

AmNat 2020 Schedule

Saturday, January 4

8:30am-10:00am: Chapel

5-minute Lightning Talks

10:40am-12:00pm

[Session 1 \(Heather\)](#): It's a microbial world and we're just living in it

[Session 2 \(Toyon\)](#): Behavior and sociality talks have the best images

[Session 3 \(Scripps\)](#): I'll evolve if you evolve too

[Session 4 \(Chapel\)](#): Energy return on investment

1:00pm-5:45pm

[Symposium I \(Chapel\)](#): Merging behavioral ecology with eco-evolutionary dynamics: lessons from the past to move current research forward

7:00pm

Keynote Speaker: Anurag Agrawal

8:00pm

[Poster Session \(Chapel\)](#)

Sunday, January 5

8:30am-12:00pm

[Session 5 \(Chapel\)](#): Can't we all get along? Coexistence in communities

[Session 6 \(Acacia\)](#): Life Histories

[Session 7 \(Heather\)](#): Genetic Basis of Adaption: Where'd you get your genes?

[Session 8 \(Scripps\)](#): Ooh, look at that evolution go!

[Session 9 \(Toyon\)](#): Speciation

1:00pm-5:45pm

[Symposium II \(Chapel\)](#): Predicting population persistence and coexistence in the Anthropocene

7:30pm

Presidential Debate: Can we study what is natural in the Anthropocene?

Michelle Afkhami, Don Levitan, Elizabeth Pringle, Jeremy Yoder

Monday, January 6

8:30am-12:00pm

[Session 10 \(Chapel\)](#): Eco meet Eco; Evo meet Eco
[Session 11 \(Scripps\)](#): The New Normal in the Anthropocene
[Session 12 \(Toyon\)](#): Two's company, three's a community
[Session 13 \(Heather\)](#): Flowers, pollinators, and herbivores, oh my

[Return to overall schedule](#)

1:00pm-3:00pm

[Session 14 \(Chapel\)](#): Hybrids: Keep six inches of dance space between those species
[Session 15 \(Scripps\)](#): Dispersal: Doesn't anybody stay in one place anymore?
[Session 16 \(Toyon\)](#): ALLLLLLL the species interactions
[Session 17 \(Heather\)](#): Host-parasite dynamics

7:30pm: Bonfire Mixer

AmNat 2020 Detailed Schedule

Saturday, January 4

8:30am-10:00am

[5-minute Lightning Talks \(Chapel\)](#)

- "The history of ecology through the lenses of its publication records: 25 years of publication"
Paula Lemos-Costa and Stefano Allesina
- "Exploring the role of multi-species interactions in community assembly and coexistence"
Michelle Marraffini and Daniel Stouffer
- "Prey identity matters in a predation model "
Lily Khadempour, Leslie Rivas Quijano, Casey terHorst
- "The role of periodic disturbance in the emergence of facilitative interactions"
Peter C. Zee and Nayan Chawla
- "Parasite ecology and pulse heat stress in a warming world"
Danielle C Claar ,Chelsea L Wood
- "Milkweed chemical cocktails respond to herbivory and water stresses"
Elizabeth Pringle, Aramee Diethelm, and Fabiane Mundim
- "Exploring the genetic basis of spatial memory in mountain chickadees (*Poecile gambeli*)"
Wagner DN, Branch CL, Pravosudov V, Taylor SA
- "Testing for evolutionary tradeoffs in plant defense across the grape genus, *Vitis*"
Marjorie Weber
- "Adaptive introgression during environmental change can weaken reproductive isolation"
Gregory L. Owens, Kieran Samuk
- "Sexual Dimorphism and Species Diversity: from Clades to Sites"
Kaoru Tsuji and Tadashi Fukami
- "An Inordinate Fondness for Clover"
Maren L. Friesen, Sharon Y. Strauss, Andrew Siefert, Colleen A. Friel, Emily Mclachlan, Richard Allen White
- "Belowground microbes as a cryptic cause of maternal effects in plants"
Jennifer A. Lau and Madeleine R. Gellinger

10:40am-12:00pm

[Session 1 \(Heather\)](#): It's a microbial world and we're just living in it

10:40am: "Selection effects on diversity and specific ecosystem functions in pitcher plant associated bacteria"

Catalina Cuellar-Gempeler, José Alejandro Bravo, Eric Malekos, Marissa Monaco, and Eli Kallison

11:00am: "Legume invasions: did rhizobia escape phage control?"

Jannick Van Cauwenberghe & Ellen Simms

11:20am: "Legacy of prior host and soil selection on rhizobial fitness in plants"

Liana T. Burghardt, Brendan Epstein, and Peter Tiffin

11:40am: "The role of tree neighborhoods in structuring plant/insect/microbe interactions"

Karin T. Burghardt

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[Session 2 \(Toyon\)](#): Behavior and sociality talks have the best images

10:40am: "Social versus genetic mating systems: the complex mating system of the lark bunting"

Bruce E. Lyon

11:00am: "Mate preference depends on developmental environment"

Meredith Censer

11:20am: "Structure and function of flexible, adaptive living ant bridges"

Helen F. McCreery

11:40am: "Drifting at dawn: how deep-diving marine mammals schedule rest"

Roxanne Beltran, Jessica Kendall-Bar, Patrick Robinson, Daniel Costa

[Session 3 \(Scripps\)](#): I'll evolve if you evolve too

10:40am: "Coevolution through subtle shifts in partially correlated traits"

John N Thompson and Magne Friberg

11:00am: "Trait coevolution in ecological networks"

Paulo R. Guimarães Jr.

11:20am: "A Bayesian methodology for estimating the distribution of coevolution within ecological communities"

Bob Week, Scott Nuismer

11:40am: "Intersexual resource competition drives the coevolution of male and female dispersal traits"

Xiang-Yi Li and Hanna Kokko

[Session 4 \(Chapel\)](#): Energy return on investment

10:40am: "Life history of sockeye salmon as a reflection of EROI (Energy Return On Investment)"

Charles A. S. Hall, James Brown, Chen Hou and Robbie Burger

11:0am: "The energetic fitness paradigm: a useful tautology?"

James H. Brown, Robert J. Burger, Charles A. S. Hall and Chen Hou

11:20am: "Thermal biology of vector-borne disease"

Erin Mordecai

11:40am: "Towards a dynamic macroecology"

Erica A. Newman

1:00pm-5:45pm

Symposium I (Chapel): Merging behavioral ecology with eco-evolutionary dynamics: lessons from the past to move current research forward

1:00pm: Welcome/Introduction

1:10pm: "Frequency-dependent processes and feedbacks prior to eco-evolutionary dynamics: historical and contemporary perspectives"

Erik Svensson

1:30pm: "Behavioral flexibility scales up to drive feedback control of ecological dynamics"

Renée A. Duckworth

1:50pm: "Movement behavior as a framework for quantifying within-population variation in selective environments."

Ambika Kamath

2:10pm: Discussion

2:20pm: "Lessons from fishes on the causes and consequences of behavioral plasticity."

Suzanne H. Alonzo

2:40pm: "Evolutionary and plastic responses to feeding under predation threat and implications for trophic cascades"

Eric P. Palkovacs, Simone Des Roches, David C. Fryxell, Rebecca A. Robinson, Zachary T. Wood, Michael T. Kinnison

3:00pm: Coffee break

3:30pm: "Behavioral shifts mediate eco-evolutionary dynamics in island ecosystems"

Oriol Lapiedra, Jason Kolbe, Jonathan Losos

3:50pm: "Evolutionary and Ecosystem Ecology: overcoming the two solitudes"

Oswald Schmitz

4:10pm: "Cuckoos, reed warblers, and behavioural drivers of coevolutionary dynamics"

Rose Thorogood, Edward Klun, Katja Rönkä

4:30pm: "How Important Is Behavior, Really?"

Andrew P. Hendry

4:50pm: Discussion

8:30pm

Poster Session! (Chapel)

"The two-lines test: an unbiased test for humped and U-shaped bivariate relationships"

Rachel Tessier and Jeremy Fox

"Climatic drivers of the flowering niche in the *Streptanthus* clade"

Megan Bontrager, Sharon Y. Strauss, Julin Maloof, Jennifer Gremer

"The role of large predators in structuring diverse communities"

McDevitt-Irwin J., Meekan, M., Taylor, B., and Micheli, F.

"Inferring recent demography from gene genealogies"

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- Matthew Osmond, Graham Coop*
 “The paradox of polyploidy: is variation in unreduced gamete formation the key missing factor?”
B. Gerstner, H.J. Wearing, K.D. Whitney
- “Evolution in extreme events: good or bad?”
Kelsey Lyberger, Matthew Osmond, Sebastian Schreiber
- “How do spatial distribution and reward quality impact pollinator-mediated associational effects?”
Francis JS, Leonard AS
- “Project Baseline: Securing genetic materials for gauging plant evolutionary response to global change.”
Arthur E. Weis, Julie Etterson, Steven J. Franks, Susan J. Mazer, Ruth G. Shaw, Nicole Soper Gordon, Heather Schneider, Jennifer J. Weber, Katie Winkler
- “Comparing insect herbivore community structure across plants' native and non-native ranges: A meta-analysis”
Daniel B. Turner and William C. Wetzel
- “The strength of selection on alternative modifiers of genetic architecture under migration selection balance.”
Stephen R Proulx, Henrique Teotonio
- “Predicting adaptive dynamics in different habitats using ancestral trait values and demographic events”
Vrinda Ravi Kumar, Arun Prakash, Shyamsunder Buddh, Deepa Agashe
- “They grow up so fast: undergraduate students investigate the impact of nutrients and genotype on *Arabidopsis thaliana* phenotype.”
Lua Lopez, 2019 Spring Semester Freshman Research Immersion Students
- “The NEON Biorepository as a tool for monitoring ecological and evolutionary responses to change”
Kelsey Yule, Edward Gilbert, Azhar Husain, M. Andrew Johnston, Laura Rocha Prado, Laura Steger, Nico Franz
- “Predation and habitat structure drive community assembly in eelgrass-associated peracarid crustaceans”
Collin Gross, Jay Stachowicz
- “Nectar yeasts better resist priority effects when previously exposed to priority effects”
Callie R. Chappell, Clara I. Kieschnick, Tadashi Fukami
- “Influence of burrowing crabs on salt marsh substrate stability and vegetation”
Sofi Courtney and Megan Tyrrell
- “Effects of urbanization on plant-pollinator interactions”
Sevan Suni
- “Toward a metabolic theory of life history”
 Joseph Robert Burger, Chen Hou, and James H. Brown
- “Sequestration and aposematism in the milkweed herbivore system.”
Amy P. Hastings and Anurag A. Agrawal.
- “Ecological consequences of genome size in an invasive plant”
 -F. Alice Cang, Katrina M. Dlugosch
- “Sexual selection via male-male competition in a polymorphic poeciliid fish”
Gita R. Kolluru, Erin M. Wojan, Susan M. Bertram, Crystal Castillo, Heather M. Neldner, Jedediah A. Fitzgerald and Nalana C. Carreiro
- “Tests of negative frequency-dependent sexual selection in a polymorphic poeciliid fish”
Samantha West, Alexander S. Willcox, Evelyn G. Teodoro, Gita R. Kolluru

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Sunday, January 5

8:30am-12:00pm

[Session 5 \(Chapel\)](#): Can't we all get along? Coexistence in communities

8:30am: "The Evolution of Coexistence in Trinidadian streams"

Ron Bassar

8:50am: "Coexistence in coevolutionary systems - effects of intraspecific variation"

Athmanathan Senthilnathan

9:10am: "Alternative states and coexistence in the evolution of a competitive community"

Lucas A. Nell, Joseph S. Phillips, Anthony R. Ives

9:30am: "On the Consequences of the Interdependence of Stabilizing and Equalizing Mechanisms"

Chuliang Song, György Barabás, and Serguei Saavedra

9:50am: "Coexistence in complex communities: some insights from a three species to competition model"

Ravi Ranjan, Thomas Koffel, Christopher A. Klausmeier

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10:10am: Coffee break

10:40am: "Barriers to coexistence restrict the poleward range of a globally-distributed aquatic plant"

David W. Armitage, Stuart E. Jones

11:00am: "Consumer sexual dimorphism promotes coexistence among competing resources"

Stephen P. De Lisle, Gonzalo Hernando, Sebastian Schreiber, Daniel I. Bolnick

11:20am: "The density dependence of mutualistic interactions"

Christopher Moore and Karen Abbott

11:40am: "Network topology influences occupancy and abundance in experimental and model metapopulations"

Paulina A. Arancibia & Peter J. Morin

[Session 6 \(Acacia\)](#): Life Histories

8:30am: "Intraspecific life history variation in an introduced plant: effects of climate and herbivory"

Jennifer L. Williams & Sophie Duncan

8:50am: "Can females differentially allocate resources to offspring sired by different males?"

David Reznick and Samantha Levell

9:10am: "The influence of microhabitat variation on life cycle expression and population growth in an invasive, clonal sea anemone"

Will H. Ryan and Stacy A. Krueger-Hadfield

9:30am: "Mating system impacts the genetic architecture of adaptation to heterogeneous environments"

Kathryn Hodgins and Sam Yeaman

9:50am: “Restricted heritability of a polymorphic life history trait between sexes and tactics avoids conflict”

Madilyn Gamble & Ryan Calsbeek

10:10am: Coffee break

10:40am: “Developing the Genotype to Phenotype arrow: how conceptualizations of development broaden evolutionary theory”

Emilie Snell-Rood and Sean Ehlman

11:00am: “The effects of maternal and paternal age on the fitness of antler flies in the wild: a field experiment”

Christopher S. Angell and Howard D. Rundle

11:20am: “Did Mother Know Best? How Spatial Patterns of Emergence by Periodical Cicadas in a Fragmented Landscape Relate to Oviposition Patterns – 17 Years Earlier”

Sarah E. Anderson, Robert H. Hagen, Robert D. Holt (presenter), Jin Yao, William M. Cook

11:40am: “Linking the effects of density dependence on individuals and populations”

Jessie Mutz

Session 7 (Heather): Genetic Basis of Adaption: Where’d you get your genes?

8:30am: “Stranger things: the chloroplast genome edition”

David R. Smith

8:50am: “Fitness maps to a known large-effect locus in introduced stickleback populations”

D. Schluter, K. B. Marchinko, M. E. Arnegard, H. Zhang, S. D. Brady, F. C. Jones, M.A. Bell, and D. M. Kingsley

9:10am: “Genetic architecture underlying evolution in a fossil stickleback lineage”

Yoel E. Stuart, Matthew E. Travis, and Michael A. Bell.*

9:30am: “Genetics of coevolution between tapeworms and threespine stickleback”

Jesse N. Weber, Natalie C. Steinel, Foen Peng, Kum Chuan, Shim, Daniel I. Bolnick

9:50am: “Global adaptation confounds the search for local adaptation”

Tom R. Booker, Samuel Yeaman, Michael C. Whitlock

10:10am: Coffee break

10:40am: “Host genomics and blood parasite infections across an elevational contact zone between chickadees”

Angela Theodosopoulos, Kathryn Grabenstein, Scott Taylor

11:00am: “Climate adaptation across space and time in a migratory songbird”

Rachael Bay, Daniel Karp, Jasmine Rajbhandary, Kristen Ruegg, Tom Smith

11:20am: “Assortative mating by genomic regions involved in plumage coloration in a rapid avian radiation”

Sheela P. Turbek, Melanie Browne, Adrián S. Di Giacomo, Cecilia Kopuchian, Scott Taylor, Rebecca Safran, Leonardo Campagna

11:40am: “Recombination rate predicts patterns of admixture and phylogenetic discordance in the “hybrid swarm” haplochromine radiation of Lake Kivu”

Chad D. Brock, Reid P. Olson,, Catherine E. Wagner, Ole Seehausen

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[Session 8 \(Scripps\):](#) Ooh, look at that evolution go!

8:30am: “Evaluating evolutionary responses to an invasive predator by resurrecting decades old populations of *Daphnia*”

Matthew R. Walsh and J. Alex Landy

8:50am: “Experimental evolution results in rapid adaptation of rhizobia to their local legume host”

R. T. Batstone, T. L. Harrison, A. M. O’Brien, & Megan E. Frederickson

9:10am: “Minimizing the evolution of antibiotic resistance using optimal scheduling”

Jeremy Van Cleve, Quiyana M. Murphy, David Murrugarra

9:30am: “When to protect: Evolution of microbe-mediated protection in *C. elegans*”

Anke Kloock, Michael Bosall, Kayla King

9:50am: “Rapid adaptation to an extreme drought cycle in *Mimulus cardinalis*”

Daniel N. Anstett, Haley Branch1 & Amy Angert

10:10am: Coffee break

10:40am: “Evolution in a community context with *Sarracenia purpurea* protozoa”

Thomas Miller, Olivia Mason, Abigail Pastore, Catalina Cuellar-Gempeler, and Erin Canter

11:00am: “Evolutionary rescue in small populations”

Dale Clement

11:20am: “Rapid sexual signal loss and maintenance of a heritable reproductive polymorphism in crickets”

Justa Heinen-Kay and Marlene Zuk

11:40am: “Selective pressures on phenotypic traits change over the course of a single flowering season”

Laura C. Leventhal, Karen J. Bai, Madeline A.E. Peters, Emily J. Austen, Arthur E. Weis, Jennifer L. Ison.

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[Session 9 \(Toyon\):](#) Speciation

8:30am: “Do strong biotic interactions lead to faster evolutionary divergence in the tropics? Case studies from our feathered friends”

Benjamin Freeman, Joseph Tobias and Dolph Schluter

8:50am: “Macroevolutionary assembly of the endemic Hawaiian insect fauna”

David Hembry (presenting author) and Patrick O’Grady

9:10am: “Rewinding the tape of biogeography in a macroevolutionary simulation of the island progression pattern”

Jesse Czekanski-Moir

9:30am: “The contribution of temperature and continental fragmentation to amphibian diversification”

Jonathan Rolland & Fabien L. Condamine

9:50am: “Repeated speciation by adaptation in sympatric lineages of extremophile fishes”

Ryan Greenway, Anthony P. Brown, Henry Camarillo, Cassie Delich, Kerry L. McGowan, Lenin Arias-Rodriguez, Joanna L. Kelley, and Michael Tobler

1:00pm-5:45pm

[Symposium II \(Chapel\): Predicting population persistence and coexistence in the Anthropocene](#)

1:00pm: Impacts of early snowmelt and level of pollen limitation on population dynamics of a subalpine plant”

Diane R. Campbell

1:30pm: “Monsoon disturbance of rhizosphere microbiomes +consequences for reproductive plant traits”

Jonathan Dickey

1:45pm: “Decoupling of plant-fungal symbioses alters plant vital rates”

Stephanie N. Kivlin, Melanie Kazenel, Joshua Lynn, D. Lee Taylor and Jennifer Rudgers

2:05pm: “The direct effects of a non-native allelopathic invader on fungal community composition and native plant population dynamics”

Lalasia Bialic-Murphy, Stephanie Kivlin, Nathan L. Brouwer, and Susan Kalisz

2:25pm: Host-symbiont interactions through the lens of stochastic demography: variance buffering as a form of mutualism”

Tom E.X. Miller, Joshua C. Fowler, Kenneth D. Whitney, Jennifer A. Rudgers

2:45pm: Coffee break

3:30pm: “Do microbes matter? Combining demographic modeling and experimental approaches to understand the role of soil microbes for persistence of imperiled plant species.”

Michelle Afkhami, Aaron David, Pedro Quintana-Ascencio, Eric Menges, Khum B. Thapa-Magar, and Christopher Searcy

3:50pm: “Nectar microbes may exacerbate the impact of climate-induced phenological shifts on pollination”

Tadashi Fukami, Zhiyuan Song, Rachel L. Vannette, Manpreet K. Dhani

4:10pm: “How interactions and scale regulate species diversity in spatially-variable environments”

William K. Petry

4:30pm: “Generalized interactions promote coexistence of plant species that vary in seed size”

J.L. Maron, K.L. Hajek, P.G. Hahn. and D.E. Pearson

4:50pm: Synthesis and Discussion

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Monday, January 6

8:30am-12:00pm

[Session 10 \(Chapel\): Eco meet Eco; Evo meet Eco](#)

8:30am: “Eco-evolutionary dynamics of trait variances”

Daniel Bolnick, Denon Start

8:50am: “Evolution in ecological communities: complex interspecific interactions underlie adaptation”

Rachel Germain

9:10am: “The evolution of competitive ability”

Jawad Sakarchi and Rachel Germain

9:30am: “The overriding dampening effect of evolution on nature”
M.C. Urban, F. Pelletier, S.M. Carlson, S.Y. Strauss, E.P. Palkovacs, L. De Meester, A.L. Angert, M.A. Leibold, A.P. Hendry, S.T. Giery

9:50am: Break

10:10am: Coffee break

10:40am: “When do factors promoting genetic diversity also promote population persistence?”

Sebastian J. Schreiber

11:00am: “Intrapopulation variation in the brown anole: are species-rich communities composed of more diverse populations?”

Sean T. Giery

11:20am: “Genetic variation influences the strength and direction of neighbor effects on fitness”

Lauren Carley, Jackson Snow, Allison Carter, Tom Mitchell-Olds

11:40am: “Evolutionary Insights from Endemic Predation: Linking Daphnia Evolution to Stickleback Phenotypes in Alaskan Lake Ecosystems.”

Michelle Packer, Matthew R. Walsh

Session 11 (Scripps): The New Normal in the Anthropocene

8:30am: “Prediction and localized control of extreme events in spatiotemporal systems”
Bethany Johnson, Steve Munch

8:50am: “Evaluating how human land disturbances influence species barriers at continent-wide and regional scales”

Grabenstein, K.C., Burg, T. M., Otter, K. A., Taylor, S. A.

9:10am: “No evidence of wide-spread agricultural death trap for a species rich community of neotropical birds.”

Leithen K. M'Gonigle, Luke O. Frishkoff, Chase D. Mendenhall

9:30am: “Coupling fisheries and climate change in the food-web dynamic of an intertidal rocky-shore South Pacific food-web.”

M.I. Ávila-Thieme, A. Pérez-Matus, S.A. Navarrete, F.S. Valdovinos, P.A. Moreno

9:50am: “Local adaptation and maladaptation entwined in roadside amphibians”
Steven P. Brady

10:10am: Coffee break

10:40am: “Failure to shift phenology may be associated with local extinction”
Meredith A. Zettlemoyer

11:00am: “Spatio-temporal shifts to maintain climatic niche in *Bombus*”
Olga Koppel and Dr. Jeremy T. Kerr

11:20am: “The interacting effects of climate change and urbanization on Threespine Stickleback evolution”

Simone Des Roches, Michael A Bell, Marina Alberti, Eric P Palkovacs

11:40am: “The Future Keepers: Assessing Effects Of Thermal Stress And Resource Limitation On Ants”

Nigel R Andrew, Sarah J Hill, Nate Sanders, Rob Dunn, Alan Andersen

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[Session 12 \(Toyon\)](#): Two's company, three's a community

8:30am: "The stability of plant functional diversity following disturbance"

Leila Z. Forsyth and Benjamin Gilbert

8:50am: "Elevation shapes the reassembly of Anthropocene lizard communities"

Luke O. Frishkoff, Eveling Gabot, George Sandler, Cristian Marte, and D. Luke Mahler

9:10am: "Ecological communities are formed by probable combinations of competing species"

Lucas P. Medeiros, Karina Boege, Ek del-Val, Alejandro Zaldivar-Riverón and Serguei Saavedra

9:30am: "Using integral projection models to understand community disease dynamics of a fungal pathogen"

A. Marm Kilpatrick, J.R. Hoyt, K.L. Parise, J.T. Foster, K.E. Langwig

9:50am: "Equation-free predictions of noisy, stochastic, and nonstationary ecological dynamics."

Stephan B Munch

10:10am: Coffee break

10:40am: "Widespread character displacement in the avian bill across a latitudinal gradient"

Sean Anderson and Jason Weir

11:00am: "A conceptual framework for predicting combined non-consumptive effects of multiple predators on individuals, populations, and communities"

William J. Reserits, Jr.

11:20am: "Reconsidering predator diversity effects: a theoretical comparison of body size, phylogenetic, and trait based definitions of functional diversity"

Michael W. McCoy, Elizabeth Hamman, James R. Vonesh, Jeremy Wojdak, and Benjamin M. Bolker

11:40am: "Ecosystem-based management using Empirical Dynamic Programming"

Antoine Brias, Steve Munch

[Session 13 \(Heather\)](#): Flowers, pollinators, and herbivores, oh my

8:30am: "Floral symmetry and specialization in pollination interactions"

Jeremy B. Yoder, Giancarlo Gomez, and Colin J. Carlson

8:50am: "Changes in flower size are associated with changes in plant size, not plant physiology, in co-occurring Californian annuals"

Katherine E. Eisen and Ellie M. Goud

9:10am: "Why advertise low quality? Explaining informative floral traits"

Carla J. Essenberg

9:30am: "Anther dimorphism as a strategy to increase male fitness when pollinators consume male gametes"

Kathleen Kay

9:50am: "Effects of pollinators on plant coexistence"

Christopher A. Johnson, Jonathan M. Levine

10:10am: Coffee break

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10:40am: “Fitness consequences of natural and anthropogenic dietary chemicals in a social bee, with insights into physiology and behavior”

Sarah K. Richman, Angela M. Smilanich, Denyse Marquez Sanchez, Anne S. Leonard

11:00am: “Understanding Floral Scent Inheritance in a Coevolved Plant-Pollinator System”

Mia T. Waters, John N. Thompson, Magne Friberg

11:20am: “Phenological Plasticity Predicts Trends in Abundance of Massachusetts Butterflies”

James Michielini, Erik Dopman & Elizabeth Crone

11:40am: “Population dynamics of insect herbivores in highly fragmented landscapes”

Elizabeth E. Crone

1:00pm-3:00pm

Session 14 (Chapel): Hybrids: Keep six inches of dance space between those species

1:00pm: “Cardinals are red, buntings are blue; because they hybridize, they’re interesting too!”

Libby Megna, Matthew D. Carling

1:20pm: “Reinforcement and ecological speciation between incipient outcrossing and selfing *Clarkia* species”

David A. Moeller and Ryan D. Briscoe Runquist

1:40pm: “The evolution of gametic compatibility within species and reproductive isolation across species”

Don R. Levitan

2:00pm: “Evolutionary dynamics of inbreeding and outbreeding in a plant-like animal”

Kevin C. Olsen and Don R. Levitan

2:20pm: “Patterns, predictors, and consequences of dominance in F1 hybrids”

Ken A. Thompson, Mackenzie J. Uquhart-Cronish, Kenneth D. Whitney, Loren H. Rieseberg, Dolph Schluter

Session 15 (Scripps): Dispersal: Doesn’t anybody stay in one place anymore?

1:00pm: “Western monarch summer range expansion slows as population declines”

Collin Edwards, Elizabeth Crone

1:20pm: “Does habitat fragmentation affect the dispersal ability of a terrestrial darkling beetle?”

Goggy Davidowitz, Natasha Tigreros, Giorgi Kozhoridze, Yaron Ziv

2:40pm: “Effects of migration on rapid adaptation and the genetic basis of dispersal behavior in natural populations of *D. melanogaster*”

Ozan Kiratli, Paul Schmidt

2:00pm: “Scale-dependent effects of niche specialization: the disconnect between individual movement and species distribution”

Shan Huang, Marlee A. Tucker, Jörg Albrecht, Alison Eyres

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Session 16 (Toyon): ALLLLLL the species interactions

1:00pm: “Antagonistic and Mutualistic Biotic Interactions Across the Geographic Range Margin of *Clarkia xantiana* ssp. *xantiana*”

John W. Benning and David A. Moeller

1:20pm: “Ecological context drives a shift from parasitism to mutualism”

Mary Rogalski, Tara Stewart Merrill, Camden Gowler, Carla Caceres, Meghan Duffy

1:40pm: “The Ecology and Evolution of Commensalism”

Judie Bronstein

2:00pm: “Cooper’s and Sharp-shinned Hawks fill discrete niches created by the relative abundances of their prey species.”

Eliot T. Miller, Oisin Mac Aodha, Emma I. Greig, David N. Bonter, Wesley M. Hochachka

2:20pm: “Mediation of the insect immune response by ecological factors: insights from a recent host expansion”

Su'ad Yoon, Joshua G. Harrison, Angela Smilanich, Matthew Forister

Session 17 (Heather): Host-parasite Dynamics

1:00pm: “The maintenance of genetic variation under host-parasite coevolution”

Ailene MacPherson, Matthew Keeling, Sally Otto

1:20pm: “Parasite recognition and resistance varies among closely related stickleback populations”

Amanda Hund, Lauren Fuess, Mariah Kenney, Meghan Maciejewski, Daniel Bolnick

1:40pm: "Sick of Eating: eco-evo-immuno dynamics of predators and their trophically acquired parasites"

Sam Fleischer, Dan Bolnick, Sebastian Schreiber

2:00pm: “Social trematode parasites allocate soldiers according to invasion threat in the field.”

Emlyn J. Resetarits, Ryan F. Hechinger and Mark E. Torchin

2:20pm: “Host energetics explain variation in parasite productivity across scales”

Rita Grunberg and David Anderson

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AmNat 2020 Abstracts

Lightning Talks

“The history of ecology through the lenses of its publication records: 25 years of publication”

Paula Lemos-Costa and Stefano Allesina

PLC and SA -- Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA; SA -- Northwestern Institute on Complex Systems, Evanston, IL, USA

We document the explosive growth of ecology in the past 25 years by examining more than 300,000 articles published by almost 400,000 researchers in 160 ecological journals. We reconstruct the publication and affiliation history of each author, and assign them a putative gender using their first name. Armed with these data of unprecedented quality and size, we document the rapid growth of the field: in a quarter century, the number of ecological journals indexed by Web Of Science doubled, the number of published documents tripled, the number of unique authors grew sixfold. Ecology is becoming increasingly collaborative, with author lists growing in size and diversity (both in terms of gender, and in number of countries represented). This tremendous growth is however uneven: few countries dominate the field when it comes to productivity and impact, and the gender publication gap although slowly closing is still strong, with women publishing fewer and less-cited articles. In light of our results, we discuss measures that can be taken to make the field of ecology as diverse as the systems ecologists study.

“Exploring the role of multi-species interactions in community assembly and coexistence”

Michelle Marraffini and Daniel Stouffer

School of Biological Sciences, University of Canterbury, NZ

Two kinds of interaction dynamics emerge when pairwise competitive interactions are embedded in a network of three species or more: intransitive loops and higher-order interactions. While research on the role of species interactions in general during the assembly process began decades ago, recent theoretical frameworks have revitalized interest on this process in a multiple species' context. Using modern coexistence theory and invasion criteria we explore how multiple species interactions, intransitive loops and higher-order interactions, form during the assembly process. Specifically, we aim to explore the importance of the order of arrival in the assembly of multispecies communities, its effects on coexistence, and the resulting interaction scheme. We will adapt existing theoretical models and frameworks, drawing on multiple fields of ecology including pairwise competition studies, food-web dynamics, and network analysis, to develop methods for simulating communities under different interaction strategies and assembly processes.

For example, we know a community with 'rock' species may be invaded by 'paper' species when 'paper' and 'scissors' invade together. Also, it is theorized that if 'rock' is imbedded in a larger community, other species act as 'scissor' allowing 'paper' to invade. Similar to this 'rock-paper-scissor' scenario, we expect to gain insight into how other multispecies interactions form during the assembly process and their role in coexistence in diverse communities.

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“Prey identity matters in a predation model”

Lily Khadempour, Leslie Rivas Quijano, Casey terHorst

California State University, Northridge, Department of Biology

The microbial community that resides inside *Sarracenia purpurea* pitcher plants is used as a model

system for studying ecology and evolution. Ciliated protozoans feed on a bacterial community that is responsible for releasing energy and nutrients from dead insects that the plant traps. Traditionally, when this system has been used for studying predator-prey dynamics, the bacterial community has been treated as a black box where all bacteria are thought to have similar effects on protist fitness. We show that this is not the case. We isolated bacterial strains from pitcher plant fluid, identified them to the genus level using 16S rRNA sequencing, and grew them with different protist genotypes. We found that strains of bacteria affect protist growth rates differently. We used this information to create synthetic bacterial communities that were designed to either promote or inhibit protist growth. These synthetic communities will be used in future studies to investigate the relationship between ecology and evolution in this system.

“The role of periodic disturbance in the emergence of facilitative interactions”

Peter C. Zee and Nayan Chawla

[University of Mississippi](#)

A body of both empirical and theoretical work has demonstrated the importance of spatial structure for the evolutionary maintenance of facilitative both within and among species. Here, we seek to understand how temporal variation in spatial structure may impact the likelihood of emergence of facilitative interactions in microbial communities. To do so, we have developed a spatially explicit model of biofilms where individual fitness is determined by extracellular compounds released by neighboring cells. In our model, we are able to track both species densities and allele frequencies simultaneously. Confirming results from previous work, we find that spatial structure and local dispersal facilitate the maintenance of mutualistic interactions in communities. However, we also find that intermittent lapses in spatial structure have the ability to promote the origin of these interactions. We test a range of parameters of disturbance, modes of dispersal, sizes of interaction neighborhoods for their impacts on composition of ecological interaction types in the community. Future work will aim extend the model include more diverse communities as well as responses to abiotic variation.

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“Parasite ecology and pulse heat stress in a warming world”

Danielle C Claar (1, 2), Chelsea L Wood (1)

[1\) University of Washington; 2\) UCAR/NOAA](#)

Although much disease ecology research has focused on gradual warming, climate change effects manifest not only via incremental temperature increases (“press” warming), but also by episodic climatic events (“pulse” warming). The effects of pulse warming are different than those of gradual warming; while gradual warming is an ‘inching-along’ process, pulse warming can instigate dramatic changes over a short period of time. Pulse warming can also instigate climate threshold events: non-linear responses that drastically alter ecosystem structure, causing coral bleaching and mass mortality events, changing kelp forest distributions, and sparking massive forest and brush fires. Because pulse warming events are expected to continue to increase in frequency and magnitude, it is urgent that we understand how such climate events are likely to influence rates of infectious disease transmission. This talk will focus on pulse warming and the abundance of disease-causing parasites. Parasites are often hidden and can be easy to overlook, but they are ecologically important and ubiquitous across all metazoan taxa and ecosystems. It is imperative that we understand the effects of pulse heat stress on parasites if we are to anticipate and counteract the effects of amplified outbreak frequency on human and wildlife health. We synthesize our current understanding of parasitism and pulse heat stress and highlight urgent research gaps.

“Milkweed chemical cocktails respond to herbivory and water stresses”

Elizabeth Pringle, Aramee Diethelm, and Fabiane Mundim

University of Nevada Reno, Department of Biology

Phytochemistry links nutrient cycles to trophic interactions. Patterns of phytochemical variation can thus be an organizing principle in ecology. Milkweeds have long been model plants for studying the chemical ecology of plant-animal interactions, but the chemical focus has primarily been on the steroidal glycosides known as cardenolides. Milkweed plants actually contain diverse cocktails of specialized compounds, which seem to mediate the plant’s response to biotic and abiotic stresses and cascade up to affect both herbivores and predators. In this talk, I will describe the roles played by some lesser known chemical components of milkweed plants in the evolutionary ecology of milkweed-animal interactions.

“Exploring the genetic basis of spatial memory in mountain chickadees (*Poecile gambeli*)”

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1University of Colorado Boulder, Department of Ecology and Evolutionary Biology

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3University of Nevada Reno, Department of Biology

Spatial memory is important for survival. Mountain chickadees (*Poecile gambeli*) are small, non-migratory, food-caching songbirds that live in alpine habitat and experience harsh environmental conditions over the winter months that can result in high mortality. Birds at higher elevations experience significantly harsher conditions, including lower temperatures, more snowfall, and reduced food availability than birds at low elevations. There are significant differences in spatial memory among mountain chickadee populations at different elevations, birds with better spatial memory are more likely to survive at higher elevations, and chickadees at higher elevations score, on average, better on tests of spatial memory than chickadees from lower elevation populations. We are using whole genome sequence data to investigate the genetic basis of spatial memory in mountain chickadees and have found that several gene regions have significant associations with the spatial memory phenotype. Excitingly, the majority of these SNPs have been associated with cognitive processes in humans or other organisms.

“Testing for evolutionary tradeoffs in plant defense across the grape genus, *Vitis*”

Marjorie Weber

Michigan State University

Plants have evolved a myriad of fascinating ways to defend themselves against pathogens and herbivores. One mechanism that has originated many times across the plant tree of life is the evolution of specialized plant traits that provide rewards (e.g., food or shelter) to bodyguard arthropods in return for protection against plant enemies. These traits, known as mutualistic or indirect defense traits, attract and retain the third trophic level to plants, thereby facilitating top-down defense from plant enemies via a tri-trophic interaction. There are many hypotheses about why some species have indirect defensive traits while others do not. Plant defense theory predicts tradeoffs among direct and indirect defensive traits, such that indirect defensive traits will be less effective in highly physically or chemically defended species. However, we lack studies aimed at understanding how multiple defensive traits interact to influence the long-term evolution of defense mutualisms and their traits. Here, we characterize the

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macroevolutionary patterns of indirect (domatia) and direct (chemical) defense trait variation across the wild grape genus, *Vitis*, testing for signatures consistent with trait trade-off hypotheses.

“Adaptive introgression during environmental change can weaken reproductive isolation”

*Gregory L. Owens*¹, *Kieran Samuk*²

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Durham, NC, USA, 27708.

Anthropogenic climate change is an urgent threat to species diversity. One aspect of this threat is the merging of species through increased hybridization. The primary mechanism for this collapse is thought to be the weakening of ecologically-mediated reproductive barriers, as demonstrated in cases of “reverse speciation”. Here, we expand on this idea and show that adaptive introgression between species adapting to a shared, moving climatic optimum can readily weaken any reproductive barrier, including those that are completely independent of climate. Using genetically explicit forward-time simulations, we show that genetic linkage between alleles conferring adaptation to a changing climate and alleles conferring reproductive isolation (intrinsic and/or non-climatic extrinsic) can lead to adaptive introgression facilitating the homogenization of reproductive isolation alleles. This effect causes the decay of species boundaries across a broad and biologically-realistic parameter space. We explore how the magnitude of this effect depends upon the rate of climate change, the genetic architecture of adaptation, the initial degree of reproductive isolation, the degree to which reproductive isolation is intrinsic vs. extrinsic, and the mutation rate. These results highlight a previously unexplored effect of rapid climate change on species diversity.

“Sexual Dimorphism and Species Diversity: from Clades to Sites”

Kaoru Tsuji and *Tadashi Fukami*

Kyoto University

A variety of relationships have been observed between sexual dimorphism and species diversity, from positive to negative and non-significant. Although many hypotheses have been developed to explain these relationships, it has proven difficult to understand why patterns are so variable. Most studies on this topic have used clades as phylogenetically independent replicates for pattern analysis, but a few recent studies took an alternative approach, using sites as spatially independent replicates. We discuss how the new, site-based studies complement the traditional, clade-based studies and argue that the combined use of the two approaches will be more powerful than either alone in understanding environmental factors that produce variation in sexual dimorphism–species diversity relationships.

“An Inordinate Fondness for Clover”

Maren L. Friesen, *Sharon Y. Strauss*, *Andrew Siefert*, *Colleen A. Friel*, *Emily Mclachlan*, *Richard Allen White*

Washington State University

Understanding the coexistence of close relatives is an important test case for evolutionary ecology. Using Californian communities of clover as a testbed, we combine long-term field observations, greenhouse studies, and genomics to explore the role of microbial symbionts, particularly rhizobial mutualists, in coexistence processes.

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“Belowground microbes as a cryptic cause of maternal effects in plants”

Jennifer A. Lau and Madeleine R. Gellinger

Indiana University

Plants live in close association with microbes, which can influence the expression of plant traits. Here, we investigate whether these microbe-effects extend to the offspring generation and influence transgenerational plasticity (maternal effects) in their plant hosts. We used *Brassica rapa* seeds from an experiment in which plants were grown in either drought or well-watered conditions in association with microbial communities that had been evolving for 16 months in either drought or well-watered conditions to determine how the maternal environment (dry or wet soil conditions and drought vs. wet adapted microbial communities) affected seedling traits and drought tolerance in the offspring. We find that most maternal effects detected in our study result not from abiotic environmental conditions, but are instead caused by the evolutionary history of belowground microbes. Our findings indicate that microbial communities may be a cryptic cause of maternal effects in plants.

Session 1

“Legume invasions: did rhizobia escape phage control?”

Jannick Van Cauwenberghe & Ellen Simms

UC Berkeley

Global trade has transported many species outside their natural range; some proliferate and negatively impact their new ecosystems. Almost 10% of the invasive plants recorded for North America are legumes (Fabaceae). Legumes benefit from access to atmospheric nitrogen (N) via a specialized mutualistic interaction with soil-dwelling bacteria called rhizobia. This dependence hampers the invasion ability of some legumes, yet rhizobia sometimes co-invade. Thus, understanding legume invasions requires elucidating factors that limit and facilitate rhizobium invasions.

The enemy escape hypothesis (EEH) is commonly invoked to explain why invading species proliferate excessively. The EEH states that non-native species become invasive because they have escaped specialized natural enemies (e.g., predators and parasites) that regulate their native-range populations, but are absent from the invaded ecosystem. We hypothesize that rhizobium genotypes associated with invasive legumes have largely escaped infection by bacteriophages, which has allowed those rhizobia to facilitate invasion by their host legumes.

To test this hypothesis, we will assess the host range of the phages associated with rhizobia from 3 Californian populations of yellow bush lupine (*Lupinus arboreus*, native Californian legume), and 3 populations of French broom (*Genista monspessulana*, invasive European legume) from each of 4 regions (California, Spain, France and Italy). We expect the host range of phages associated with invaded communities to be more similar to the host range of phages from the European communities than to phages associated with native communities.

“Legacy of prior host and soil selection on rhizobial fitness in plants”

Liana T. Burghardt, Brendan Epstein, and Peter Tiffin

Department of Plant and Microbial Biology, University of Minnesota, Twin Cities

Measuring selection acting on microbial populations in natural or even seminatural environments is challenging because many microbial populations experience variable selection. The majority of rhizobial

bacteria are found in the soil. However, they also live symbiotically inside nodules of legume hosts and each nodule can release thousands of daughter cells back into the soil. We tested how past selection (i.e., legacies) by two plant genotypes and by the soil alone affected selection and genetic diversity within a mixed inoculum of scores of strains of *Ensifer meliloti*. In addition to imposing direct selection on rhizobia populations, soil and host environments had lasting effects across host generations. Host presence and genotype during the legacy period explained 22% and 12% of the variance in the strain composition of nodule communities in the second cohort, respectively. Although strains with high host fitness in the legacy cohort tended to be enriched in the second cohort, the diversity of the strain community was greater when the second cohort was preceded by host rather than soil legacies. Our results indicate the potential importance of soil selection driving the evolution of these plant-associated microbes.

“Selection effects on diversity and specific ecosystem functions in pitcher plant associated bacteria”

Catalina Cuellar-Gempeler, José Alejandro Bravo, Eric Malekos, Marissa Monaco, and Eli Kallison
[Humboldt State University](#)

For decades, studies have supported a positive correlation between biodiversity and ecosystem function. While most studies focus on broad community functions, such as productivity, specific functional pathways have received less attention. These pathways are particularly important for microorganisms involved in nutrient cycling. We studied the role of diversity in driving specific functions within the pitcher shaped leaves of the Cobra Lily (*Darlingtonia californica*). This carnivorous plant relies on the microorganisms within its pitcher leaf fluid to degrade its prey and release its nutrients. We hypothesized that diversity correlates with the broad function of prey degradation but not with specific functions in the nitrogen cycle, because these can associate with unique taxa. We used pitcher plant bacteria to inoculate microcosms with gradients of diversity by applying three selective gradients: (1)dilution-to-extinction, (2)nutrient concentration and (3)antibiotic dilution. Using distinct selective gradients, we can better separate the effects of community composition from diversity in natural microbial communities. Carbon metabolism had positive correlations with diversity, reflecting patterns of the broader function of degradation. In contrast, nitrification, chitin degradation, and aminoacid pathways had neutral or negative relationships with diversity. We propose a framework to integrate diversity-specific function relationships into ecosystem models of multiple nutrient cycles.

“The role of tree neighborhoods in structuring plant/insect/microbe interactions”

Karin T. Burghardt

[Department of Entomology, University of Maryland, College Park, MD](#)

Sometimes referred to as the “great unseen”, we now know that hidden actors like bacteria and fungi are actively altering plant phenotypes, potentially with effects on ecosystem function rivaling those of macro-organism diversity. However, despite some targeted work on pairwise plant-microbe interactions, we lack a comprehensive understanding of how the plant microbiome affects plant phenotype, plant-plant interactions, and interactions with herbivores. Here I present data from an establishing tree biodiversity experiment—BiodiversiTREE—at the Smithsonian Environmental Research Center (SERC) linking the taxonomic, phylogenetic, and functional diversity of tree planting neighborhoods to both insect community and fungal endophyte community composition on a set of the same 540 focal trees across 15 tree species and 3 diversity treatments. There are strong signals of

increasing insect diversity paired to decreases in fungal endophyte diversity when trees grow in diverse neighborhoods although outcomes are dependent of which aspects of diversity are considered. Multi-trophic interactions dependent on the spatial arrangement of potential host trees may underlie biodiversity ecosystem function relationships in forests.

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Session 2:

“Social versus genetic mating systems: the complex mating system of the lark bunting”

Bruce E. Lyon

Department of Ecology and Evolutionary Biology, University of California, Santa Cruz and
Alexis S. Chaine, Station d'Ecologie Théorique et Expérimentale du CNRS, Moulis, France

Social and genetic mating systems are often uncoupled in a species. For example, many socially monogamous birds have high levels of genetic polygamy due to extra-pair paternity (EPP). However, the cryptic nature of extra-pair copulations in most species makes it difficult to determine their social and evolutionary causes and consequences, and they are therefore often relegated to a minor role in the social mating system. In the socially monogamous lark bunting we found that behaviors associated with acquisition of extra-pair copulations are a major driver of the social system during the breeding season. Male buntings show classic territoriality until they attract a female, at which point they completely cease defending their territory and switch to mate guarding. Prior to clutch completion, most females are closely attended by readily observable ‘mobs’ of up to six additional males seeking extra-pair copulations, with little overt physical aggression shown by the social mate. Behavioral observations revealed complex social interactions between males in mobs, the existence of subtle tactics for enhancing success at mobbing suggest that EPP in lark buntings are often forced by males rather than driven by female choice. Genetic analysis confirms high rates of EPP in our population and selection analyses on this component of fitness indicate that success in EPP is non-random with respect to male plumage and size traits. Mobbing is a key component of the mating system of the lark bunting and plays a significant role in the evolution of their social behavior and plumage signaling.

“Structure and function of flexible, adaptive living ant bridges”

Helen F. McCreery

Harvard University, School of Engineering and Applied Sciences

Eciton hamatum army ants forage along trails with many thousands of workers. To facilitate high traffic flows, workers link together to form temporary bridges over gaps or rough terrain. These bridges are adaptive and agile; they form rapidly and adjust quickly to changes in traffic flow and to changes in the geometry of the micro-environment. The living bridges adjust as attachments points – leaves and twigs – shift. I explored how these collectives respond dynamically to changing structural requirements by inducing bridges on an apparatus which allowed me to adjust the size of the gap. I changed the gap size repeatedly, forcing the expansion, modification, and disassembly of existing bridges, and recorded the structures from two angles to get detailed structural information, including bridge volume, asymmetry and curvature, throughout trials. I combine these data with behavioral data, including the number of ants in the bridge and timing of ant “joining” and “leaving” events. These structural and behavioral data allow me to explore how individual actions interact with the mechanics and stability bridges to understand how these flexible, agile living structures emerge and adapt.

“Mate preference depends on developmental environment”

Meredith Censer

University of Chicago

Prezygotic isolating factors, one of the most important of which is mate choice, are thought to be among the fastest evolving barriers in the origin of reproductive isolation. However, behavioral isolation can also be highly plastic, particularly when genetic differentiation between populations is weak. In locally adapted populations, plastic preferences that depend on the developmental habitat have the potential to enhance or mask behavioral isolation between populations.

I used the red-shouldered soapberry bug, a classic example of local adaptation between an ancestral and an introduced host plant, to assess the role of the developmental host on mating behavior. I find that populations from the ancestral host have a strong preference for males who developed on the ancestral host, but that populations from the introduced host have no preference at all. This may indicate that soapberry bugs have lost preference during the process of adaptation to the novel host. It may also be a more recent adaptation in populations on the ancestral host to avoid mating with non-local migrants in response to increased gene flow over the last 30 years.

“Drifting at dawn: how deep-diving marine mammals schedule rest”

Roxanne Beltran, Jessica Kendall-Bar, Patrick Robinson, Daniel Costa*

*Department of Ecology and Evolutionary Biology, University of California Santa Cruz

Sleep is a critical daily activity for wild animals but comes at the cost of increased predation. This is particularly true for species with long-distance migrations and aquatic life histories that have infrequent access to safe resting grounds. Elephant seals undergo a seven-month foraging trip each year, during which they dive continuously (on average 23-minute dives followed by 2-minute surface intervals). About 6% of dives are spent passively drifting through the water column which is thought to enable sleep. Our objective was to use tracking and diving data from adult female seals (N=203) to determine how these drift dives are scheduled within and across days. We found that during the outbound migration when animals are in poor body condition, drifting begins at dawn. In contrast, during the inbound migration when animals are in good body condition, drifting ends at dawn. These dynamics likely reflect a shift in the risk-reward tradeoff, as seals in poor body condition prioritize resource acquisition over avoidance of visual predators. Our future efforts will seek to characterize the distribution of food resources and predators across time and 3-dimensional space such that optimal diving decisions can be modeled.

Session 3:

“Coevolution through subtle shifts in partially correlated traits”

John N Thompson and Magne Friberg

University of California, Santa Cruz

Much of the signal of coevolution may often be in subtle shifts in the relative sizes, shapes, number, or concentration of traits that are partially correlated with each other, rather than through the evolution of fundamentally novel traits. We evaluated how the geographic mosaic of coevolution is shaped in saxifragaceous plants and their coevolved prodoxid moth pollinators through a combination of partially correlated morphological and chemical traits. The results suggest that a focus on only a few traits would underestimate the extent of local coadaptation in these interactions. More generally, the results suggest that ongoing coevolution among species may be more pervasive than often suspected, because it is

often difficult to know in advance which of the many possible trait combinations are under coevolutionary selection.

“Trait coevolution in ecological networks”

*Paulo R. Guimarães Jr.*¹

¹Departamento de Ecologia, Universidade de São Paulo, São Paulo, Brazil

A central problem in evolutionary ecology is to understand the evolutionary dynamics of species-rich networks. I will use the work of my research group to address this problem by integrating empirical data, coevolutionary models, and network science. Our studies reveal three potential consequences of network structure to the coevolution of ecological assemblages through indirect effects. First, indirect effects propagate across weak but numerous pathways connecting species, shaping trait evolution at the network level. Second, indirect effects may partially explain trait patterns in mutualisms across simple landscapes. In a two-site model, the interplay between gene flow and indirect effects cancel out contrasting selective pressures not related to mutualisms and favor trait matching between mutualistic partners at the landscape level. Third, indirect effects may affect the spatial diversification of complex phenotypes. In a two-traits model, indirect effects mediated by mutualistic networks buffer the diversifying effects of genetic architectures of complex phenotypes. Collectively, these results suggest that coevolution in network structure can be mapped to the theory describing information flow in networks, indicating a potential unifying theoretical framework for how evolutionary effects may cascade across species, traits, or sites in ecological systems.

“Intersexual resource competition drives the coevolution of male and female dispersal traits”

Xiang-Yi Li and Hannah Kokko

Institute of Biology, University of Neuchâtel, Switzerland and University of Zürich Switzerland

Resource competition is a major driver of dispersal: an emigrating individual leaves more resources to its kin. Existing models of sex-biased dispersal rarely consider intersexual competition for resources. Instead, male reproductive success is often solely assumed to depend on female availability, implying a tacit assumption that male presence never depletes resources, such as food, that are of interest to female kin. In reality, both male and female offspring typically consume resources on their natal site before departing to consume resources elsewhere, and sexually dimorphic body sizes imply that the resource needs can differ. The goal of our study is to investigate how intersexual competition for resources can affect the evolution of sex-specific dispersal, via competition between kin of the same sex or different sexes and the subsequent success elsewhere. Our individual-based simulation model allows not only the dispersal probability but also its timing to evolve. We consider dispersal timing because later dispersal yields a longer period of kin competition than dispersal that occurs soon after independence. We also highlight the role of sex-specific income/capital breeding strategies, which is understudied in both empirical and theoretical literature of sex-specific dispersal. We show that sex biases in dispersal probability and timing are sensitive to the presence of intersexual competition, sexual differences in capital vs. income breeding strategies, and sexual dimorphism in the quantity of resources consumed. Males may evolve to disperse earlier if they also consume more food, as a result of selection to reduce intersexual kin competition. Alternatively, males may evolve to disperse less as well as later than females, if male fitness depends more on resource accumulation (e.g., building a large body to succeed in mating competition under polygyny) whereas female fitness depends more on reliable income (e.g., in species that require extended periods of maternal foraging), even if both sexes are equally competitive in consuming resources. Although the more dispersive sex is often the earlier

departing sex, we also find cases where the only clear dimorphism is found in dispersal timing. We thus encourage more studies on the timing aspect of sex-biased dispersal.

“A Bayesian methodology for estimating the distribution of coevolution within ecological communities”

Bob Week, Scott Nuismer

University of Idaho

Coevolution has long been thought to influence trait distributions and patterns of interaction within ecological communities. Because available methods for measuring coevolution are designed for species pairs, however, we are currently unable to reliably evaluate the role of coevolution in structuring ecological communities. Here I present a new Bayesian methodology that combines mathematical models of coevolution with interaction network and phenotypic data to estimate coevolutionary selection for each pair of species in a community. The performance of this new method is evaluated using simulated data sets and estimates for the strength of coevolution are computed for a subalpine plant-pollinator community located near the Rocky Mountain Biological Research Station in Gothic, Colorado. Applying this Bayesian approach more broadly will help to resolve long-standing debates in ecology and evolution over the importance of coevolution for the structure and function of ecological communities.

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Session 4:

“The energetic fitness paradigm: a useful tautology?”

James H. Brown, Robert J. Burger, Charles A. S. Hall and Chen Hou

James H. Brown, University of New Mexico (retired); 636 Piney Way, Morro Bay, CA 93342

The equal fitness paradigm (EFP) of Brown, Hall and Sibly (Nature Ecol Evol 2018, 2:262) holds that organisms are approximately equally fit, because energetic fitness, $E = GBQF$, where G is generation time, B is the mass-specific rate of biomass production, Q is the energy density of biomass, and F is the fraction of production incorporated into surviving offspring. On the one hand, the EFP is a tautology, because at steady state the average parent replaces itself with one offspring in one generation. On the other hand, the EFP offers powerful insights into ecology and evolution, because it: 1) requires that generation time and production rate have equal but opposite scalings with body mass and temperature; 2) calls attention to how production, in the form of offspring growth and parental investment, imposes fundamental biophysical constraints on life history (e.g., variation in mortality with age); 3) highlights universal characteristics of life (e.g., the near-constant energy density of biomass: $Q \approx 22.4$ kJ/g dry weight); 4) provides a biophysical basis for Red Queen coevolution; 5) offers insights into departures from steady state due to natural and artificial selection; and 6) demonstrates the central importance of energy – and metabolism, scaling relations and power-time tradeoffs – in life history, ecology, and evolution.

“Life history of sockeye salmon as a reflection of EROI (Energy Return On Investment)”

Charles A. S. Hall, James Brown, Chen Hou and Robbie Burger

Why do animal migrations exist? The life histories of Sockeye Salmon give good evidence that it is a consequence of strategies for maximizing Energy Return On (energy) Investment, or EROI. Adult female migratory sockeye, which have invested considerable energy into migrations of tens of thousands of kilometers in rivers and oceans, weigh 5 KG and have 3000 eggs. Con specific, non-migratory kokanee of

the same age may share the same spawning grounds but weigh but 0.4 KG and have only 400 eggs. Obviously the salmon at sea have found much richer food resources than those in home nursery waters that more than compensates for the energy required to undertake their migration. We have constructed energy models of the salmon and their ecosystems to examine energy investments and costs associated with a migratory life style. Preliminary results indicate that more energy is gained from the migration than is lost in undertaking it. We speculate further on EROI as a much more general procedure for understanding mechanistically animal life histories.

“Thermal biology of vector-borne disease”

Erin Mordecai

[Stanford University](#)

Temperature profoundly affects the physiology of nearly all organisms, including the mosquitoes that transmit pathogens. Because temperature nonlinearly affects rates of development, survival, and reproduction in both the vector and pathogen, it affects vector-borne disease transmission. We characterized the thermal responses for traits and transmission for 11 different pathogens in 15 mosquito species and validate them with field observations. Temperature physiologically limits transmission below 9-23°C and above 32-38°C and optimizes it at 23-29°C for temperate (e.g., West Nile) and tropical (e.g., dengue and malaria) diseases. Temperate pathogens had broader thermal ranges and more potential for warming-driven expansion than tropical pathogens, some of which may decline with climate warming. Field data and multiple modeling approaches support predicted temperature effects on transmission over space and time. Simple mechanistic models can therefore powerfully predict thermal responses and the potential for shifts, expansions, and declines in disease driven by climate change.

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“Towards a dynamic macroecology”

Erica A. Newman

[Department of Ecology & Evolutionary Biology, University of Arizona](#)

We search for generality across ecosystems, and the patterns that remain constant tend to be the macroecological ones, which incorporate scaling, but are independent of any particular mechanism within any given ecosystem. Instead, patterns like the Species Area Relationship, the Species Abundance Distribution, and body-size distributions within a community emerge due to statistical aggregation. A recent form of information-based macroecology called the Maximum Entropy Theory of Ecology (METE) makes two important advances; first, it unites spatial patterns, species diversity, and metabolic distributions within a single mathematical framework; and second, it allows us to parameterize real ecosystems and the potential parameter space they occupy. With METE, we now have the opportunity to advance beyond categorizing forms of mathematical distributions that describe biodiversity patterns and move into a predictive framework where the true constraints on ecosystems and their dynamics emerge. To date, all real biological communities that have been measured fall into a fairly narrow range of available parameter space. I will discuss the parameter space of real ecosystems, the constraints that govern them, and implications for ecosystem dynamics at large scales.

Poster Session!

“The two-lines test: an unbiased test for humped and U-shaped bivariate relationships”

Rachel Tessier and Jeremy Fox

[University of Calgary](#)

Many ecological and evolutionary theories propose humped or U-shaped bivariate relationships. Examples include the intermediate disturbance hypothesis, the diversity-productivity hypothesis, and stabilizing and disruptive selection. However, these theories rarely specify the precise quantitative form of the hump or U-shape, raising the question of how best to test for humped or U-shaped relationships without assuming a specific form. Quadratic regression is the most common method for testing for humped or U-shaped bivariate relationships, but we show that it is prone to bias because it misdiagnoses nonlinear asymptotic relationships as humped or U-shaped. We show a newly-developed alternative approach, the two-lines test. The two-lines test is a modified breakpoint regression in which the two regression lines are not forced to meet at the breakpoint. Using simulated data, we show that the two-lines test is an unbiased test for humped or U-shaped bivariate relationships. We reanalyze published data and show that humped diversity-disturbance and diversity-productivity relationships are even rarer than previously thought.

“Climatic drivers of the flowering niche in the *Streptanthus* clade”
Megan Bontrager (presenter), Sharon Y. Strauss, Julin Maloof, Jennifer Gremer
[University of California, Davis](#)

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Plants use a diversity of cues to align the timing of flowering with the most favorable conditions for subsequent reproduction. The particular cues that plants use may differ among species or populations if optimal conditions for reproduction differ across species' ranges or among local environments. Alternatively, phenological cues may be conserved if favorable conditions are consistent across environments (perhaps differing only in seasonal timing). Under climate change, phenological responses may fail to enhance fitness if cues are no longer reliably aligned with conditions that maximize reproduction. Here, we use detailed assessments of phenology and reproductive effort from over 1200 herbarium specimens to identify climate conditions associated with flowering and subsequent reproductive success. Our work focuses on the *Streptanthus* clade, a group that occupies a diversity of geographic and climatic spaces in the California Floristic Province. We test whether the climatic conditions associated with flowering and reproductive success are phylogenetically conserved across this clade. We also examine whether the conditions that promote reproductive success are reliably aligned with flowering cues in contemporary and future climate scenarios.

“The role of large predators in structuring diverse communities “
*McDevitt-Irwin J.1**, *Meekan, M.2*, *Taylor, B.2*, and *Micheli, F.1*
[1- Stanford University](#), [2- Australian Institute of Marine Sciences](#)

Ecosystems around the world, terrestrial to marine, are experiencing losses of apex predators, resulting in trophic downgrading. Large predators are critical drivers of community structure and ecosystem function, having both direct (e.g. changes in prey abundance) and indirect (e.g. trophic cascades) consequences on the ecosystem, but their effects can be hard to capture as you can't directly manipulate large predators. Sharks are prominent predators on coral reefs but are continuing to decline worldwide, primarily due to over-harvesting by humans, therefore, it's imperative to evaluate the broader ecological consequences of their loss. Here, we aim to further understand the role of large predators in structuring natural communities and the ecological consequences of losing these top predators due to human impacts. Specifically, we asked, how do sharks influence coral reef fish community structure and ecosystem function? We hypothesized that spatial variation in shark abundance correlates with changes in reef fish abundance, functional traits and trophic composition.

We used diver operated video (DOV) surveys, baited remote underwater videos (BRUV) surveys, stable isotopes of carbon and nitrogen, and morphometric analysis in the Chagos Archipelago in the British Indian Ocean Territory, a wilderness area that contains some of the highest fish biomass in the world as a no-take MPA. We evaluated spatial variation in shark abundance and how this correlates with reef fish abundance, functional traits and trophic composition at the community level; and at the individual level, reef fish diet, eye size and fin size. Our study provides further insight into the role of large predators, currently declining worldwide, and the ecological consequences of their loss on diverse and complex ecosystems.

“Inferring recent demography from gene genealogies”

Matthew Osmond, Graham Coop

[Center for Population Biology, UC Davis](#)

Demography is central to both ecology and evolution, but is often unknown. Inferring demography from genetic data has been a longstanding pursuit since Wright and Malecot, with substantial advances in the last decade due to the newfound ability of characterize blocks of genomes that are identical-by-descent (IBD). In just the last couple years it has become possible to characterize not just blocks of IBD but the entire genealogical history of a large set of DNA sequences — the ultimate description of the genetic variation within a sample. Here we explore what this information can tell us about recent demography. For any site within the genome we can build the genealogy and use this, together with the locations of the sample, to infer the locations of the genetic ancestors back to the most recent common ancestor. This allows direct inference of migration rates at every locus and, based on rates of coalescence within particular geographic regions, a map of effective population size. We show how this method performs in a wide range of simulated circumstances, including range expansion, and discuss promising empirical applications.

“The paradox of polyploidy: is variation in unreduced gamete formation the key missing factor?”

B. GERSTNER, H.J. WEARING, K.D. WHITNEY

[Department of Biology, University of New Mexico](#)

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The primary method for formation of polyploids, in plants, is through the formation and joining of unreduced gametes. Their production is affected by genetic and environmental factors that result in variable formation rates of unreduced gametes (FRUG) within and between populations. Once formed, neo-polyploids face minority cytotype exclusion (MCE) due to a lack of viable mating opportunities. More than a dozen theoretical models have explored factors that could permit neopolyploids to overcome MCE. Until now, however, none have explored variability in FRUG and its consequences for the rate of polyploid establishment. In this work, we: (1) determine the distribution that best fits available empirical data on FRUG; (2) explore the consequences of using stochastic draws from this FRUG distribution on an existing model’s behavior. We found that FRUG is best fit by a log-normal distribution. Stochastic draws for FRUG decrease the time to overcome MCE and, in some instances, make overcoming MCE possible when it was not otherwise. These results may help reconcile previous modeling results (indicating that polyploid establishment should only occur under a restrictive set of conditions) with the observation that polyploids are common in nature.

“Evolution in extreme events: good or bad?”

Kelsey Lyberger, Matthew Osmond, Sebastian Schreiber

UC Davis

Climate change is predicted to lead to more severe environmental perturbations, including storms and droughts. Such disturbances act as strong selective agents on organisms. Many of the best documented cases of natural selection in action are during short-lived extreme climatic events. For example, a severe storm selected on body size in house sparrows, hurricanes select on limb length in lizards, and droughts select for earlier flowering time in *Brassica rapa*. We praise these as charismatic examples of how evolution can promote adaptation to the environment because we typically focus on documenting how evolution can prevent extinction in the context of press disturbances where rapid adaptation is always beneficial. But extreme climatic events act as pulse disturbances, where the new environment is transitory and faster evolution results in greater maladaptation when the pulse ends. We show how genetic variance and heritability affect population size and the chance of persistence under a pulse disturbance. Interestingly, we find genetically-based trait change can, under certain conditions, promote extinction.

“How do spatial distribution and reward quality impact pollinator-mediated associational effects?”

Francis JS, Leonard AS

University of Nevada Reno, Department of Biology

Co-flowering plants that share pollinators can experience associational effects ranging from facilitation to competition via the receipt of conspecific and heterospecific pollen. Despite growing interest in these plant-plant interactions, predicting their outcome is difficult because it is unclear what properties of floral communities shape pollinator behavior and pollen movement. Here we asked how two aspects of floral communities impact pollen movement among bumblebee-visited (*Bombus*) co-flowering plants: 1) plants' fine scale spatial distribution, and 2) the quality of two floral resources that are critical for bumblebees, pollen and nectar. Using unmanned aircraft imagery, we created high-resolution floral maps of High Sierra (CA) meadows at pollinator-relevant scales (~3 pixels/cm; 3000–5000 m² plots). In each plot we collected stigmas from five plants of the most dominant plant bumblebee-visited species (>20 open inflorescences, N= 155 individual plants from seven genera), and characterized con- and heterospecific pollen receipt. To quantify floral rewards, we measured pollen protein: lipid ratio and nectar sugar content of each plant species. Using this unique dataset we will be able to determine how the nutritional landscape surrounding a plant impacts its interaction with co-flowering species. By combining large-scale floral mapping with a community-level analysis of a critical functional trait for determining bee foraging, this study will help connect the growing fields of bee nutritional ecology and pollinator-mediated interactions between plants ecology.

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“Project Baseline: Securing genetic materials for gauging plant evolutionary response to global change.”

Arthur E. Weis¹, Julie Etterson², Steven J. Franks³, Susan J. Mazer⁴, Ruth G. Shaw⁵, Nicole Soper Gorden⁶, Heather Schneider⁴, Jennifer J. Weber⁷, Katie Winkler²

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Rapid environmental change is imposing selection on ecologically important traits. Project Baseline has gathered and stored genetic materials that will enable future researchers to effectively estimate evolutionary responses through resurrection experiments. With this approach, dormant ancestors of known age are revived and reared in a common garden with their contemporary descendants. When ancestors and descendants are grown in the same environment, phenotypic differences between them can be attributed to genetic change.

Between 2012 and 2015, we amassed a collection of seed from 65 plant species across the USA for future resurrection experiments. On average, each species was collected from 15 sites through its range, with 100 maternal lines collected per site. Sampling protocols were designed to obtain an unbiased sample of the segregating genetic variation. The collection is stored at the USDA National Center for Genetic Resources Preservation under conditions that will maintain seed viability of over the next 50 years.

At 5-year intervals, Project Baseline seed will be released to researchers submitting proposals taking advantage of this unique resource. Proposals must include detailed plans for collecting descendant generations, and must use a resurrection approach. The first call for proposals will be announced in 2020-21.

“Comparing insect herbivore community structure across plants' native and non-native ranges: A meta-analysis”

Daniel B. Turner and William C. Wetzel

Department of Entomology, Michigan State University

Across invasion ecology research, many hypotheses have been developed to describe patterns of natural enemy pressure on plants in their non-native ranges, including the enemy release and evolution of increased competitive ability hypotheses. For example, we have learned that many non-native species may have a competitive advantage against native species by escaping specialist herbivores that may cause significant decreases in fitness. However, we do not broadly understand how the ratio of specialist to generalist enemies nor the functional trait composition of insect herbivore communities shift upon introduction to a novel range. Therefore, in order to understand how these dynamics change, we require broad and quantitative comparisons of insect community diversity between a plant's native and non-native ranges. Here, we collected insect herbivore community data on plants in their native and non-native ranges and use insect and plant functional traits, geographic distribution, and time since introduction to a novel range to describe herbivore community and functional differences across these ranges. We present our findings that describe the variation and patterns in insect herbivore community structure on multiple plant species across the globe.

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“The strength of selection on alternative modifiers of genetic architecture under migration selection balance.”

Stephen R Proulx, Henrique Teotonio

UCSB

Migration between habitats can generate large sustainable fitness load. Selection can drive the spread of alternative modifiers that reduce these negative effects because they canalize habitat specific fitness.

We compare selection for modifiers of migration, recombination, dominance, and epistasis. We find that selection on recombination is typically weak, while selection for epistasis is generally strongest. These results suggest that recombination modifiers are less likely to evolve than other modifiers of genetic architecture.

“Predicting adaptive dynamics in different habitats using ancestral trait values and demographic events”
Vrinda Ravi Kumar, Arun Prakash, Shyamsunder Buddh, Deepa Agashe
National Centre for Biological Sciences, Bangalore, India

Rapid and widespread environmental change worldwide has raised concern about the ability of natural populations to adapt to novel conditions. Ancestral population phenotypes and population dynamics should predict successful adaptation - but which specific phenotypic traits and demographic events matter? And finally, might different founding traits and demographic events explain adaptation to different environments?

To answer this, we experimentally evolved 10 distinct wild-collected populations of the red flour beetle. From each population, we founded three replicate laboratory lines, selecting for performance on the optimal ancestral resource, wheat flour, and two novel resources - finger millet and corn. We collected census data every generation for 40 generations during adaptive evolution and asked which ancestral traits correlate with adaptive dynamics. We find that adaptation to finger millet versus corn involves contrasting population dynamics that are correlated with distinct ancestral parameters. While population sizes correlate with starvation resistance and intraspecific competition, population stability is harder to predict. Importantly, phenotypic traits measured in the ancestral environment typically do not correlate with population performance in a novel environment. This suggests that phenotypic traits of natural populations measured in an optimal environment may not be useful for predicting persistence in a new, stressful environment.

Studying the real-time adaptive evolution of these lines across different habitats have allowed us to test a range of hypotheses that have not been tested in a single experimental system. These results bring us closer to making predictions about the adaptive potential of wild populations during major changes in their natural environment.

“They grow up so fast: undergraduate students investigate the impact of nutrients and genotype on *Arabidopsis thaliana* phenotype.”

Lua Lopez, 2019 Spring Semester Freshman Research Immersion Students

Freshman Research Immersion/Biology Department, Binghamton University (SUNY), NY

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Understanding how phenotypic variation arises through interactions between genetics and the environment is a challenging concept for first year college students to grasp. To facilitate a deeper understanding of this important concept in ecological genetics, students in the Binghamton University Freshman Immersion Program researched changes in fitness-related traits among eleven genetic lines (six natural ecotypes and five knocked out mutants) of *Arabidopsis thaliana* growing in two nutrient conditions. Students observed differences in flowering time among genetic lines, namely, natural ecotypes from drought prone climates flowered earlier compared with ecotypes from milder climates suggesting adaptation to their climate or origin. Regarding the knocked-out lines, none of the silenced genes had a large phenotypic effect illustrating how complex, ecological relevant traits are usually not controlled by a single gene. Finally, students observed an increase in plant size and fruit production

under nutrient addition showing the effect that environment has on the phenotype. This course improved student understanding of complex evolutionary processes, both clarifying concepts they were familiar with and increasing knowledge of previously unknown concepts. During this program, students gained experience analyzing data, presented results during a poster presentation, discussed their conclusions in the context of relevant literature, and were exposed to scientific writing with a final research paper. Overall, this kind of research project-based approach is an effective tool to help students understand complex evolutionary interactions. Finally, since the research was carried out under the unPAK (Undergraduate Phenotyping of Arabidopsis Knockouts), students contributed to a larger data collection effort, now publicly available, providing them with a final purpose and a collaborative scientific experience.

“The NEON Biorepository as a tool for monitoring ecological and evolutionary responses to change”
Kelsey Yule, Edward Gilbert, Azhar Husain, M. Andrew Johnston, Laura Rocha Prado, Laura Steger, Nico Franz
Arizona State University

Although closely related to other natural history collections that are centered on documenting biodiversity, biorepositories are change-focused and reflect a highly-structured and self-referential sampling strategy. Operated by and located at Arizona State University, the National Ecological Observatory Network (NEON) Biorepository houses all physical samples and specimens associated with the NEON project, which aims to monitor biological responses to global change over the next 30 years. With the intent to collect samples that are representative of within and between species variation and community composition, collection protocols are standardized across all 81 NEON terrestrial and freshwater aquatic sites spanning the continental United States, Hawaii, and Puerto Rico. The Biorepository is growing by more than 100,000 samples per year of over 40 organismal, environmental, and genomic classes. Specimen records can be explored and sample requests can be made in the Symbiota-based NEON Biorepository Data Portal (<https://biorepo.neonscience.org>). Researchers can actively view, manage, and publish open and easily accessible sample-associated data directly within the portal. In line with the primary goal of monitoring change, preservation of sample data and data potential are prioritized over preservation of individual specimen integrity. Although any current sample use must be weighed against the potential future value of the sample, samples are meant to be used frequently and destructive or invasive sample can be appropriate.

“Predation and habitat structure drive community assembly in eelgrass-associated peracarid crustaceans”
Collin Gross, Jay Stachowicz
University of California, Davis

Empirical studies of community assembly processes typically focus on two major functional trait patterns at small plot-level or site-level scales. Communities with traits that are clustered relative to a null distribution are thought to be structured primarily by abiotic environmental filters, and overdispersed communities structured primarily by biotic interactions such as competitive niche partitioning. However, the patterns and drivers of community assembly may vary across different spatial scales and species pools. Using species abundance and trait data from 42 sites across the northern hemisphere spanning 37 degrees of latitude, we examined the assembly patterns of eelgrass (*Zostera marina*) -associated peracarid crustacean communities according to several abiotic and biotic environmental predictors. Specifically, we compared functional diversity distributions across global and ocean-specific species pools, using subsite (50 km), and plot (1 m) as replicates in separate analyses.

Across all species pools in site-level analyses, predation emerged as an important predictor in models of dispersion – high predation intensity sites were more overdispersed and low predation intensity sites were more clustered. Ocean basin (east vs. west) and Latitude also emerged as strong predictors of dispersion at the global scale. At the plot level, dispersion was best modeled as a function of microhabitat variables as well as predation across species pools, along with food availability in the Atlantic. In taking a global approach to understanding community assembly processes, our study allows us to pinpoint mechanisms common to all eelgrass communities, as well as detect where and how these mechanisms differ worldwide.

“Nectar yeasts better resist priority effects when previously exposed to priority effects”

Callie R. Chappell (1), Clara I. Kieschnick (1), Tadashi Fukami (1)

[\(1\)Department of Biology, Stanford University](#)

The initial relative density of competing species can affect final species abundances in local communities, the phenomenon known as priority effects. Most studies assume that species traits that determine the strength of priority effects are static, but these traits can evolve rapidly in the metacommunity within which the local communities are embedded. Using nectar microbes, we investigated whether prior exposure to priority effects could cause populations to evolve resistance to priority effects. We used nectar microbes for our experiments that exert strong negative priority effects on each other: yeast, *Metschnikowia reukaufii*, and bacteria, *Acinetobacter nectaris*. Over three months, corresponding to a typical flowering season, we sequentially transferred the yeast in three types of artificial nectar: (1) nectar where pH was 6, simulating fresh real nectar; (2) nectar where pH was 3, simulating pH reduction caused by growth of the bacterium, *Acinetobacter nectaris*; and (3) nectar where pH was initially 6, but then conditioned by growth of *A. nectaris*. Then, using the yeast strains from these three treatments, we manipulated the initial density of a given yeast strain relative to a co-inoculated standard bacterial strain and measured abundances after three days of growth. Strains that had grown in bacteria-conditioned nectar were suppressed to a lesser extent by the initially dominant bacteria than their ancestral counterparts. The strains that had grown in low-pH nectar showed the same weakening of priority effects, suggesting that pH explains the results. These findings indicate that the historical exposure to priority effects can cause species to evolve to resist priority effects, thereby making priority effects appear insignificant when only their contemporary, not historical, importance was considered.

“Influence of burrowing crabs on salt marsh substrate stability and vegetation:

Sofi Courtney and Megan Tyrrell

[Sofi Courtney, NOAA Hollings Scholar, Drexel University, and the Academy of Natural Sciences](#)

Coastal marshes across the Northeastern United States have been documented to be declining. Causes for this decline likely include both biotic and abiotic factors due to changes from accelerated sea level rise and other anthropogenic disturbances. A possible biotic factor in marsh decline is increased perturbation from burrowing crabs. *Uca* species’ (fiddler crabs) populations have been shown to be increasing in many marshes in the eastern US, likely due to disruptions in food webs and expanding habitat from sea level rise. High densities of fiddler crab burrows have been shown to contribute to creek bank erosion and possibly in other factors of marsh instability. In this study, we experimentally test the impact of fiddler crabs on marsh substrate stability and marsh vegetation distribution in the high marsh by excluding crabs from some sections of a micro-tidal back-barrier marsh on Cape Cod, Massachusetts, and allowing them into others. We then compare vegetation cover, soil organic matter,

elevation, and various soil stability metrics between manipulated crab burrow densities and un-manipulated densities.

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“Effects of urbanization on plant-pollinator interactions”

Sevan Suni

Pollinators are responsible for about one-third of all food consumed and are essential for the reproduction of almost 90% of flowering plants. Understanding how urbanization alters functional interactions among pollinators and plants is thus critically important given ongoing increasing anthropogenic land use. Pollinators often exhibit short-term specialization, and visit plants of the same species during one foraging bout. This facilitates plant receipt of conspecific pollen, defined as pollen on a pollinator that is the same species as the plant on which the pollinator was visiting. Conspecific pollen receipt facilitates plant reproductive success, and is thus important to plant and pollinator persistence. We tested the hypothesis that urbanization decreases short term specialization, by comparing the proportion of conspecific pollen on pollinators in urban fragments and natural areas. The urban sites had been restored with native plants or contained remnant native plant communities. We also explored how urbanization affects plant-pollinator network specialization. Surprisingly, we found a higher proportion of conspecific pollen on pollinators in urban fragments relative to natural areas, and that network specialization differed between urban and natural areas. We argue that that lower species diversity, and higher floral density in urban habitat fragments drives higher short-term specialization in urban areas.

“Toward a metabolic theory of life history”

Joseph Robert Burger (a), Chen Hou (b), and James H. Brown (c)

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The life histories of animals reflect the allocation of metabolic energy to traits that determine fitness and the pace of living. Here we extend metabolic theories to address how demography and mass-energy balance constrain allocation of biomass to survival, growth, and reproduction over a life cycle of one generation. We first present data for diverse kinds of animals showing empirical patterns of variation in life history traits. These patterns are predicted by new theory that highlights the effects of two fundamental biophysical constraints: demography on number and mortality of offspring; and mass-energy balance on allocation of energy to growth and reproduction. These constraints impose two fundamental tradeoffs on allocation of assimilated biomass energy to production: between number and size of offspring, and between parental investment and offspring growth. Evolution has generated enormous diversity of body sizes, morphologies, physiologies, ecologies, and life histories across the millions of animal, plant and microbe species, yet simple rules specified by general equations highlight the underlying unity of life.

“Sequestration and aposematism in the milkweed herbivore system.”

Amy P. Hastings and Anurag A. Agrawal.

[Department of Ecology and Evolutionary Biology, Cornell University.](#)

How strong are the associations between toxin sequestration and warning coloration (aposematism) within a community of specialized herbivorous insects? While these two traits are generally thought to be tightly-linked (honest signaling), frequent co-existence may increase opportunity for Batesian

mimicry. Common milkweed (*Asclepias syriaca*) produces toxic cardenolides and is known for its community of specialized, and often brightly-colored, insect herbivores, including the monarch butterfly. We measured cardenolide sequestration in nine co-occurring species of insects, spanning four orders, that feed on various tissues of *A. syriaca*. Sequestration was measured in terms of concentration per unit body mass, total content per insect, as well as concentration relative to the food source (particular plant tissue type). Of these nine species, seven are aposematic during at least one developmental stage. On average, species with warning coloration did tend to sequester more toxins than cryptic species, however, there is evidence for mimicry in 2 aposematic species (1 moth, 1 beetle) which show either no sequestration or passive storage of very low concentrations of toxins. There was no evidence of active sequestration in the three cryptic species, and insects feeding on milkweed seeds were able to sequester the greatest concentrations of cardenolides.

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“Ecological consequences of genome size in an invasive plant”

F. Alice Cang, Katrina M. Dlugosch

[University of Arizona](#)

Evolutionary drivers responsible for the extraordinary genome size variation across angiosperms remain largely unknown and biological invasions present unique opportunities to clarify the population-level processes that shape this variation. Genome size shifts have occurred in association with successful colonization events in some plants, suggesting phenotypic consequences of variation. If it imposes functional constraints, a potential invader may benefit from reduced genome sizes that promote "weedy" traits. Potential mechanisms also include selection along environmental clines, and founder effects that allow larger genomes to drift to high frequency. In the invasive thistle, *Centaurea solstitialis*, we found larger genomes were significantly associated with slower vegetative growth and later flowering times, with lower lifetime biomass and flower production. We also observed a negative relationship with elevation, suggesting support for a hypothesis of selection for earlier flowering time, potentially due to shorter growing seasons at higher elevations. Despite these potential ecological consequences, we found no evidence of selection for smaller genomes during range expansion. Instead, we saw a significant, negative relationship with population age, consistent with the prediction that small founding populations permit neutral or detrimental increases in genome size to rise to higher frequencies. Current work employs Oxford Nanopore long-read sequencing to characterize the molecular mechanisms that underlie patterns of genome size variation, such as differences in transposable element content.

“Sexual selection via male-male competition in a polymorphic poeciliid fish”

Gita R. Kolluru, Erin M. Wojan, Susan M. Bertram, Crystal Castillo, Heather M. Neldner, Jedediah A. Fitzgerald and Nalana C. Carreiro

[California Polytechnic State University, San Luis Obispo, CA](#)

Color polymorphism requires an evolutionary explanation, often involving sexual selection. Although female choice receives much attention, male-male competition may be equally important. *Girardinus metallicus* is a polymorphic Cuban poeciliid fish. Rare “black morph males” are black and yellow and persistently follow females while displaying, whereas common “plain morph males” are drab and almost exclusively sneak copulations. Both morphs also compete aggressively for mating opportunities. Females prefer either plain morph or familiar morph males, and do not pay attention to the coloration traits of black morphs, calling into question the role of the black morph display. We predicted that: 1) black morph males are more aggressive; 2) in black morphs, more colorful males are more aggressive; 3) females eavesdrop on fights to select more aggressive males; and 4) mating success is lower in black

morph pairs than in mixed morph pairs, possibly because of increased harassment of females and aggressive interference in black morph pairs. All of these predictions received support, suggesting that the display may be a signal of aggressive mate guarding or a species indicator, performed to secure access to mating opportunities given the rarity of black morph males. Black morphs may be rare because of reduced mating success when they are common.

“Tests of negative frequency-dependent sexual selection in a polymorphic poeciliid fish”

Samantha West, Alexander S. Willcox, Evelyn G. Teodoro, Gita R. Kolluru

California Polytechnic State University, San Luis Obispo

Explanations for polymorphism persistence typically involve some form of balancing selection. *Girardinus metallicus* is a color polymorphic poeciliid fish with a rare black morph and a common plain morph. The polymorphism extends to behavior: black morph males display during mating, whereas plain morph males almost exclusively sneak copulations. We hypothesized that this polymorphism is maintained by negative frequency dependent sexual selection (NFDSS), using two experiments. In experiment 1, we habituated females to one morph for several weeks and subsequently tested their morph preference in dichotomous choice tests. Contrary to NFDSS, females preferred the familiar morph. In experiment 2 we tested females who were housed with both morphs, but this time using groups of males differing in morph frequencies as the stimuli, with the prediction that females would prefer mixed-morph groups to a control group of only plain morph males. This prediction tended to be upheld, but only if the group was plain morph-biased. The results of experiment 2 may rescue the idea of NFDSS and suggest that more realistic test scenarios reveal important patterns. Indeed, the social environment may contribute to the maintenance of the polymorphism via indirect genetic effects, such that the mating success of males depends on the morph frequencies in their social groups.

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SYMPOSIUM 1

“Lessons from fishes on the causes and consequences of behavioral plasticity.”

Suzanne H. Alonzo

University of California Santa Cruz

Increasingly, we are realizing that organismal plasticity is fundamentally important yet poorly understood. Yet, the importance of understanding the biological causes and consequences is increasing, as we need to predict how organisms will respond to rapidly changing environments. Plasticity generates eco-evolutionary feedbacks which have been shown to hinder, accelerate and even alter the direction of adaptive evolutionary change. Recent developments in neurobiology and genomics are also revealing a complex mix of conservation and innovation in the genetic and physiological mechanisms underpinning behavioral plasticity and consistency. Extensive research on phenotypic plasticity has focused on an organism’s response to extrinsic environmental conditions (e.g. temperature or resources). Yet, animals also exhibit striking plasticity in response to changes in their social environment (e.g. interactions with members of the same species). While there is a general recognition that a better understanding of plasticity and the resulting eco-evolutionary dynamics it generates is needed, I will first argue that this will require a more integrative approach. I will then illustrate some of what we are learning about the cause and consequences of behavioral plasticity from empirical work on a few species of fish.

“Behavioral flexibility scales up to drive feedback control of ecological dynamics”

Renée A. Duckworth

[University of Arizona](#)

One of the greatest challenges in evolutionary ecology is determining when ecological dynamics are driven by built-in flexibility of pre-existing adaptations or eco-evolutionary feedbacks. Meeting this challenge requires unification of behavioral biology, ecology, and evolutionary biology and holds the promise of providing unique insight into such disparate problems as species' stasis, predictability versus contingency of evolution and identifying species most at risk of extinction in response to environmental change. Specifically, population dynamics depend on the feedback between individual decisions and extrinsic factors that influence demographic change. I will suggest that behavioral responses and adaptive plasticity in general, form feedback loops that drive dynamics of ecological systems, ultimately influencing evolutionary patterns at multiple scales.

“How Important Is Behavior, Really?”

Andrew P. Hendry

[McGill University](#)

At various times, scientific disciplines large or small are criticized for failure to properly (or at least promptly) consider new paradigm-shifting, new-synthesis-requiring concepts. Yet, for instance, does evolutionary biology really require a major re-organization as a result of epigenetics or microbiomes or development or niche construction? Behavior often has been cast in this potential new-synthesis-requiring role. Yet, does a consideration of behavior fundamentally change our understanding of invasion biology or inheritance or - now - eco-evolutionary dynamics? I will argue that this determination requires definitive tests of whether behavioral understanding alters the directions or strengths of established effects, or reveals fundamentally new and important effects. If not, perhaps behavior belongs into the ever-expanding dustbin of "high enthusiasm and low r-squared" ideas that, while still with us, really didn't have a big effect on our field. Fluctuating asymmetry anyone? I will describe potential observations and experiments that will help to make this determination for behavior in the context of eco-evolutionary dynamics.

“Movement behavior as a framework for quantifying within-population variation in selective environments.”

Ambika Kamath

[Miller Institute, UC Berkeley](#)

In this presentation, I will first talk about within-population variation in selective environments as an important piece of the eco-evolutionary dynamics puzzle, and then discuss how movement behavior can be used as a window into understanding and quantifying variation in the selective environments experienced by individuals and groups. After developing this idea conceptually, I will illustrate this using my empirical research on sexual selection in *Anolis sagrei* and on collective hunting/foraging behavior in social spiders and tent caterpillars.

“Behavioral shifts mediate eco-evolutionary dynamics in island ecosystems”

Oriol Lapiedra, Jason Kolbe, Jonathan Losos

[CREAF \(Center for Ecological Research and Applied Forestries\)](#)

Understanding how animal behavior mediates ecological and evolutionary processes is crucial to unravel

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how animal populations cope with rapid environmental changes. We set up a large scale, manipulative field experiment to assess whether individual variation in behavior influences the success of animals confronted with new selective pressures. Specifically, we quantified natural selection on risk taking behavior of brown anoles in the presence or absence of a well-known ground predator, the curly tailed lizard. On experimentally established island populations with the ground predator, brown anoles with a tendency to avoid the ground survived better. On islands without the predator, lizards that were quick to begin exploring survived better. Selection on behavior occurred in parallel with selection on morphological traits and the selective benefit of behavioral traits is context-dependent. In the presence of predators, the observed behavioral shifts have led to modifications in several dimensions of the ecological niches of brown anoles such as habitat use and diet. These changes have led to top-down cascading effects on prey taxa. Overall, our ongoing field experiment provides evidence that behaviorally-driven ecological niche shifts can alter ecosystem functioning.

“Evolutionary and plastic responses to feeding under predation threat and implications for trophic cascades”

Eric P. Palkovacs (presenter), Simone Des Roches, David C. Fryxell, Rebecca A. Robinson, Zachary T. Wood, Michael T. Kinnison

[University of California, Santa Cruz](#)

Prey behavior is shaped by predators and, in turn, can shape ecological interactions. We investigated the role of evolution and plasticity in shaping the feeding behavior (feeding rate) of mosquitofish under predation threat by largemouth bass. Then, we tested the relative strength of the trophic cascade driven by mosquitofish populations that had evolved in the presence or absence of largemouth bass predators. Results show that evolutionary effects on feeding behavior were stronger than plastic effects. Trophic cascade strength was similar between populations that had evolved with versus without predators; however, cascades were driven by different mechanisms (behaviorally-mediated versus density-mediated) depending on the population's evolutionary history. Thus, the evolution of behavior may shape the dominant mechanism underlying trophic cascades.

“Evolutionary and Ecosystem Ecology: overcoming the two solitudes”

Oswald Schmitz

[Yale University School of Forestry and Environmental Studies.](#)

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The presentation will discuss how adaptive evolutionary thinking can inform ecosystem ecology when you can't directly measure or observe evolution happening. The presentation will focus on using a linked behavioral and physiological functional traits perspective to understand how plasticity and local adaptation can shape species interactions within food webs and drive biogeochemical cycling and ecosystem functioning. The presentation will elaborate on how prey adaptive foraging-predator avoidance trade-off behavior is influenced by prey physiological state and prey population-level ability to respond adaptively to environmental and biotic stressors, as determined by evolutionary history of the population. It will be shown how the nature of population-level prey trait responses determines prey stoichiometric balance and implications for ecosystem nutrient cycling. Understanding such population-level dependency on ecosystem functioning calls for using experimental approaches not normally used in community and ecosystem ecology. This includes especially population-level geographic scale reciprocal transplant experiments to fully understand the evolutionary states of interacting consumers and resources and the implication for resilience of ecosystem functioning in the face of global changes

"Frequency-dependent processes and feedbacks prior to eco-evolutionary dynamics: historical and contemporary perspectives"

Erik Svensson

Department of Biology, Lund University, SE-223 62 Lund, SWEDEN

The increasing growth and popularity of eco-evolutionary dynamics as a research field calls for some reflections about the historical origins of its foundations and the roots of feedbacks between ecological and evolutionary processes. In this talk, I will discuss some of these historical roots which can be found in the empirical traditions of population ecology and density-dependence (e. g. David Lack's work) and in the theoretical ideas of primarily Sewall Wright and Fisher, who were both interested in various frequency-dependent processes and their feedbacks on population growth, genetic composition and evolutionary consequences (e. g. Fisher's Fundamental Theorem, sex ratio evolution, evolution of population mean fitness). Frequency-dependent selection later became popular in the game theoretical tradition of behavioural ecology, but surprisingly its importance and scope has been underestimated in empirical research, beyond its generally accepted role in maintaining genetic polymorphisms within populations. Today, frequency-dependent processes are increasingly being recognized as important also in several other contexts from within-species interactions (e. g. sexual selection, sexual conflict and intraspecific coevolutionary arms races) but also in between-species interactions, co-evolution and community ecology. The frequency-dependent processes operate on genetic polymorphisms within species share many parallels with the similar frequency-dependent processes within local ecological communities that shape species diversity. I will illustrate my talk with various empirical examples from work in my own research lab on the various frequency-dependent processes operating on damselflies (Odonata: Zygoptera) in natural settings.

"Cuckoos, reed warblers, and behavioural drivers of coevolutionary dynamics"

Rose Thorogood (presenter), Edward Klun, Katja Rönkä

HiLIFE Helsinki Institute of Life Science & the Faculty of Biological and Environmental Sciences, University of Helsinki, Finland

Cuckoos and their hosts are a classic example of how we can use field studies to explore the role of behaviour in coevolution, and feature in both behavioural ecology and evolutionary biology textbooks. From over 30 years of work, we now know that behaviour evolves to both defend against cuckoos and outmanoeuvre hosts. As a consequence, behavioural defences in hosts exert selection on behavioural offences in cuckoos, and vice versa. However, here I'll use them as a case study to explore how behaviour of both parties interacts with ecological change to generate plasticity. By comparing how social information use varies across populations, our experiments suggest that behavioural plasticity in reed warbler hosts may shape geographic selection mosaics and therefore drive coevolutionary dynamics. In so doing, I'll argue that eco-evo dynamics are implicit in behavioural ecology (and evolutionary ecology more broadly) whenever we consider how behavioural interactions alter selection environments experienced by others.

Session 5:

"The density dependence of mutualistic interactions"

Christopher Moore and Karen Abbott

Colby College

Mutualism is an interspecific interaction where two or more species reciprocally increase each other's fitness. Contemporary theory on the population ecology of mutualism focuses on how fitness benefits are conferred from a mutualist to a focal population, which depends on the mutualist partner's density (i.e., functional response). This framework implicitly assumes that the benefit received by the focal population is independent of its own density, an unrealistic assumption. In this study we bridge examining intraspecific and interspecific densities to investigate their roles on the population dynamics of mutualism. We created a two-species dynamic model that allowed us to modify both how benefits are received as a function of intraspecific density and how benefits are conferred by a partner as a function of interspecific density. We also synthesized empirical work on mutualism that explicitly took focal or partner densities into account. Our principal finding was that mutualistic benefits either conferred or received at low densities, irrespective of the strength of the mutualistic benefit, resulted in stable coexistence. We also found that very few empirical studies considered population densities, but most show mutualistic benefits being received or conferred most strongly at low or mid densities. Receiving benefits, and consequently increasing growth, at low densities is a key trait for population and community ecology because its central to promoting coexistence, strengthening resilience, etc. As population models act as the foundation of other, more complex models, it is important to ensure that the foundation is soundly based on empirical observation and ecological realism.

“On the Consequences of the Interdependence of Stabilizing and Equalizing Mechanisms”

Chuliang Song, György Barabás, and Serguei Saavedra

[Department of Civil and Environmental Engineering, Massachusetts Institute of Technology](#)

We present an overlooked but important property of modern coexistence theory (MCT), along with two key new results and their consequences. The overlooked property is that stabilizing mechanisms (increasing species' niche differences) and equalizing mechanisms (reducing species' fitness differences) have two distinct sets of meanings within MCT: one in a two-species context and another in a general multispecies context. We demonstrate that the two-species framework is not a special case of the multispecies one, and therefore these two parallel frameworks must be studied independently. Our first result is that, using the two-species framework and mechanistic consumer-resource models, stabilizing and equalizing mechanisms exhibit complex interdependence, such that changing one will simultaneously change the other. Furthermore, the nature and direction of this simultaneous change sensitively depend on model parameters. The second result states that while MCT is often seen as bridging niche and neutral modes of coexistence by building a niche-neutrality continuum, the interdependence between stabilizing and equalizing mechanisms acts to break this continuum under almost any biologically relevant circumstance. We conclude that the complex entanglement of stabilizing and equalizing terms makes their impact on coexistence difficult to understand, but by seeing them as aggregated effects (rather than underlying causes) of coexistence, we may increase our understanding of ecological dynamics.

“Barriers to coexistence restrict the poleward range of a globally-distributed aquatic plant”

David W. Armitage, Stuart E. Jones

[Department of BioSciences, Rice University](#)

Species' poleward ranges are thought to be primarily limited by climatic constraints, rather than by biotic interactions such as competition. However, theory suggests that the negative effects of competition can be amplified as environments harshen. This implies that under certain conditions, interspecific competition near species' range margins can prevent the establishment of populations in otherwise tolerable habitats, leading to truncated realized geographic distributions. We test this

mechanism by using empirically-parameterized competition models to predict the latitudinal range boundaries of two globally-distributed, widely co-occurring, and ecologically-similar aquatic duckweed plants, *Lemna minor* and *Spirodela polyrhiza*. Using a spatially-explicit reciprocal invasion analysis, we identify geographic regions where stable coexistence is predicted to break down. We found evidence that interspecific competition from the resident competitor, *L. minor*, constrains the predicted latitudinal limits of the weaker competitor, *S. polyrhiza*, compared to when *L. minor* is absent. Our mechanistic species distribution model outperformed a widely-used correlative species distribution model in predicting the true distributions and range limits of both species. Finally, a partitioning of model-predicted growth rates into coexistence-promoting mechanisms uncovered a crucial role for relative nonlinearity in competitors' thermal growth curves for coexistence at the range boundary. Our results highlight how accounting for environmental variation, species interactions, and coexistence mechanisms can clarify the factors shaping species' geographic distributions.

“Alternative states and coexistence in the evolution of a competitive community”

Lucas A. Nell, Joseph S. Phillips, Anthony R. Ives

[Department of Integrative Biology, University of Wisconsin, Madison, Wisconsin](#)

Recent studies have shown the usefulness of incorporating trait evolution into models of competition in the context of community assembly. In these and other models, competition is often treated implicitly, as a side-effect of, for example, interactions with external resources. Here, we used a simple community model where members' evolving traits directly affect competition experienced by all members of the community. We evaluated how evolving competition affects outcomes of community assembly, including the conditions under which coexistence occurs and the equilibria at which communities ultimately arrive. Treating competition as an abstraction also allowed us to examine complex patterns relating to community equilibria. We find that coexistence occurs only when evolution is non-conflicting or neutral and that community "saturation" affects the shape of fitness landscapes. Trait non-additive effects influence whether more than one evolutionarily stable community exists, and complex patterns such as alternative stable states and neutrally stable attractor manifolds are possible.

“Coexistence in complex communities: some insights from a three species competition model”

Ravi Ranjan, Thomas Koffel, Christopher A. Klausmeier

[1. Kellogg Biological Station, Michigan State University, 3700 E Gull Lake Dr., Hickory Corners, MI 49060, USA](#)

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Competition is a ubiquitous interaction between organisms that structures communities worldwide. Our current understanding of competition derives mostly from two-species models – either mechanistic or phenomenological. This understanding has led to a lot of progress in understanding coexistence of species in communities. While these insights are fairly robust and hold across more complex communities, some of them break down as communities get more complex. Complex communities, however, are harder to manipulate and study. Thus, it is crucial to understand the ways in which the insights from pairwise competition break down in complex communities and the factors causing this. We address this question by studying a three-species competitive community following the Lotka-Volterra (LV) competition model. We use ideas from the structural approach to coexistence theory to classify the model into 38 different scenarios based on the pairwise niche differences of the species pairs. Further, we use previously known dynamical outcomes of three-species LV competition and correlate them with these scenarios to understand how knowledge about pairwise coexistence translates into predictions

about three-species coexistence. Not surprisingly, if the pairwise niche differences allow pairwise coexistence of all three pairs, coexistence is easiest and can occur in several different dynamic forms. Surprisingly, we found that three species coexistence is possible in a multitude of cases even without pairwise coexistence being possible for all pairs. These results show that scaling up from two-species to more diverse communities may prove challenging.

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“The Evolution of Coexistence in Trinidadian streams”

Ron Bassar

“Consumer sexual dimorphism promotes coexistence among competing resources”

Stephen P. De Lisle, Gonzalo Hernando, Sebastian Schreiber, Daniel I. Bolnick

[University of Connecticut](#)

Within-species variation is a salient feature of natural populations, of substantial importance for species interactions. However, the community consequences of sexual dimorphism, one of the most ubiquitous sources of within-species variance, remains poorly understood. Here, we extend classical models of consumer-resource dynamics to explore the ecological consequences of consumer sexual dimorphism. We show that sexual dimorphism in consumer attack rates on two different resource species promotes coexistence between those resources, mitigating the effects of both apparent competition and direct interspecific competition. Consumer sexual dimorphism can prevent exclusion of a resource with inferior growth rates because reduction in any of the two resources reduces consumer density, generating negative frequency dependence that stabilizes coexistence between resources. Our work highlights ecological sex differences as a potentially key factor governing the assembly of ecological communities, illustrating that the specific source of within-species variance can have important implications for community ecology.

“Coexistence in coevolutionary systems - effects of intraspecific variation”

Athmanathan Senthilnathan

[University of Tennessee, Knoxville](#)

Differences between individuals of a population is a part of the diversity we see in nature. Mechanisms of maintenance of intraspecific variation has been a major focus in evolutionary biology for a long time. Intraspecific variation plays a crucial role in understanding the ecology of different organisms and communities. With dramatic changes to the environment due to climate change and human land-use changes, many species evolve rapidly and intraspecific variation changes along with it. To understand the relevance of these changes, we need a mathematical framework which would capture the ecological consequences of intraspecific variation in the backdrop of the evolutionary processes affecting it. In this study, I develop an eco-evolutionary model of two species with their trait distributions as the state variables allowing for the quantification of the dynamics of variance as well as the means. I use this model to demonstrate the importance of intraspecific variation to two-species interactions, such as (i) competition, (ii) exploiter-victim interactions and (iii) mutualisms. I find that with heritable trait variation, the classical conditions for coexistence in competition and exploiter-victim interaction hold only when stabilizing selection is stronger than intraspecific competition. Exploiter-victim models produce results consistent with earlier adaptive dynamics, multi-locus population genetics, and individual based models. Evolving intraspecific variation could limit the positive feedback due to mutualistic benefits leading to finite population sizes.

“Network topology influences occupancy and abundance in experimental and model metapopulations”

Paulina A. Arancibia & Peter J. Morin

Graduate Program in Ecology & Evolution, Rutgers University

Biodiversity loss due to habitat fragmentation is one of the biggest concerns in ecology. Biological populations are rarely isolated in space and interact with others via migration in metapopulations. Network connectivity patterns can have critical effects on network robustness, as some topologies can promote resilience after perturbations. However, at present, experimental evidence of how these patterns affect population persistence in a metapopulation framework is lacking. In this study, we used the aquatic protist *Paramecium tetraurelia* to determine how network topology influences its regional persistence. We created metapopulations engineered to be comparable in terms of linkage density, but differing in their degree distribution. We compared metapopulations arranged as random networks to power-law networks by evaluating local population persistence and abundance throughout ~30 protist generations. In parallel, we ran simulations to explore differences between topologies. Random metapopulations of *P. tetraurelia* reached higher densities and higher occupancy (proportion of occupied patches) compared to power-law systems in both experimental and simulated systems. The two types of networks also showed opposite patterns of temporal occupancy or “incidence” when related to other node metrics. These contrasting results highlight the fact that node metrics alone are not good predictors of occupancy if topology is not accounted for.

Session 6:

“Can females differentially allocate resources to offspring sired by different males?”

David Reznick and Samantha Levell

Department of Evolution, Ecology and Organismal Biology, University of California Riverside

The Viviparity Driven Conflict Hypothesis posits that females in placental species can exercise post mating choice among males in fertilization success and/or by allocating different amounts of resources to offspring from different males. We test this hypothesis by artificially inseminating females with sperm from males from two populations. Doing so enables us to quantify differential success in the siring of offspring and in the resources mothers allocate to developing offspring. Our experimental species is *Heterandria formosa*, a small, freshwater fish in the family Poeciliidae from the southeastern US that has placental reproduction. We performed reciprocal crosses between fish from populations of *H. formosa* that produced either small (SO) or large (LO) offspring. Offspring size is a measure of post-fertilization provisioning; the LO population allocates more resources to each offspring during development. Prior results from single male-female crosses between these populations revealed reduced viability in crosses between SO females and LO males, presumably as a consequence of the imbalance in how intergenomic conflict is resolved in the two populations. Here we report on the relative success of males in siring offspring, which can be a property of either sperm competition or sperm-egg interactions, and on how resources are allocated to offspring as a function of their genotype.

“Intraspecific life history variation in an introduced plant: effects of climate and herbivory”

Jennifer L. Williams & Sophie Duncan

Department of Geography & Biodiversity Research Centre, University of British Columbia

All organisms must allocate resources to reproduce and survive. The study of intraspecific life history

variation can provide insight into how different selective pressures, such as herbivory or climate, can favor different life history strategies and constrain others depending on which life stages are most vulnerable. We examined how variation in herbivory and climate influence variation in the flowering size of plants and the occurrence of semelparity versus iteroparity in the introduced range of an invasive plant, houndstongue (*Cynoglossum officinale*). Houndstongue is a short-lived semelparous perennial in its native range. In its introduced range, we earlier documented increased rates of iteroparity and a higher threshold flowering size compared to the native range. Here we hypothesized that the recent introduction of a specialist biocontrol root-boring insect (*Mogulones crucifer*) would decrease threshold flowering size, and reduce the proportion of iteroparous plants. We surveyed 24 sites across the northwestern United States to quantify the frequency of semelparity versus iteroparity and to estimate abundance of *M. crucifer*. We found that the proportion of iteroparous plants varied across sites and that those with greater precipitation and no weevils had a higher frequency of iteroparity. With demographic data collected from six sites, we found that threshold flowering size was smaller at sites with a higher attack rate by weevils. The variation in frequency of flowering and threshold flowering size that we observed driven in part by the recent colonization of a specialist insect highlight how quickly life history strategies can shift.

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“Restricted heritability of a polymorphic life history trait between sexes and tactics avoids conflict”

Madilyn Gamble & Ryan Calsbeek

Intralocus sexual conflict arises when a trait has different optima in males and females. Recently, evolutionary biologists have realized that intralocus conflict can exist between morphs or tactics within a sex as well, and that intralocus tactical conflict can constrain tactical dimorphism in the same way intralocus sexual conflict can constrain sexual dimorphism. However, theory regarding how each kind of tactic interacts with the other is lacking, and little work has focused simultaneously on both intralocus sexual and tactical conflict. We use Coho salmon (*Oncorhynchus kisutch*), for which length at maturity is sexually and tactically dimorphic, to ask whether sexual and/or tactical conflict could constrain evolution toward sexual and tactical phenotypic optima. Male Coho exhibit heritable alternative reproductive tactics that differ in age and size at maturity (and consequently degree of sexual dimorphism) and affect reproductive success. We performed selection analysis on length at maturity to test for antagonistic selection between sexes and among tactics, and then calculated phenotypic correlations for length between sexes and among tactics to determine if and where intralocus conflict exists. Selection on length was antagonistic between sexes but not among tactics. Length was heritable between dams and daughters and between the large male tactic and their large morph sons. However, no other intertactical heritabilities were significantly different from zero. Perhaps most intriguingly, the length of small tactic sires was not significantly correlated with that of any of their offspring, regardless of tactic or sex. This suggests that the breakdown of intersexual and intertactical correlations in this system may avoid conflict.

“The influence of microhabitat variation on life cycle expression and population growth in an invasive, clonal sea anemone”

Will H. Ryan and Stacy A. Krueger-Hadfield

[University of Alabama at Birmingham](#)

Understanding environmental predictors of population growth is a key goal of ecology, particularly in

the case of an invasive species. For clonal species, abiotic conditions can also determine the relative contribution of asexual and sexual reproduction to population growth. Patterns of body size, population density, gamete production, and fission rate have all been tied to latitudinal variation in temperature and salinity on a continental scale in the sea anemone *Diadumene lineata*. However, the influence of abiotic variation among sites within latitudinal regions is also critically important for understanding the persistence of the species. We tracked body size, gamete production, and population density across seasons at 12 sites along both sides of the Delmarva peninsula, which divides the Chesapeake Bay from the Atlantic Ocean, that varied dramatically in substrate type, tidal exposure, temperature, and salinity. Site-level environmental variation was predictive of many key population characteristics, including the degree to which individuals engage in gamete production and asexual proliferation. Understanding the connections among environmental variation, population density, and patterns of life cycle expression are important for understanding the eco-evolutionary processes of local adaptation and patterns of genetic diversity arising in species with partially clonal life cycles.

“Developing the Genotype to Phenotype arrow: how conceptualizations of development broaden evolutionary theory”

Emilie Snell-Rood and Sean Ehlman

Dept. Ecology, Evolution and behavior, University of Minnesota

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A key directive in evolutionary biology is to explain the breadth of biological diversity on Earth, and yet most evolutionary theory excels at only predicting microevolutionary change. While the field of ‘evodevo’ has advanced our understanding of mutational variance, evolvability, robustness, and macroevolutionary patterns, our theoretical conceptions of evolution still fail to capture the complexities of development that have yielded such insights. We review recent advances in fields from developmental and molecular biology to artificial intelligence and biomedical engineering that have developed quantitative models that capture diverse features of development. Specifically, we highlight four features of development, a) responsiveness to the environment (plasticity), b) networks of interactions, c) growth and morphogenesis, and d) selection and evolution of developmental environments. Models of evolutionary processes that capture these features of development reveal novel insights relative to simpler models that map phenotypes from genotypes without developmental processes. We discuss the costs and benefits of increasing the level of complexity and realism in evolutionary models that incorporate development. In reviewing this existing toolbox of conceptualizations of development, we strive to provide a way forward in resolving current debates within biology on how to integrate development and evolutionary biology. We conclude by highlighting a range of evolutionary questions – from aging to evolutionary rescue -- that could benefit from incorporating different features of development.

“The effects of maternal and paternal age on the fitness of antler flies in the wild: a field experiment”

Christopher S. Angell and Howard D. Rundle

Department of Biology, University of Ottawa

Growing evidence suggests that age-related declines in survival and performance may be widespread among wild insects, as they are in laboratory populations. However, little is known about whether costs are passed from aging insects to their offspring in nature, as has been reported in vertebrates. Such costs may include increased mortality, decreased reproductive success, or accelerated aging, and could be mediated by a combination of accumulated germline mutations, reduction in provisioning of

offspring, or epigenetic factors. Using the antler fly, an insect species whose high site fidelity makes them well suited to ecological studies of aging, we investigated the fitness consequences of parental age at reproduction. We reared young and old parents of both sexes in the laboratory and mated them in a factorial design. Their offspring were then released in Algonquin Provincial Park, where they were monitored to determine whether parental age influenced their survival, mating success, and aging rates in a natural forest environment.

“Did Mother Know Best? How Spatial Patterns of Emergence by Periodical Cicadas in a Fragmented Landscape Relate to Oviposition Patterns – 17 Years Earlier”

Sarah E. Anderson, Robert H. Hagen, Robert D. Holt (presenter), Jin Yao, William M. Cook

How an organism experiences the environment is governed by its life history and movement, which modulate how environmental variability influences fitness. At locations across much of eastern North America, broods of the iconic periodical cicada *Magicicada* emerge in massive numbers every 13 or 17 years. Adult females have a brief few weeks to sample their landscape as they mate, oviposit, and die, after which their offspring live attached to woody plant roots, until the next emergence. How accurately do a female’s oviposition choices predict the long-term survival and fitness of its offspring? We examined this in a long-term fragmentation experiment in eastern Kansas, where the last half century has seen three emergences. In 1981, a dramatic emergence occurred in a woodland, but not in an adjacent agricultural field – which harbored no woody plants (required for oviposition and underground feeding). In 1984, a fragmented landscape was superimposed on that field; patches differing in size and distance from the woodland were created (maintained by mowing the interstitial matrix). By the 1998 emergence, rapid succession towards woody vegetation in the patches provided abundant woody hosts suitable for cicada colonization via short-distance flight -- with strong patch size and distance effects on oviposition. This talk will report how spatial patterns in the 2015 emergence corresponded (or not) to the spatial pattern of oviposition, 17 years earlier. Our results shed light on the conceptual issue of understanding maladaptation in long-lived organisms, and more broadly illustrate the importance of long-term experiments in ecology.

“Linking the effects of density dependence on individuals and populations”

Jessie Mutz

[Department of Biological Science, Florida State University](#)

Linking species interactions that occur among individuals with patterns of population-level change is critical to understanding the sensitivity of populations to changes in the biotic community and the contribution of particular interactions to fitness. For example, interaction outcomes often depend on density at small spatial scales (e.g., the scale at which predators perceive or respond to prey density), and density at these scales can vary substantially within a population. While theory shows that such variance in density can affect population growth and carrying capacity, we lack examples of how the spatial scale and ontogenetic context of density dependence affect the scaling process.

I built a stage-density structured population model for the leaf beetle, *Leptinotarsa juncta*, and estimated parameters using data from field experiments. I used these models to investigate (1) consequences of small-scale density dependence for population dynamics and spatial structure, (2) selection on density-related life history traits (e.g., clutch size and movement) within a full demographic context, and (3) how these results depend on the spatial scale at which density is defined.

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I analyzed the stage-density models using *L. juncta* density on a single plant or within a multi-plant patch. In the plant-scale model, equilibrium density was most sensitive to density-dependent survival of early-instar larvae and predicted density distributions closely matched observational data. Selection on clutch size was much stronger than selection on among-plant movement. In contrast, the patch-scale model showed strongly cyclic dynamics.

Together these results demonstrate the importance of spatial scale in mediating the effects of local density dependence on population-level outcomes and, more generally, of addressing biological aspects of any scaling process.

“Mating system impacts the genetic architecture of adaptation to heterogeneous environments”

Kathryn Hodgins and Sam Yeaman

[Monash University](#)

Self-fertilization has consequences for variation across the genome as it reduces effective population size, effect recombination rates and pollen flow, with implications for local adaptation. We conducted simulations of divergent stabilizing selection on a quantitative trait with drift, pollen flow, mutation, recombination and different outcrossing rates. We quantified trait divergence and the genetic architecture of adaptation. We conducted an FST outlier analysis to identify candidate loci and quantified the impact of mating system on detectability. Selfing promoted trait divergence mainly through reductions in pollen flow. Moreover, trait architecture became more diffuse with selfing. Average effect size of trait loci was lower, while the number of loci, and their clustering distance increased. The genetic architecture of selfers was also more diffuse than outcrossers for equivalent migration rates. However, when deleterious alleles were included, architectures became more concentrated in selfers, likely because of reductions in population size caused by mutational meltdown and impacts of background selection on N_e . Our simulations demonstrate that mating system has important impacts on adaptive divergence of traits and the genetic landscape underlying that divergence. Selfing has a significant effect on detectability of regions of the genome important for adaptation because of neutral divergence and diffuse trait architecture.

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Session 7:

“Stranger things: the chloroplast genome edition”

[David R. Smith](#)

I have always been intrigued by and attracted to strange genomes, genomes that break all the rules and leave researchers scratching their heads. It is no surprise, then, that I have devoted my career as a researcher to exploring organelle genomes, many of which seem to show no bounds in their propensity for peculiar and noncanonical characteristics. The past five years, in particular, have been exciting times for studying unusual organelle DNAs, especially those of chloroplasts. Recent high-profile studies have uncovered some of the most interesting chloroplast DNAs on record, including ones with massive or miniature sizes, unprecedented conformations, such as single-stranded hairpins, and other surprising features, including outright genome loss. Here, I look closely at the varying extremes in chloroplast genomic architecture, with a particular focus on those from the Chlamydomonadales, comparing them to other types of genomes, and discuss how these data are changing our understanding of organelle genome evolution.

Both theoretical and empirical work has highlighted the role of hybridization in introducing genetic variation that can facilitate evolutionary radiations. The ‘Lake Victoria Region Superflock’ (LVRS) provides an important example for ancient hybridization between distinct lineages consistent with the ‘hybrid swarm’ model of diversification. Here, we use whole-genome re-sequencing data from 78 individuals to estimate phylogenomic relationships and to characterize patterns of historical introgression between the Upper Nile, Congo and LVRS cichlids, focusing primarily on the Lake Kivu radiation. We find evidence for a minimum of 3 introgression events between the Upper Nile and LVRS lineages. We show that Upper Nile admixture varies extensively across the genome in LVRS species and is especially elevated in regions with higher recombination rates and regions of low gene density, consistent with widespread selection against introgression. This complex history of admixture has generated extensive phylogenomic discordance across the genome regarding the relationships between the Upper Nile, Congo and LVRS lineages, and we employ a suite of analyses to distinguish the true historical branching order for these clades. Our results suggest the history of admixture within the LVRS radiation is more complex than previously recognized, and highlight that while hybridization may provide key genetic variation that spurs diversification, it can simultaneously lead to an overall pattern of strong negative selection against hybrid ancestry.

“Genetic architecture underlying evolution in a fossil stickleback lineage”

Yoel E. Stuart, Matthew E. Travis, and Michael A. Bell.*

**Department of Biology, Loyola University Chicago*

Microevolutionary process and macroevolutionary pattern have been poorly integrated because it is difficult to observe population-level mechanisms acting across evolutionary time. Here, we address this problem by inferring the genetic architecture of phenotypic evolution in a well-preserved fossil lineage of a Miocene stickleback fish (*Gasterosteus doryssus*). We do so by comparing observed pelvic reduction across ~18,000 years of the fossil sequence to known relationships between pelvic reduction and genetic architecture in the extant, closely-related Threespine Stickleback (*G. aculeatus*). We find that reduction in pelvic score, a categorical measure of pelvic structure, followed a multi-modal pattern in *G. doryssus*. This suggests a single Mendelian gene of large effect. Reduction was also asymmetric and left-biased. These patterns together implicate the action of *Pitx1*, a gene whose deletion generates similar pelvic reduction in *G. aculeatus*. Additionally, continuous traits like pelvic girdle length and pelvic spine length reduced independently of pelvic score in *G. doryssus*, suggesting a suite of minor-effect genes also contributing to pelvic reduction. Such genes for pelvic reduction are known in *G. aculeatus*. Thus, it appears that similar genetic architectures explain shared macroevolutionary patterns across 10 million years of stickleback evolution.

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“Global adaptation confounds the search for local adaptation”

Tom R. Booker, Samuel Yeaman, Michael C. Whitlock

University of British Columbia

Spatially varying selection promotes variance in allele frequencies, increasing genetic differentiation between the demes of a metapopulation. For that reason, outliers in the genome wide distribution of summary statistics measuring genetic differentiation, such as F_{ST} , are often interpreted as evidence for alleles which contribute to local adaptation. However, in spatially structured populations, the spread of beneficial mutations with spatially uniform effects can also induce transient genetic differentiation and numerous theoretical studies have suggested that species-wide, or global, adaptation makes a substantial contribution to molecular evolution. In this study, we ask whether such global adaptation affects the genome-wide distribution of F_{ST} and generates statistical outliers which could be mistaken

for local adaptation. Using forward-in-time population genetic simulations assuming parameters for the rate and strength of beneficial mutations similar to those that have been estimated for natural populations, we show the spread of globally beneficial in parapatric populations can readily generate FST outliers, which may be misinterpreted as evidence for local adaptation. The spread of beneficial mutations causes selective sweeps at flanking sites, so the effects of global versus local adaptation may be distinguished by examining patterns of nucleotide diversity along with FST. Our study suggests that global adaptation should be considered in the interpretation of genome-scan results and the design of future studies aimed at understanding the genetic basis of local adaptation.

“Fitness maps to a known large-effect locus in introduced stickleback populations”

D. Schluter, K. B. Marchinko, M. E. Arnegard, H. Zhang, S. D. Brady, F. C. Jones, M.A. Bell, and D. M. Kingsley

University of British Columbia

Beneficial mutations with large fitness effects are expected to contribute to adaptation under certain conditions. Genes and genomic regions with large effects on phenotypes are known, but their fitness effect sizes in natural populations have rarely been estimated. We mapped fitness over a generation in a marine x freshwater stickleback cross introduced to a freshwater pond. Number of surviving offspring per female mapped to a single, large-effect locus near the Ectodysplasin (Eda) gene, which is known to have an ancient freshwater allele causing reduced bony armor. Females homozygous for the freshwater allele had twice the number of surviving F3 offspring as homozygotes for the marine allele, producing a large selection coefficient on the locus, $s = 0.50 \pm 0.09$ SE. This contributed to an increase in the frequency of the freshwater allele from 0.50 in mothers to 0.58 in surviving offspring. We compared these results to observed allele frequency changes at the same gene in an Alaskan lake population colonized by marine stickleback in the 1980's. The frequency of the freshwater Eda allele rose steadily over multiple generations and reached 95% within 20 years, yielding a similar estimate of selection, $s = 0.49 \pm 0.05$. These findings are consistent with other studies suggesting strong selection on this gene (and/or linked genes) in fresh water. Selection on ancient genetic variants carried by colonizing ancestors is likely to increase the prevalence of large-effect fitness variants in adaptive evolution.

“Genetics of coevolution between tapeworms and threespine stickleback”

Jesse N. Weber, Natalie C. Steinel, Foen Peng, Kum Chuan, Shim, Daniel I. Bolnick

Dept of Biological Sciences, University of Alaska Anchorage

Coevolutionary processes can influence how the prevalence and intensity of parasite infections vary over space and time. However, the genetic basis of most traits related to host-parasite interactions is unknown. This makes it difficult to determine whether infection variation is due to ecological, evolutionary, or stochastic factors. The Weber Lab explores the evolutionary genetics of host-parasite interactions using stickleback fishes and stickleback tapeworms. In particular, our experiments show that marine sticklebacks are ancestrally susceptible to tapeworms, but when lineages of fish colonize freshwater they evolve distinct forms of parasite resistance or tolerance. Moreover, tapeworms seem to respond by countering the resistance of their local hosts, leading to host-specialized lineages of parasites. These heritable differences in both species seem to explain much natural infection variation. I will present recent genomic data that we have gathered to identify the molecular basis of tapeworm resistance by stickleback. I will also describe our landscape-level approach to understanding how patterns of gene flow between tapeworm populations influences coevolutionary outcomes.

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“Host genomics and blood parasite infections across an elevational contact zone between chickadees”

Angela Theodosopoulos, Kathryn Grabenstein, Scott Taylor

Blood parasites are known to infect a diverse number of bird species. Advances in genomic tools have shown that there are significantly more strains of avian blood parasites than previously thought. Studies of blood parasites in the Rocky Mountains have shown there to be multiple strains of parasite that can infect a single avian host. However, few studies have examined the role that contact between two closely related host species, and host hybridization, may play in the presence and diversity of blood parasite infections. I will present research on blood parasite infections in two species of chickadee captured in regions where their ranges overlap and hybridization may occur, across a 2000m elevation gradient. My work will explore the role that host immune gene heterozygosity may play in blood parasite infections, in addition to characterizing blood parasite strains found in both chickadee species.

“Climate adaptation across space and time in a migratory songbird”

Rachael Bay, Daniel Karp, Jasmine Rajbhandary, Kristen Ruegg, Tom Smith

Negative effects of anthropogenic climate change on biodiversity have led to an increased interest and urgency to understand mechanisms of adaptation to local climate conditions. For migratory species, investigating local adaptation is particularly complicated as selection pressures might drastically differ across different stages. We previously identified genomic signals for selection associated with climate gradients on the North American breeding grounds for the neotropical migratory bird, Yellow warbler. We now use genetic markers to examine migratory connectivity between breeding and wintering grounds, testing whether birds tend to migrate to regions with similar climate regimes. Additionally, we examine the potential for climate change-induced shifts in allele frequencies by genotyping historical specimens collected on the breeding range over the past century. Together, this information provides a more complete picture of local adaptation and the capacity for evolutionary response to climate change in this migratory species.

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“Assortative mating by genomic regions involved in plumage coloration in a rapid avian radiation”

Sheela P. Turbek, Melanie Browne, Adrián S. Di Giacomo, Cecilia Kopuchian, Scott Taylor, Rebecca Safran, Leonardo Campagna

Ecology and Evolutionary Biology, University of Colorado, Boulder, CO USA

Post-zygotic isolation often takes longer to evolve than the time to speciation of many taxa, and pre-mating isolation has therefore been proposed as a powerful reproductive barrier maintaining sympatric species early in divergence. However, the ease with which assortative mating can break down has called into question the importance of pre-mating isolation during incipient speciation. We combined whole-genome and double digest restriction-site associated DNA (ddRAD) data with fine-scale behavioral analyses from two years of detailed field study to quantify assortative mating between two sympatric species of capuchino seedeaters (*Sporophila hypoxantha* and *Sporophila iberensis*). Capuchino seedeaters comprise a recent, rapid avian radiation characterized by striking differences in male plumage coloration and song despite remarkably little ecological or genomic divergence. We found that the two species exhibit an extremely low level of background differentiation (genome-wide $F_{st} = 0.006$) that is punctuated by three narrow regions of elevated genomic divergence. These peaks, ranging from 5-50 kb long, encompass 11 genes, two of which are known to be involved in the regulation of

coloration. Though *S. hypoxantha* and *S. iberaensis* lack temporal or spatial barriers to reproduction, and the rate of extra-pair paternity was extremely high, we documented complete assortative mating with regard to both social and extra-pair mates by the genomic regions that underlie differences in male plumage patterning. Given that females of the two species are phenotypically indistinguishable, our findings provide strong evidence that pre-mating isolation related to male sexual signaling may be sufficient to maintain species boundaries extremely early in divergence.

Session 8:

“When to protect: Evolution of microbe-mediated protection in *C. elegans*”

Anke Kloock, Michael Bosall, Kayla King

Department of Zoology, University of Oxford

Microbes living with hosts can protect them against pathogen infection. Although microbes can have great evolutionary potential, the conditions under which they might evolve to protect their host remain elusive. It is hypothesized that a high risk of infection favours the evolution of protective traits by microbes, but infection is often temporally heterogeneous in nature (e.g., seasonality). We thus tested the effect of temporal heterogeneity in infection on the evolution of microbe-mediated protection. We experimentally coevolved protective microbes, *Enterococcus faecalis*, with populations of *Caenorhabditis elegans* nematode hosts, in treatments varying the infection frequency with pathogenic *Staphylococcus aureus*. Temporal heterogeneity involved pathogen exposure every host generation, alternating host generations, every fifth host generation or never, and we additionally investigated the effect of initial pathogen presence. Our results show that microbe-mediated protection evolved in those sympatric host-*E. faecalis* associations that were exposed to the pathogen *S. aureus* in the evolution experiment, while neither the interval of pathogen exposure nor initial pathogen exposure conditions had an effect. No fitness costs could be detected for the evolution of this microbe-mediated detection. Overall, our results indicate, that pathogen presence is required to drive the evolution of microbe-mediated protection. The results from this study illuminate the relationship between temporal variation in pathogen infection and selection for host-protection by an organism’s resident microbiota.

“Evaluating evolutionary responses to an invasive predator by resurrecting decades old populations of *Daphnia*”

Matthew R. Walsh and J. Alex Landy

University of Texas at Arlington

The role that environmentally-induced phenotypic plasticity plays in adaptive evolution has been debated for decades. Does plasticity shield genotypes from selection following a novel shift in the environment and, in turn, impede adaptation? Or does phenotypic plasticity accelerate the rate at which populations attain new fitness peaks and thereby facilitate adaptation? Multiple lakes in Wisconsin were recently invaded by a novel invertebrate predator (spiny waterflea). Comparisons across contemporary populations show that invasion by spiny waterfleas is associated with rapid evolution of *Daphnia* prey. Here we tracked evolutionary shifts in trait values and trait plasticity by resurrecting historic propagules of *Daphnia* over the past three decades. We hatched multiple species of *Daphnia* from three replicate lakes and reared all clones in the presence and absence of spiny waterflea chemical cues to assess temporal changes in life history and behavioral plasticity. Our preliminary results revealed a rapid loss of plasticity as *Daphnia* adapted to invasion by a novel predator.

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“Evolutionary rescue in small populations”

Dale Clement

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As anthropogenic changes accelerate and species continue to go extinct, the need to understand of why some species are able to respond to environmental change while other fail to respond has become increasingly urgent. Evolution is an important component of this response, and there are a growing number of studies demonstrating that if a species can evolve rapidly enough, it may recover from otherwise inevitable extinction. While our theoretical understanding of this phenomenon, known as evolutionary rescue, is developing rapidly, few studies have examined how a population behaves during the critical phase when it is no longer declining, but remains small and vulnerable to extinction. Predicting extinction in small populations is inherently fraught because not only are evolutionary and demographic dynamics increasingly subject to random chance as population size declines to zero, but evolution and demography also become highly coupled. Population size influences the efficacy of selection through genetic drift and inbreeding, while evolutionary fitness governs the survival and reproduction of individuals. This complex, stochastic interaction makes it challenging to predict the combined effect of genetic drift, inbreeding, and demographic stochasticity on evolutionary rescue. In order to better understand how these three processes interact to determine population fate and extinction risk, I use a mix of mathematical and simulation-based models to partition the effects of demographic stochasticity, evolutionary stochasticity, and their interactions on the demographic and evolutionary dynamics of small populations.

“Rapid adaptation to an extreme drought cycle in *Mimulus cardinalis*”

Daniel N. Anstett¹, Haley Branch¹ & Amy Angert¹⁻²

¹ Department of Botany, Biodiversity Research Centre, University of British Columbia, Canada

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Plant populations are under increasing pressure to adapt to extreme variation in precipitation. Though rapid evolution is known to occur, its effectiveness at tracking drought cycles has not been assessed across the entire geographic range of a species. Here we study rapid evolution in *Mimulus cardinalis* to a record-breaking drought and subsequent reversal in California and Southern Oregon. From 2010 to 2016, we collected mature fruits from 12 populations throughout the range of the plant throughout the drought cycle. We carry out a greenhouse experiment, where we grow all collected genotypes in drought and well-watered conditions. Drought adaptation is assessed at each site/year combination by measuring flowering time, leaf water content, stomatal conductance, carbon assimilation, biomass and the plasticity of these traits. We describe the impacts of the drought cycle and its variability within sites on multivariate trait evolution. We then associate these adaptations with demographic changes in all 12 populations throughout the drought cycle. This work represents one of the largest tests of rapid evolutionary effects across the range of a single organism with implications for the long-term survival of these populations to current and future droughts.

“Minimizing the evolution of antibiotic resistance using optimal scheduling”

Jeremy Van Cleve, Quiyana M. Murphy, David Murrugarra

University of Kentucky

Persistent use of common antibiotics has led to the evolution of resistant pathogen strains that are difficult to treat. Evolutionary and ecological theory has provided important insights into how some antibiotic treatment strategies may actually promote the evolution of resistance. Specifically, theory suggests that cycling between different antibiotics, rather than applying multiple antibiotics at once, can

more rapidly lead to the evolution of highly resistant strains. Given empirical data that suggests cycling can be clinically effective, it remains unclear under what scenarios cycling is most effective. In this work, we combine empirical data on *E. coli* growth rates in 15 different beta-lactam antibiotics with population genetic and stochastic control theory to determine optimal antibiotic treatment strategies. We show that antibiotic cycling can minimize total microbial growth rates only when antibiotics can be switched any time a new more resistant strain invades. A single antibiotic is the optimal treatment strategy when antibiotics cannot be switched rapidly. Moreover, we find that the best cycling strategy, which produces the lowest total microbial growth rate, is limited by the lowest local fitness peak among the 15 antibiotic. This work suggests important limits on the effectiveness of antibiotic cycling and provides a quantitative framework for determining the optimal schedule of antibiotics given an empirical fitness landscape for resistance.

“Experimental evolution results in rapid adaptation of rhizobia to their local legume host”

R. T. Batstone, T. L. Harrison, A. M. O’Brien, & Megan E. Frederickson

[Carl Woese Institute for Genomic Biology, University of Illinois at Champaign-Urbana, Urbana, IL, 61801, USA](#)

[Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, ON, M5S 3B2, Canada](#)

Biotic interactions among species are major drivers of adaptive evolution. While antagonistic interactions often result in coevolutionary arms races that generate an extensive amount of genetic variation in traits underlying the interaction, mutualisms are predicted to result in evolutionary stasis, as traits converge on an optimal value for both partners. Yet, genetic variation in mutualistic traits is extensive in nature, calling into question the mechanisms that govern (co)adaptation in mutualisms. Here, we combined an evolution experiment, a manipulative cross-inoculation experiment, and whole-genome sequencing, to test whether nitrogen fixing bacteria (i.e., rhizobia) adapt to their legume hosts, and if so, what genetic mechanisms underlie such adaptation. Even though we initially inoculated all plants with two strains of rhizobia, one strain quickly went extinct from all treatments, while the other evolved novel isolates that differed in their benefit to hosts within five plant generations. We found that rhizobia can rapidly adapt to their local host, and that genetic variants (single nucleotide polymorphisms, indels) associated with local adaptation were mostly limited to genes involved in transcriptional regulation, as well as plasmid and metabolite transfer. What emerges from our results is a new model of adaptation in mutualisms: partners can rapidly adapt to a particular host by evolving *de novo* mutations that are often neutral or deleterious on non-local host genotypes, generating variation in mutualistic traits observed in nature.

“Evolution in a community context with *Sarracenia purpurea* protozoa”

Thomas Miller, Olivia Mason, Abigail Pastore, Catalina Cuellar-Gempeler, and Erin Canter

[Department of Biological Science, Florida State University](#)

Niche theory remains the basis for our expectations about evolution driven by species interactions. Yet the niche is an over-simplistic concept, and there are very few experimental studies of evolution in communities where indirect effects and diffuse interactions may complicate our understanding of evolution. We conducted selection experiments by growing 4 species of protozoa in monocultures and the four species mixture, as well as all pairwise combinations in *Sarracenia purpurea* leaves, then comparing growth characteristics before and after selection. Simultaneously, we used iTag sequencing to quantify the use, and evolution of use, of bacterial resources in these combinations. There are significant differences in resources use by different protozoa, with subordinate species appearing to evolve more rapidly in response to competition than do dominant competitors and evolution occurring

more slowly in multispecies mixtures than in pairs. These results have implications for community diversity, as rare species will be more likely to evolve to persist, but diversity itself may slow evolution.

“Rapid sexual signal loss and maintenance of a heritable reproductive polymorphism in crickets”

Justa Heinen-Kay and Marlene Zuk

Dept. of Ecology, Evolution and behavior; University of Minnesota

Diversification of sexual communication is constrained by the need for continued coordination between the signaler and receiver. One way this can occur is if signal expression and preference are pleiotropically controlled by a single gene, but evidence supporting this hypothesis is limited. We used the case of rapid signal loss in the Pacific field cricket, *Teleogryllus oceanicus*, to investigate the role of genetic coupling during sexual signal evolution. Many males on the Hawaiian Island of Kauai have rapidly lost the ability to sing. The silencing mutation, flatwing, is favored by natural selection because it provides protection against a deadly acoustically-orienting parasitoid fly. We discovered an association between the locus underlying male silence and female likelihood of mating, but not in a direction that favors the evolution of signal loss. Flatwing-homozygous females were more discriminating than wild-type females and exhibited a lower rate of mating, particularly in the absence of courtship song. Females of both genotypes were more likely to mate in the presence of courtship song, and showed a preference for wild-type males. While our results do not support a role for genetic coupling during the evolution of signal loss in *T. oceanicus*, they do help explain why flatwing has not gone to fixation. We have demonstrated that a genetic association between obligate male silence and female mating behavior can constrain the evolution of sexual signal loss and contribute to the maintenance of a male reproductive polymorphism.

“Selective pressures on phenotypic traits change over the course of a single flowering season”

Laura C. Leventhal, Karen J. Bai, Madeline A.E. Peters, Emily J. Austen, Arthur E. Weis, Jennifer L. Ison.

University of California Davis, College of Wooster

Over the course of a flowering season, plants mate repeatedly as they open and close successive flowers. This raises the possibility that selection—i.e., the covariance between phenotype and mating success—is stronger during some time intervals but weaker at others. However, few studies have observed pressures and therefore, selection, changing within a breeding season. Our study examines the changing strength and direction of selection on three phenological traits in the annual self-incompatible, *Brassica rapa*, at eight different time intervals within a single flowering season. A novel field manipulation in which potential dams were moved in and out of experimental plots at certain points in time enabled us to examine the genepool over discrete time intervals. To gain insight on how small-scale spatial distribution impacted pollen movement, we aggregated donors into dense clusters in two plots, but uniformly distributed in the others. We genotyped 860 pollen donors, 287 dams, and 2064 offspring at ten microsatellite loci and used a full probability maximum likelihood framework to calculate donor siring success, and thus selection via male fitness. We evaluated the strength and direction of selection via selection gradients on start date, total number of flowers, and duration of flowering. We calculated pairwise spatial distance between father-offspring pairs. We found directional selection via male fitness towards a late start date late in the season and directional selection towards more total flowers and longer duration of flowering during peak and late season. Finally, we found that pollen moved farther in aggregated spatial plots than in even spatial plots. Together, our research provides a novel method for

evaluating within season selection and provides insight into the presence and effects of spatial and temporal structures.

Session 9:

“Macroevolutionary assembly of the endemic Hawaiian insect fauna”

David Hembry (presenting author) and Patrick O'Grady

Department of Entomology, Cornell University

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The Hawaiian Archipelago is the most remote island group on the planet, located 3,200 km from the nearest continent. This isolation has allowed a few colonizing species to evolve into an impressive biota, with over 1000 species of plants and an estimated 10,000 species of insects, roughly 90% of which are thought to be endemic. The endemic Hawaiian biota has inspired many classic studies in speciation, phylogenetic biogeography, and the links between clade diversification and community assembly. Here, using a dataset of recent molecular phylogenetic studies of endemic Hawaiian insect radiations, we revisit many central questions in the evolution of the Hawaiian biota. First, we show that few radiations perfectly mirror the geological formation of the islands (known as the “progression rule”) as has long been hypothesized. The progression rule hypothesis may have less utility for Hawaiian biogeography than has been previously assumed. Second, we show that a substantial fraction of the Hawaiian insect biota may have colonized the archipelago before the formation of the current suite of high islands beginning c. 5 Ma, in contrast to the conclusions of previous studies. Since many insect clades may be older than the current high islands but most endemic plant clades are younger than the same islands, this suggests that insect and plant macroevolution may be partially decoupled in Hawai'i. Finally, we find no evidence for an clade age-species richness relationship in the Hawaiian insect fauna, although two of the oldest insect radiations are also the most species-rich today.

“Rewinding the tape of biogeography in a macroevolutionary simulation of the island progression pattern”

Jesse Czekanski-Moir

State University of New York College of Environmental Science and Forestry

Department of Environmental and Forest Biology

Many taxa in hot-spot archipelagos (e.g., Hawaii) exhibit phylogeographic patterns that are concordant with island age. The oldest islands contain the earliest-branching taxa, and younger islands in the archipelago have younger clades that are paraphyletic or reciprocally monophyletic with respect to the assemblages on the older islands. This pattern is usefully true as an approximation for many taxa, but there are also many exceptions. How replicable should we expect geographic patterns of diversity to be? I discuss this question in the context of a spatially explicit macroevolutionary simulation of speciation within a four-island "archipelago" with “islands” emerging at different points throughout the simulation. By varying different parameters, including dispersal ability, the age of each island, and the importance of competitive exclusion, I explore the conditions that seem most conducive to the emergence of a more rule-like island progression pattern. Notably, there are many simulation runs that had similar parameters that result in very different outcomes in terms of the overall diversity of the system, underscoring the potential for very different outcomes in diversification patterns in the absence of meaningful biological differences.

“The contribution of temperature and continental fragmentation to amphibian diversification”

Jonathan Rolland & Fabien L. Condamine

Department of Zoology, University of British Columbia, Vancouver, British Columbia, Canada

Abiotic factors such as global temperature or continental fragmentation may favour speciation through the ecological and geographical isolation of lineages. Here, we propose to use biogeographical estimations and palaeoenvironmental diversification models to estimate whether and how palaeotemperature and the sequential break-ups of Pangaea, Gondwana and Laurasia have affected the diversification of amphibians through time. Using a time-calibrated phylogeny for 3,309 amphibian species and a genus-level fossil record, we estimated the diversification rates of the group with birth–death models allowing rates to depend on the temporal variations of the environment or continental fragmentation. We also estimated the biogeographical history based on a time-stratified parametric model informed by the global palaeogeography. The diversification analyses on the whole amphibians showed that temperature-dependent models are better supported than tectonic-dependent, time-dependent and constant-rate models for both the fossil and phylogenetic data. The best-fitting temperature-dependent model indicated a positive dependence of both speciation and extinction rates with the temperature through time. Biogeographical analyses indicated a Pangaeian origin for amphibians and also showed that allopatric speciation (vicariance) explained important phases of the evolution of geographical ranges in the Mesozoic. Our results support that palaeotemperatures have positively impacted amphibian diversification. Our study provides additional insights into how to quantify the effect of the landmass fragmentation on the diversification processes and shows with biogeographical reconstruction that continental fragmentation is linked to allopatric speciation in the early history of the clade.

“Repeated speciation by adaptation in sympatric lineages of extremophile fishes”

Ryan Greenway, Anthony P. Brown, Henry Camarillo, Cassie Delich, Kerry L. McGowan, Lenin Arias-Rodriguez, Joanna L. Kelley, and Michael Tobler

Division of Biology, Kansas State University; Department of Fish Ecology and Evolution, Swiss Federal Institute of Aquatic Science and Technology

Divergent selection along ecological gradients can lead to speciation with gene flow, but it remains unclear whether the same mechanisms underlie this phenomenon when multiple evolutionary lineages are exposed to the same selective regimes. We analyzed evolutionary responses in three species of poeciliid fishes occurring in sympatry in an extremely toxic, hydrogen sulfide (H₂S)-rich spring and an adjacent freshwater stream. Despite different demographic histories in each population pair and extremely small spatial scales, we found strong genetic differentiation between populations in sulfidic and non-sulfidic habitats. In addition, analyses of morphology, physiology, and genome-wide patterns of gene expression and molecular evolution indicated clear patterns of convergent evolution across species, with evidence for modification of mitochondrial processes associated with H₂S toxicity and detoxification. These results suggest that adaptation to local environmental conditions drives the emergence of reproductive isolation in this system, which was corroborated experimentally by documenting strong selection against migrants between habitat types. Contrary to predictions of speciation theory, however, analyses of genome-wide patterns of divergence neither revealed evidence for clear genomic islands of speciation or congruence of outlier regions across population pairs. Instead, consistently high levels of divergence across the genome suggest the rapid evolution of high levels of reproductive isolation. Overall, our results demonstrate evidence for the repeated evolution of adaptation and reproductive isolation in sympatric lineages exposed to the same source of divergent selection.

“Do strong biotic interactions lead to faster evolutionary divergence in the tropics? Case studies from our feathered friends”

Benjamin Freeman, Joseph Tobias and Dolph Schluter

[University of British Columbia](#)

The “biotic interactions” hypothesis proposes that stronger interspecific interactions in the tropics drive faster evolution and ultimately speciation, explaining in part why there are so many more species in the tropics. At present there is an active debate about whether rates of biotic interactions are indeed highest in the tropics, but data on latitudinal rates of divergence in traits linked to biotic interactions is scant. Here we present two analyses to begin to fill this gap. First, we investigate a canonical example of a strong tropical biotic interaction - nest predation - and show that daily rates of nest survival experienced by land birds vary minimally with latitude. We attempt to explain this surprising result by invoking adaptation, and suggest that adaptation to latitudinal differences in species interactions may potentially flatten latitudinal gradients in interaction rates. Second, we analyze rates of beak divergence at a global scale, and show that beak evolution is fastest in the temperate zone. We conclude with a general call to measure both latitudinal patterns in interaction strength and evolutionary responses to these interactions.

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SYMPOSIUM 2

“Nectar microbes may exacerbate the impact of climate-induced phenological shifts on pollination”

Tadashi Fukami, Zhiyuan Song, Rachel L. Vannette, Manpreet K. Dhani

[Stanford University](#)

Climate change can negatively affect pollination when it causes a phenological mismatch between plants and pollinators, but factors affecting the extent of this effect remain unclear. Here we argue that one overlooked factor is the microorganisms, including bacteria and yeasts, that colonize floral nectar. We highlight three observations: bacteria rely less on pollinators than yeasts for flower-to-flower dispersal; microbial communities in nectar are dominated by either bacteria or yeasts, and rarely both, owing to priority effects; and once dominance is established, bacteria, but not yeasts, discourage pollinators from visiting flowers. Based on these observations, we develop a mathematical model of nectar microbial community assembly. Numerical simulation of this model shows that bacteria benefit from an earlier onset of flowering relative to pollinators, which in turn exerts a long-lasting influence on plant-pollinator interactions, reducing pollination to a greater extent than normally expected, especially if the activity of the associated pollinators is also seasonal. Our analysis suggests that many of the observed shifts in flowering phenology that have been attributed to climate change are large enough to have caused substantial reduction in pollination via nectar microbes. This study points to the importance of microbial mediation of plant-animal interactions for understanding ecological consequences of climate change.

“Host-symbiont interactions through the lens of stochastic demography: variance buffering as a form of mutualism”

Tom E.X. Miller (presenting), Joshua C. Fowler, Kenneth D. Whitney, Jennifer A. Rudgers

[Rice University](#)

Microbial symbioses are widespread in nature and notoriously context-dependent, spanning a continuum from mutualism to parasitism depending on environmental conditions. Most symbioses are subject to temporal fluctuations in environmental conditions, and this is increasingly the case under

global climate change. This context-dependency means that symbionts may be most beneficial to hosts in harsh years but neutral or even costly in benign years. Therefore, in the long term, symbiosis with microbes may reduce demographic variance in the host. This talk will explore the hypothesis that symbiotic microbes function as mutualists by reducing variability, even if their fitness effects are neutral, on average. Our work leverages a long-term field experiment in which plant populations were established with or without vertically transmitted fungal symbionts, replicated across seven host-symbiont pairs. We built population projections models based on 10 years of data and decomposed the overall fitness effect of symbiosis into contributions from the means and temporal variances of multiple demographic rates integrated across the life cycle. We show that variance buffering is a critical element of host-symbiont mutualism, but one that cannot be detected with short-term studies. Considering interaction outcome as a random variable opens up new ways of thinking about context-dependency in ecology.

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“Do microbes matter? Combining demographic modeling and experimental approaches to understand the role of soil microbes for persistence of imperiled plant species.”

Michelle Afkhami, Aaron David, Pedro Quintana-Ascencio, Eric Menges, Khum B. Thapa-Magar, and Christopher Searcy

University of Miami

Microbes are increasingly recognized as ubiquitous, hidden players that can dramatically affect the functioning of plants and animals. Despite how commonly microbes influence individual-level plant fitness, our understanding of whether these effects scale up to impact host population growth rates and persistence comes predominantly from studies of tightly coevolved, mutualistic fungi or studies that largely do not consider vital rates. Research investigating how diverse soil microbial communities affect plant population dynamics is therefore urgently needed to advance our understanding of how microbes influence plant species distributions and ultimately their persistence. Here, we use an integrative approach combining multidecadal data, manipulative experiments, and integral projection modeling to quantify 1) the effect microbes have on 12 plant species from the imperiled Florida scrub ecosystem and 2) the role of these microbial effects play in maintaining populations of the endangered plant *Hypericum cumulicola* or contributing to their decline. Our experiments documented significant effects of microbes on plant vital rates across the all species, and our demographic models found that the microbiome boosted population growth rates of *H. cumulicola* by 13% on average, the difference between population growth versus decline in 76% of patches. The greatest benefit (47% increase in λ) occurred in low nutrient habitats, suggesting that the soil microbiome may help expand *H. cumulicola*'s distribution to include these stressful habitats. Overall, our results illustrate the importance of considering interactions with diverse soil microbial communities for understanding plant population dynamics and making informed conservation decisions for threatened species.

“The direct effects of a non-native allelopathic invader on fungal community composition and native plant population dynamics”

Lalasia Bialic-Murphy, Stephanie Kivlin, Nathan L. Brouwer, and Susan Kalisz

Department of Ecology and Evolutionary Biology, University of Tennessee Knoxville, Knoxville, Tennessee, USA.

A primary trait common to the worst exotic invaders is the production of allelochemicals, which can

inhibit spore germination of beneficial arbuscular mycorrhizal (AM) fungi. An unanswered question in invasion biology is to what extent such invaders affect native plants population dynamics, which commonly rely on root-fungal mutualisms for soil resource acquisition (i.e. nutrients and water). We present a novel approach drawing on network theory and innovative demographic models to shed light on processes underpinning shifts in native plant fitness following perturbations in complex plant-fungal integrations. Using six years of demographic data in a size-dependent integral projection model, we show that the allelochemical-producing invader, *Alliaria petiolata*, can directly and negatively influence the population growth rate of a native understory perennial. In additional experiments, we find that *Alliaria* invasion results in hyper-diversity of AM fungi and higher photosynthetic rate relative to *Alliaria* removal plots, counter to expectations. However, enhanced photosynthetic rate does not increase plant growth. We find that *Alliaria* invasion alters the bipartite network structure of root-fungal interactions and increases turnover of the fungal community in native plant roots. Together, these results suggest that mutualism disruption of root-fungal networks leads to reduced plant discrimination of fungal partners and an imbalance in carbon allocation and nutrient acquisition.

“How interactions and scale regulate species diversity in spatially-variable environments”

William K. Petry

[Princeton University](#)

“Monsoon disturbance of rhizosphere microbiomes +consequences for reproductive plant traits”

Jonathan Dickey

[Department of Ecology and Evolutionary Biology, University of Tennessee Knoxville](#)

While often overlooked, diffuse trophic interactions among plants and their soil microbiomes can have large effects on aboveground plant traits as they regulate nutrients for plant uptake. For example, variation in bacterial richness within soil surrounding the roots (i.e., rhizosphere) can have selective effects on photosynthetic biomass. However, the extent of microbial selection on floral traits and phenology is currently unknown. Host specific microbial composition is dynamic and can be dependent on environmental and biotic interactions. Therefore, the first step to understand the outcome of varying microbial selection on floral traits is to examine how annual changes in the abiotic environment affect the structure of rhizosphere microbial communities. Linking environmentally mediated shifts in microbial composition to changes in floral traits will give realistic insight on variation in plant fitness and how mutualisms respond to multiple selective agents. *Lupinus neomexicanus*, a native to the Sky Islands, provides a unique system for plant-microbiome studies due to an elongated flowering state and large fleshy root system. Here I address the following questions: How does microbial community structure associated with the plant rhizosphere correlate with plant phenology, reproductive traits, and relative fitness? Does the intensity of seasonal monsoonal rainfall alter community structure of plant rhizospheres and contribute to variation in phenological shifts and plant fitness? By examining *L. neomexicanus* at different developmental stages (n=35 each), I will address how variation in rhizosphere microbial structure covaries with phenology, variation in floral abundance, and seed pod development. To directly test to what extent rhizospheric microbial structure changes due to monsoon events, I removed monsoon disturbance on a subset of plants by adding rainout shelters as protection. Abundance and diversity of soil microbiota will be quantified through bacterial 16S rRNA and AMF 18S sequencing using the Illumina MiSeq workflow. I predict that rhizosphere microbiomes with more diverse communities favoring nitrogen fixation will lead to a quicker response in flowering time of plants disturbed by heavy rainfall. Accordingly, plants that receive fewer resources from the rhizosphere

microbiome will have fewer flowers, diminished corollas, and higher reproductive cost. Linking environmentally and biotically mediated shifts in microbial composition to changes in floral traits will help give realistic insight on variation in plant fitness and how plant soil feedback loops are further reinforced.

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“Generalized interactions promote coexistence of plant species that vary in seed size”

J.L. Maron, K.L. Hajek, P.G. Hahn. and D.E. Pearson

Maron, Hajek, Hahn: University of Montana

Pearson: U.S. Forest Service

Understanding the mechanisms enabling coexistence and the traits through which these mechanisms operate has been a pivotal challenge for ecologists. We examined the role of bunchgrass competition and seed predation by mice in equalizing fitness differences among 17 co-occurring perennial forb species that varied in seed size. Seeds of focal species were added to plots where interactions were manipulated at 9 grassland sites across a productivity gradient. Three years after seed addition, the abundance of small-seeded species was lower in the presence versus absence of bunchgrass whereas the abundance of large-seeded species was lower in the presence versus absence of mice. Experimentally assembled communities exposed to interactions (i.e. bunchgrass competition and seed predation) had mean trait values indicative of a more resource acquisitive strategy compared to community trait values in plots with no interactions. In the presence of interactions, resource acquisitive traits increased with increasing site productivity, but not in the absence of interactions. Whereas variation in fecundity among species predicted final abundance without interactions, in the presence of interactions, species abundances were more equalized, and fecundity did not predict abundance. These results indicate that generalized interactions can equalize fitness differences among species, influencing community trait values and promoting coexistence.

“Impacts of early snowmelt and level of pollen limitation on population dynamics of a subalpine plant”

Diane R. Campbell

Department of Ecology and Evolutionary Biology, University of California, Irvine, CA, USA, and Rocky Mountain Biological Laboratory, Crested Butte, CO, USA

Climate change could impact the dynamics of a plant population by changing abiotic conditions or by influencing interactions with other organisms, such as animal pollinators. These processes are poorly understood, as few plant studies have measured response of vital rates to abiotic or biotic variables and modeled the impact on population growth. I used 25 years of demographic data to analyze how survival, growth, and fecundity respond to date of spring snow melt for the subalpine plant *Ipomopsis aggregata*. Integral projection models predicted that earlier snowmelt with warming will lead to negative population growth within 2 to 4 decades, driven especially by reduced seedling establishment and reduced seed production. Those population impacts are likely due to low soil moisture, a hypothesis now under experimental test. Seed production is also limited by low pollen transfer, primarily by hummingbirds, although extent of pollen limitation is not strongly associated with snowmelt date. Incorporating 7 years of data from supplemental pollinations into the models suggests that reduced pollination impacts population growth to a similar extent as a 1 to 2 week difference in snowmelt. These results illustrate the potential for strong population impacts of environmental change, even in the absence of more commonly reported visual signs, like changes in floral display.

Session 10:

“Eco-evolutionary dynamics of trait variances”

Daniel Bolnick (1), Denon Start (2, 3)

(1) Ecology and Evolutionary Biology, University of Connecticut

(2) Center for Population Biology, University of California at Davis

(3) Previous address: Ecology and Evolutionary Biology, University of Toronto

Species interactions generate selection on traits that modulate those interactions. As a result, ecological dynamics can drive rapid evolutionary change that feeds back to change ecology. Such 'eco-evolutionary dynamics' appear to be widespread, and can serve an important role in stabilizing species coexistence. The literature on eco-evolutionary dynamics has focused heavily on changes in trait means in response to directional selection. Yet, ecological interactions can also drive stabilizing or disruptive selection, or even higher-moment shapes (e.g., asymmetric selection), which should act to change trait variances. These variances, in turn, can have profound effects on ecological dynamics. In principle, therefore, eco-evolutionary dynamics could proceed via shifts in trait variances, that may be overlooked by studies tracking trait means. In this talk, we synthesize theory and data to argue that trait variances are also subject to eco-evolutionary dynamics that warrant more attention.

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“The Joint Consequences of Ecological and Evolutionary Stochasticity”

Denon Start, Arthur Weis, Benjamin Gilbert

Department of Ecology & Evolutionary Biology at the University of Toronto, and the Center for Population Biology at UC Davis.

The distribution of biodiversity depends on the combined and interactive effects of ecological and evolutionary processes. The joint contribution of these processes has focused almost exclusively on deterministic effects, even though mechanisms that increase the importance of random ecological processes are expected to also increase the importance of random evolutionary processes. We explore these ideas using a series of experiments in a gall forming fly and its enemies, and mathematical models. Traits and communities were more variable in smaller patches. However, because of the preference of some enemies for some trait values (gall sizes), random variation in population mean trait values exacerbated differences in community composition. The random distribution of traits and interactions created predictable but highly variable patterns of natural selection. In a separate study, we show that seemingly random enemy loss can also drive changes in mean directional selection, demography, and local adaptation. Our work highlights how stochastic processes can affect ecological and evolutionary processes structuring the strength and direction of selection locally and at larger scales.

“The evolution of competitive ability”

Jawad Sakarchi and Rachel Germain*

The University of British Columbia

Competition is a driving force for evolutionary change across taxa but our understanding of how competitive differences among species drive the evolution of interspecific interactions remains incomplete. Verbal models assume that interspecific competition selects for weaker interspecific responses (α_{ij}) of each species to the other. However, these models ignore the potential for other

demographic components of competitive ability to evolve: interspecific effects (α_{ji}), intraspecific interactions (α_{ii}), and intrinsic growth rates (λ_i). Here, I test two hypotheses: that (a) α_{ij} , α_{ji} , α_{ii} , and λ_i can evolve in response to interspecific competition, and (b) the evolution of each is constrained by a trade-off. I tested these hypotheses by competing 31 population pairs of annual grasses that occur in California. I competed sympatric and allopatric lineages of *Vulpia microstachys* to their dominant invader--*Bromus hordeaceus*--which have potentially coevolved in the field for ~200 years. Our preliminary results for *Vulpia* reveal both λ_i and α_{ii} are greater in sympatry ($p = 0.06$, $p = 0.18$ respectively). Surprisingly, we found no evidence that α_{ji} differed between histories. Further, we find λ_i is positively correlated to both α_{ij} ($R^2 = 0.68$, $p < 0.01$) and α_{ii} ($p < 0.01$) in sympatry. Our data suggests that the evolution of increased interspecific competitive ability (λ_i , α_{ij}) of the inferior species comes at the cost of increased intraspecific competition (α_{ii}). Overall, I show the complexity that which demographic components evolve to interspecific competition, resulting in distinct ecological consequences (eg. population persistence, size).

“The overriding dampening effect of evolution on nature”

M.C. Urban, F. Pelletier, S.M. Carlson, S.Y. Strauss, E.P. Palkovacs, L. De Meester, A.L. Angert, M.A. Leibold, A.P. Hendry, S.T. Giery

Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT.

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Historically, many biologists assumed that evolution and ecology acted independently because evolution occurred over distances too great to influence most ecological patterns. Today, evidence indicates that evolution can operate over a range of spatial scales, including fine spatial scales, and frequently interacts with the mechanisms that determine spatial ecological patterns. We synthesize recent insights and develop a predictive framework that highlights how 14 mechanisms mediate if evolution amplifies, dampens, or creates ecological patterns. Most often, evolution dampens environmental gradients, thus obscuring the underlying heterogeneity in nature. We highlight the need for future research to inform a fully integrated and predictive biology that accounts for eco-evolutionary interactions in both time and space.

“Evolution in ecological communities: complex interspecific interactions underlie adaptation”

Rachel Germain

The University of British Columbia

Natural populations are embedded in diverse ecological communities, but despite the potential to have dramatic effects on individual fitness, it is unknown if and how interactions with community members evolve. Most hypotheses are based on tests of a small number of pairs of competitors under lab conditions, and predict a weakening of competitive interactions through co-evolution. Evolutionary outcomes, however, are likely more complex in multispecies communities because evolution of species interactions may not be evenly distributed among all community members, and the presence of other species might affect the interaction strengths among any given species pair. To test the evolution of interaction strengths in natural communities, we performed common garden experiments with *Bromus hordeaceus* in grassland communities in Northern California. In doing so, we fit multi-species competition models to our fitness data, estimating interaction strengths between our focal *B. hordeaceus* populations and each of seven common species in the neighbourhood. We found that interaction strengths with the local *B. hordeaceus* population evolved with two of seven neighbourhood species, increasing competition with one and decreasing it with the other. Fitness of local populations decreased when neighbours were removed, causing local maladaptation, whereas all populations

performed equally when neighbours were left intact. Together, our results demonstrate how species interactions evolve to determine fitness in complex communities, providing a richer view of adaptation in natural systems.

“Evolutionary Insights from Endemic Predation: Linking Daphnia Evolution to Stickleback Phenotypes in Alaskan Lake Ecosystems.”

Michelle Packer, Matthew R. Walsh

University of Texas at Arlington

Predation is known to elicit phenotypic plasticity, such as inducible defenses, shifts in traits and behavioral changes in multiple species. Studies suggest that prey express predator-specific responses, however, it is unclear if morphological differences, such as those represented by predator ecotypes, impact the evolution of their prey (but see Palkovacs and Post 2009). Lakes in Alaska contain divergent populations of ‘benthic’ and ‘limnetic’ populations of predatory fish (Threespine Stickleback, *Gasterosteus aculeatus*). ‘Benthic’ sticklebacks, are classified by deep bodies and heads, with few/short gill rakers, that allow for efficient foraging on benthic invertebrates, while ‘limnetic’ sticklebacks have shallow bodies/heads, and many/long gill rakers, which are specific for foraging on pelagic zooplankton.

Predation by these distinct morphs of stickleback presents the opportunity for divergent predatory selection on their prey, Daphnia. To test this, Daphnia were collected from three lakes containing each morph. We measured divergence in life-history traits and plastic responses to fish predation cues to determine if phenotypic variation among stickleback has driven evolutionary divergence in Daphnia. Daphnia are primarily pelagic, thus predatory selection should be stronger on populations that experience predation from limnetic sticklebacks, and should therefore evolve earlier maturation, increased reproductive effort and a smaller size.

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“Intrapopulation variation in the brown anole: are species-rich communities composed of more diverse populations?”

Sean T. Giery

Department of Biology, The Pennsylvania State University, University Park, PA 16802

Interest in speciation with gene flow has fueled a desire to understand the behavioral and ecological mechanisms that reduce gene flow within diversified populations subject to divergent selection. How phenotypically diversified populations arise is, however, less well understood. The prevailing model of adaptive ecological diversification generally includes some version of ecological release. Essentially, the model predicts increased population size, expanded population niche width, and higher interindividual variation when a population exploits an ecological opportunity-usually relaxed interspecific interactions. Here, I evaluate the latter two predictions with range-wide patterns of resource use in the brown anole, *Anolis sagrei*. Specifically, I address whether population niche width (PNW) is inversely correlated with species richness, and whether intrapopulation niche variation (NV) decreases with species richness. Our results do not match the ecological release paradigm: PNW expands with community richness, and individuals are more generalized and less similar in species rich communities. But while the pattern of intrapopulation variation emerging from our data is clear, the eco-evolutionary underpinning is not. I’ll briefly discuss alternative models of adaptive diversification, but without additional analyses and experimental tests, I can only speculate as to the eco-evolutionary mechanism(s) underlying the observed pattern.

“When do factors promoting genetic diversity also promote population persistence?”

Sebastian J. Schreiber

Department of Evolution and Ecology, University of California, Davis

Classical stochastic demography predicts that environmental stochasticity reduces population growth rates and, thereby, can increase extinction risk. In contrast, J.H. Gillespie demonstrated that environmental stochasticity can promote genetic diversity. Extending Gillespie's diploid model to account for demography, I examine the simultaneous effects of environmental stochasticity on genetic diversity and population persistence. Consistent with Gillespie's analysis, if the log-fitness function is concave and allelic responses to the environment are not perfectly correlated, then genetic diversity is maintained. This diversity is maintained through a genetic storage effect. If the log-fitness function is convex, then all alleles but one are eventually lost. In particular, alleles at higher frequency are more likely to be the last allele left standing. Unlike its effect on the frequency of rare alleles, concavity of the log-fitness function negatively impacts population growth. Moreover, allelic diversity, via a form of genetic bet-hedging, increases the population's per-capita growth rate despite decreasing the per-capita growth rate of rare alleles. Collectively, these results (i) highlight how mechanisms promoting population persistence may be at odds with mechanisms promoting genetic diversity, and (ii) provide conditions under which population persistence relies on existing standing genetic variation.

“Genetic variation influences the strength and direction of neighbor effects on fitness”

Lauren Carley, Jackson Snow, Allison Carter, Tom Mitchell-Olds

Duke University Program in Ecology

Understanding the factors that influence whether neighbors increase fitness via facilitation or decrease fitness via competition is a critical component in gaining a mechanistic understanding of species coexistence in communities. Classic theory predicts that environmental stress should inform whether neighbor interactions result in net benefits or costs. Although often invoked, this prediction is broad and fails to consider how individual trait variation and its underlying genetic variation influence the outcomes of these ecological interactions with neighbors. We performed common garden studies and manipulative field experiments using the ecological model species *Boechera stricta* (Brassicaceae) to investigate the role of genetic variation, trait variation, and environmental stress in determining whether the density of heterospecific neighbors conferred facilitative or competitive effects on focal plants. By growing >300 *B. stricta* genotypes in a common garden environment, we found significant genetic variation in the relationship between heterospecific neighbor density and reproductive output. Furthermore, these interactions varied among years, suggesting that environmental variation modifies the impact of genotype on the level of competition or facilitation experienced. To tease apart effects of microclimate and naturally occurring neighbor density, which may be correlated, we also manipulated the density of a heterospecific neighbor in potted *B. stricta* transplants of the same genotypes. Here, one genotype experienced greater competition from neighbors, while the other benefited from neighbor density, possibly due to associational defenses. Together, these results provide mixed evidence for the general applicability of the stress gradient hypothesis in predicting the magnitude and direction of species interactions, and emphasize the contributions of genetic and trait variation, in addition to environmental conditions, to ecological outcomes among close neighbors.

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Session 11:

“Prediction and localized control of extreme events in spatiotemporal systems”

Bethany Johnson, Steve Munch

University of California, Santa Cruz

Extreme events are ubiquitous in complex systems. Ecological extremes, such as pest outbreaks and harmful algal blooms often have severe impacts on their surrounding environment. Despite nearly a century of research efforts to forecast and mitigate these events, effective control remains a challenge. This stems, in part, from incomplete knowledge of the mechanisms that drive extreme events. Empirical dynamic modeling (EDM) approaches may be used to circumvent structural uncertainty but have not been applied to controlling extreme events in ecology. Here we extend EDM to spatially extended systems and apply this approach to predicting outbreaks in a simulated host-parasitoid system. Using EDM predictions, localized control rules effectively suppress future outbreaks. Our results provide a management framework that has potential to decrease environmental impacts of management and reduce losses resulting from ecological extremes.

“Evaluating how human land disturbances influence species barriers at continent-wide and regional scales”

Grabenstein, K.C., Burg, T. M., Otter, K. A., Taylor, S. A.

The University of Colorado, Boulder

Determining how species boundaries are maintained is critical for conserving biodiversity and understanding speciation. Hybridization following anthropogenic habitat disturbances (e.g., urbanization) has been detected globally in both terrestrial and aquatic species, and highlights the break-down of species barriers. However, while we have numerous records of the occurrence of disturbance-mediated hybridization, we lack information on the mechanisms by which disturbance breaks species barriers in most cases. Black-capped (*Poecile atricapillus*) and mountain (*P. gambeli*) chickadees are non-migratory birds that, despite broad range overlap, appear to hybridize predominantly in disturbed areas (e.g. logging sites or urban centers), including Colorado’s Front Range. Using whole genome data from chickadees in Colorado, paired with reduced representation sequencing of a broader and larger set of samples spanning the majority of range overlap between mountain and black-capped chickadees, we are comparing patterns of human-mediated habitat disturbances with hybridization rates. This allows me to assess if disturbance is driving hybridization. Assessing the conditions that correlate with broken species boundaries between black-capped and mountain chickadees will provide insight into the barriers that may be important for reproductive isolation. Characterizing how human-altered landscapes change species interactions will expand our understanding of the mechanisms by which anthropogenic changes promote hybridization in a rapidly changing world.

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“No evidence of wide-spread agricultural death trap for a species rich community of neotropical birds.”

Leithen K. M’Gonigle, Luke O. Frishkoff, Chase D. Mendenhall

Simon Fraser University (LKM), University of Texas, Arlington (LOF), Carnegie Museum of Natural History (CDM)

Rapid environmental change as a result of human activity can reduce habitat quality while leaving in tact cues that wildlife use to identify suitable habitat. This decoupling of quality habitat from cues leads to what has been called an “ecological trap”; individuals preferentially occupy patches where fecundity is lower and/or mortality is higher. There are few published studies of ecological traps, making their prevalence difficult to assess. Here, we utilize a long-term data-set of bird captures and recaptures in

the countryside of Costa Rica to ask how species in a diverse community in the tropics respond to agricultural landscapes in terms of both habitat affinities and habitat-dependent mortality rates. To address this goal we first test the hypothesis that mortality rates in agriculture are greater than in natural forest, a necessary condition if agriculture is creating an ecological trap. We then identify which species traits correlate with higher or lower rates of mortality and ask whether those traits are affiliated with occupancy in natural versus anthropogenic habitats, thereby helping identify species-level drivers of population dynamics and community structure in landscapes that represent an ever-growing fraction of the planet.

“Coupling fisheries and climate change in the food-web dynamic of an intertidal rocky-shore South Pacific food-web.”

M.I. Ávila-Thieme, A. Pérez-Matus, S.A. Navarrete, F.S. Valdovinos, P.A. Marquet*
[Ecology Doctoral Program of Pontificia Universidad Católica de Chile.](#)

Fisheries are threatening marine biodiversity, but global warming might worsen their adverse effects due to an expected reduction in the global biomass of the most basal species of food-webs, plankton. We use an allometric trophic network model to analyze the independent and combined effects of small-scale artisanal fisheries and climate change on the dynamic of an empirical intertidal rocky-shore food web of the Central Coast of Chile. We simulate the food-web dynamic under different exploitation rates (fisheries impact) and depleting the plankton subsidy biomass (climate change impacts). We simulate each perturbation separately (independent effect) and also, we coupled them in one single simulation (combined effects). At the end of the simulations, we quantify the species biomass change between before and after perturbation. Both perturbations were propagated through the entire food-web. After fishing, all harvested species decrease their biomass while mostly all non-harvested species grow. Harvested macroalgae were vulnerable to very low exploitation rates. After depleting plankton subsidy, the biomass of filter-feeders, carnivores, and top predators strongly decreased while the biomass of omnivores, herbivores, and macroalgae increased weakly. Fisheries and climate change together, intensified the independent effects more than their simple additive effects, especially in harvested species.

“Local adaptation and maladaptation entwined in roadside amphibians”

Steven P. Brady

[Biology Department, Southern Connecticut State University](#)

Roads can mediate natural selection and other evolutionary forces, modifying trait distributions and fitness in road-adjacent populations. I investigated local population responses to roads in two species of pool-breeding amphibians—the wood frog (*Rana sylvatica*) and spotted salamander (*Ambystoma maculatum*). Local population responses to road proximity varied considerably between these two species. Whereas spotted salamanders showed clear evidence for local adaptation to roads, wood frogs in these same habitats showed mixed effects. Compared to populations away from roads, aquatic-staged wood frogs from roadside populations survived and developed at lower rates and accrued more malformations, while adults showed high rates of edema (presumably induced by road salt). However, adult wood frogs from roadside populations also showed increased locomotor performance and fecundity, and these populations tended to be older than those away from roads. We lack comprehensive estimates of fitness for these populations and are unable to resolve these contrasting outcomes. Thus, whether or not roadside wood frogs are locally maladapted or adapted remains to be determined.

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Regardless of exact outcomes and mechanisms, roadside amphibian populations are clearly differentiated from neighboring populations located away from roads.

“Failure to shift phenology may be associated with local extinction”

Meredith A. Zettlemoyer

Kellogg Biological Station, Michigan State University

Phenology is a harbinger of climate change, with many species advancing flowering in response to rising temperatures. However, there is tremendous variation among species in phenological response to warming, with native species demonstrating limited ability to track rising temperatures and adjust flowering time under global warming. Prior work at a few well-studied sites suggests that these non-responding species may be more susceptible to population declines. However, whether a failure to shift phenology in response to global change is linked to extinction events remains to be seen. We used herbarium records from across the Midwestern US to examine how the flowering phenology of 9 confamilial pairs of locally extinct and non-extinct native species once found in Michigan prairies has shifted over the last 155 years (ca. 1860-2015) and in response to temperature over this time period. Locally extinct species tended to flower earlier than non-extinct species ($\chi^2=0.56$, $p<0.0001$). However, non-extinct species flowered earlier while locally extinct species flowered later at warmer monthly temperatures (status \times temperature $\chi^2=47.18$, $p<0.0001$). These results support the hypothesis that the inability to shift flowering phenology may influence population declines, but also suggest that locally extinct species may have shifted their phenologies in the wrong direction predicted under climate warming. This study potentially implicates phenology as a mechanism underlying local extinction events.

“Spatio-temporal shifts to maintain climatic niche in *Bombus*”

Olga Koppel and Dr. Jeremy T. Kerr

University of Ottawa

Unprecedented floral and faunal declines over the past two decades have been attributed to rapid global climate change. Bee populations are shrinking across North America and Europe as a result of these climate shifts. Species' survival is threatened when shifting climate pushes them beyond their tolerable environmental conditions. Changes in distribution and phenology are observed in the direction of global warming patterns, but some species fail to respond at the rate of climate change. To reliably assess extinction risks posed for different *Bombus* species, it is important to understand the interactions between their climate change responses. In this talk, I discuss how distribution and phenology shifts interact to alter *Bombus* species' persistence. I investigate whether phenological change may compensate for range loss and negative environmental effects for certain *Bombus* species. Clarifying these spatial and temporal shift patterns of *Bombus* species will be vital in improving predictions of their climate change responses.

“The interacting effects of climate change and urbanization on Threespine Stickleback evolution”

Simone Des Roches, Michael A Bell, Marina Alberti, Eric P Palkovacs

Urban Ecology Research Lab , Department of Urban Design and Planning, University of Washington

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Both climate change and urbanization can shape spatial and temporal variation within species. Still, few studies have investigated how potential interactions between these two drivers affect contemporary adaptive trait change. We resurveyed populations of Threespine Stickleback sampled from Californian

estuaries in the last 40-100 years. Previous research demonstrated that stickleback lateral plate number, a defensive, streamlining trait with substantial genetic and environmental associations, declined with decreasing latitude and precipitation. Plate number is linked to a single Mendelian-inherited gene (“EDA”). The derived “low plated” phenotype, associated with two copies of the “low” EDA allele, often evolves rapidly in lentic (“lake-like”) habitats where plates hinder manoeuvrability in densely-vegetated, slow-moving water. We provide evidence that the low EDA allele may be increasingly selected for in estuaries that have become more lentic with decreased precipitation and streamflow. This habitat transformation is likely responsible for increases in low-plated stickleback over time and with decreasing latitude. Stickleback from estuaries surrounded by extensive urbanization, however, highlight a notable exception: plate number has increased in estuaries that have undergone significant hydromodification – including the channelization and dredging that tend to increase streamflow and reduce biological habitat complexity. Variation in stickleback plate phenotype and genotype, therefore, may reflect divergent selection in estuary habitats that are transforming under urbanization versus climate change.

“The Future Keepers: Assessing Effects Of Thermal Stress And Resource Limitation On Ants”

Nigel R Andrew (University Of New England, Australia),

Sarah J Hill (University Of New England, Australia),

Nate Sanders (University Of Vermont, United States),

Rob Dunn (North Carolina State University, United States),

Alan Andersen (Charles Darwin University, Australia)

Across Australia, different regions have experienced climatic changes to varying degrees, both seasonally and annually. One of the most fundamental issues is how our biota will respond to rapid changes in climate. Changes in population abundances, modified via changing behaviour, physiology or competition for food resources, could cause major population restructuring of currently common species, leading to the collapse of trophic interactions and depletion of ecosystem function. AIMS: To predict how key species (ants) that provide core ecosystem functions may change under thermal stress and resource limitation. QUESTION 1: What influence does differential resource limitation have on ant food preference and biological traits along biogeographical gradients? QUESTION 2: Does differential resource limitation change ant foraging along the gradients under increased temperatures? QUESTION 3: How do physiological traits of ants collected from more arid zones of Australia compared with more coastal populations. PREDICTIONS: More ants found on salt diet up to 100km from coastal areas, but not further inland. Ant foraging strategies may change along gradients and with seasonal changes. In chambers – more ants attracted to salt food sources. In extreme temperature sites – summer thermophilic taxa will be more active in the chambers. Sites with greater seasonal variation, will see a bigger change in nutritional preferences. CTmax and thermolimit responses will not change along transects. CONCLUSION: Understanding how ants respond to temperature and moisture changes will help determine the impact of climate change on ecosystem engineers: answers to the questions posed here will address this.

Session 12:

“The stability of plant functional diversity following disturbance”

Leila Z. Forsyth and Benjamin Gilbert

Species of the same trophic level are hypothesized to competitively exclude one-another when functionally similar and co-occur when functionally distinct. Dominant species are predicted to have key

traits closest to an abiotic optimum, while species farther from the optimum persist in lower abundance. This provides explicit predictions for the mean and variance of trait distributions based solely on biotic interactions but lacks predictions for the stability of communities following disturbance, which can significantly alter the diversity of a system.

In 2018, we manipulated the mean and/or variance of a key functional trait (specific leaf area; SLA) in 56 plant communities by removing 20% biomass across four treatments. Within one growing season, both the trait means and variances responded to our perturbations, but their rates of return differed and varied among treatments. Communities that had both trait tails removed (a decrease in trait variation) met with the strongest increase in variation this season, whereas communities with removal of a single tail responded with no increase or even a decrease in trait variation. Trait means showed a different pattern, with loss of high SLA species causing an increase in SLA in response, whereas all others decreased. Overall, these results suggest that the stability of trait distributions (means and variances) depends not just on the magnitude of the perturbation, but also its directionality. Thus, disturbances may differently impact not only the diversity and stability of a community, but potentially the range of functional strategies and the biotic interactions they govern.

“Elevation shapes the reassembly of Anthropocene lizard communities”

Luke O. Frishkoff, Eveling Gabot, George Sandler, Cristian Marte, and D. Luke Mahler
[University of Texas at Arlington](#)

Human impacts, especially land-use change, are precipitating biodiversity loss. Yet anthropogenic drivers are layered atop natural biogeographic gradients. We ask whether the effects of anthropogenic habitat conversion depend on climatic context. We studied the structure of *Anolis* lizard communities in intact and human-modified habitats across natural climate gradients in the northern Dominican Republic. Using community-wide mark–resight methods to control for detection bias, we show that the effects of habitat conversion reverse with elevation (and thus macroclimate temperature). Deforestation reduces abundance and biomass in lowland communities but has no such effect at high elevations. In contrast, forest loss results in no compositional change in the lowlands, but complete community turnover between habitats in the highlands. These contrasting community-level patterns emerge from consistent responses of individual species based on their thermal niches. Community reorganization in the highlands stems from thermal niche tracking and habitat switching by abundant lowland species. We find no support for the hypothesis that climate generalists outperform specialists to succeed in anthropogenic habitats. Instead, warm-climate specialists dominate anthropogenic habitats, even in cool macroclimates. Human impacts interact with pre-existing environmental gradients to reorganize biodiversity. Leveraging a biogeographic perspective will provide insight into the future communities of life on Earth.

“A conceptual framework for predicting combined non-consumptive effects of multiple predators on individuals, populations, and communities”

William J. Resetarits, Jr.
[Department of Biology, University of Mississippi](#)

The world is a dangerous place, and running the gauntlet of predators is a critical time and energy consuming occupation, as all species are vulnerable to one or, typically, more predators at some life stage. Animals use a vast array of mechanisms to avoid predation, from morphological adaptations for speed, weaponry, camouflage, or distastefulness, to behavioral mechanisms of reduced activity, flocking, temporal activity shifts, and habitat use patterns. Predators, likewise, come in a bewildering

variety of shapes, sizes, offensive weaponry, hunting behaviors, sensory abilities, etc., and defensive adaptations are rarely one size fits all. A large body of work has addressed multiple predator consumptive effects, but predators can also generate non-consumptive effects (NCEs) that equal or exceed consumptive effects on prey individuals, populations, and by extension, communities. NCEs can be manifested as behavioral, phenotypic, or life history responses, and may be driven by stress responses, or by evolved or learned behavioral algorithms that function outside the stress complex. As a result each type of non-consumptive effect generates its own set of complexities for predicting the combined effects of multiple predators. Thus, while consumptive effects are straightforwardly quantified and compared by determining survival rates in the presence of individual and combined predator species, non-consumptive effects pose a more complex version of this problem. Here I present relevant experimental data and attempt to provide a conceptual framework for exploring the role of the non-consumptive effects of multiple predators on prey individuals and populations, and how that may affect the assembly and dynamics of communities.

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“Ecological communities are formed by probable combinations of competing species”
Lucas P. Medeiros, Karina Boege, Ek del-Val, Alejandro Zaldivar-Riverón and Serguei Saavedra
[Massachusetts Institute of Technology, Department of Civil and Environmental Engineering](#)

Despite the rich biodiversity found in nature, it is unclear the extent to which some combinations of competing species while conceivable in a given place and time may never be realized. Yet, solving this problem is important in order to understand the role of randomness and predictability in ecology. Following a structural approach, we show that observed combinations of competing species forming ecological communities have a probability of persistence higher than the expected probability associated with potential combinations that could be formed from a regional species pool. Additionally, we show that this bias in the probability of persistence is associated with observed combinations having a lower average competition strength than potential combinations. We validate our theoretical results using a 10-year observational study recording 88 plant-mediated competition communities of herbivores across three different successional stages. Our findings suggest that observed combinations of species are among the most probable outcomes of community dynamics under changing environments.

“Equation-free predictions of noisy, stochastic, and nonstationary ecological dynamics.”
Stephan B Munch
[UC Santa Cruz, EEB and NOAA Fisheries](#)

The complex dynamics of ecosystems are governed by the interactions of many species and the environment. The available ecosystem data are rarely complete; there are almost always species, traits, and other variables that are unobserved or left out of our models for other reasons. Rigorously specifying the interactions among all components is a difficult task. These ‘structural uncertainties’ are the primary impediments to practical ecosystem forecasting. Empirical dynamic modeling (EDM) approaches, in principle, allow us to circumvent structural uncertainty using lags to account for hidden states and nonparametric methods to recover the dynamics from the observed time series. However, EDM typically assumes noise-free data from stationary deterministic systems. Here, I describe several extensions to the EDM toolkit that explicitly handle noisy observations from stochastic, nonstationary systems.

“Ecosystem-based management using Empirical Dynamic Programming”

Antoine Brias, Steve Munch

UCSC

Conceptually, ecosystem management allows us to balance conservation and management goals across competing objectives. However, ecosystem models are often strongly sensitive to assumptions about species interactions, making it difficult to assess the robustness of conservation and management plans that depend on them. To circumvent this problem, we present the Empirical Dynamic Programming framework as a tool for trading-off conservation and management goals without parametric models. We construct and evaluate near-optimal policies by coupling recently developed tools from machine learning and nonlinear dynamics. A non-parametric model is built from the data and used to feed a temporal difference learning algorithm which approximates the optimal policy. We illustrate this approach for the Pacific sardine ecosystem in the Gulf of California, producing relatively simple and robust policies to ensure a long-term sustainable development.

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“Widespread character displacement in the avian bill across a latitudinal gradient”

Sean Anderson and Jason Weir

University of Toronto

Character displacement, or the evolution of trait differences between lineages in response to competition, has been a central concept linking ecology with diversification from Darwin to modern adaptive radiation theory. Detailed studies on model species pairs have provided strong evidence that trait divergence can indeed be driven by competition, but recent analyses using comparative datasets have found no compelling support for a wider role of character displacement in trait differentiation. This is potentially due to the difficulty in distinguishing alternative processes. While sympatric species are typically more differentiated than their allopatric counterparts, they are also typically older, and their greater disparity may be explained by greater evolutionary time over which to accumulate differences. Furthermore, ecological sorting during community assembly may preferentially select previously-diverged lineage pairs for a given locale, creating the false appearance of an effect of competition. To tease apart these alternative processes, we designed evolutionary models to explicitly test for signatures of character displacement and ecological sorting in lineage pair datasets. From a novel set of 207 pairs of new world forest birds, here we report the first evidence for widespread character displacement in the avian bill. Our results suggest that allopatric lineages are more similar than expected by chance alone, and that divergence is driven primarily by jumps in divergent selection that correspond with the establishment of secondary sympatry. Additionally, we find evidence for a latitudinal gradient in the strength of character displacement, with more severe increases in divergent selection occurring toward the tropics. These results are consistent with a general role of interspecific competition driving trait divergence between closely related lineages, and they help shed light on biogeographic patterns in species-rich Amazonia.

“Reconsidering predator diversity effects: a theoretical comparison of body size, phylogenetic, and trait based definitions of functional diversity”

Michael W. McCoy, Elizabeth Hamman, James R. Vonesh, Jeremy Wojdak, and Benjamin M. Bolker

Department of Biology, East Carolina University

Predicting how changes in predator communities trickle down to affect ecosystems has been a challenge for ecologists, in part because of the highly context dependent nature of predator and prey interactions.

Nevertheless it is generally accepted that the functional diversity of predator communities is more important than species richness for predicting the cascading effects of predators on prey dynamics and ecosystem functions. However, because current approaches for quantifying functional diversity are descriptive (e.g. based on morphometric traits) or idiosyncratic to systems (e.g. phylogenetic distance) and not linked to relevant theory our ability to predict how changes in diversity will impact ecosystem function remains limited. Here we propose and test a new index for quantifying predator functional diversity. Specifically, we use randomly generated phylogenetic trees to evolve predator communities with different phylogenetic relationships, body sizes and functional traits using Brownian motion evolutionary models. We then compare the relative predictive value of different metrics of functional diversity. We find that our proposed trait-based approach is anchored to relevant consumer-resource models provides better predictive power and a means to decompose mechanisms leading to observed diversity effects than approaches that use body size or phylogenetic distance to quantify functional diversity.

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“Using integral projection models to understand community disease dynamics of a fungal pathogen”

A. Marm Kilpatrick, J.R. Hoyt, K.L. Parise, J.T. Foster, K.E. Langwig

Dept. Ecology & Evolutionary Biology, University of California, Santa Cruz

Emerging infectious diseases have caused enormous population declines and species extinctions. Understanding the role of different species in both transmission and impacts of disease remains a key challenge in disease ecology. The emergence of several multi-host fungal pathogens in the past few decades, including chytridiomycosis in frogs and salamanders and white nose syndrome in bats, has made this challenge especially important for this pathogen type with its unique biological traits. We used integral projection models to describe the relatively slow pathogen dynamics of white-nose syndrome on individual bat hosts and the transmission among species and the environmental reservoir. We find that species play highly disparate roles in transmission due to differences in within-host pathogen dynamics, and these differences have cascading impacts on population impacts of disease. As a result, sites with different community compositions had disparate disease dynamics and differential impacts. The integration of models and rich data streams from multiple years and sites provided unique insight into the underlying ecology of this devastating disease.

Session 13:

“Why advertise low quality? Explaining informative floral traits”

Carla J. Essenberg

Bates College

Availability of floral resources such as nectar and pollen can vary substantially within plant species and even within individual plants. A variety of floral traits, including petal color, morphology, and size, floral volatiles, and color and scent of the rewards themselves, are now known to provide accurate information to pollinators about this intraspecific variability in rewards. These informative traits likely play an important role in many pollination mutualisms and could provide insights into how communication between cooperative partners evolves and is maintained. In this talk, I shall describe the main types of informative floral traits documented in the literature, discuss the mechanisms by which informative floral traits could influence plant fitness, and present hypotheses that could explain their evolution and maintenance. While pollinators often use informative floral traits when selecting flowers, little is known yet about their effects on plant fitness. Researchers have proposed a variety of

explanations for their evolution, but evidence needed to test those hypotheses is still scarce. I argue that it is time to deepen our understanding of this common element of plant reproductive ecology.

“Floral symmetry and specialization in pollination interactions”

Jeremy B. Yoder, Giancarlo Gomez, and Colin J. Carlson

[CSU Northridge](#)

Botanists have long identified angiosperm species with bilaterally symmetrical (zygomorphic) flowers as having more specialized pollination interactions than species with radially symmetrical (actinomorphic) flowers. Zygomorphic flowers have been shown to facilitate more specific points of contact with pollinators, guide pollinator behavior, and exclude less effective pollinators. However, to our knowledge, the basic idea that species with zygomorphic flowers interact with a smaller subset of available pollinators has not been broadly evaluated. We compiled data on 32,901 plant-pollinator associations in 159 natural communities around the world, classified the floral symmetry of the plant taxa, and compared the number of pollinator associations recorded for taxa with different floral symmetry. Both at the global level and within individual plant-pollinator networks, we found that species with zygomorphic floral symmetry are associated with fewer pollinators. We also find that the structure of plant-pollinator networks differ for plants with different floral symmetry, in ways that may arise from this difference in pollinator diversity. These results explain associations between zygomorphy and diversification, and imply that species with zygomorphic flowers may face greater risks of extinction due to pollinator loss.

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“Anther dimorphism as a strategy to increase male fitness when pollinators consume male gametes”

Kathleen Kay

[University of California Santa Cruz](#)

The presence of two types of anthers within the same flower is common among bee-pollinated plants and typically involves one set of easily-accessible, brightly-colored anthers and another set of cryptic anthers. Although perplexing to Darwin, it is now commonly accepted as a division of labor between feeding and pollinating functions of bee-pollinated flowers. I examine the evolution of dimorphic anthers across the genus *Clarkia* and find that it is indeed associated with bee pollination. I then test the division of labor hypothesis by assessing whether 1) one set of anthers is cryptic to bees whereas the other is conspicuous, 2) bees primarily collect pollen from conspicuous anthers, and 3) pollen from cryptic anthers is more likely to be transferred to stigmas. Although one set of anthers is cryptic to bees, I do not find division of labor between cryptic and conspicuous anthers. Instead, I find that cryptic anthers are held in reserve until conspicuous anthers are depleted by bees, at which point they move into a conspicuous position in the flower, release pollen, and are harvested by bee visitors. Trials with bumble bees show this strategy increases pollen export, potentially increasing siring success. My results support pollen presentation theory and highlight intricate floral adaptations to cope with pollen consumption by bees.

“Population dynamics of insect herbivores in highly fragmented landscapes”

Elizabeth E. Crone

[Tufts University](#)

Abundance of herbivorous insects is often assumed to be determined by the abundance of food

resources. In the case of butterflies, these are usually larval host plants, i.e., food resources for growing caterpillars. One common assumption is that the larval host plants determine the carrying capacity. For example, past models of population dynamics of butterflies have implemented density dependent survival of caterpillars, and in some cases, assumed strict ratio dependence of the number of adult butterflies based on the availability of their larval hostplants. An alternative assumption is that population growth rates are limited by the time it takes adult insects to move through the landscape and encounter host plants. For example, at landscape scales, milkweed cover for monarch butterflies is about 0.01-1%, suggesting significant search-time limitation. In this talk, I use simple integrodifference equation models (parameterized with field and lab data for monarch butterflies) to explore population dynamics of monarch butterflies in these highly fragmented landscapes. I contrast the predictions of these models, which are based on time limitation, to past modeling efforts. For example, if host plants regulate populations in a density dependent manner, stopping habitat destruction will cause populations to stabilize. However, if search time for host plants affects population growth rate in a density independent manner, then populations will continue to decline, even if habitat destruction is stopped.

“Understanding Floral Scent Inheritance in a Coevolved Plant-Pollinator System”

Mia T. Waters, John N. Thompson, Magne Friberg*

Department of Zoology, University of British Columbia; Vancouver, British Columbia, Canada

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Floral scent is a complex trait essential for signaling and communication with pollinators. The genus *Lithophragma* (Saxifragaceae) is one of the most extreme examples of inter- and intra-specific variation of floral scent profiles. Species within this genus have coevolved in a geographic mosaic with moths in the genus *Greya*, which are both specialized pollinators and seed parasites for these plants. Here I begin to disentangle the genetic basis for the evolution of this complex signaling trait through the chemical analysis of F1, F2, and backcross hybrid generations crossed in a common garden from two *Lithophragma* sister species (*L. affine* and *L. parviflorum*) with highly divergent floral chemistry. Floral scent was collected from each generation across 7 genetically different lineages and analyzed using gas chromatography–mass spectrometry. The results reveal that floral scent in the hybrid generations vary widely in relation to their parental populations. This study sets a foundation for future research to assess how variation in signaling traits might affect coevolved interactions as locally adapted populations hybridize. Because the distributions of many plant species are rapidly changing, altered interactions with pollinators through such novel trait combinations in hybrids could become common in many species-rich taxa capable of hybridization.

“Effects of pollinators on plant coexistence”

Christopher A. Johnson, Jonathan M. Levine

Department of Ecology and Evolutionary Biology, Princeton University

Plants in nature must compete for pollinators as well as other limiting factors such as abiotic resources. We integrate theory with field experiments to investigate how pollinators affect the coexistence of competing annual plants. We systematically varied intra- and inter-specific plant densities in the field and experimentally manipulated pollen limitation. Using the coexistence theory framework, we used our field data to estimate niche and fitness differences and predict the outcome of competition. We find that competition for pollinators affects both niche and fitness differences such that pollinators can change the outcome of competition, potentially promoting or eroding plant coexistence.

“Changes in flower size are associated with changes in plant size, not plant physiology, in co-occurring Californian annuals”

Katherine E. Eisen^{^} and Ellie M. Goud^{^°}*

[^]Department of Ecology and Evolutionary Biology, Cornell University

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Flowering is a critical but costly part of the life cycle of annual plants. Where species co-occur and share pollinators, increased investment in flowers (producing more or larger flowers) may increase pollinator attraction and consequently reproductive success. However, investment in flowers may also be limited by the abiotic environment, namely water availability, such that the potential advantages of increased floral investment may come at a physiological cost. In the southern Sierra Nevada foothills, *Clarkia cylindrica* produces larger flowers it co-occurs with *C. unguiculata*. We assessed whether the production of larger flowers in *C. cylindrica* is correlated with a change in physiological strategy or biomass allocation. In communities where these species occur alone and in communities where they co-occur, we measured floral, functional, and biomass allocation traits and estimated water loss via leaves and flowers using carbon and oxygen stable isotope analyses. We found species-level differences in physiology, but these physiological strategies did not vary with community context. This suggests that the observed shifts in flower size do not reflect changes in a plant’s primary metabolic strategy. Flower size of *C. cylindrica* is less strongly correlated with biomass allocation to reproduction where *C. cylindrica* co-occurs with *C. unguiculata* relative to where *C. cylindrica* occurs alone. This pattern may result from increases in plant size of *C. cylindrica* where the species co-occur, which suggests that competition for light and space may influence the evolution of trait differences.

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“Phenological Plasticity Predicts Trends in Abundance of Massachusetts Butterflies”

James Michielini, Erik Dopman & Elizabeth Crone

Tufts University

Though phenological shifts have been well-documented in the ecological literature, relatively few studies have identified their significance for changes in demography and abundance. We use records from a citizen science group, the Massachusetts Butterfly Club, to quantify trends in phenology and relative abundance across ~90 species. We calculated shifts phenology using quantile regression, an underappreciated technique in phenological research. Trends in mean observation date and in first observation were not correlated with trends in relative abundance. However, increases in total flight period were associated with increases in relative abundance. These changes may be driven in part by plasticity in voltinism, as this association was stronger in multivoltine species. Some species, like the Zabulon skipper *Poanes zabulon*, appear to be adding a generation early in the year, indicating a shift from vagrant to resident. Others, like the Appalachian brown, *Satyroides Appalachia*, were adding a second generation later in the year, indicating a possible shift from univoltine to bivoltine. Our results emphasize the overall importance of evaluating phenological changes throughout the activity period of a species, rather than focusing on trends of first or median dates.

“Fitness consequences of natural and anthropogenic dietary chemicals in a social bee, with insights into physiology and behavior”

Sarah K. Richman¹, Angela M. Smilanich¹, Denyse Marquez Sanchez², Anne S. Leonard¹

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Human activities may reshape nutritional resources in ways that scale up to affect fitness via effects on behavior and physiology. For example, pollinator diets consist of floral resources (nectar and pollen), which besides macronutrients, also contain alkaloids, terpenoids, and other compounds. These nectar chemicals can have positive and negative effects on physiology and behavior. Under global change, pollinators such as bees are increasingly exposed to dietary pesticides, which generally have a negative impact on fitness components. While there is a considerable amount of research on the fitness effects of secondary metabolites and of pesticides in pollinator diets conducted in parallel, we know almost nothing about their combined effects. We address this knowledge gap in a laboratory experiment using the bumble bee *Bombus impatiens*. We ask whether bees that consume artificial nectars offering field-realistic levels of caffeine (an alkaloid) and thymol (a terpenoid), exhibit higher immune function and experience a higher probability of survival after an acute dose of imidicloprid, a widely used neonicotinoid pesticide. We find that bees' immune systems respond differently to pesticides if they consumed a diet supplemented with nectar chemicals than if they had consumed a sugar-only diet. Surprisingly, we did not find large differences in survival, even though bees exposed to pesticides consumed significantly less nectar per day. behavioral assays shed light on this phenomenon: pesticide-exposed bees were significantly less active than non-exposed bees. While our results show little implication for worker survival, they bring up important questions about the effects of diet on colony-level fitness.

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Session 14:

“Reinforcement and ecological speciation between incipient outcrossing and selfing *Clarkia* species”

David A. Moeller and Ryan D. Briscoe Runquist

University of Minnesota

Studies of reproductive isolation often find that prezygotic barriers evolve more rapidly than postzygotic barriers between incipient species. However, it has been challenging to determine whether selection has directly resulted in elevated assortative mating (reinforcement) or whether reproductive isolation has occurred as a by-product of adaptation to alternative environments. In *Clarkia xantiana*, there is a pronounced pattern of reproductive character displacement (RCD) between incipient plant species that remain cross-compatible, a key signature of reinforcement. Mating is mediated by interactions with specialized bee pollinators whose population dynamics and evolution are linked to that of *Clarkia* populations. Here, we test whether reinforcement selection has directly caused the evolution of RCD in quantitative floral traits using a series of field experiments. In particular, we examined whether assortative mating was stronger between sympatric populations than allopatric populations. Our results show that assortative mating is very high between sympatric genotypes resulting in few hybrids. Whereas, assortative mating is weaker between allopatric genotypes and hybridization is approximately twice as likely, consistent with the reinforcement hypothesis. Pollinator discrimination largely determines the likelihood of hybridization. We also tested the alternative hypothesis that RCD developed as by-product of adaptation to contrasting pollination environments in the allopatric and sympatric regions. However, we found no evidence for this hypothesis. Overall, these results are novel in demonstrating a contribution of mating system divergence to the speciation process in plants.

“The evolution of gametic compatibility within species and reproductive isolation across species”

Don R. Levitan

Reproductive isolation is central to speciation, but how do isolating mechanisms evolve? The proliferation of initially rare genotypes becomes particularly puzzling for traits associated with reproductive compatibility. How can a mutation, that by definition results in reduced compatibility with mates, have a fitness advantage over commonly available competitors that have high compatibility with those same mates? Here I show how within species sexual conflict and across species reinforcement might interact to influence the evolution of reproductive isolation in two sympatric sea urchin species. Conflict driven by the risk of polyspermy can produce a balanced polymorphism in gamete recognition loci. This variation in sperm and egg recognition proteins not only influence reproductive success within species, but also can explain variation in conspecific sperm precedence across species. Phylogenetic analysis suggests sexual conflict might generate the variation in these recognition proteins that allow for reinforcement selection to operate.

“Cardinals are red, buntings are blue; because they hybridize, they’re interesting too!”

Libby Megna, Matthew D. Carling

Dept of Zoology & Physiology, Program in Ecology, University of Wyoming, Laramie, WY, USA

Understanding how reproductive isolation arises between populations is critical to understanding the process by which species diverge. However, when two species are completely reproductively isolated, it is difficult to assess which isolating mechanisms are operating. Hybridization between species reveals information on which isolating mechanisms have failed upon secondary contact. Furthermore, one of the most salient questions in evolutionary biology is whether we can predict evolutionary processes; can we find overarching patterns in how reproductive isolation is maintained among passerine species? Here, we determine if there are repeated patterns of trait divergence for species in the family Cardinalidae, and if those patterns can predict hybridization between species. Twelve of the 48 species in Cardinalidae hybridize. We quantified several traits for each species: plumage coloration, climatic niche, bill morphology, and song. We used phylogenetically informed GLMMs to examine the association between trait values and hybridization. Our preliminary results indicate that Neotropical migrant species are more likely to hybridize than tropical resident species; that species with greater frequency bandwidth songs are more likely to hybridize; and that species with redder plumage are more likely to hybridize, whereas species with more blue are less likely to hybridize. It is generally thought that each instance of hybridization between species has its own evolutionarily unique history, and thus dynamics of hybridization between two species pairs cannot be generalized to other species pairs. However, our results suggest that there are overarching patterns in how reproductive isolation arose within Cardinalidae.

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“Evolutionary dynamics of inbreeding and outbreeding in a plant-like animal”

Kevin C. Olsen and Don R. Levitan*

Department of Biological Science, Florida State University

The degree of coancestry between mates and the extent to which this varies has important implications for how genetic variation is structured among populations. Variation in inbreeding has predominately been studied under the dichotomy of self-fertilization versus outcrossing in seed plants, with the notion that selfing affords inclusive fitness advantages and may reduce inbreeding depression, leading to the evolution of inbred mating systems. However, this dichotomy limits the utility of theory on inbreeding and outbreeding to self-compatible taxa, and there are relatively few examples assessing variation in the magnitude of biparental inbreeding and the purging of inbreeding depression. My dissertation evaluates

biparental inbreeding in a sessile marine invertebrate with limited potential for dispersal. I've found that individuals in isolated habitats have a greater degree of relatedness and harbor genetic indicators of inbreeding compared with those in less secluded populations. I am currently estimating inbreeding depression to test if biparentally inbred populations purge their genetic load as expected from theory. I suggest that marine invertebrates with short lifespans, sessile reproductive stages, and who mate via the release of gametes into the environment are likely to evolve plant-like mating systems and represent an opportunity to expand our understanding of mating systems to incorporate a broader range of phenomena.

"Patterns, predictors, and consequences of dominance in F1 hybrids"

Ken A. Thompson, Mackenzie J. Uquhart-Cronish, Kenneth D. Whitney, Loren H. Rieseberg, Dolph Schluter
[University of British Columbia - Vancouver](#)

Although the phenotype of otherwise viable and fertile hybrids determines their fate, little is known about the general patterns, predictors, and consequences of phenotype expression in hybrids. To address this empirical gap, we compiled data from nearly 200 studies where traits were measured in a common environment for two parent populations and F1 hybrids. We find that hybrid phenotypes tend to resemble one parent about 50% more than the other but also have substantial 'mismatch' due to dominance in opposing directions among traits. No variable (phylogeny, genetic distance, etc.) was associated with dominance. Using data from an experimental array of recombinant hybrid sunflowers, we illustrate that dominance for traits in the same direction has positive fitness consequences while dominance in opposing directions ('mismatch') has negative fitness consequences. In sum, our study suggests that hybrids formed between ecologically divergent natural populations are typically not phenotypically intermediate but resemble one parent more than the other while also displaying novel trait combinations similar to individual recombinant hybrids. Such patterns of dominance are likely determined by population-specific processes rather than general rules. Finally, ecology-mediated selection against F1 hybrids is expected to result from both selection against intermediacy and also against incompatible trait combinations.

Session 15:

"Effects of migration on rapid adaptation and the genetic basis of dispersal behavior in natural populations of *D. melanogaster*"

Ozan Kiratli, Paul Schmidt
[University of Pennsylvania](#)

One of the main forces that shapes evolution is gene flow. Three questions have yet to be understood: 1) How much does migration of individuals result in actual gene flow? 2) What are the effects of the resulting gene flow on rapid adaptive responses in natural populations? 3) What is the genetic basis of dispersal behavior? I conducted two separate experiments to address these questions. First, I tested whether a single event of migration could change the rate and/or direction of the adaptive response to thermal regime. I used outbred populations of *Drosophila melanogaster*, created from isofemale lines that were collected from Florida (FL), Pennsylvania (PA) and Maine (ME); the response of isolated populations (PA, FL, and ME) was contrasted with a PA population subject to migration from FL or ME. After 5 generations of exposure to different seasonal temperature regimes, populations subject to the initial migration were observed to have increased the rate and magnitude of adaptive response compared to the isolated ones. Next, I tested whether dispersal is non-randomly associated with variants genome-wide, and whether dispersal behavior is heritable. To achieve this, I adopted a tail-

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based sampling method to collect the earliest dispersing flies in large scale mesocosms, and conducted GWAS analysis as well as measured dispersal- and fitness-related phenotypes in their F2 progeny.

“Scale-dependent effects of niche specialization: the disconnect between individual movement and species distribution”

Shan Huang, Marlee A. Tucker, Jörg Albrecht, Alison Eyres

[Senckenberg Biodiversity and Climate Research Centre \(SBIK-F\), Frankfurt, Germany](#)

Understanding the relationship between niche specialization and species distribution dynamics is important for evaluating the impact of environmental changes. In this study, we use phylogenetic comparative analyses to show that in terrestrial mammals, occurrences at individual and species levels are both connected to species niche specialization but the specific mechanisms are scale-dependent. We considered species specialization in terms of diet breadth and habitat breadth. Diet breadth is primarily associated with distribution patterns at the individual level such as short-term movements and the average home range size, with body size and primary productivity as important covariates, suggesting a significant role of energy budget. In comparison, habitat breadth is more relevant to distribution at the species level such as the geographic range size, supporting the hypothesis of a trade-off between specialization and dispersal ability that might contribute to shaping the pervasive latitudinal diversity gradient in global biogeography. Overall, individual movement and home range size only explain a small portion of variation in species geographic range size, indicating that species maintain their gene pool over broad geographic space through complex mechanisms. Our findings highlight the scale-dependency of biological mechanisms in shaping biodiversity patterns, and specifically, that species geographic range cannot be easily explained by individual behaviors.

“Does habitat fragmentation affect the dispersal ability of a terrestrial darkling beetle?”

Goggy Davidowitz, Natasha Tigreros, Giorgi Kozhoridze, Yaron Ziv

[Department of Entomology, University of Arizona](#)

Agricultural and urban intensification has resulted in fragmented natural habitats. While a number of studies indicate that habitat fragmentation can lead to a quick loss in biodiversity and ecosystem services, recent studies also suggest that some organisms may be able to adapt and persist in fragmented landscapes. Understanding what makes some organisms better (or worse) at enduring habitat fragmentation may allow us to better understand the consequences of modern agricultural and urban practices. We used satellite imagery to select patches of different sizes, vegetation cover and degrees of isolation. We then compared locomotion performance –mobility rate, speed, and metabolic rate during locomotion– of beetles from the different patches to test whether variation in locomotion efficiency in the darkling beetle *Zophosis punctata* explains their ability to persist, or not, in a highly fragmented landscape. Preliminary results indicate a complex relationship between beetle locomotion performance (speed and metabolic rates) and their abundance across the fragmented landscape.

“Western monarch summer range expansion slows as population declines”

Collin Edwards, Elizabeth Crone

[Tufts University](#)

Western monarch populations declined dramatically in abundance during the past 40 years. Overwintering counts were millions of individuals in the 1900s, 200,000 to 300,000 in the 2000s, and then crashed to ~28,000 in the winter of 2018/2019, with very low abundance apparent on the breeding

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grounds in 2018 and 2019. We used more than 100 years of citizen science data to compare summer range expansion of monarchs in three specific time periods: (1) historic (20th century) data, (2) recent (21st century) data, and (3) summers of 2018 and 2019, when the population was extremely small. Comparing historic and recent data could indicate potential factors associated with long-term decline. Comparing recent and post-crash data could indicate potential Allee effects. Based on a combination of quantile regression and nonlinear models, monarch range expansion rates in the 21st century were similar to but possibly slightly slower than in the 20th. Range expansion was dramatically slower in 2018 and 2019 than either previous period. Our findings suggest that expansion rates are one of the key population processes that can fall apart as this populations declined. The breeding population did not decline dramatically from 2018 to 2019, suggesting that monarchs mitigate Allee effects by slower movement in small populations, rather than experiencing lower fecundity throughout the range.

Session 16:

“Antagonistic and Mutualistic Biotic Interactions Across the Geographic Range Margin of *Clarkia xantiana* ssp. *xantiana*”

John W. Benning and David A. Moeller

University of Minnesota, Plant & Microbial Biology

Species’ geographic distributions have already shifted during the Anthropocene. However, we often do not know what aspects of the environment drive range dynamics, much less which traits mediate organisms’ response to these environmental gradients. Most studies focus on possible climatic limits to species’ distributions and have ignored the role of biotic interactions, despite theoretical support for their importance in setting large-scale distributional limits. We have used a variety of field experiments to quantify the contributions of multiple biotic interactions to a geographic range boundary in the California annual plant *Clarkia xantiana* ssp. *xantiana*.

We show that a steep gradient of increasing probability of herbivory occurs across the boundary, and that herbivory drove several-fold declines in lifetime fitness of transplants beyond the boundary. We also showed that a specific trait, phenology, is strongly associated with *C. xantiana* ssp. *xantiana*’s susceptibility to herbivory and low fitness beyond its border. Pollen limitation of reproduction also increases outside the range limit, where pollinator visitation drops off precipitously. Overall, our results provide some of the most comprehensive evidence to date of how the interplay of demography, traits, and spatial gradients in species interactions can produce a geographic range limit, and lend empirical support to recent developments in range limits theory.

“Cooper’s and Sharp-shinned Hawks fill discrete niches created by the relative abundances of their prey species.”

Eliot T. Miller, Oisín Mac Aodha, Emma I. Greig, David N. Bonter, Wesley M. Hochachka

Cornell Lab of Ornithology, Ithaca, New York

In this paper we address two broad questions that guide our interpretation of species’ niches in the face of a growing trove of citizen science data. The first is one of basic biology, “do discrete niches exist?” The second is one of observer expertise and its statistical ramifications, “how good are observers at distinguishing similar species, and how does this vary with expertise?” These questions are inextricably linked—if we cannot be sure of the identity of our study organisms, then we cannot be sure of the strength of our conclusions. The decisions made by top predators over what prey to target have traditionally been detailed after painstaking observation in the field by trained biologists. Here, we take

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an alternative approach and use reports submitted by citizen scientists to quantify niche partitioning between two broadly sympatric congeneric avian predators, Cooper's and Sharp-shinned Hawks. We find that the resource base, as quantified by feeder bird body mass abundance, is multimodal and approximately lognormal. Cooper's and Sharp-shinned Hawks appear to fill these modes in the resource base, with Sharp-shinned Hawks focusing their hunting efforts on abundant small prey items, and Cooper's Hawks taking prey from the two most abundant peaks in the resource base (both the small body mass peak and a lesser peak at medium body mass). To some degree, therefore, these hawks partition niche space as defined by prey body mass, and habitat differences presumably further minimize niche overlap. Through online testing with known gold standard images of the study species and potential confusion species, we find that citizen scientists struggle to distinguish these similar looking predators from one another, but our simulations show that citizen scientists' observation skills are sufficient to allow us to reach our conclusions.

"The Ecology and Evolution of Commensalism"

Judie Bronstein

[University of Arizona and Kate Mathis, Clark University](#)

Studies of competition and antagonism (predation, herbivory, parasitism, and host/pathogen interactions) lie at the heart of our field. Recent decades have seen a surge of interest in mutualism and facilitation as well. Other forms of interaction, however, remain minimally investigated. Our goal here is to promote the ecological and evolutionary study of commensalism, interactions that benefit one partner and that neither benefit nor harm the other. We first survey how and where commensalism has been documented, or at least claimed to exist. Based on these data, we argue that commensalism is not a single type of interaction; rather it is a suite of distinct phenomena characterized by different ecological processes and evolutionary consequences. For each of these, we discuss evidence for how, where, and why it occurs. Finally, we offer a set of synthetic predictions regarding the ecology and evolution of commensalism, with suggestions for how they might be tested. One major conclusion is that commensalism is commonly a tipping point between beneficial and harmful interactions that might be paused at or passed through regularly. As such, we argue, understanding commensalism is key to understanding the ecological and evolutionary dynamics of species interactions as a whole.

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"Mediation of the insect immune response by ecological factors: insights from a recent host expansion"

Su'ad Yoon, Joshua G. Harrison, Angela Smilanich, Matthew Forister

[University of Nevada, Reno](#)

My dissertation focuses on expanding our knowledge of ecological immunology; the goal of this particular field of ecology is to determine how components of ecological variation can affect immunological variation in the wild. Specifically, I seek to understand how ecological factors such as nutrition, resource use, plant chemistry, and microbial communities can affect the immune response of insects in natural populations. In order to address these questions, I have conducted observational and experimental projects on wild populations of the Melissa blue butterfly (*Lycaeides melissa*) in the Great Basin Desert located in Northern Nevada. This specialist plant-feeding butterfly is of interest from an evolutionary ecology standpoint because it has recently undergone a host expansion; it has incorporated a novel host plant into its diet. I have used this host expansion as a comparative framework to understand how ecological components can change the immune response; the novel host plant represents a novel nutritional, chemical, and microbial resource, all factors that can potentially

impact the insect immune response. By comparing immune strength on the novel and ancestral host plants, I seek to further the field of ecological immunology by quantifying the relative strength of ecological variation in the wild, and shedding light on how this variation impacts immunity. Further, by quantifying different levels of ecological variation simultaneously, I can test for potential interactions between these factors. The fields of ecological immunology and plant-microbe-insect interactions are both relatively new areas of research, yet they hold great potential to inform our knowledge of coevolution, integrated pest management, and the relationship between microbes and overall health.

“Ecological context drives a shift from parasitism to mutualism”

Mary Rogalski, Tara Stewart Merrill, Camden Gowler, Carla Caceres, Meghan Duffy

[Bowdoin College](#)

Interspecific interactions can shift along a mutualism to parasitism continuum. While there are many studies of flexible species interactions examining dynamics typically considered to be mutualistic that sometimes shift towards parasitic, little is known about conditions underlying shifts from parasitism towards mutualism. We observed a robust field pattern where infection by a microsporidian gut symbiont (MicG) was associated with reduced host fecundity under some circumstances but became more and more beneficial to the host when other much more virulent parasites (e.g. *Metschnikowia*, *Spirobacillus*, *Pasteuria*) were more abundant. One possibility is that MicG modifies the gut in some way that makes it harder for other parasites to infect the host. Experimental manipulation showed that MicG infection does reduce gut penetrability. These dynamics have the potential to interact with resources as well – gut penetrability tends to be higher when resources are high and the difference between MicG vs. uninfected gut penetrability increases with increasing resources. In Michigan lakes, but not in Indiana lakes, MicG infection was most beneficial when resources are high. Taken together, these findings suggest that the fitness impacts of this symbiont (MicG) likely depends on both the multiparasite environment and the resource environment. This work highlights the importance of considering ecological context in host-parasite studies and opens the door for future research into conditions under which organisms that typically act as parasites might benefit their hosts.

Session 17:

“The maintenance of genetic variation under host-parasite coevolution”

Ailene MacPherson, Matthew Keeling, Sally Otto

[University of British Columbia](#)

How genetic variation is maintained is a fundamental question in evolutionary biology, inspiring some of the earliest models in theoretical population genetics. To date however, these results have focused primarily on the dynamics of genetic variation within a single species. We explore the effect of host-parasite coevolution and the associated ecological and epidemiological effects on the maintenance of genetic variation in finite populations. In the simplest case where population size is forced to remain constant, genetic variation in the classic matching-alleles model behaves as expected under neutral drift alone. The introduction of eco-evolutionary dynamics results in the net maintenance of genetic variation relative to neutral drift, a pattern that is accentuated in the presence of epidemiological dynamics. These results highlight the importance of incorporating species interactions into our understanding of the maintenance of genetic variation.

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“Parasite recognition and resistance varies among closely related stickleback populations”

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It has long been recognized that parasites can generate strong selective pressures that can shape host evolution, which is often characterized by tight coevolutionary cycles between hosts and parasites. However, we still do not have a good understanding of how these cycles might vary between closely related populations and how this can shape variation in parasite resistance or tolerance mechanisms. Using a novel method where we injected immune adjuvant and/or parasite protein into the site of infection, we compared the timing and strength of a parasite-resistance response (fibrosis) in three populations of three-spine sticklebacks: one that has strong resistance to a common cestode parasite, one that has weak resistance, and a marine ancestral population with a history of rare cestode exposure. We found that the resistant population had a faster and stronger response and was uniquely able to recognize and respond to parasite antigens alone in the absence of an immune adjuvant. The resistant population was also able to better clear fibrotic tissue once it had developed. This study provides evidence that host parasite-interactions can vary dramatically in closely related populations, in small geographic areas, and under short evolutionary time scales.

"Sick of Eating: eco-evo-immuno dynamics of predators and their trophically acquired parasites"

Sam Fleischer (UC Davis), Dan Bolnick (U Conn), Sebastian Schreiber (UC Davis)

"When predators consume prey, they risk becoming infected with their prey's parasites, which can then establish the predator as a secondary host. For example, stickleback in northern temperate lakes consume benthic and/or limnetic prey which are often parasitized by nematodes and/or cestodes, respectively. These worms then establish the stickleback as a secondary host and can cause behavioral changes linked to increased predation by birds. We use a quantitative genetics framework to consider the simultaneous evolution of predator ecomorphology and predator immunity when alternative prey may confer different parasite exposures. We explore the relationship between the evolution of food preference and immunity, and find conditions for when the evolution of these two traits are correlated. We also show that the evolution of immunity can cause a negative correlation between parasite intake and infection."

"Social trematode parasites allocate soldiers according to invasion threat in the field."

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Eusociality involves allocating resources between multiple, specialized castes, such as reproductives, workers, and soldiers. Due to trade-offs between defense and reproductive investment, theory posits that colonies should alter caste allocation in response to environmental conditions. However, few studies have examined the role of species interactions in shifting allocation between reproductive and soldier castes, likely because of the difficulty in quantifying or manipulating interaction strength (e.g. competition or predation) and censusing total colony investment. Social castrating trematode parasites in the California Horn Snail represent a novel system to test resource allocation theory in terms of response to invasion threat because we can easily quantify the risk of invasion through mean infection prevalence. In this study, we examine how invasion threat across a latitudinal gradient alters soldier investment within focal trematode species. We find that soldier investment by these species positively correlates with invasion threat across sites, consistent with the hypothesis that caste allocation adaptively responds to the threat of invasion in this guild.

“Host energetics explain variation in parasite productivity across scales”

Rita Grunberg and David Anderson

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Parasites are thought to play a significant role in ecosystem energy flow, but the amount of energy used by parasite communities, and the relationship of parasite communities to host energetics, remain unclear. Here, we extend ideas in the metabolic theory of ecology to describe the energetic cost of parasitism across hosts and ecosystems. First, we develop and test theory that links host metabolism to the energy flux of parasitic communities spanning 28 host taxa. We test whether the fraction of a host's energy budget that is allocated to parasitism is invariant with respect to host metabolic rate, and based off this prediction parasites will use a constant proportion of a host's metabolism across host taxa. Our data affirm an allometric relationship between host metabolic rate and parasite community flux, although the slope of the relationship was shallower than the expected isometric relationship. This relationship suggests the fraction of energy taken by parasites declines with host metabolic rate. Finally, we extend this framework to explain the scaling of host and parasite community energetics at the ecosystem scale. Across three riverine ecosystems, we found strong relationships between parasite and host productivity. A common scaling exponent describes host and parasite energy flux within all three ecosystems, but intercept values varied based on ecosystem identity. This implies variation in parasite productivity across systems is driven in part by differences in host and ecosystem productivity.