Beans **G V**

Rice with Fresh Cilantro and Lime Zest **G V**

Mini Bean Burritos **V**

Desserts & Beverages

Strawberry Shortcake Wedge
Lemon Meringue Pie
Regular Coffee, Decaf, and Tea Service

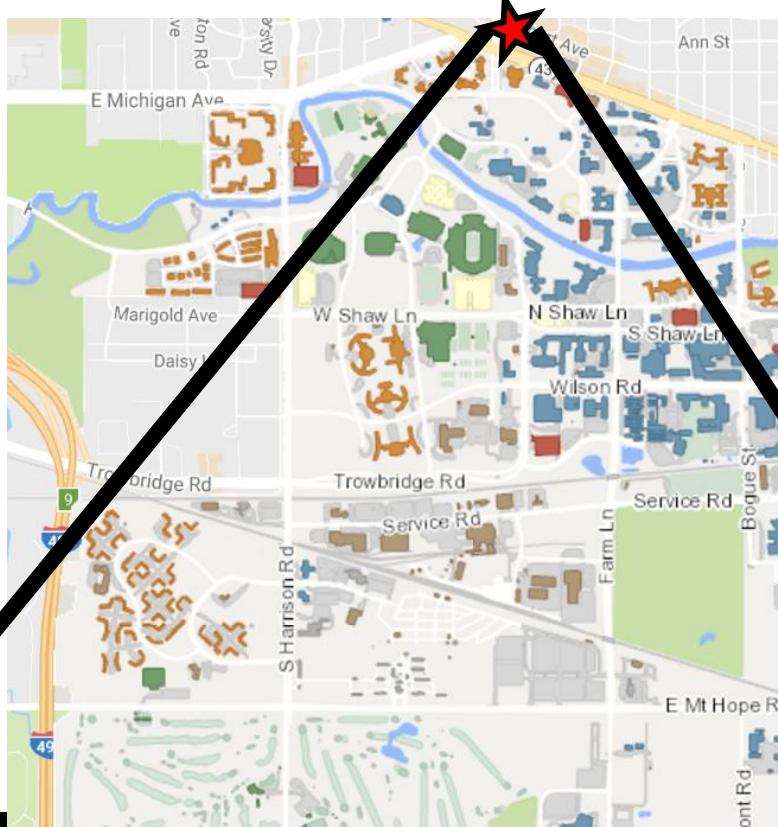
Symbol Key:

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

Beggar's Banquet

[218 Abbot Road, East Lansing, MI](https://www.google.com/maps/place/218+Abbot+Road,+East+Lansing,+MI)

(517) 351-4540



Directions:

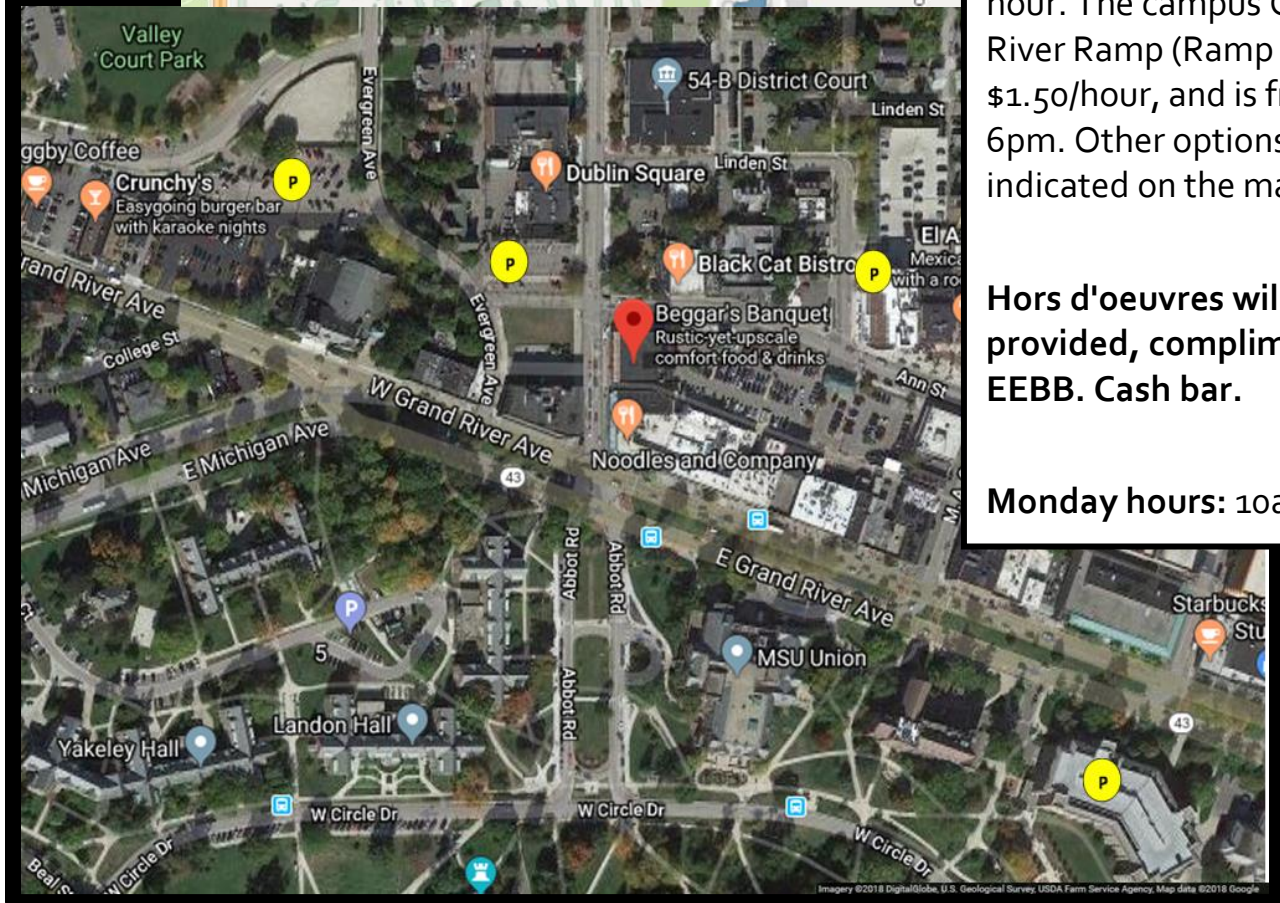
From the Henry Center, travel east on Forest Rd. toward Harrison Rd. Turn left on Harrison Rd, right on Michigan Ave, left on Abbot Rd. Beggar's Banquet is on the first block and will be on your right.

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.

Stronger anti-herbivore defense at lower latitudes in a widespread temperate herb

Carina Baskett¹, Doug Schemske¹, Tony Schillmiller², Marjorie Weber¹

¹Department of Plant Biology, Michigan State University, ²Mass Spectrometry and Metabolic Core, Michigan State University

Biotic interactions are hypothesized to play a greater role in driving adaptation at lower latitudes where abiotic selection pressures are weaker. We tested whether plants from lower latitudes are better defended against herbivores along a gradient from 27°N to 42°N in *Phytolacca americana* (pokeweed, Phytolaccaceae), an herbaceous, perennial pioneer species native to the eastern US. Previous results have found higher herbivory rates in the field in the southern half of its range. We planted a greenhouse common garden of 13 *P. americana* populations to quantify latitudinal variation in functional defense and identify defensive traits. We quantified defense by conducting palatability experiments using a naïve generalist Lepidopteran (*Spodoptera exigua*). Caterpillar biomass was greater at higher latitudes for both young and mature leaves, indicating that lower-latitude leaves are better defended, consistent with the biotic interactions hypothesis. Palatability in mature leaves may be driven by a negative correlation between latitude and toughness or nutrition (carbon:nitrogen). Young leaves were less palatable than mature leaves. Patterns of palatability for young leaves are not explained by toughness or nutrition, and are likely due to chemical defenses, which we are quantifying with LC-MS.

Microbial Puppeteers in a Changing World: How Much Are They Pulling the Strings in Plants?

Lana G. Bolin

Department of Plant Biology

Plant productivity is largely contingent upon water and nutrient availability, and it is often implicitly assumed that plant growth is only responding to water and nutrient levels *directly*. However, plant responses are likely mediated by changes to the soil microbial community as well, but the relative importance of these microbial-mediated effects is unknown. Microbes can evolve rapidly due to their short generation times and their ability to share genetic material via horizontal gene transfer, and their community composition can shift quickly in response to environmental changes. These microbial responses, in turn, can improve or diminish plant growth, with the direction of these effects potentially depending on contemporary environmental conditions.

Plants show phenotypic plasticity in response to abiotic factors that include water and nutrient availability, but they also respond to the presence of soil microbes in a changing environment. Microbes can either increase or decrease the degree of plant phenotypic plasticity, and these shifts can improve plant fitness in new environments. Microbe-mediated changes to plant plasticity have been detected in a handful of traits when comparing nutrient or temperature environments, but no known studies to date have looked at trait plasticity responses to water availability, nor have any investigated interacting environmental gradients. If microbes are causing beneficial changes to plant plasticity in the face of globally changing water and nutrient levels, current estimates of plant resilience to global change may be low.

This summer I will conduct two parallel experiments to assess how belowground microbial communities mediate soybean plant productivity and phenotypic plasticity in response to irrigation and fertilization. I will manipulate the historical water and nitrogen environment of soil microbial communities, and inoculate those communities onto soybean plants growing under concomitant contemporary water and nitrogen levels in the greenhouse. I will then measure plant productivity and fitness traits, as well as a battery of traits shown to respond to water and nitrogen levels. I will also measure differences in soil microbial community composition and the rate of *Rhizobia* nodulation in soybean to determine how the soil microbial community has been altered by irrigation and fertilization. This information will provide some mechanistic understanding of why these communities are differentially affecting plant productivity and plasticity. Because water and nutrient dynamics are shifting under global change, understanding the mechanisms by which plant productivity and resilience are responding to these shifts will help us manage for more resilient ecosystems and agricultural systems in a changing climate.

Odyssey of Strange Fish: Investigating Fish Genomes and Development to Illuminate Vertebrate Evolution

Ingo Braasch

Fish Evo-Devo-Geno Lab, Department of Integrative Biology

In this Lightning Talk, I will give an overview of the research in the Fish Evo-Devo-Geno Lab in the Department in Integrative Biology. Our research addresses fundamental questions about the genomic and developmental basis of major transitions during the course of vertebrate evolution. We study genomic and morphological novelties in vertebrates at the levels of genome structure, gene family dynamics, and gene regulation and combine comparative genomics with analyses of molecular evolution and developmental genetic approaches using spotted gar (*Lepisosteus oculatus*) and teleost fishes such as zebrafish as model systems.

Teleost fishes like zebrafish are commonly used to investigate vertebrate developmental and genomic evolution. However, teleosts are derived from a teleost-specific genome duplication (TGD) that had major impact on their genome and gene function evolution. This complicates vertebrate macroevolutionary comparisons: the 'big bang' of vertebrate genome duplications led to lineage-specific genome reshuffling and gene losses, obscuring the distinction of orthologous vs. paralogous genes and hiding the origins of vertebrate gene functions. We show that gar and other representatives of 'ancient fish' lineages provide connectivity among vertebrate genomes and inform the ancestry and evolution of vertebrate development. The gar genome is representative of the bony vertebrate ancestor, retained

many genes differentially lost in other vertebrate lineages, and facilitates the identification of gene regulatory elements. We furthermore rear gars here at MSU to developmentally test hypotheses about the evolutionary origins of vertebrate gene functions. Gar in comparison to the more derived zebrafish system is thus a powerful new model to study the genomic foundation of vertebrate Evo-Devo.

Toward prediction in restoration ecology

Lars Brudvig

Department of Plant Biology

By repairing ecosystems damaged by human activities, restoration ecology is widely viewed as a critical tool for biodiversity conservation. To meet this potential, however, restoration practitioners must be able to reliably meet goals, such as reestablishment of a diverse, native-dominated community. In practice, restoration outcomes are notoriously variable - some even argue unpredictable - and the causes of this variation remain poorly understood. Working within a system of tallgrass prairie restoration, my lab confronts this issue by asking: What explains variation among restoration projects? We have shown that variation arises from the details of how, when, and where restoration projects take place. Together, these insights point the way toward an era of prediction in restoration, whereby practitioners might reliably forecast the outcomes of their restoration efforts at the onset of projects.

An –omics approach to assess emergent properties within a 3-member synthetic microbial community

John Chodkowski and Dr. Ashley Shade

Department of Microbiology and Molecular Genetics

Though most microorganisms live within a community, we have modest knowledge about microbial interactions and their implications for community properties and ecosystem functions. To advance understanding of microbial interactions, we describe a straightforward synthetic community system that can be used to interrogate exometabolite interactions among microorganisms. The filter plate system (also known as the Transwell system) physically separates microbial populations, but allows for chemical interactions via a shared medium reservoir. Exometabolites, including small molecules, extracellular enzymes, and antibiotics, are assayed from the reservoir using sensitive mass spectrometry. Community member outcomes, such as growth, productivity, and gene regulation, can be determined using flow cytometry, biomass measurements, and transcript analyses, respectively. The synthetic community design allows for determination of the consequences of microbiome diversity for emergent community properties and for functional changes over time or after perturbation. Because it is versatile, scalable, and accessible, this synthetic community system has the potential to practically advance knowledge of microbial interactions that occur within both natural and artificial communities.

Modeling degrees of genetic redundancy among paralogs in *Arabidopsis thaliana*

Siobhan A. Cusack¹, Fanrui Meng², Peipei Wang^{2,3}, Bethany M. Moore^{2,4}, Paityn E. Donaldson⁵, Melissa D. Lehti-Shiu², Jeffrey K. Conner^{2,6}, Patrick J. Krysan^{7,8}, Shin-Han Shiu^{2,4,9}

¹Cell and Molecular Biology Program, Michigan State University

²Department of Plant Biology, Michigan State University

³Great Lakes Bioenergy Research Center, Michigan State University

⁴Ecology, Evolutionary Biology, and Behavior Program, Michigan State University

⁵Department of Microbiology and Molecular Genetics, Michigan State University

⁶Kellogg Biological Station, Michigan State University

⁷Genome Center of Wisconsin, University of Wisconsin-Madison

⁸Department of Horticulture, University of Wisconsin-Madison

⁹Genetics Program, Michigan State University

Genetic redundancy refers to paralogous genes maintaining seemingly redundant functions; a single gene mutant (single mutant) may not show an apparent phenotype until additional paralogs are knocked out in combination (i.e. double or higher-order mutants). In *Arabidopsis thaliana*, many single mutants have no reported phenotype. This may be due to genetic redundancy or because they have conditional or extremely subtle phenotypes, among other possibilities. Here, a machine-learning approach is applied to build a model for prediction of the extent to which an *A. thaliana* gene pair is genetically redundant based on evolutionary conservation, duplication patterns and mechanisms, epigenetic and post-translational modifications, gene expression patterns, and network properties of paralogous gene pairs. The predictions are then tested using hold-out, published phenotype data and a library of *A. thaliana* Mitogen Activated Protein Kinase single and double mutants. To capture subtle and/or conditional phenotypes in single mutants, we impose low-level abiotic stress and examine growth rate, photosynthetic efficiency, and most importantly, lifetime fitness estimates that measure the combined impact of subtle phenotypes on reproductive success. With this comprehensive phenotyping, a fine-scale measure of the degree of genetic redundancy between these gene pairs is generated. The genetic redundancy model sheds light on characteristics that may contribute to long-term maintenance of paralogs that are seemingly functionally redundant. It additionally allows for more targeted generation of functionally informative double mutants, advancing the study of gene functions.

Ecology from space!

Kyla Dahlin

Department of Geography, Environment, & Spatial Sciences

Why do plants grow where and when they grow? At the landscape scale we know that vegetation patterns are controlled by a combination of environmental gradients, dispersal limitation, fecundity, disturbance, species interactions, and feedbacks. The relative importance of these factors, however, remains a question. At the global scale, we would also like to know what level of detail is necessary to accurately represent the land surface in Earth system models. In the Ecological Remote Sensing and Modeling (ERSAM) Lab we use remotely sensed data from space- and airborne platforms to better understand present-day spatiotemporal ecosystem processes and to help predict how ecosystems may change in the future.

Ecological Communities in Evolutionary Computation

Emily Dolson and Charles Ofria

Department of Computer Science and Engineering, BEACON

In evolutionary computation, evolutionary principles are used as a form of machine learning. A population of possible solutions to a problem are selected, duplicated, and mutated, with selection based on how well they solve the problem. Ensuring that this population is diverse is critical to successfully solving challenging problems. As such, over the past few decades, various ecological dynamics have been imported into evolutionary computation to help maintain diversity. At first glance, many of their implementations seem entirely divorced from biology. Upon further inspection, however, many are analogous (or even mathematically identical) to scenarios in biology. For instance, the equations that govern coexistence in the popular “fitness sharing” evolutionary computation algorithm are identical to the equations of Chesson’s modern coexistence theory in ecology. In this talk, I will discuss how various evolutionary computation algorithms (fitness sharing, Eco-EA, Lexicase Selection, and MAP-Elites) map to different ecological scenarios. Specifically, fitness sharing mirrors competition for a single continuously varying resource (e.g. seeds of different shapes), Eco-EA implements standard resource competition (with the wrinkle that only some resources are substitutable), and both Lexicase selection and MAP-Elites can be thought of as harsh abiotic environments that impose geographic species range constraints. By understanding these connections, we will be able to import findings from evolutionary computation directly into biology research on eco-evolutionary dynamics. Given the vast frontier of open questions in eco-evolutionary dynamics, we believe that drawing on evolutionary computation research as essentially a large body of pilot data will be an incredibly useful tool for formulating hypotheses and choosing productive research directions.

The ghost of trees past: how long do plant-soil feedbacks persist to influence current tree seedling dynamics?

Clarice Esch

Department of Forestry

Individual trees directly modify the soils they occupy, which in turn can affect survival and growth of tree seedlings—a process known as plant-soil feedbacks (PSFs). PSFs critically influence tree species composition and diversity. Despite their importance, persistence of PSFs after tree death remains virtually unstudied. Our preliminary work used *Prunus serotina*, which has shown strong negative PSFs, to examine PSFs at a range of times since tree death (0.5, 1.5, 3.5 & ~15 years since harvest) and found a release from prior negative PSFs between 0.5 and 1.5 years. Building upon this work, we collected soil cores from the vicinity of *P. serotina* stumps (spanning 0.5–1.5 years since harvest) and live trees and assessed PSF persistence by growing conspecific seedlings in soil cores under two light levels (5% & 30% full sun) and monitored survival for 12 weeks. We also identified potential soil pathogens causing the PSF by baiting field collected soils, culturing on selective media, and sequencing the ITS 4 and 6 regions for identification. To confirm pathogenicity, *P. serotina* seedlings grown in sterile potting media will be inoculated with each isolate and seedling survival and growth will be monitored.

Negative PSFs persisted after tree removal, but only for 0.5 years after harvest and under 5% full sun, typical of light levels in a single tree fall gap. Seedlings were released from negative PSFs at 1.5 years after tree harvest, despite the potential for fungal and oomycete components of PSFs to persist long term in resting forms. Three dominant potential pathogens were identified: *Phytophthium vexans*, *Pythium irregulare*, and *Pythium intermedium*. *Phytophthium vexans* was detected at all live trees and stumps regardless of time since harvest, while *P. irregulare* and *P. intermedium* were detected at all live trees and stumps harvested 0.5 years prior, but only found at two stumps harvested 1.5 years prior. Interestingly, seedling survival at these two stumps was poorer than seedling survival at other stumps harvested 1.5 years prior where *P. irregulare* and *P. intermedium* were not detected. Results of the pathogenicity trial, where *P. serotina* seedlings are inoculated with each isolate, will illuminate which of these potential pathogens is driving seedling survival responses and the PSF legacy effect. Though PSF legacies were short-lived, this study provides estimates of PSF persistence after tree death, demonstrates their importance, and identifies particular agents of early seedling death.

Mechanisms of Adaptive Weed Evolution

Ava Garrison and Jeff Conner

Department of Plant Biology

Wild radish (*Raphanus raphanistrum*) is a winter annual native to the Mediterranean, but it has evolved a distinct weedy ecotype that is an aggressive agricultural pest on every continent except Antarctica. We are investigating the rapid adaptation of weedy radish to agricultural habitats, particularly the frequent and severe disturbances of plowing and harvesting. Previous work suggested that weeds evolved a rapid life-cycle compared to their native ancestors by flowering rapidly and reducing investment in rosette leaves. To investigate the relative contributions of genetic differentiation and plasticity to differences between weedy and native radish in these key traits, we conducted a simulated reciprocal transplant. Growth chambers were used to mimic environmental conditions in Spain (the native range) during a winter annual growth season and Michigan (part of the weedy range) during a spring annual growth season. Weeds flowered faster and produced fewer rosette leaves in both environments. In addition, the spring annual environment caused accelerated flowering of both weedy and native ecotypes relative to the winter annual environment. This suggests that plastic earlier flowering upon initial invasion of agricultural fields enabled annual radish to produce some seeds and establish in the fields, and subsequent adaptive differentiation of both flowering time and rosette investment made it possible for radish to become a damaging weed. Current work is focused on the genetic mechanisms underlying these processes, particularly the involvement of the Gibberellin signalling pathway, as well as the environmental cues for plasticity.

The scent of a pathogen: An avian chemosignal predicts host infection status in feral chickens (*Gallus gallus*)

Eben Gering¹, Kathryn Fiedler, Hans Cheng², Thomas Getty¹, Danielle Whittaker³

¹Department of Integrative Biology

²USDA-ARS

³BEACON

Preen oil is secreted by most living birds, and functions as both a feather protectant and social signal. We sought to determine the sources of variation in preen oil chemistry in rapidly evolving, hybrid feral chickens (*Gallus gallus*). Here, we test how PrC differs between 1) domesticated vs. feral populations, 2) male vs. female feral chickens, 3) ecologically divergent (feral) habitats, 4) individuals that differ in condition indexes (residual body mass and/or infection status), 5) individuals with different genetic backgrounds (MHC and/or unlinked markers), and 6) individuals that differ in sexual ornamentation and/or weaponry (e.g. combs and spurs). Together, these comparisons reveal how variation in a complex trait (preen oil chemistry), covaries with rapid, recent changes in the social, biotic, and physical environments of a colonizing species. Among our most interesting findings thus far is that, in infected birds, preen oil chemistry predicts antibody titers for locally prevalent protozoan and bacterial pathogens. Thus, a chemically complex social signal could encode detailed information about

immunological costs of infections, even in rapidly evolving hosts inhabiting novel, non-native environments.

Trait-based community assembly and succession across an infant gut metacommunity

John Guittar^{1,2}, Ashley Shade^{2,3}, Elena Litchman^{1,4}

1. Kellogg Biological Station, Michigan State University, Hickory Corners, MI 49060, USA
2. Department of Microbiology and Molecular Genetics, Department of Plant, Soil and Microbial Sciences, and The Plant Resilience Institute, Michigan State University, East Lansing MI 48840, USA
3. Program in Ecology, Evolutionary Biology and Behavior, Michigan State University East Lansing MI 48840, USA
4. Department of Integrative Biology, Michigan State University, East Lansing, MI 48824, USA

Ecological primary succession in the human gut occurs over the first three years of life, during which time infants acquire and cultivate gut microbiota that train their immune systems, synthesize B and K vitamins, and aid in the digestion of otherwise indigestible food. Despite our familiarity with the general patterns of gut community succession, it is unclear the degree to which gut succession is shaped by dispersal limitation relative to host physiology and behavior. Here, we combine phenotypic and genotypic information and phylogenetic inference to characterize trait-based changes in the gut microbiome over the first three years of human life in a cohort of 58 Scandinavian infants, with an aim to unpack the ecological mechanisms underlying primary succession. We find early succession to be dominated by taxa with traits related to active dispersal (i.e., they have flagella) and general environmental tolerance (i.e., tolerance of oxygen, ability to form biofilms), which gives way to taxa that lack these adaptations but are well suited for the stable environment of the human gut (i.e., are obligate anaerobes, are tolerated by the human immune system). Intriguingly, we see an increase in the abundance of sporulating taxa, an adaptation that may be important for dispersal among human hosts. We find convergence in taxonomic and trait-based composition within and among infants over time, consistent with a deterministic community assembly process potentially limited by dispersal, rather than one dominated by historical contingencies or strong host differences. Our results suggest that alleviating dispersal limitation could be an effective way of promoting healthy gut community development in infants.

Quantifying Impacts of Floodplain Availability on Chinook Salmon (*Oncorhynchus tshawytscha*)

Sara Hugentobler and Mariah Meek
Department of Integrative Biology

Water quality and quantity can be highly variable in California's Central Valley Region due to environmental and anthropogenic changes. This presents unique challenges for the federally listed Central Valley Chinook Salmon (*Oncorhynchus tshawytscha*), which use the limited floodplain in the Central Valley as rearing habitat. Flood plains, such as the Yolo Bypass, can be disproportionately affected by drought and stream flow changes, affecting the fitness of Chinook salmon. We are interested in understanding how different water years (drought versus flood) influence the run composition and abundance of juvenile Chinook salmon in the floodplain (Yolo Bypass) versus the mainstem of the Sacramento River. Chinook from the Yolo Bypass and areas along the Sacramento River were sampled and genotyped with an innovative genetic panel and identified at the run level (Fall, Late Fall, Winter, and Spring) from 1998-2017. These genetic data can help answer important questions about the impact of drought and flood years, and if specific runs are adversely affected by different water conditions. This study will also provide important information on the loss of genetic diversity due to environmental or anthropogenic changes in the Sacramento River. Chinook are of enormous economic, cultural, and ecological value in California, making a better understanding of how these changes are affecting this species of special importance.

Predictors of innovation in spotted hyenas

Lily Johnson-Ulrich¹, Zoe Johnson-Ulrich², Kay Holekamp¹

¹Department of Integrative Biology, Michigan State University, ²Department of Psychology, Oakland University

Innovation is a widely studied phenomenon in animals that is influenced by cognitive factors, such as inhibitory control, in addition to non-cognitive factors. To compare their relative influence on innovation we used a multi-access box (MAB) to measure the number of unique innovations learned across trials by 10 captive spotted hyenas (*Crocuta crocuta*). Spotted hyenas are highly innovative and display striking variation in behavioral traits, making them a good model organism for examining the relationship between the two. We measured persistence, motor diversity, motivation, activity, efficiency, inhibitory control, and neophobia demonstrated by hyenas while interacting with the MAB. We also independently assessed inhibitory control with a detour cylinder task. Interestingly, neither measure of inhibitory control predicted innovation. Instead, innovation was predicted by a proactive syndrome of behavioral traits that included high persistence, high motor diversity, high activity and low neophobia. Our results suggest that this proactive behavioral syndrome may be more important than inhibitory control for successful innovation with the MAB.

Phytohormones can resuscitate dormant environmental bacteria

Patrick J. Kearns^{1,2}, Nejc Stopnisek^{1,2}, Ashley Shade^{1,2,3,4}

1. Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing MI
2. Plant Resilience Institute Michigan State University, East Lansing MI
3. Program in Ecology, Evolution, and Behavior Michigan State University, East Lansing MI
4. DOE Great Lakes Bioenergy Research Center, Michigan State University, East Lansing MI

Interactions between bacteria and plants are important for plant wellness and productivity. Assembly and maintenance of rhizosphere communities are primarily driven by root exudates that provide carbon and nutrients. Changes in root exudates can occur when plants experience biotic or abiotic stress, including the production of phytohormones such as salicylic acid (SA) or abscisic acid (ABA). While the bacteria in rhizosphere communities are abundant and diverse, the soil also harbors a sizeable pool of inactive (dormant) taxa that can act as a reservoir of metabolic diversity and resuscitate to provide pulses of activity under specific environmental conditions. Despite the importance of bacteria to plant health, the importance of dormant taxa in the assembly of plant microbiomes and for plant fitness is unknown. In particular, the effect of phytohormones on dormant taxa and the activity of rhizosphere taxa is unclear. We hypothesized that phytohormones resuscitate dormant bacterial taxa and signal their recruitment to the rhizosphere. To begin to test this hypothesis, we first examined changes in growth, resuscitation, and behavior (motility and biofilm production) of several environmental bacterial strains when exposed to the stress phytohormones SA, jasmonic acid (JA), ABA, and the growth phytohormone auxin (IAA). We tested strains that associate with plants (both pathogenic and beneficial), and compared them to strains that are common in soils but not known to associate with plants. We found that many plant-associated bacteria have a relative increase in growth rate and biomass production, and they can also be resuscitated from a state of nutrient starvation-induced dormancy. We also observed changes in motility and biofilm production in some of these strains when they were exposed to phytohormones. In general, growth and resuscitation responses were very consistent within and across strains to SA, JA, and IAA, but responses to ABA were more variable and strain-specific. Additionally, we conducted an *in situ* experiment in which we added SA to rhizosphere soil and measured changes in microbiome activity using 16S rRNA sequencing. We found that phytohormone treatment to rhizosphere soil stimulated that activity of bacteria commonly associated with plants, including *Burkholderia* and *Bacillus*. Overall, our results suggest that phytohormones produced by plants under biotic and abiotic stress can resuscitate bacteria that are potentially beneficial. Furthermore, these observations point to an important role of dormant soil bacteria as a reservoir of functions significant for plant wellness, and an evolutionarily conserved relationship between soil bacteria and plants that is mediated through phytohormones.

Variation in rodent predatory behavior and preference for biochemically defended prey

Lauren Koenig

Department of Integrative Biology

Pain sensation allows an organism to perceive danger, respond appropriately, and avoid additional harm. Some prey organisms capitalize on the pain pathway of their predators by using painful venoms or sprays. Predators, in turn, may evolve resistance to those toxins. These adaptations represent an evolutionary paradox. Selection for higher pain thresholds is likely constrained by the necessity of feeling pain. Predatory grasshopper mice (*Onychomys torridus*) and pinacate beetles (*Eleodes longicollis*) are an ideal system for examining an evolutionary arms race showcasing counter-selection against prey defenses through modifications to the pain pathway. Pinacate beetles evolved a benzoquinone spray that is intolerable for most mammalian predators, but ineffective in deterring grasshopper mice. We recorded predator-prey interactions in a behavioral arena, in which a beetle was paired with one of three closely related species of rodents: a grasshopper mouse (an obligate carnivore), a deer mouse (a facultative insectivore), or a pocket mouse (a granivore). We found that grasshopper mice are much more successful and effective predators compared to deer mice, whereas pocket mice showed no interest in the beetles. Using a two-bottle choice test, we found that grasshopper mice are more willing to drink benzoquinone than house mice, but they are also more likely to drink greater quantities of water. Both mice demonstrated similar drinking behavior when offered six different concentrations of benzoquinone. Taken together, these results suggest predatory behavior may be modified by genetic and/or physiological variability in the pain receptors targeted by benzoquinone.

Identity-dependent of Plant Traits in Responding to Grazing

Maowei Liang^{1,2}, Jiquan Chen², Cunzhu Liang¹

¹School of Ecology and Environment, Inner Mongolia University, Hohhot 010021, P. R. China

²Center for Global Change and Earth Observations, Department of Geography, Environment, and Spatial Sciences, Michigan State University, East Lansing 48824, USA

Grazing effects on plant communities are fundamentally related to plant morphological and physiological traits in the grassland. However, how grazing influence on plant intraspecific traits and their functional linkages, and whether this rule is consistent at interspecific scale or not remain unclear. Our objective was to explore how does grazing alter the plant morphological (i.e. plant canopy height and plant dominance), foliar stoichiometry (i.e. foliar C, N, P content), and regrowth (i.e. plant growth rate and resilience) traits and influence on their relationships. A rotational grazing experiment has been conducted in the growing season since 2013, we collected these data from 4 species (i.e. *Stipa grandis*, *Leymus chinensis*, *Anemarrhena asphodeloides*, and *Cleistogenes squarrosa*) in the plant community. We found that: 1. Grazing consistently decreased the plant canopy height in all 4 plants; however,

grazing optimized *S. grandis*'s dominance (42.6–134.9%, $P < 0.0001$) in contrasting with decreased *L. chinensis* within 20.8–84.4% ($P < 0.0001$) and *A. asphodeloides* by 78.6–89.6% ($P < 0.0001$), but no changes were found in *C. squarrosa* ($P = 0.517$). 2. Grazing enriched foliar N ($P = 0.005$) and P ($P = 0.003$) content while did not change foliar C content ($P = 0.468$). Meanwhile, grazing declined foliar C: N and C: P or change N: P ($P < 0.05$). Specifically, grazing only changed N content both in *A. asphodeloides* ($P = 0.017$) and *C. squarrosa* ($P = 0.001$), as a result of changing ratio of C: N, C: P and N: P of them ($P < 0.05$). 3. Grazing, plant species, and their interactions did not alter ($P > 0.05$ in all cases) plant growth rate. However, grazing significantly ($P = 0.004$) affected the resilience of *A. asphodeloides* that was in contrast with another 3 plants. Consequently, the effects of grazing on plant resilience were strongly associated with plant species ($P = 0.007$). 4. The PLS-SEM showed that grazing and plant species significantly ($P < 0.05$ in all cases) affected foliar stoichiometry (foliar C, N, P content) and volume of plant (plant canopy height and dominance) in the communities, but these endogenous and exogenous variables poorly explained the variation of plant regrowth traits ($R^2 = 0.09$). Our results highlight that the responses of plant traits to grazing and the functional linkages among these traits maybe identity-dependent, suggesting that the plant morphological and physiological trait might be a key element to explore how grazing shape ecosystem structure and functioning in the grasslands.

Fast and accurate inference of phylogenetic networks using large-scale genomic sequence data

Kevin Liu

Department of Computer Science and Engineering

Advances in next-generation sequencing technologies and phylogenomics have reshaped our understanding of evolutionary biology. One primary outcome is the emerging discovery that interspecific gene flow has played a major role in the evolution of many different organisms across the Tree of Life. To what extent is the Tree of Life not truly a tree reflecting strict "vertical" divergence, but rather a more general graph structure known as a phylogenetic network which also captures "horizontal" gene flow? The answer to this fundamental question not only depends upon densely sampled and divergent genomic sequence data, but also computational methods which are capable of accurately and efficiently inferring phylogenetic networks from large-scale genomic sequence datasets. Recent methodological advances have attempted to address this gap. However, in the 2016 performance study of Hejase and Liu, state-of-the-art methods fell well short of the scalability requirements of existing phylogenomic studies.

The methodological gap remains: how can phylogenetic networks be accurately and efficiently inferred using genomic sequence data involving many dozens or hundreds of taxa? In this study, we address this gap by proposing a new phylogenetic divide-and-conquer method which we call FastNet. Using synthetic and empirical data spanning a range of evolutionary scenarios, we demonstrate that FastNet outperforms state-of-the-art methods in terms of computational efficiency and topological accuracy.

The Sensory Space of the Threespine Stickleback

Robert B. Mobley, Janette W. Boughman

Department of Integrative Biology

Animals make use of multiple sensory systems to mediate behaviors. Studies of sensory systems typically consider adaptations of a single sense to the environment, without regard to the interactions between senses. We quantified the relationships between visual, chemical and mechanosensory organs in marine, as well as freshwater benthic and limnetic ecotypes of threespine sticklebacks using morphometrics. Across habitats, we found a strong correlation between eye size and neuromast number, with benthic fish possessing larger eyes and more neuromasts than limnetic and marine fish. No interactions between the size of the olfactory epithelium and other sensory organs were found, nor did olfactory epithelium differ across habitats.

Predicting specialized metabolism genes using a machine learning approach in *Arabidopsis thaliana*

Bethany Moore^{1,2}, Peipei Wang¹, Pengxiang Fan³, Bryan Leong¹, Craig A. Schenck³, John P. Lloyd¹, Melissa Lehti-Shiu¹, Robert Last^{1,3}, Eran Pichersky⁴, Shin-Han Shiu^{1,2}

¹Department of Plant Biology, ²Ecology, Evolutionary Biology, and Behavior program, ³Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI 48824, USA, ⁴Department of Molecular, Cellular and Developmental Biology, University of Michigan, Ann Arbor, MI 48109, USA

Specialized metabolism (SM) genes in plants are responsible for producing lineage-specific metabolites with important ecological, evolutionary, and biotechnological implications. Using *Arabidopsis thaliana* as a model, we identified distinguishing characteristics of SM and GM (general metabolism, traditionally referred to as primary) genes through a comprehensive study of gene features relevant to duplication patterns, sequence conservation, transcription, gene function, and gene network properties. Using gene ontology (GO) and AraCyc annotated SM and GM genes as benchmarks, we found SM genes tend to be tandemly duplicated, less conserved, more narrowly expressed at lower levels, more highly co-expressed with their paralogs, and less connected in gene networks relative to GM genes. Although the values of each of these features significantly differed between SM and GM genes, any single feature was ineffective at distinguishing them. Using machine-learning methods to integrate all features, a well performing prediction model was established with a true positive rate of 0.84 and a false positive rate of 0.23. In addition, this model identified 82% known SM genes not used to train the model, further demonstrating model accuracy. Importantly, application of the prediction model led to the identification of 1,817 likely novel *A. thaliana* SM genes, providing a global estimate of SM gene content in any plant genome.

The role of temporal niche in mammalian sensory brain evolution

Andrea Morrow^{1,2,3}, Paul Meek⁴, Laura Smale^{1,2,3,5}, and Barbara Lundrigan^{1,2,3,6}

¹Department of Integrative Biology MSU

²Ecology, Evolutionary Biology, and Behavior Program MSU

³BEACON Center for the Study of Evolution in Action MSU

⁴NSW Department of Primary Industries and Invasive Animals

⁵Department of Psychology MSU

⁶MSU Museum

Temporal niche refers to the time at which an animal is most active across a 24-hour period and has an enormous influence on the biotic and abiotic factors to which it is regularly exposed. This environmental variation produces distinctly different sensory environments for nocturnal versus diurnal animals. To optimize fitness, nocturnal and diurnal animals should differ in the extent to which they rely on different sensory modalities, and because brain tissue is metabolically expensive, tradeoffs in investment for processing different kinds of sensory information are expected. While the earliest mammals were nocturnal, evolutionary transitions between different temporal niches have occurred multiple times within Class Mammalia. Here we examine sensory adaptations in the brain that coincide with evolutionary transitions in temporal niche, focusing specifically on auditory and visual investments. We test the hypothesis that the ratio of investment in auditory to visual brain regions will be higher in the most nocturnal than diurnal species. We collected brain tissue from 24 individuals, representing four nocturnal species (*Glaucomys volans*, *Rattus norvegicus*, *Rattus fuscipes*, *Onychomys torridus*) and four species exhibiting varying levels of diurnality (*Tamiasciurus hudsonicus*, *Arvicanthis niloticus*, *Rattus lutreolus*, *Myodes gapperi*) from the Order Rodentia, capturing four independent evolutionary transitions in temporal niche. To estimate the relative investment in tissues supporting auditory versus visual functions, we measured the volumes of two auditory processing structures (medial geniculate nucleus, inferior colliculus) and two visual processing structures (lateral geniculate nucleus, superior colliculus) in the brain. Preliminary data suggest that evolutionary transitions in temporal niche prompt changes in the utilization of sensory information and associated tradeoffs in the allocation of brain tissues that function in audition and vision. This research was supported by BEACON: An NSF Center for the Study of Evolution in Action.

Variable impacts of habitat context on monarch butterfly (*Danaus plexippus* L.) oviposition and egg survival

Andrew Myers¹, Christine Bahlai², Douglas Landis¹

¹Michigan State University Department of Entomology and Program in Ecology, Evolutionary Biology, and Behavior

²Kent State University Department of Biological Sciences

The eastern North American population of monarch butterflies (*Danaus plexippus*) has become a major conservation concern as overwintering populations in Mexico have declined dramatically during the past two decades. Efforts to increase monarch populations have included restoring milkweed host plants in the breeding range lost through the adoption of herbicide-resistant row cropping systems. To maximize conservation efforts, it is important understand which habitats are most attractive to egg-laying monarchs and support the greatest survival of eggs and larvae. Through two summers of sentinel host plant experiments, we found oviposition site selection varied between years with corn as the most attractive habitat in 2016 and prairie in 2017. We found a strong effect of predation egg survival, with a sharp drop during the first 24 hours and variable, but at times particularly low survival in prairies. Our findings have important implications for monarch conservation and indicate that targeting grasslands for milkweed host plant restoration may support very low monarch butterfly survival compared with milkweed historically growing in corn fields.

Evaluating the effects of contrasting management regimes on tropical mammal diversity

Valentina Oberosler^{1, 2}, Francesco Rovero¹, Simone Tenan³, and Elise Zipkin⁴

¹Tropical Biodiversity Section, MUSE—Museo delle Scienze, Corso del Lavoro e della Scienza 3, 38122 Trento, Italy

²Dipartimento di Scienze della Terra e dell'Ambiente, Università degli Studi di Pavia, via Ferrata 1, 27100 Pavia, Italy

³Vertebrate Zoology Section, MUSE—Museo delle Scienze, Corso del Lavoro e della Scienza 3, 38122 Trento, Italy

⁴Department of Integrative Biology and Ecology, Evolutionary Biology and Behavior Program, Michigan State University

Understanding the effects of human disturbance on species richness, community composition, and population abundance is of critical conservation concern, especially in high biodiversity regions. We evaluated how two contrasting management regimes influence ecologically similar mammal communities in forested areas of the Udzungwa Mountains of Tanzania, Mwanihana (MW) and Uzungwa Scarp (US). These forests differ only in their protection status, with US experiencing significantly higher levels of illegal hunting and habitat destruction. We deployed systematic camera trap surveys and evaluated differences in species richness, community composition, and species-specific occupancies using a hierarchical multi-region community model. Model results demonstrate that the mammal community in US is degraded

compared to that in MW. Estimated species richness was 29 (95% CI: 25-39) in MW and only 21 in US (95% CI: 19-29). Occupancy for most species was significantly reduced in US, and some species, especially large-bodied mammals, were absent in US, the forest with higher disturbance levels. Functional community diversity was also altered in US, with an increase in omnivores and loss in carnivores and insectivores. Our results suggest that reserve management in US is partially ineffective and that protection of species and habitat should be enforced to maintain biodiversity in this region.

Exploring isolate variability in *Macrophomina phaseolina*, the causal agent of charcoal rot: temperature adaptation, fungicide sensitivity and pathogenicity

Viviana Ortiz Londono, H. Sang, H.X. Chang, Z. Noel, M.I. Chilvers
Department of Plant, Soil and Microbial Sciences

Charcoal rot caused by *Macrophomina phaseolina* can significantly reduce yield and seed quality in soybean and dry bean, especially under hot and drought conditions. Consequently, production is affected mainly in tropical and subtropical regions. However, the incidence and severity of charcoal rot in soybean has recently been increasing in the northern US in which pathogen temperature adaptation may be involved. The objectives of this study were to test the hypothesis that *M. phaseolina* isolates from the northern US may be adapted to cold temperatures contributing to the increase in disease incidence and severity, and to characterize *M. phaseolina* isolates for fungicide sensitivity and pathogenicity on soybean. To address this a collection of 96 *M. phaseolina* isolates, collected from soybean grown in 11 US states, and from dry bean grown in MI, Puerto Rico and Colombia, were phenotyped and whole-genome sequenced. Sequencing consisted of 23X coverage using a 150 base-pair paired-end strategy on the Illumina HiSeq 4000 platform. Mycelial dry weight at 15°C relative to 35°C was used to evaluate the influence of temperature on fungal growth. Isolates that grew faster at 15°C were collected from the northern US. To assess fungicide sensitivity, the relative mycelial growth of *M. phaseolina* isolates challenged against representatives of three different classes of fungicides, boscalid (SDHI), iprodione (dicarboximide) and prothioconazole (DMI) was used to determine EC₅₀ values. Most isolates were sensitive to boscalid, iprodione and prothioconazole, with EC₅₀ distributions means of 1.2, 0.83 and 0.16, and ranges of 0.16 – 28.31, 0.54 – 1.49 and 0.06 - 1.17 µg ml⁻¹, respectively. To evaluate pathogenicity and virulence of isolates on soybean, experiments were conducted at 35 °C using the detached leaf method. Preliminary results indicate isolates vary in virulence. Combined phenotypic and genomic approaches and population genomics are being used to identify genomic regions and candidate genes involved in temperature adaptation, fungicide sensitivity and pathogenicity.

LTR_retriever: a highly accurate and sensitive program for identification of LTR retrotransposons

Shujun Ou and Ning Jiang

Department of Horticulture, Michigan State University, East Lansing, MI, 48824, USA

Long terminal-repeat retrotransposons (LTR-RTs) are prevalent in plant genomes. Identification of LTR-RTs is critical for achieving high-quality gene annotation. Based on the well-conserved structure, multiple programs were developed for *de novo* identification of LTR-RTs; however, these programs are associated with low specificity and high false discovery rate (FDR). Here we report LTR_retriever, a multithreading empowered Perl program that identifies LTR-RTs and generates high-quality LTR libraries from genomic sequences. LTR_retriever demonstrated significant improvements by achieving high levels of sensitivity (91%), specificity (97%), accuracy (96%), and precision (90%) in rice. LTR_retriever is also compatible with long sequencing reads. With 40k self-corrected PacBio reads equivalent to 4.5X genome coverage in Arabidopsis, the constructed LTR library showed excellent sensitivity and specificity. In addition to canonical LTR-RTs with 5'-TG...CA-3' termini, LTR_retriever also identifies non-canonical LTR-RTs (non-TGCA), which have been largely ignored in genome-wide studies. We identified seven types of non-canonical LTRs from 42 out of 50 plant genomes. The majority of non-canonical LTRs are *Copia* elements, with which the LTR is four times shorter than that of other *Copia* elements, which may be a result of their target specificity. Strikingly, non-TGCA *Copia* elements are often located in genic regions and preferentially insert nearby or within genes, indicating their impact on the evolution of genes and potential as mutagenesis tools.

The relative roles of genetic variance and phenotypic plasticity on *Ixodes scapularis* emergence timing in the eastern United States.

Genevieve Pang¹, Jean Tsao¹, Howard Ginsberg², Nicholas Ogden³, and Graham Hickling⁴.

¹Fisheries and Wildlife, Michigan State University

²Department of Plant Sciences and Entomology, University of Rhode Island

³National Microbiology Laboratory, Public Health Agency of Canada

⁴Department of Forestry, Wildlife, and Fisheries, University of Tennessee

The seasonal emergence patterns of immature *Ixodes scapularis* vary geographically and may play a key role in observed geographical gradients in pathogen transmission patterns. However, in regions with relatively low disease incidence, *I. scapularis* emergence is not well characterized, and many questions still exist about the cues and processes driving these emergence patterns. We conducted a multi-year microcosm experiment at four field sites distributed throughout this species' broad geographical range, in order to investigate the relative roles of genetics and phenotypic plasticity on *I. scapularis* emergence. *Ixodes scapularis* larvae and adults were collected from sites, fed to repletion under standardized laboratory conditions, and transplanted to sites at different periods during their active seasons. Replete

specimens were housed in containers that provided exposure to ambient conditions, and observed from the emergence of the molted stage until cessation of activity. The results of this study provide novel insights regarding how site-specific emergence patterns of the immature stages of *I. scapularis* may contribute to current regional patterns of Lyme disease risk. An analysis of transplanted ticks indicates that both genetics and phenotypic plasticity have significant effects on emergence timing. An enhanced understanding of current patterns of *I. scapularis* emergence, as well as the factors driving these patterns, advances our ability to understand current geographical patterns of pathogen prevalence and predict how these patterns may be affected by changing abiotic conditions.

Evolution of Sensory Systems across Novel Environments

John G. Phillips and Janette W. Boughman

Department of Integrative Biology, Ecology, Evolutionary Biology and Behavior Program, and BEACON Center for the Study of Evolution in Action

Organisms radiating into novel environments can offer insight into adaptive evolution. We are using a fish model, the Three-spined Stickleback (*Gasterosteus aculeatus*) to test differential patterns of selection on different sensory systems across a variance in ecological parameters. As an anadromous fish, stickleback can inhabit both fresh and saltwater habitats, and across their range have repeatedly colonized freshwater habitats from a saltwater ancestor. One topologically diverse region that serves as a natural laboratory to study *G. aculeatus* is the island of Iceland, whose landscape contains hundreds of lakes that were recently formed (on a scale of 100s to 1000s of years ago). Some lakes are spring fed and clear, and others are glacially fed and turbid. Stickleback have colonized a number of both glacial and spring-fed lakes, offering a unique opportunity to study how this closely related populations can undergo phenotypic divergence when faced with different ecological pressures. We examine visual, olfactory, and mechanosensory systems in *G. aculeatus* to test for trade-offs between sensory systems. Due to turbidity, sensory adaptations to glacial lakes have potential to reveal novel sensory function. Most studies of sensory adaptation are limited in scale, so we attempt to address this by incorporating multiple sensory modes. This work will be completed by phylogeographic work to establish divergence among populations and to further estimate the temporal scale over which evolutionary change occurs in this system.

Evaluating the role of herbivory and salt spray on the evolution of locally adapted intraspecies ecotypes of Seep Monkeyflower (*Mimulus guttatus*) across a coast-inland moisture gradient

Damian Popovic and David B. Lowry

Department of Plant Biology, Michigan State University

Over the past century, local adaptation has been shown to be a prime generator of ecologically significant intraspecies diversity. Despite attempts to demystify the scope and manifestations of local adaptation, little work has been done to elucidate the variable selective pressures that result in this divergence. Here we used an emergent model system, the Seep Monkeyflower (*Mimulus*

guttatus), to explore what external biotic and abiotic factors select for local adaptation across CA's coast-inland moisture gradient. *M. guttatus* presents a tractable species complex replete with phenotypic and ecological diversity, proving invaluable to the study of evolutionary ecology. Though local adaptation has previously been confirmed in coast-inland ecotypes of *M. guttatus*, no studies have sought to manipulate field conditions to determine the climatic and/or biotic regimes that have historically driven this distinction. In this study we enacted a field reciprocal transplant experiment with manipulations. Numerous exclosures were implemented in both coastal and inland Sonoma County, CA with the intent of excluding herbivore pressure and oncoming salt spray among *M. guttatus* plantings. An Aster model series was subsequently used to analyze survival and dry aboveground biomass as fitness proxies for comparison across site and treatment. We found that among our coastal exclosures, inland replicates were significantly more fit than their control counterparts, essentially rescuing inland fitness outside their native range. It is likely that herbivory and salt stress play a continuing role in the evolution of coastal *M. guttatus* populations and – as conjecture – the resiliency of entire coastal communities.

How landscape composition affects honey bee colony growth and survival

Gabriela Quinlan¹, Meghan Milbrath¹, Rufus Isaacs¹, Clint Otto²

¹Michigan State University Entomology Department ²Northern Prairie Wildlife Research Center, USGS

Michigan is a critical state in the commercial beekeeping migratory circuit as an area for feeding and recovery from pollination contracts. Broad-scale landscape composition may impact forage availability and therefore influence where beekeepers choose to put their bees. However, there is currently no model for optimizing apiary location choice in Michigan. Therefore, we examined the variation among 12 different landscapes within southern Michigan in relation to hive growth and survival of commercially managed honey bees, *Apis mellifera*. We found that pollinator conservation land, wetlands and ditches were positive land covers, while open-unmanaged land and forests were negative land covers for promoting colony productivity. We also observed the beneficial effects of pollinator conservation land and ditches at a finer, floristic scale. Understanding the value of these land covers to colony growth and survival can contribute to more effective management and habitat restoration decisions.

Benbow Lab: Novel microbiome research for human health, forensics and environmental science

JP Receveur¹, CE Larson¹, S Kaszubinski², N Babcock¹ and ME Benbow^{1,3}

¹ Department of Entomology, MSU

² Department of Integrative Biology, MSU

³ Osteopathic Medical Specialties, MSU

This is the lab poster summarizing information about the research that is conducted in the Benbow Lab at MSU.

Hogs Gone Wild: Ecology and Behavior of Feral Swine in Michigan

Gary J. Roloff

Applied Forest and Wildlife Ecology Laboratory, Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI

The Applied Forest and Wildlife Ecology Lab (AFWEL) at Michigan State University conducts research on a variety of topics with a primary focus on forest-wildlife relationships. We also have conducted research on invasive species. Russian boar and hybrids (*Sus scrofa*) were brought to Michigan for fenced shooting opportunities approximately 20 years ago, however their escape and intentional release caused Michigan Department of Natural Resources (MDNR) to recently designate them as an invasive species that are illegal to possess. With a free-ranging population, AFWEL was asked to study the spatial ecology and behaviors of feral swine in Michigan, with a focus of producing research results that could inform eradication efforts. In this presentation, I will highlight the feral swine problem in Michigan and present our research results.

Microbiome diversity and assembly in the phyllosphere of perennial bioenergy crops

Jackson Sorensen¹, Nejc Stopnisek^{1,2}, Keara Grady¹, Ashley Shade^{1,2}

¹Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing MI

²Plant Resilience Institute, Michigan State University, East Lansing MI

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 growing season at the Great Lakes Bioenergy intensive cropping sites (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. The leaves harbored relatively simple communities of less than 100 taxa, and had a core microbiome (persistent and abundant taxa) that included several Proteobacteria. 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 vagabonds randomly assembling from the air or soil. The highest numbers of taxa were observed early and late in the growing season, and the lowest at mid-summer. Miscanthus and switchgrass phyllosphere communities became more

differentiated over time, indicating an influence of host on the late-season phyllosphere community. 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.

What enables populations to colonize a novel environment?

Marianna Szucs

Department of Entomology

Large founding groups are more successful at founding new populations than are small groups. However, it is not clear whether this pattern is driven more by demographic processes such as buffering against stochastic fluctuations in population size and Allee effects or by genetic processes given that larger groups will harbor more genetic variation, masking genetic load and facilitating adaptation to new environments. Laboratory studies using a model system, red flour beetles and a factorial experimental design where populations of different genetic backgrounds (inbred – outbred) were introduced at different founding sizes found important and independent roles for both demographic and genetic processes. Now I am trying to test the importance of these mechanisms in the field during the release of a new biological control agent, *Hypena opulenta*, against swallowwort species in Michigan.

The effects of solar installations on desert plants

Miranda Wade

Department of Integrative Biology

Increasing demand for sources of alternative energy has led to a rise in the popularity of solar thermal facilities, where large mirrors are lined up in rows to concentrate solar rays on a collection point. While there is an increasing prevalence of these arrays across the desert regions of the United States, the ecological impact of such facilities is mostly unknown. The Mojave Desert region is an ideal location for solar installations due to its landscape and weather patterns. However, this region is also a hotspot of environmentally-sensitive rare plantlife. One such plant is the Mojave milkweed (*Asclepias nyctaginifolia*), which is listed in the California Rare Plant Bank. This milkweed serves as an important component of the desert ecosystem, serving as a food source for several organisms, including the charismatic Monarch butterfly (*Danaus plexippus*). The Ivanpah Solar Electric Generating System (ISEGS), located in the Mojave Desert of California, provides an excellent study system for understanding how such a development can affect Mojave milkweed populations. It is currently the largest solar installation in the world, and, uniquely, the ground was not graded beneath the solar panels, so the plant community within the array is still intact. Additionally, the construction plans attempted to limit the impact on the plants by including halo-like gaps in the array around the milkweed patches. While this prevented the milkweed from being destroyed during construction, the milkweed population is now growing in a sea of solar mirrors. It is not clear what the long-term effect will be on the milkweed. The habitat disturbances and resulting changes in natural water and light patterns

resulting from the development of these arrays has led to a unique opportunity to understand the effects of anthropogenic and climate change on environmentally sensitive desert habitats.

Factors influencing gene family size variation among related species in a plant family

Peipei Wang¹, Bethany M. Moore^{1,2}, Nicholas L. Panchy³, Fanrui Meng¹, Melissa D. Lehti-Shiu¹, and Shin-Han Shiu^{1,2,3} *

¹Department of Plant Biology, ²Ecology, Evolutionary Biology, and Behavior Program, ³Genetics Program, Michigan State University, East Lansing, MI 48824

Gene duplication and loss contribute to gene content differences as well as phenotypic divergence across species. However, the extent to which gene content varies among closely related plant species and the factors responsible for such variation remain unclear. Here, we used the Solanaceae family as a model to investigate differences in gene family size and the likely factors contributing to these differences. We found that genes in highly variable families have high turnover rate and tend to be involved in processes that have diverged between Solanaceae species, whereas genes in low-variability families tend to have housekeeping roles. In addition, genes in high- and low-variability gene families tend to be duplicated by tandem and whole genome duplication, respectively. This finding together with the observation that genes duplicated by different mechanisms experience different selection pressures suggests that duplication mechanism impacts gene family turnover. We explored using pseudogene number as a proxy for gene loss but discovered that a substantial number of pseudogenes are actually products of pseudogene duplication, contrary to the expectation that most plant pseudogenes are remnants of once-functional duplicates. Our findings reveal complex relationships between variation in gene family size, gene functions, duplication mechanism, and evolutionary rate. The patterns of lineage-specific gene family expansion within the Solanaceae provide the foundation for a better understanding of the genetic basis underlying phenotypic diversity in this economically important family.

Genetic mechanisms underlying desiccation resistance in desert fruit flies

Zinan Wang^{a,b}, Jian Pu^a, Mei Luo^a, Henry Chung^{a,b}

^aDepartment of Entomology, Michigan State University, East Lansing, MI, USA

^bProgram in Ecology, Evolutionary Biology and Behavior, Michigan State University, East Lansing, MI, USA

Organisms evolve different mechanisms to adapt and survive in extreme environments. For example, desert species are able to tolerate warmer and drier conditions in the desert. However, the genetic mechanisms underlying such adaptations are rarely dissected at the molecular level. The cactophilic fruit fly, *Drosophila mojavensis*, has adapted well to several deserts in the United States and Mexico with the highest desiccation resistance among all *Drosophila* species tested. How do insects deal with desiccation? The use of cuticular

hydrocarbons (CHCs), a waxy layer on the cuticle, is widely reported for insects preventing water from evaporating out of the body. The rate of water evaporation depends on the composition and melting temperature of this waxy layer, which is determined by the saturation and carbon-chain lengths of these CHCs. Previous studies have shown that a subset of these CHCs, the methyl-branched CHCs (mbCHCs), are involved in desiccation resistance in other *Drosophila* species. *Drosophila mojavensis* has longer mbCHCs than other tested fruit flies, suggesting that these longer mbCHCs could be the basis of higher desiccation resistance than other species. In our study, we investigated the genetic basis underlying the syntheses of these longer mbCHCs (30 – 32 carbons) in *D. mojavensis*. In invertebrates, the syntheses of CHCs share part of the fatty acid synthesis pathway but occurring only in insect-specific cells oenocytes, and the carbon-chain length of CHCs depends on fatty acid elongases. Using a RNAi screen and a candidate gene approach, we identified a cluster of two elongase genes contributing to medium length mbCHCs (26 – 28 carbons) in *D. melanogaster*, a model species with genetic tools. Bioinformatics analyses revealed that this cluster contained four elongase genes in *D. mojavensis*, suggesting that the cluster has experienced gene duplication events. We hypothesized that these extra copies in *D. mojavensis* could contribute to the syntheses of longer mbCHCs in this species. To test this hypothesis, we made different transgenic *D. melanogaster* strains in the laboratory that capable of overexpressing each of these elongases from *D. mojavensis*. We will test whether overexpression of these elongases will elongate mbCHCs in *D. melanogaster* and investigate if these longer mbCHCs contribute to higher desiccation resistance in *D. melanogaster*. Once we identify our candidate gene, we will use the CRISPR/Cas9 system to disrupt its expression in *D. mojavensis* and then investigate if this will lead to reduced desiccation resistance. Our study will lead to better understanding of the genetic basis of adaptation to the rapidly changing environment around us.

Responses to contemporary climate suggest that *Quercus rubra* will respond similarly to ongoing climate change throughout a latitudinal gradient in the Great Lakes region

Scott M. Warner¹, Andrew M. Jarosz^{1,2}, and Frank W. Telewski^{1,3}

¹Dept. of Plant Biology and Ecology, Evolutionary Biology and Behavior Program, Michigan State University (MSU); ²Dept. Of Plant, Soil and Microbial Sciences, MSU; ³W.J. Beal Botanical Garden, MSU

The long-term consequences of climate change remain unresolved, however, modern change has already begun to influence plants, including their rate of growth, mostly in marginal environments. In more benign environments, however, recent change has generally been too minor to effect an overall change in growth. Nonetheless, in these regions, observed relationships between growth and climate can aid in projecting future climate-change responses, which is particularly important for foundation species such as *Quercus rubra*. How will this species respond to ongoing climate change, and how will latitude affect responses? Will populations near the species' northern limit fare better than mid-range populations? We took increment cores from four *Q. rubra* populations along a latitudinal gradient from southern Lower Michigan to Upper Michigan. Tree rings were measured and filtered with a

cubic smoothing spline to attenuate the influence of confounding variables. Principal-component regression was conducted on the filtered data to quantify growth responses to climate.

Throughout the gradient, there were two consistent signals among populations. The first was a positive response to April temperature in the year preceding the year of ring formation. The second was a signal of summer moisture stress (negative responses to temperature and positive to precipitation). Differences among populations were minor with no consistent pattern.

Thus, responses to climate were similar along the gradient, in spite of *Q. rubra* being near its northern limit at the northern-most site, suggesting the species will respond similarly to ongoing climate change throughout the region, unless a climatic-tolerance threshold is passed for some populations, but not others.

Uncovering Student Conceptions About Randomness

Michael Wisner, Louise Mead, Jim Smith, Robert Pennock
EEBB and BEACON, MSU

One of the most significant stumbling blocks students face when learning about evolution is how to reconcile that many features of living systems seem intricately fitted together – even, to some, engineered – yet they arise from random mutations. Previous work in our group has established that students who are exposed to certain pieces of curriculum are much more likely than others to say that mutations are random. But this is from survey data. What do students mean when they say that mutations are random? Can they explain randomness in mathematical terms? Can they apply randomness appropriately in an evolutionary context? To address these questions, I have been interviewing students in both introductory level biology classes, and an upper-division evolution course, both pre- and post-instruction. These semi-structured interviews consist of a core set of questions asked of all students, with additional probing and clarification questions based on student responses to other questions. Results thus far indicate that students' ability to explain randomness mathematically and their ability to apply it appropriately in an evolutionary context are almost orthogonal; many individuals struggle with one while excelling at the other, and in both directions. Perhaps most surprisingly, a substantial percentage of students do not understand that dice rolls or shuffled cards are random. These results suggest that it is important to explain to students what we actually mean when we tell them that mutations are random; simply referencing other random events may not adequately convey the information if the students don't know that these other events are themselves random.

Fast and Accurate Introgression Detection using Statistical Phylogenomic Inference

Qiqige Wuyun, Kevin J. Liu

Department of Computer Science & Engineering

Introgression is the movement of genes from one species to the gene pool of another by recurrent backcrossing of hybrid. Introgression is thought to play an important role in genome evolution throughout the Tree of Life, the evolutionary history of all life on Earth. To quantitatively investigate this hypothesis, a variety of state-of-the-art techniques have been developed for detecting introgression from genomic sequence data. However, no existing method is capable of fast and accurate introgression detection on datasets with many dozens of genomic sequences. In this work, we develop an improved introgression detection approach which enables scalable analysis of large-scale datasets. Our approach combines the multi-species network coalescent model with hidden Markov models (HMMs) to tease apart the effects of incomplete lineage sorting (ILS) from those of introgression. Using simulated and empirical data, we perform a large-scale comparative assessment of our new method with other state-of-the-art introgression detection methods such as PhyloNet-HMM and CoalHMM. Our experiments explore a wide range of factors that may influence the performance of introgression detection, including the number of taxa, the number of alleles sampled from each taxa, sequence length, migration probability, and starting time of migration.