EVOLUTION 2026

Society of Systematic Biologists
Society for the Study of Evolution
American Society of Naturalists

EVOLUTION 2026

June 20-24, 2026

Cleveland, OH

CONFERENCE PROGRAM

OVERVIEW

	Sat June 20	Sun June 21	Mon June 22	Tue June 23	Wed June 24
8:00-9:15		ASN Presidential Address	SSE Presidential Address	SSB Presidential Address	
9:30-10:45		ASN VP Symposium & Concurrent Sessions	Symposium/Research Synthesis Working Group: Impacts of Genome Architecture on Polygenic Adaptation during Rapid Environmental Change Session One & Concurrent Sessions	Genetic diversity in ecological communities: A new biodiversity pattern that unifies ecological and evolutionary timescales & Concurrent Sessions	Concurrent Sessions
10:45-11:15	**Full Day Workshop** • Writing Effective Op-Eds	Coffee break & Flying solo mixer	Coffee break & Neurodivergent Mixer	Coffee break International Mixer & Fieldwork Mixer	Coffee break & UCE Social Disabilities Mixer
11:15-12:30	**AM Workshops/Meetings** • Joint council entrance • Storytelling Workshop • Navigating Scientific Publishing (Part 1)	ASN VP Symposium & Concurrent Sessions	Symposium/Research Synthesis Working Group: Impacts of Genome Architecture on Polygenic Adaptation during Rapid Environmental Change Session Two	Genetic diversity in ecological communities: A new biodiversity pattern that unifies ecological and evolutionary timescales	Tri-Society AICC Symposium Session One & Concurrent Sessions
12:30-2:30	• NSF BIO Info Session • Undergraduate Community Workshop **PM Workshops/Meetings** • Imageomics	Lunch (not included) ASN Members Meeting SSE Members Meeting SSB Members Meeting Postdoc fellowship lunch	Lunch (not included) Postdoc networking lunch Faculty-student networking lunch Systematic Biology journal American Naturalist journal	Lunch (not included) LGBTQIA+ Networking Lunch Black at Evolution Networking lunch ASN Grad Mixer Evolution Journal Joint Council Exit	Lunch (not included) ASN exit Meeting SSE Exit Meeting SSB Exit Meeting
2:30-3:45	• Diverse Careers • Navigating Scientific Publishing (Part 2) • SSE Council entrance • ASN council entrance • SSB Council entrance	ASN Early Career Awards & Concurrent Sessions	Symposium/Research Synthesis Working Group: Impacts of Genome Architecture on Polygenic Adaptation during Rapid Environmental Change Session Three & Concurrent Sessions	Concurrent Sessions	Tri-Society AICC Symposium Session Two & Concurrent Sessions
3:45-4:15		Coffee break & LGBTQIA+ mixer	Coffee break & BIPOC mixer	Coffee break & Latines in Evolution mixer Asians in Evolution mixer Africans in Evolution mixer	Coffee break & PUI mixer SSB Early Career Mixer
4:15-5:30		ASN Early Career Awards/ Dobzhansky Award & Concurrent Sessions	Presidential Symposium & Concurrent Sessions	Concurrent Sessions	Concurrent Sessions
5:45-6:30/7		Poster session 1	Support Social Mixer	Poster session 2	
7:00-8:00	Gould Lecture (open to public)				Super Social (Banquet) GLSC
Evening	Opening reception				

In-Person Program

Gould Award Talk

06/20/26: 7:00 PM - 8:00 PM

7:00 PM - 8:00 PM
Gould Lecture

Neil Shubin, University of Chicago

Oral Presentations

ASN Presidential Plenary

06/21/26: 8:00 AM - 9:15 AM

8:00 AM - 9:00 AM
Light does more than illuminate: the role of lighting environment in shaping phenotypic evolution

Rebecca Fuller, University of Illinois

Abstract:

Lighting environments are among the most powerful selective forces in nature, yet their effects on organismal biology are more pervasive than is commonly appreciated. Sensory ecology focuses on how animals acquire information from their environment through their sensory systems, and how that shapes their behavior, ecology, and evolution. Endler's 1992 American Naturalist paper introduced sensory drive to ecological and evolutionary biologists and provided a powerful lens for examining these effects. In killifish, populations inhabiting tannin-stained swamps and clear-water springs differ dramatically in their lighting environments, and nearly every component of the sensory drive framework is shaped by those differences. Surprisingly, the lighting environment operates through multiple distinct pathways: it drives genetic differentiation among populations, shapes phenotypic development through rearing environment effects, and immediately alters perception in real time. These pathways have different effects on different traits, and their interactions are complex and sometimes counterintuitive. The effects of lighting environment extend well beyond color, shaping visual system properties, foraging preferences, and competitive outcomes, and the lessons from fish extend broadly across taxa.

In this address, I will discuss the multifaceted roles of lighting environment in shaping phenotypic evolution and reflect on the role of the American Society of Naturalists in fostering integrative and

conceptually driven science. I will also speak to the broader value of scientific societies: the benefits of community, of publishing in the American Naturalist, and the irreplaceable role of meetings in generating the exchange of ideas that moves science forward.

Adaptation I

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

I'm still standing: the genetic basis of Spinosad resistance in the melon fly, Zeugodacus cucurbitae (Diptera: Tephritidae)

Haley Arnold, USDA REE-ARS
Sheina Sim, USDA-ARS

Abstract:

The rapid evolution of insecticide resistance in insect pests is one of the most financially and environmentally concerning issues in modern agriculture. Historical overuse of chemical pesticides has spurred an arms race of evolution. Understanding the mechanisms by which resistance evolves is essential predicting the potential for cross-resistance, developing diagnostic tools for detecting resistance, and for understanding the repeatability and predictability of evolution. In Hawaii, the tephritid melon fly Zeugodacus cucurbitae is invasive and attacks specialty cucurbit crops such as cucumbers, honeydew, and watermelons in addition to non-cucurbits such as tomato and papaya. Melon fly infestations are managed using Spinosad, an insecticide produced from the naturally synthesized products of bacteria Saccharopolyspora spinosa. However, growers on the island of Oahu have observed continued infestation and suspect that flies have developed a resistance to Spinosad. Previous studies revealed target site mutations in the nicotinic acetylcholine receptor (nAChR) genes as the genetic basis for Spinosad resistance in other insects. To determine the genetic basis for Spinosad resistance in melon fly, we evaluated field populations for resistance, performed artificial selection to increase the allele frequency of the resistance alleles in the wild-collected populations, and performed a genome-wide association study to identify loci associated with resistance. In addition, we performed population genetic analysis to characterize insecticide susceptible colonies, wild-caught flies suspected of resistance, and flies selected for increased resistance. Results from Fst and DAPC studies show SNPs within the nAchR are relevant. Further interrogation of whole-genome sequencing data revealed other candidate genes and different candidate genes across colonies including cytochrome P450 and other genes potentially involved in metabolism.

9:45 AM - 10:00 AM

Network rewiring underlies adaptive variation at Epas1 in highland deer mice

Lacey Conrad, The University of Denver
Rena Schweizer, USDA ARS
Zachary Cheviron, University of Montana
Jon Velotta, University of Denver

10:00 AM - 10:15 AM

Adaptation to marginal habitats provides resilience to future warming at the rear edge

Antoine Perrier, University of Virginia
Laura Galloway, University of Virginia

Abstract:

Rear-edge populations, relicts of glacial refugia, often persist in marginal habitats at the warmer edge of species distributions. Persistence in these habitats likely required adapting to postglacial climate warming. The resulting local adaptation may affect success in changing climates depending on whether adaptative strategies align or conflict with future conditions. We explored how rear-edge populations persist in their marginal habitats, and whether any adaptations affect responses to future warming in the North American herb Campanula americana. We raised plants from 23 rear-edge and central populations in a common garden experiment spanning their climatic gradient. We evaluated performance across sites and life stages to identify key traits underlying adaptation to rear-edge conditions. We then predicted the expression of key traits under future climates. Local adaptation at the rear edge was mainly driven by whether plants were able to transition from vegetative growth to reproduction, i.e. bolting. Rear-edge populations exhibited high bolting frequency under local warm winters, while more northern populations failed to bolt in these conditions. Bolting is cued by winter cold (vernalization) in the species, but rear-edge climates provide only few days sufficiently cold for effective vernalization. We found that rear-edge populations have adapted to these conditions by evolving reduced vernalization requirement and sensitivity. Under projected warmer winters, bolting is expected to decline at mid-latitudes, whereas rear-edge populations are predicted to maintain high bolting. Our findings highlight that adaptation to marginal rear-edge habitats can hinge on a single trait, and this adaptation may buffer rear-edge populations against future climates.

10:15 AM - 10:30 AM

Repeated convergent evolution of semiaquatic adaptations in the largest superfamily of Neotropical lizards (Squamata: Gymnophthalmoidea)

Juan Vásquez-Restrepo, Department of Ecology & Evolutionary Biology
Daniela Garcia Cobos, American Museum of Natural History
Santiago Sanchez-Pacheco, Universidad Nacional de Colombia

Tiago Simões, Princeton University

Abstract:

Gymnophthalmoid squamates (Alopoglossidae, Gymnophthalmidae, Teiidae) are a diverse radiation of New World lizards that provide a powerful system to study repeated ecological transitions. Several lineages have independently evolved a semiaquatic lifestyle and exhibit a so-called Crocodile-Like Morphology (CLM), including heterogeneous dorsal scales, longitudinal crests, and laterally compressed tails. Despite its widespread use, CLM has traditionally been treated as a single qualitative character complex and assumed to represent a direct adaptation to aquatic habitats, yet this relationship has never been rigorously tested in a phylogenetic framework.

Here, we compiled the most comprehensive dataset to date of external morphology and habitat use for 288 species (97% of genera) and reconstructed a new fossil-informed time tree for Gymnophthalmoidea using a combined inference strategy, with maximum-likelihood phylogenetic reconstruction followed by a posteriori time calibration in BEAST2. We decomposed CLM into discrete traits and used Random Forest aiming to predict it as a probabilistic character. We subsequently evaluated their evolutionary dynamics and association with semiaquatic behavior using Bayesian stochastic character mapping and hidden-state models implemented in corHMM.

We recovered at least 11 independent transitions to semiaquatic habits since the Eocene, representing the highest number known for any non-snake squamate clade. Although several morphological traits strongly correlate with freshwater use, they do not evolve as a single integrated body plan, and semiaquatic behavior can occur in the absence of CLM. Our results therefore reveal a decoupling between morphology and realized ecology and indicate that ecological shifts toward aquatic habitats have repeatedly arisen through multiple evolutionary pathways. Together, these findings highlight gymnophthalmoids as a key system for understanding convergent evolution and functional diversification across the land–water interface.

10:30 AM - 10:45 AM

The rapid evolution and expansion of insecticide resistance in the invasive arboviral vector Aedes albopictus in USA, a region without centralized mosquito control

Martha Burford Reiskind, North Carolina State University

Abstract:

In urban mosquito populations, determining the factors that initiate and drive the evolution of insecticide resistance is critical to managing susceptible populations. Maintaining susceptible mosquito populations is important for vector mosquitoes such as Aedes albopictus, which can transmit dengue, chikungunya, Zika, and yellow fever viruses to protect public health. Over a decade, we have conducted a longitudinal, spatial study of the rapid arrival and expansion of a nonsynonymous, point mutation in the voltage-gated sodium channel (vgsc) gene that confers

resistance to pyrethroids in this in a rural/suburban/urban landscape mosaic in a county in North Carolina, USA (mutation F1534S). We documented the first appearance of F1534S in 2018, then observed its steady rise and expansion to 50% prevalence in 2025. We found that the prevalence of resistance is spatially correlated with home wealth and age, which points to private mosquito control at the household level as the main driver. In addition, we have conducted a similar study in Augusta, Georgia and Boston, Massachusetts and found evidence of the same mutation at a lower prevalence in a few locations. We confirmed that this mutation confers insecticide resistance in bioassay trials of individual mosquitoes. In addition, we deep sequenced the entire vgsc gene to investigate any additional non-synonymous mutations associated with insecticide resistance. The evolution and rise of insecticide resistance in vector mosquitoes in regions without centralized mosquito control is a threat to public health, as our front-line, emergency response to outbreaks of arboviral disease includes insecticides targeting biting adults for immediate intervention.

ASN Vice presidential Symposium: Evolutionary dynamics across scales I

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:55 AM

Evolutionary dynamics: How flexible responses maintain stability yet drive change

Renee Duckworth, University of Arizona

Abstract:

9:55 AM - 10:20 AM

Origin of life from a multilevel selection perspective

Eugene Koonin, NIH

Abstract:

There are two fundamentally distinct but inextricably linked types of biological evolutionary units, reproducers and replicators. Reproducers are cells and organelles that reproduce via various forms of division and maintain the physical continuity of compartments and their content. Replicators are genetic elements (GE), including genomes of cellular organisms and various autonomous elements, that both cooperate with reproducers and rely on the latter for replication. All known cells and organisms comprise a union between replicators and reproducers. Thus, origin of life and subseqeunt major transitions in evolution can be adequately analyzed only within the multilevel

selection framework whereby selection occurs at different levels and during evolutionary transitions, the agency of selection is transferred from a lower to a higher level of organization. I will explore a model in which cells emerged via symbiosis between primordial "metabolic" reproducers (protocells) which evolved, on short time scales, via a primitive form of selection and random drift, and mutualist replicators. Mathematical modeling identifies the conditions, under which GE-carrying protocells can outcompete GE-less ones, taking into account that, from the earliest stages of evolution, replicators split into mutualists and parasites. Analysis of the model shows that, for the GE-containing protocells to win the competition and to be fixed in evolution, it is essential that the birth-death process of the GE is coordinated with the rate of protocell division. At the early stages of evolution, random, high-variance cell division is advantageous compared with symmetrical division because the former provides for the emergence of protocells containing only mutualists, preventing takeover by parasites. Critically, in this model, selection initially affects individual reproducers and replicators but, with the origin of cells, the selective pressure is transferred to reproducers-replicator holobiont. These findings illuminate the likely order of key events on the evolutionary route from protocells to cells.

10:20 AM - 10:45 AM
Between Chance and Necessity: On the dynamic origins of specificity in evolution

Alex Badyaev, University of Arizona

Comparative Biology I

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM
Functional Implications of Ear Loss in Sand Lizards

Kelsey Jenkins, Smithsonian National Museum of Natural History
Kevin de Queiroz, National Museum of Natural History

Abstract:

Despite its advantages, tympanic hearing was secondarily lost multiple times within tetrapods. Loss of a sensory structure often implies a shift to new environments. However, the loss of tympanic hearing within North American sand lizards (Callisaurini) has eluded explanation. To explore the evolutionary reduction and loss of tympanic hearing within this clade, we created 3D models of the stapes to analyze morphological differences. Then, we determined if those morphological differences impact stapedial movement using harmonic response analysis (HRA). We also included the stapes of the callisaurin sand lizards along with those of a diversity of other

squamatans in phylogenetic linear discriminant analyses to determine if stapes of tympanic and atympanic species differ morphologically, and if the presence or absence of limbs, lifestyle, or diet influence stapedial morphology. We found that earless taxa (Cophosaurus, Holbrookia) have stapes that resemble those of other atympanic squamates, while the eared taxon Uma has stapes that resemble those of tympanic squamates. However, the eared taxon Callisaurus possesses an intermediate stapes between those of Uma and the atympanic species. Similarly, it was less prone to displacement within the HRA than other eared species. We found that neither lifestyle nor diet could explain differences in ear morphology within this clade. This suggests that ear loss in this clade is either due to a relaxation of selection on the ear, or more likely, differences in substrate use resulted in selection on the ear that influences both stapedial shape and tympanum loss, perhaps for the transmission of low-frequency vibrations through substrate.

9:45 AM - 10:00 AM
Comparative Genomics of Pine Needle-Associated Fungi

Gabriel Silva, Auburn University CFWE

10:00 AM - 10:15 AM
Rostral suture complexity and digging mode importance in rodents

Saxton Strassberg, University of Chicago
Kenneth Angielczyk, Field Museum of Natural History

Abstract:

Mammalian cranial ecomorphology is well studied, but the effects of locomotion and ecology on cranial suture shape and complexity have received less attention. Suture morphology is highly variable across both suture types and taxa and has been demonstrated to correlate with diet or function in certain groups (e.g., horn clashing in male wild sheep). Outside laboratory rats and mice, rodent suture morphology is especially poorly studied. Fossoriality, particularly the usage of chisel-tooth and/or head-lift digging, may increase biomechanical demands on rodent crania and thus influence suture morphology. We surveyed premaxillofrontal (PMF) and nasofrontal (NF) suture morphology across 107 rodent species representing all suborders and 24 families, using sinuosity index (SI) and short-time windowed Fourier transform with a power spectrum density (PSD) calculation as metrics of complexity. The NF consistently exhibits greater intraspecific variance than the PMF, indicating potential differences in morphological lability across the two sutures. Relationships between suture complexity and digging mode importance differ across clades. Murids have consistently elevated SI, especially of the PMF, possibly reflecting uniform structural stresses rather than ecomorphological differences. Higher PMF SI values tend to correlate best with scratch digging, rather than chisel-tooth or head-lift digging, across Rodentia and within most suborders, but within Hystricomorpha, both SI and PSD strongly reflect chisel-tooth digging usage. Spalax leucodon, the sole specialized head-lift digger, exhibits elevated PMF PSD but significantly reduced NF PSD, suggesting suture-specific functional demands imposed by

this digging mode. Rodent suture morphology and complexity vary widely, even within species, and phylogeny may mediate how fossoriality-related stresses influence aspects of suture morphology.

10:15 AM - 10:30 AM
The impact of degenerate sex chromosomes (Y|W) on sex-specific survival in insects

Calvin Belton, The University of Kansas (KU)
James Walters, University of Kansas
Arjen van 't Hof, Institute of Entomology

Abstract:

Among animals, one sex typically is shorter lived than the other, but which sex is shorter lived differs across taxa. For taxa with XX/XY sex-determination systems the males tend to be shorter lived, whereas taxa with ZZ/ZW sex-determination systems the females are typically shorter lived. So while the shorter-lived sex changes, it appears consistent that the sex with heterogametic sex-chromosomes is typically shorter lived. This pattern may reflect the "toxic Y hypothesis", which suggests that the degenerate sex chromosome (e.g. Y or W) causes a shorter lifespan in the sex that possesses it. We have tested this hypothesis with experiments within two study species, D. affinis (a fruit fly) and B. anynana (a butterfly), both with natural variation in the presence of the degenerate sex chromosome. In D. affinis, XY males outlived XO males, but in B. anynana ZO females outlived ZW females. This suggests that while the degenerate sex chromosome may negatively affect longevity across some species, in other species its impact may be beneficial, or offset by other species-specific factors that also influence longevity.

10:30 AM - 10:45 AM
Janzen's Hypothesis in the Understory

Martha Muñoz, Yale University

Abstract:

Classic ideas about climate adaptation often assume that organisms experiencing similar climates should evolve in similar ways. Yet species do not experience climate passively. Through behavior, habitat use, and movement, organisms can alter their exposure to environmental conditions, potentially reshaping both the strength and direction of selection. This talk revisits these ideas through the lens of Janzen's hypothesis and related theory on climatic specialization in the tropics. Using reptiles and amphibians as model systems, I explore how behavioral interactions with the environment influence evolutionary responses to climate across contemporary and macroevolutionary timescales. Drawing on long-term resurveys and comparative physiological datasets, I illustrate how closely related species exposed to similar regional climates exhibit markedly different physiological trajectories depending on how they use their environments. Some lineages appear to track warming through physiological adjustments, whereas others remain

comparatively stable despite substantial environmental change. Thermal ecology, not phylogenetic or geographic proximity, predicts physiological evolution at micro- and macroevolutionary scales.

Evolutionary Ecology I

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Microhabitat and Climatic Niche Evolution in Frogs

Julia Laterza Barbosa, Yale University
Martha Muñoz, Yale University
Laura Alencar, Yale University

9:45 AM - 10:00 AM

The pace and scale of climatic niche divergence in woodland salamanders

Brian Waldron, Yale University
Nathalie Alomar, Yale University
Martha Muñoz, Yale University

Abstract:

Climatic niche divergence may be an important driver of diversification. However, tests often rely on occurrence data with strong spatial and phylogenetic patterns that may or may not result from climatic causes. Using the woodland salamanders as a model system, we used a variety of comparative methods to address whether clades with strongly parapatric or allopatric distributions show evidence of climatic niche divergence, while accounting for availability of climates in environmental space.

10:00 AM - 10:15 AM

Rare today, common tomorrow: Evolutionary transitions and non-equilibrium dynamics shape species rarity

Alivia Nytko, University of Tennessee
Brian O'Meara, University of Tennessee - Knoxville

Abstract:

Common species are alike, but each rare species is rare in its own way. By using ecological and evolutionary factors to characterize these differences, we can identify species that are geographically rare in their range size, functionally rare in their traits, and/or phylogenetically rare in their evolutionary history across regional and local scales. There are many ecological and

anthropogenic drivers of modern rarity, but there are also key evolutionary processes that have contributed to the existence of multidimensional rarity through time. Using the regional and local geographic, functional, and phylogenetic rarity of 1,011 British plant species, we applied univariate and bivariate hidden state speciation and extinction models to 1) investigate the ancestral origins of rarity, 2) predict the equilibrium frequency of rarity, 3) characterize evolutionary transitions between rarity and commonness, and 4) examine the diversification processes associated with rarity. Looking at one dimension of rarity alone, rare lineages tended to have lower net diversification rates, but when looking at pairs of rarity dimensions, results were mixed and lineages rare in two dimensions often diversified faster than those rare in only one dimension. While rarity represented the most probable ancestral state for most dimensions, rarity was predicted to occur in very low frequency at equilibrium. The current prevalence of rare species is likely driven by a combination of ecological factors and non-equilibrium dynamics; however, state changes between rarity and commonness occurred very rapidly. Unexpectedly, rare lineages were more likely to become common rather than go extinct. Taken together, these results suggest that rarity has likely existed as an ecologically important, but ephemeral state driven by a combination of anthropogenic factors, non-equilibrium evolutionary dynamics, and rapid transitions from commonness, rather than differential diversification.

10:15 AM - 10:30 AM
Bioclimatic predictors, not latitude, explain global wMel Wolbachia frequency variation in Drosophila melanogaster

Nitin Ravikanthachari, University of Montana

10:30 AM - 10:45 AM
Longitudinal, multi-species approaches reveal conserved and divergent mechanisms of disease resilience

Lauren Fuess, Texas State University
Erin Shilling, Texas State University
Alex Veglia, University of Puerto Rico Mayaguez
Ashely Rossin, NOAA Atlantic Oceanographic & Meteorological Laboratory
Grace Klinges, Island Conservation

Abstract:

Increasing evidence suggests that metazoan immune systems are exceptionally diverse and capable of significant evolutionary diversification. However, understanding of the evolution of these defenses has been limited due, in part, to taxonomic bias in historical immunological studies. Indeed, understanding of the diversity of immune responses within and amongst early diverging metazoans is limited, impacting understanding of both the diversity of these traits across the metazoan tree of life, and the evolutionary origins of complex immunological processes. Here, we leverage a multi-species natural experiment to quantify diversification of immune responses in reef-building corals (Phylum Cnidaria). Using repeated-sampling approaches, we assessed

differences in gene expression among four species of coral through the onset of a novel disease outbreak (Stony Coral Tissue Loss Disease). We identified transcriptomic signatures of both disease resistance and response, using an orthogroup-based approach to identify conserved and divergent signatures. Results indicate the mechanisms of disease resistance are highly divergent amongst species, whereas response to disease is largely conserved. Furthermore, preliminary analyses found no association between gene family size variance and specificity of responses, suggesting adaptive changes in copy number variation play a limited role in immune variation. Combined, these results significantly enhance our understanding of the mechanisms and consequences of variation in immune responses and inform understanding of the evolution of metazoan immunity.

Genomics: Bioinformatics and Molecular Evolution

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Poolseq analysis of color in Chelymorpha alternans

Sam Kubica, Boston University
Lynette Strickland, Boston University

Abstract:

One in every four described species is a beetle, but they remain understudied, especially the largest suborder Polphaga, which includes the diverse family of leaf beetles, Chrysomelidae. Chelymorpha alternans is a tropical species of tortoise beetle (Coleoptera: Chrysomelidae: Cassidinae) with five color phenotypes. The color phenotypes are Rufipennis (beetles with solid red elytra and black pronotums), Militaris-a (beetles with red elytra and pronotums both striped in black), Militaris-b (beetles with red elytra striped in black with solid black pronotums), Veraguensis (beetles with solid red elytra and pronotums) and Metallic (beetles with red elytra and pronotums both with metallic gold stripes). The inheritance pattern of these phenotypes has already been determined, but the exact gene has yet to be. Rufipennis results from the dominant Rufipennis allele which is codominant to the Militaris phenotype. Militaris-b results from both alleles. Both Rufipennis and Militaris are dominant to Veraguensis, while the Metallic allele is fully recessive. Based on samples collected at four sites in Panama (San Lorenzo n=18, Gamboa n=27, Santa Rita Ridge n=27, Darien n=28), I have utilized a PoolSeq pipeline to identify regions of variance between two color phenotypes of C. alternans. The two phenotypes are Metallic and Rufipennis. I then used BLAST to identify candidate genes from these regions. Results suggest that populations of the two color phenotypes at the four sites exhibit a high degree of relatedness, except for one population—the rufipennis population from Gamboa— which shows a distinct genetic structure. This research elucidates more about the genetics of color in a diverse, but understudied clade.

9:45 AM - 10:00 AM
Sex Chromosome Identification by Negating Kmer Densities (SCINKD)

Brendan Pinto, Milwaukee Public Museum

Abstract:

In most animal species, the sex determining pathway is typically initiated by the presence/absence of a primary genetic cue at a critical point during development. This primary genetic cue is often located on a single locus—referred to as sex chromosomes—and can be limited to females (in a ZZ/ZW system) or males (in an XX/XY system). One hallmark of sex chromosomes is a restriction or cessation of recombination surrounding the sex-limited region (to prevent its inheritance in the homogametic sex). This may lead to—through a variety of mechanisms—higher amounts of genetic divergence within this region, i.e. between the X/Z and Y/W chromosomes, especially when compared to their autosomal counterparts. Recent advances in genome sequencing and computation have brought with them the ability to resolve haplotypes within a diploid individual, permitting assembly of previously challenging genomic regions like sex chromosomes. Leveraging these capabilities, researchers can rapidly and robustly identify and characterize sex chromosomes across diverse lineages using as few as one to four individuals. The original Sex Chromosome Identification by Negating Kmer Densities (SCINKD) framework has begun to see broad adoption for both sex chromosome identification and genome curation. We are now expanding SCINKD to support systems and datasets for which the original tool is insufficient, developing multiple workflows that share a common conceptual foundation but provide the flexibility needed to accommodate diverse data types and numbers of individuals.

10:00 AM - 10:15 AM
Evolution and specialization of mammalian skeletal muscle myosins

Caroline Kauh, The Ohio State University
James Pease, The Ohio State University
Christina Harvey, Wake Forest University

10:15 AM - 10:30 AM
Transposable element and gene family evolution across Rhabditomorpha

Victoria Eggers, Florida International University
Janna Fierst, Florida International University
Jason Pienaar, Florida International University

Abstract:

Transposable elements (TEs) are mutable loci in a genome which may replicate independently from the genome. TEs vary greatly with over 40 known superfamilies and specific families can increase or decrease the mutability of a surrounding genomic region. TEs may also interact with one another

(autonomous and nonautonomous) or proteins meant to suppress TEs, such as Argonaute proteins. Yet theoretically, the persistence and spread of TEs within populations depends on patterns of effective recombination, which is connected to species traits like mating system. To test some of these patterns we re-annotate the genomes of 85 Rhabditidae nematodes using BRAKER3 and EarlyGrey. Orthofinder, KinFin, and CAFE5 are used to assess gene and repeat content across the phylogeny. Multivariate Ornstein-Uhlenbeck models are implemented to statistically analyze how the genomic features affect the evolution of nematode genomes.

10:30 AM - 10:45 AM
Strong Overdominance Explains the Persistence of the In(2L)t Inversion

Jingqi Liu, University of Virginia
Alan Bergland, University of Virginia

Abstract:

Chromosomal inversions are involved in many important evolutionary processes by suppressing recombination and preserving gene combinations. In Drosophila melanogaster, In(2L)t is a 11Mb paracentric inversion that contains ~1500 protein-coding genes, and is maintained at an average global frequency of 15 - 20%. While this inversion has been linked with an activity-survival tradeoff contributing to seasonal adaptation, ecological selection alone may not fully explain its persistence. Heterozygote advantage could also play an important role, arising through a mixture of true overdominance, where heterozygotes carry an intrinsic advantage, and associative overdominance, where heterozygosity masks recessive, linked deleterious mutations. Supporting hypothesis of overdominance, we found that In(2L)t remains heterozygous in isolated lineages established from one wild-caught female even after more than 100 generations of laboratory maintenance. This persistence is unexpected given the small population size of these lines, where genetic drift should drive a single arrangement to fixation.

To investigate whether these forms of heterozygote advantage can explain the observed persistence of In(2L)t, I integrated SLiM 5 forward genetic simulations with inversion genotype and frequency data from our lab and published resources, and estimated the strength of heterozygote advantage and the distribution of deleterious fitness effects using Approximate Bayesian Computation. We show that the observed global frequency of In(2L)t and the high heterozygosity in lab-maintained isofemale lines were best explained by models with strong true overdominance, with a 5–10% heterozygote fitness advantage associated with the inversion. These results suggest that an intrinsic heterozygote advantage is likely required for the maintenance of In(2L)t in small laboratory populations.

Molecular Evolution I

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM
Disulfides in deep time

Riley DeHority, Louisiana State University - Biological Sciences
Jeremy Brown, Louisiana State University

9:45 AM - 10:00 AM
Convergent and lineage-specific evolution at different genetic levels in arid-adapted Thamnophilus antbirds

Kelsie Lopez, Harvard University
Gustavo Bravo, Harvard University
Scott Edwards, Harvard University

Abstract:

Repeated, independent habitat transitions into similar environments provide powerful systems for investigating the genetic basis of adaptation and assessing convergent responses to shared environmental challenges. However, we still lack a clear understanding of the genetic levels of organization (e.g., nucleotide, gene, regulatory element, or pathway) at which adaptive molecular convergence occurs. Thamnophilus antbirds have repeatedly colonized South American Seasonally Dry Tropical Forests (SDTFs), which are characterized by intense, highly seasonal drought. To assess convergence across genetic levels, we generated 11 new genomes and 202 tissue-specific transcriptomes from five key tissues (liver, heart, muscle, kidney, and brain) in five independently evolved dry-forest lineages and their humid-forest sister taxa of Thamnophilus antbirds. Phylogenetic comparative analyses revealed repeated signatures of selection in both protein-coding and regulatory regions of genes associated with metabolism and oxidative stress, overlapping gene candidates previously implicated in desert-adapted mammals. Integrating tissue-specific gene expression with their putative regulatory elements, we found convergent changes across different components of the Renin-Angiotensin-Aldosterone-System signaling pathway, a central regulator of blood pressure and sodium balance, pointing to pathway-level convergence in osmoregulatory and cardiovascular function. Finally, we identified convergent regulatory evolution near ATP1A1, an ion transport gene whose regulatory region in antbirds overlaps a genomic region previously associated with variation in eggshell thickness and strength in birds. This gene has also been implicated in thermal and aridity adaptation in mammals, suggesting potential pleiotropic roles in avian egg structure and physiological responses to aridity. Together, our results demonstrate that repeated adaptation of Thamnophilus antbirds to SDTFs involves convergent evolution at multiple genetic levels, from individual genes to pathways, and reveals shared

molecular solutions with other arid-adapted vertebrates alongside lineage-specific mechanisms for coping with extreme seasonal drought.

10:00 AM - 10:15 AM
Investigating the evolution of epigenetic aging and longevity across mammals

Adeyemi Akinade, Clemson University
Shyamalika Gopalan, Clemson University

Abstract:

Why individuals age, and why species differ in their rates of aging, is an evolutionary puzzle. A major barrier to resolving this puzzle is our limited understanding of the underlying mechanisms of aging. However, recent advances in DNA methylation (DNAm) technology have created new avenues to address this long-standing problem. DNAm at thousands of genomic loci changes with age in a clock-like manner, enabling accurate prediction of individual age. While many regions of the genome exhibit age-association in multiple species, their rates of change differ, reflecting variation in species longevity. Here, we applied phylogenetic comparative methods to test how DNAm rates co-evolve with longevity across mammals. We analyzed DNAm data from 61 mammalian species, profiling ~37,500 methylated loci (i.e. CpG sites) across two tissues, whole blood and skin. We used linear regression to estimate DNAm aging rates at each CpG site and tested for evolutionary correlation with maximum lifespan, corrected for body size. CpG sites exhibiting negative correlation (i.e., where slower DNAm rate was associated with longer lifespan) were enriched near genes involved in development, cellular maintenance, autophagy, oxygen sensing, and metabolism. Interestingly, two of these genes – ELP4 and HIF1AN – have previously been identified as playing a role in modifying longevity in model organisms but have not yet been directly implicated in mammalian aging. Collectively, these findings demonstrate that DNAm rates represent a suite of molecular traits that, when analyzed within a phylogenetic framework, can uncover conserved pathways and novel genetic regulators of aging biology.

10:15 AM - 10:30 AM
The appearance of divergent noncoding transcripts from coding promoters in lobe finned fish

Brent Basso, Cornell University
Edward Rice, Cornell University
Charles Danko, Cornell University
John Lis, Cornell University

Abstract:

Mammalian cis-regulatory elements (CREs), including promoters and enhancers, are transcribed by RNA polymerase II in a manner which produces a pair of divergently oriented transcripts; one in the coding (sense) direction and another in the reverse (antisense) direction. However, antisense transcripts are absent in the model species D. melanogaster and other clades. Here we sample 46 species and demonstrate that divergent transcription first appeared in a common ancestor of lobe finned fishes, predecessors to the earliest tetrapods. This change could be mediated by the cis-

regulatory function of DNA sequence at CREs or by trans-regulatory changes driven by proteins involved with transcriptional initiation; these options are not mutually exclusive, and we explore both. Using conventional and machine learning techniques, we show that DNA sequence may drive nucleosome positioning around CREs in the many species with unidirectional promoters. A change in this architecture, coinciding with changes in the structure of core initiation factor TAF3 and its new binding partner CTCF, may have been permissive to the divergent transcription we observe ubiquitously in the lobe finned lineage.

10:30 AM - 10:45 AM

Genomic diversification shapes the regulatory deployment of a key innovation across chemical environments

Paula Fernandez Begne, University of Chicago

Abstract:

Key innovations, traits that open new ecological opportunities and fuel diversification, are central to explaining biodiversity patterns across the tree of life. Yet the genomic mechanisms that allow these innovations to persist and diversify across heterogeneous environments remain poorly understood. Gene duplication is a primary source of such innovations, but the downstream genomic changes that shape how duplicates are retained, organized, and deployed across environments are rarely characterized. Pierinae butterflies evolved nitrile-specifier proteins (NSPs) to neutralize the glucosinolate chemical defenses of their Brassicales host plants, a key innovation that enabled one of the most successful adaptive radiations in phytophagous insects. Here we leverage this system to examine how genomic and regulatory mechanisms govern the deployment of a key innovation across chemically heterogeneous environments. We generated high-quality genomes and characterized copy-number variation (CNV) in NSPs across 40 taxa, revealing extensive variation across Pierinae. Notably, two lineages that independently colonized Brassicaceae, the largest and most chemically diverse family within Brassicales, did so through distinct genomic trajectories: gene duplication and divergence, and copy number expansion. To dissect the regulatory consequences of these divergent genomic trajectories, we applied integrative RNA-seq and ATAC-seq in Pieris and Anthocharis, two representative taxa of each trajectory. NSPs in Pieris exhibit paralog-specific chromatin accessibility and transcriptional induction across divergent glucosinolate profiles, while NSPs in Anthocharis show no plastic response. Region-specific transcriptomics further reveals a functional division of labor along the gut axis, with detoxification programs (including NSPs) enriched in the anterior midgut, suggesting that spatial deployment of key innovations is as important as their induction in enabling herbivore success. Our results demonstrate that convergent ecological shifts can be mediated by different regulatory architectures. Together, these results demonstrate that the genomic history of a gene family shapes the regulatory solutions available to lineages navigating chemical complexity.

Pathogens

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Genome-wide association of nutrient-use and pathogenicity in grey mold (Botrytis cinerea)

Belinda Kincade, Louisiana State University

Abstract:

Botrytis cinerea is a generalist necrotrophic fungal pathogen capable of infecting thousands of plant species, potentially requiring high metabolic flexibility to acquire nutrients, tolerate stress, and overcome host defenses. Despite the ecological and economic importance of host-generalist pathogens, the genetic basis of nutrient-use strategies and their relationship to virulence remains poorly understood. This project investigates how variation in nutrient-use diversity correlates with virulence traits. Using 96 wole-genome-resequenced B. cinerea isolates, we quantified in vitro growth and metabolic activity across 31 carbon sources, using fluorescence imaging and resazurin-based respiration assays. Genome-wide association (GWA) and phenotype correlations with existing virulence trait data identified co-localized loci underlying nutrient-use diversity and pathogenicity, indicating potential trait trade-offs. By linking metabolic flexibility to pathogenic fitness, this work aims to reveal the evolutionary pressures shaping trait variation in generalist pathogens and understand novel elements of pathogenicity.

9:45 AM - 10:00 AM

Population connectivity and weak genomic structure of a dominant fungal associate of brown spot needle blight

Temitope Folorunso, Auburn University
Gabriel Silva, Auburn University CFWE
Janna Willoughby, Auburn University
Rabiu Olatinwo, USDA
Lori Eckhardt, Auburn University

10:00 AM - 10:15 AM

Narrow roads of gene loss: evidence for predictable genome streamlining in Dictyostelium-associated endosymbionts

Calum Stephenson, Washington University in St. Louis
Laura Walker,
Suegene Noh, Colby College

Joan Strassmann, Washington University in St. Louis
David Queller, Washington University in St. Louis

Abstract:

Under prolonged relaxed selection, bacterial genomes can become remarkably small, a process known as genetic streamlining. This is common among endosymbiotic bacteria that spend substantial time inside host cells, where a simple and stable environment can relax selection for traits necessary for survival alone. But is gene loss predictable?

We tested whether genes later lost during host-driven genome reduction were already unusually variable in related lineages that still retain them, using independently derived Paraburkholderia symbionts at different stages of adaptation to the same amoeba host, Dictyostelium discoideum. One lineage, composed of P. bonniea and P. hayleyella, has undergone significant gene loss and genome size reduction, while the other, P. agricolaris, has not. We hypothesized that genes uniquely lost in the reduced lineages would show signs of incipient loss in other Paraburkholderia, and especially in the unreduced symbiont, P. agricolaris. To test this, we constructed a genus-wide pangenome with 19 Paraburkholderia species and used it to define three gene sets: core genes shared by all, genes lost early in both reduced species, and genes lost late in only one reduced lineage. We then calculated within-species nucleotide divergence and modeled pN/pS for each set using multiple representative isolates of three free-living Paraburkholderia species, three broadly symbiotic Paraburkholderia species, and P. agricolaris. All groups showed elevated nucleotide divergence and pN/pS among lost genes relative to core genes. However, only P. agricolaris was more likely to show detectable pN/pS in genes lost early than in genes lost late, consistent with parallel evolutionary dynamics during initial host adaptation. Together, these results show that genome reduction in Paraburkholderia is non-random. Genes lost in reduced symbionts are drawn from a variable subset of the core genome, and the order of loss is already detectable in P. agricolaris, an unreduced D. discoideum symbiont following a similar evolutionary path.

10:15 AM - 10:30 AM

Ancestral state reconstruction of MRSA transmission over 17 years in Chicago

Stephanie McGimpsey, University of Michigan

Abstract:

Staphylococus aureus is a common cause of community- and healthcare-acquired bacterial infections. USA300 is a methicillin-resistant S. aureus strain that is prevalent in the USA and has been shown to disproportionately affect underserved urban populations in settings such as Chicago. Therefore, it is important to understand the transmission of USA300 between distinct socioeconomic areas in Chicago so social and health initiatives can be put in place to reduce transmission to lower the healthcare burden. Using a dataset of ~3,000 Chicago USA300 cases collected from 2004-2020 I will discuss the use of ancestral state reconstruction tools to determine

how USA300 is transmitting within Chicago and the changes over time. I will also use ~9,000 publicly available USA300 genomes from around the world to identify the potential import or export of sublineages of USA300. I will also show how gene and plasmid acquisitions are impacting transmission. Together, these analyses paint a picture of MRSA USA300 transmission in Chicago communities.

Species Delimitation

06/21/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

High resolution micro-CT data elucidate species boundaries in morphologically conserved yellow bats

Sydney Decker, The Ohio State University
Bryan Carstens, The Ohio State University

9:45 AM - 10:00 AM

Localised hybridisation events explain the genetic structure and morphological variants in a widely distributed ginger within the Indian subcontinent: understanding species complexes in the tropics

Vinita Gowda, Indian Institute of Science Education and Research Bhopal
Aleena Xavier, IISER Bhopal
Ajith Ashokan, University of Naples Federico II

Abstract:

Widely distributed (WD) species often exhibit phenotypic and genotypic variations across their distributional range, typically attributed to selection or neutral evolutionary processes. However, the role of hybridisation in intraspecific genetic variations have been rarely investigated. We tested if range-wide variation in WD species emerge from dispersal constraints or from localised hybridisations with syntopic congeners, or both.

We tested this in the morphologically variable ginger, Hedychium spicatum, a WD understory herb of the Asian tropical montane region. Our previous studies have extensively studied the interspecific reproductive incompatibilities, morphological trait variations and cases of cryptic species and taxonomic boundaries using standard phylogenetic methods. Here, we used single-nucleotide polymorphisms and simple sequence repeats, to assess whether genetic variability is explained by dispersal constraints (IBE, IBD and IBR), demographic history, and hybridisation events.

Our analyses reveal genetic heterogeneity among populations, with gene flow identified between H. spicatum and at least five co-occurring congeners, which explained the morphological intermediates and syngameons. Population differentiation was shaped by demographic fluctuations linked to Himalayan glaciations, and geographic barriers such as the Brahmaputra gap. The disjunct Western Ghats population represents a long-distance dispersal event from the Himalayas that shows signs of progenitor–derivative speciation facilitated by hybridisation.

In summary, we identified emergent-system-like characteristics in the genetically and taxonomically complex WD H. spicatum, and show speciation on a spatial scale aided by hybridisation, dispersal, and historical processes. We propose that patterns identifed in the Spicatum complex are probably common among many plant groups from the Indo-Malesian region that are known to have recent origin and where interspecific reproductive barriers are absent. Therefore, the natural outcome of hybridisation in the wild are: presence of fertile intermediates with higher genetic admixtures than those expected from older lineages and lack of taxonomic boundaries. We propose that both higher taxonomic diversity and presence of species complexes may be linked, and need to be carefully examined in the tropics to understand speciation events, and maintenance of genetic diversities.

10:00 AM - 10:15 AM
Biomonitoring 2.0 Refined: observing local change through metaphylogeography using a community-based eDNA metabarcoding monitoring network

Andrew Riley, University of Guelph

Abstract:

Multiple layers of biological data are necessary to inform and support actions combatting the ongoing biodiversity crisis. DNA metabarcoding is a widely used approach for the detection of organism at the species and genus level. Biomonitoring 2.0 Refined showcases how intraspecific diversity can be accessed for multiple species from bulk DNA metabarcoding data. Understanding intraspecific diversity is essential for tracking population distribution and movement, which supports conservation planning. However, extracting reliable intraspecific information from metabarcoding data remains challenging due to qualitative and quantitative limitations that can affect the accuracy of inferences.

An analysis of intraspecific genetic variation on benthic arthropods was performed using samples collected by the STREAM community-based monitoring project. DNA metabarcoding data included results for two non-overlapping amplicons that were used to evaluate reproducibility. Samples were collected from the eastern Rocky Mountains and were divided into four groups separated by mountain ranges. Using a PERMANOVA analysis, significant separation was observed between the regions at both the community and intraspecific-level, matching the expectation that mountains

will act as a barrier to dispersal over multiple timescales. At the intraspecific level, two regions exhibited significant spatial structuring, while all regions showed significant structuring at the community level. These patterns were consistent across both genetic markers.

Our findings demonstrate that DNA metabarcoding can be effectively applied to intraspecific diversity analyses and produce robust results across different amplicons. This approach allows probing intraspecific and community based genetic variation for a large number of species directly from bulk samples, setting the stage for linking biodiversity monitoring and conservation planning at scale.

10:15 AM - 10:30 AM

The genomic complexity of invasion: cryptic lineages, founder effects, and polygenic sex determination in armored catfish

Wynne Radcliffe, University of Chicago

Abstract:

Genetic biocontrol approaches offer promising tools for managing invasive species. However, their success depends on species identity, demographic history, and the genomic architecture of sex determination, which remain poorly resolved for many non-model taxa. We integrated high-quality genome assembly, whole-genome resequencing, and population genomics to evaluate biocontrol feasibility in invasive suckermouth armored catfish (Loricariidae) in Texas. Mitochondrial phylogenies and genome-wide SNPs revealed cryptic diversity, with distinct lineages from at least two genera (Hypostomus and Pterygoplichthys) exhibiting strong drainage-level genetic differentiation. Effective population size estimates were exceptionally low, consistent with founder effects and moderate inbreeding. Genome-wide association analyses detected no large-effect loci for sex in either genus, despite high statistical power in Hypostomus, suggesting that sex determination is polygenic and/or environmentally influenced. These results identify key biological constraints for sex-ratio-based biocontrol and underscore the importance of genomic assessments prior to management interventions. More broadly, our study highlights how integrating genomic resources, demographic inference, and evolutionary context can guide invasive species control strategies.

10:30 AM - 10:45 AM

Integrative Systematics of Calcarea: A New Species from the Eastern Pacific

Raisa Campos Rizzieri, Stony Brook University
Robert Thacker, Stony Brook University

Abstract:

As part of a broad investigation of calcareous sponges (Class Calcarea) from the Pacific Coast of North America, we are using an integrative taxonomic approach to study specimens collected at the University of Washington Friday Harbor Laboratories. Previously identified as Sycon raphanus

(de Laubenfels, 1961), these specimens exhibit distinct morphological and molecular characteristics that distinguish them from currently recognized species.

We examined the specimens' exteriors and histological sections using light microscopy. We isolated spicules by digesting sponge tissue with bleach, then imaged and measured them using scanning electron microscopy. We extracted genomic DNA using Qiagen's DNeasy PowerSoil Pro Kit. We amplified the most commonly used genetic marker for subclass Calcaronea, the large ribosomal subunit (LSU or 28S). We pooled equimolar amounts of indexed amplicons to construct a sequencing library, which was sequenced using an Oxford Nanopore Technologies platform, following the manufacturer's protocol. We aligned and edited sequences with sequences previously deposited in GenBank using MAFFT. We constructed a maximum-likelihood phylogenetic tree using the best-fitting evolutionary model, with 1000 bootstrap replicates.

Our analyses indicated that these Sycon specimens are distinct from other described taxa in the genus. This work contributes to improving taxonomic resolution in calcareous sponges and the relevance of combining morphological and molecular data in sponge systematics. Our study supports broader efforts to document marine biodiversity and refine species delimitations in understudied groups.

Adaptation and Ecology I

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Range-wide pangenomics reveals vulnerability and adaptation in a sedentary bird

Jong Yoon Jeon, Purdue University

Abstract:

Structural genetic variants play key roles in evolution, but their contributions to adaptation have never been evaluated across the entire geographic range of a species in a conservation context. The Montezuma quail (Cyrtonyx montezumae), a ground-dwelling bird inhabiting arid and montane habitats from southern Mexico to the southwestern United States, provides an opportunity to address this gap. Habitat degradation, fragmentation, and climate-driven shifts threaten the species across much of its range, and isolated peripheral populations in Texas exhibit reduced genetic diversity that limits evolutionary potential.

Here we construct a species-wide pangenome and integrate structural variant (SV) diversity with phenotypic and environmental data in an landscape-level framework to characterize adaptation profiles, identify SVs associated with local adaptation, and infer environmental vulnerability. We

identify profiles of local adaptation driven primarily by winter climate and overall climate variability, distributed along an east–west gradient. Patterns of adaptive variation, population structure, and genomic diversity support a ring-like historical range expansion consistent with the central–marginal hypothesis and glacial refugia theory, whereby diversity was greatest in the core south of the species' range and reduced in the peripheral north. SV-based genomic offset analyses and forward-time simulations consistently indicate that isolated Central Texas populations are particularly vulnerable under projected climate scenarios, but those threats could be alleviated by genetic rescue should authorities decide to pursue proactive conservation strategies.

Our results highlight the importance of structural variation in shaping adaptive potential and suggest that proactive genetic rescue could alleviate climate-associated risk in fragmented peripheral populations of this secretive bird.

11:30 AM - 11:45 AM
Characterizing adaptive CBF2-dependent transcriptomic responses during cold acclimation

Stephen Mills, Purdue University
Samuel Mantel, Purdue University
Emily Lancaster, Purdue University
Christopher Oakley, Purdue University

11:45 AM - 12:00 PM
Genomic basis of adaptation to salinity gradients in a high dispersal marine keystone species

Abdul Ada, Louisiana State University
Morgan Kelly, Louisiana State University

Abstract:

A major goal of evolutionary biology is to understand how broadly distributed species adapt to heterogeneous environments despite gene flow. In this study, we used a low-coverage whole-genome sequencing approach to compare oyster populations across natural salinity gradients in the Gulf of Mexico (Louisiana and Texas). Changes in salinity disrupt water and ion balance, resulting in osmotic stress, and ultimately impacting oyster fitness, and imposing selection for performance under local salinity regimes. In our sampling sites in the Gulf of Mexico, salinity increases from east to west (Louisiana to Texas), reflecting differences in freshwater input and evaporation. Population structure analyses revealed major genetic breaks between Louisiana and Texas populations, and a minor genetic break between Texas populations. Genotype–environment association analysis of over 4 million SNPs found 183 SNPs that were significantly associated with salinity. These SNPs were not randomly distributed across chromosomes, more than 50% of the SNPs were clustered in chromosomes 4 and 5. We found a major salinity association peak in chromosome 4 where one of the SNPs was in the LOC111128509 gene encoding the sodium

channel protein. This SNP is a nonsynonymous amino acid change between alanine (non-polar) and asparagine (polar) at the protein surface. We tested for recent positive selection in the regions surrounding the candidate SNPs using selective sweep scans. We detected areas under selection in high salinity and low salinity environments. We further tested whether coding or non-coding regions were overrepresented for the salinity SNPs, we found that coding regions were enriched for the salinity SNPs. Additionally, GO enrichment analysis found many terms associated with membrane activity, signaling regulation, and cytoskeleton remodeling. Our results provide insight into the mechanisms of adaptation to osmotic stress and improve predictions of how this ecosystem engineer will respond to future climate change.

12:00 PM - 12:15 PM

Hard sweeps, soft sweeps, and supergenes underlie post-glacial climate adaptation in a boreal moth

James Lewis, Clemson University
Karin van der Burg, Clemson University

Abstract:

Understanding how, when, and where species adapt to variation in climate is increasingly important as the impacts of climate change become more apparent. The precise genetic architecture of climate adaptation, the origin of adaptive alleles, and the role of historical population size and structure in climate adaptation are subjects that remain poorly studied. Here we investigate the genetic basis of climate adaptation in the Eastern Spruce Budworm, Choristoneura fumiferana. Using hundreds of whole-genome sequences from samples across North America, we show that C. fumiferana populations have adapted to local climates, such as variation in winter temperature and precipitation. Unexpectedly, we find that local climate adaptation occurred through a combination of selection on novel and standing genetic variants, and through the evolution of supergenes associated with diapause and cold hardiness. We also show that fragmentation of C. fumiferana into ice-age refugium populations was critical to this adaptive process. Taken together, these findings suggest that Eastern Spruce Budworm may represent an ideal benchmark for climate adaptation and future climate resilience.

12:15 PM - 12:30 PM

Artificial selection for larval heavy metal resistance on adult phenotypes in Drosophila melanogaster

Charlton Miller, University of Oklahoma
Elizabeth Everman, University of Oklahoma

Abstract:

Pollution and pesticide use are leading causes of insect decline (Quandahor et al. 2024). Additionally, many common pesticides contain heavy metals that are toxic to insects (Husak 2015).

Also, exposure to heavy metals during developing stages can have lasting impacts into adulthood and future generations (Halmenschelager and da Rocha 2019; Pölkki and Rantala 2021). Furthermore, heavy metal resistance can be selected for (Martins et al. 2007; Yang et al. 2020), and selection for resistance to one stressor, can lead to increased resistance to other stressors (Harshman et al. 1999; Arnold and Everman 2026). Previously, I found a significant increase in developmental CuSO4 resistance after artificially selecting a wild-caught population of D. melanogaster. To determine whether selection for developmental resistance also led to changes in adult life-history and stress resistance, I measured lifespan, fecundity, adult CuSO4 resistance, and starvation resistance, in a selection population and control population, as well as including treatments where developmental exposure to CuSO4 did or did not occur. There was no effect of selection on fecundity, but selection did lead to significant increases in lifespan. Additionally, there was a significant interaction between developmental selection and developmental exposure, where selection led to significant increases in resistance to adult CuSO4 exposure and starvation in flies without CuSO4 exposure, but when flies were exposed to CuSO4 there was no increase in resistance from selection. These results support that developmental exposure may lead to increases in resistance later in life without having a life-history trade-off, and increases in resistance to CuSO4 may lead to increases in resistance to other stressors.

ASN Vice presidential Symposium: Evolutionary dynamics across scales II

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:40 AM

Social feedbacks alter the genomic consequences of evolution in D. melanogaster

Julia Saltz, Indiana University

Abstract:

Evolutionary feedbacks occur when evolution in one generation alters the environment experienced by subsequent generations and are an expected result of indirect genetic effects (IGEs). Despite the expected importance of feedbacks, it has been difficult to pinpoint the effects of feedbacks in the face of other simultaneous population processes, leaving open questions about the frequency and impacts of feedbacks. Recently, we used experimental evolution investigate evolutionary feedbacks. We experimentally selected 9 replicate populations of fruit flies, D. melanogaster, for increased male aggression alongside unselected controls. Selection treatments differed in the social environment in which aggression was expressed and selected, resulting in replicate populations evolving under positive, negative, or no feedbacks. Here, we tested how these

evolutionary feedbacks influenced the genomic underpinnings of the observed evolutionary changes in behavior. By resequencing pools of flies from each selected and control population to high coverage, we tested hypotheses about how feedbacks influenced patterns of diversity and divergence. We further tested whether feedbacks alter the putative allelic targets of selection by identifying genetic variants whose frequencies differed from that of unselected controls across all replicates. Our results show [some interesting stuff]. These findings suggest that feedbacks may be important to consider when conducting population genomics inference.

11:40 AM - 12:05 PM
Losses, gains, and restructuring of biodiversity currencies: mass extinctions and the times between

David Jablonski, The University of Chicago
Stewart Edie, National Museum of Natural History

Abstract:

Mass extinctions fundamentally alter the biodiversity equation. By definition these rare events drive severe depletions in taxa, but an accounting of extinction should involve multiple currencies, for example: taxonomic richness across hierarchical levels, functional variety comprising different modes of life, morphological disparity as measured in terms of discrete traits or in a continuous multivariate space, and phylogenetic diversity, a measure of evolutionary distances among branches. We focus on the last three of the Big Five mass extinctions (end-Permian at the end of the Mesozoic Era; end-Triassic within the Mesozoic; and end-Cretaceous at the end of the Mesozoic Era), each removing 60-75% of known genus diversity in the oceans, to quantify the decoupling among taxonomic, phylogenetic, and functional diversity lost in these events relative to the longer and more stable intervals in Earth history. In a model system for macroevolutionary analysis, marine bivalves, we find that although more clades and higher taxa are lost summing over “background” times overall, the abrupt loss of taxa at mass extinctions decisively disrupts the functional and phylogenetic structure of the biota. This global reset of biodiversity currencies at the extinction event is generally maintained, not just through the ensuing rebound but until the next mass extinction, 10s of millions of years later.

12:05 PM - 12:30 PM
Towards a modern synthesis of ecology and evolution

Rachel Germain, The University of British Columbia

Comparative Biology II

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Learning to paint a lizard: Uncovering the genetic basis of the red head brown anole, Anolis sagrei

Ben Wortman, University of Georgia

Abstract:

Pigmentation displays remarkable diversity in colors and patterns that play crucial roles in species survival. In vertebrates, this diversity is produced by three major chromatophores (pigment cells): melanophores, iridophores, and xanthophores. However, not all vertebrates possess all three cell types; both mammals and birds lack xanthophores and iridophores. As a result, genetic research on pigmentation has focused primarily on melanophores. Our objective is to advance understanding of pigmentation variation in animals that retain all three chromatophore types. To accomplish this, I am studying natural pigment variations in Anolis sagrei, specifically a red head (RH) morph that occurs at low frequency in both invasive and native populations. This study seeks to understand the biological basis of this trait. To determine whether the RH trait has a clear genetic component, we performed a preliminary GWAS study using RAD-seq data generated from a previous study. This data set comprises several hundred male A. sagrei and includes non-red head (NRH) and RH individuals sampled across Florida. The GWAS results suggest that the RH trait follows Mendelian inheritance and is associated with a 5 Mb region on chromosome 5 containing 30 genes. To further narrow the candidate region and recapitulate initial findings we generated both whole genome sequence and RNA-seq datasets. With this data we narrowed the interval from 5 to 1.3 Mb and identified a single, strong candidate gene. This gene is a novel duplicate of kdr (VEGFR2 protein) which has both non-synonymous mutations associated with RH and is the only gene in the interval that is differentially expressed between RH and NRH (brown head) animals. Moving forward, functional experiments are planned to confirm our results and to determine what cellular changes accompany phenotypic differences in head coloration. This work is supported by NHGRI R01HG013006.

11:30 AM - 11:45 AM

Adaptive obesity and the evolution of bear hibernation

Blair Perry, Michigan State University
Heiko Jansen, Washington State University
Charles Robbins, Washington State University
Joanna Kelley, University of California Santa Cruz

Abstract:

Hibernation is a complex physiological adaptation that enables survival during seasonal resource scarcity. In brown bears (Ursus arctos), hibernation is preceded by a period of hyperphagia in which bears consume massive amounts of food and accumulate large fat stores. Metabolism of accumulated fat sustains bears through the ensuing hibernation season, during which metabolic rates decrease by 75%, multiple tissues become insulin resistant, and bears exhibit pronounced inactivity. Following emergence in the spring, insulin sensitivity is restored. Remarkably, bears experience no adverse effects from this annual cycle of extreme weight gain, inactivity, and metabolic depression. In contrast, obesity in many non-hibernating mammals triggers local and systemic inflammation that leads to metabolic dysregulation, systemic insulin resistance, further weight gain, and numerous pathological conditions. Using single-nuclei RNA-seq from brown bear adipose and comparative genomic analyses across extant bear species, we test the hypothesis that "adaptive obesity" and metabolic flexibility in hibernating bears are enabled, in part, by the evolutionary modification of obesity-induced inflammatory cascades. Broadly, we find coordinated downregulation of pro-inflammatory pathways across multiple adipose cell types during hibernation, many of which sharply contrast with responses observed in non-hibernating models of obesity. Further, we find preliminary evidence for selection on non-coding regulatory sequences associated with key inflammatory genes during bear evolution. Collectively, this work provides evidence that the retooling of inflammatory signaling may have played a critical - and perhaps underappreciated - role in the evolution of bear hibernation and adaptive obesity. Moving forward, investigation of inflammatory pathway activity and evolution across diverse hibernating species may reveal new insight on the evolution of metabolic flexibility and extreme physiological traits.

11:45 AM - 12:00 PM

Elucidating the evolutionary history of the water scavenger beetle beetle subfamily Enochrinae using ultraconserved elements

Peter Willadsen, University of Kansas
Robert Moyle, University of Kansas
Andrew Short, University of Florida

Abstract:

Enochrinae is one of the six subfamilies of Hydrophilidae, the second largest family of primarily aquatic beetles. Enochrinae consists of four genera containing a total of 300 with a cosmopolitan distribution. The relationships among these genera are unresolved and it remains unclear whether the largest genus, Enochrus, represents a monophyletic group. Elucidating the relationships among these lineages will allow us to explore several interesting outstanding questions pertaining to the biogeographic and evolutionary history of this subfamily. We developed a novel ultraconserved element (UCE) probeset and skimmed UCEs from low coverage whole genomes, with representative sampling from across all putative enochrine genera, to reconstruct the first genome-scale molecular phylogeny for this group. This phylogeny represents an important framework for investigating questions about the evolution of morphological and behavioral traits, as well as habitat preferences, within Enochrinae.

12:00 PM - 12:15 PM

Molecular evolution and intraspecific variation of repeat-rich spider silk genes

Amanda Markee, American Museum of Natural History
Richard Baker, American Museum of Natural History
Andrew Mongue, University of Florida
Joseph Arguelles, American Museum of Natural History
Cheryl Hayashi, American Museum of Natural History

Abstract:

Orb-weaving spiders produce multiple functionally distinct silk types, each synthesized in specialized glands. The properties of these silks are determined by spidroins, a complex gene family encoding the primary structural proteins of silk fibers. Spidroins are characterized by their extreme length (20–90 kbp), glycine-rich composition, and highly repetitive structure– features that have historically limited sequence recovery using short-read technologies. Recent advances in long-read sequencing, particularly PacBio HiFi, now enable the generation of haplotype-resolved genomes and the recovery of full-length spidroin sequences, providing new opportunities to investigate the evolutionary dynamics of this important trait. To assess baseline genetic variation in spidroins across genes, individuals, and populations, we generated 15 high-quality long-read genome assemblies for the silver garden spider (Argiope argentata), producing 30 haplotype-resolved genomes. Using a combination of ab initio and homology-based gene prediction approaches, we annotated 993 full-length silk genes and characterized both length and structural variation among paralogs, representing the largest silk gene set for a single species to date. This resource enables detailed analysis of spidroin gene architecture and variation across multiple biological scales. Our study provides a foundation for understanding the molecular evolution of silk, and establishes Argiope argentata as a key system for studying how complex, repetitive gene families evolve.

12:15 PM - 12:30 PM

Urban-tolerant butterflies are more resilient to contemporary demographic decline

Sarah Diamond, Case Western Reserve University
Isabelle Todd, Case Western Reserve University

Evolutionary Ecology II

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

The evolutionary consequences of behavioral plasticity

Carlos Botero, University of Texas at Austin

Abstract:

When environments change and phenotypes become suboptimal, organisms often mitigate the costs of maladaptation with behavioural adjustments. Although this “buffering” of natural selection is widespread, its evolutionary consequences are poorly understood. Here, I use evolutionary simulations to explore how behavioural plasticity shapes the tempo and mode of adaptive evolution. My results indicate that this fast-acting form of plasticity enhances persistence under suboptimal conditions and facilitates the accumulation of genetic variation within populations. Over short timescales, or when opportunities for niche expansion are limited, the combined action of these effects leads to slower evolution of morphology and physiology. Over longer timescales, or when ecological opportunities abound, it can instead lead to a “Goldilocks” pattern, where evolution is fastest in moderately plastic lineages, whose medium buffering capacity enables persistence in suboptimal conditions without severely constraining subsequent optimizing selection. These findings expose key differences in scope and mechanism relative to other forms of phenotypic plasticity and suggest that behavioural plasticity may more broadly influence the evolutionary trajectories of individual lineages. More generally, they help clarify our understanding of how short-term flexibility shapes long-term adaptation and underscore the need to reassess current risk-assessment frameworks that equate slower evolutionary rates with greater vulnerability to environmental change.

11:30 AM - 11:45 AM

Size trait scaling relative to two-fold expectations following ploidy elevation from diploid to synthetic neopolyploid Spirodela polyrhiza

Briante Najev, University of Pittsburgh
Keila Jellings, University of Pittsburgh
Martin Turcotte, University of Pittsburgh
Tia-Lynn Ashman, University of Pittsburgh

Abstract:

Polyploidy (whole genome duplication) is the phenomenon of an organism having more than 2 chromosome sets. A consequence of polyploidy is the Gigas effect, the enlargement of traits linked to polyploidy; one of the causes of which is polyploids requiring more nuclear volume to harbor a larger genome than their diploid counterparts. If an organism experiences ploidy elevation from

diploidy (2 chromosome sets) to tetraploidy (4 chromosome sets) we would expect traits linked to genome size to experience a two-fold increase, however while trait sizes increase with polyploidy, they rarely increase two-fold. We will examine how size-related traits vary with ploidy level and whether they scale proportionally between ploidy levels. We will fill these gaps of knowledge by characterizing phenotypic and functional traits of Spirodela polyrhiza (duckweed), from the molecular level to the population level, using diploids and synthetic neo-autotetraploids across genetic backgrounds. So far, we have 1) quantified genome size using flow cytometry, 2) measured cell area and volume using confocal microscopy imaging, and 3) characterized population dynamics from our mesocosm experiment. As expected, genome size and cell volume almost doubled in the tetraploids compared to diploids, genome size correlates with cell volume, and diploids have a higher relative growth rate compared to tetraploids. Once we complete analyses, we will address whether scaling relationships between size-related traits are consistent between ploidy levels or if there are deviations from two-fold expectations.

11:45 AM - 12:00 PM
A holistic framework to assess the impacts of auxinic herbicide drift on non-target plants and pollinators

Veronica Iriart, University of Michigan

12:00 PM - 12:15 PM
Using whole genome sequence data to detect pesticide resistance

Nathan Backenstose, Purdue University
Allison Nalesnik, Purdue University
Dien-Yu Tsai, Purdue University
Aaron Jubar, U.S. Fish and Wildlife Service
Erin Dunlop, Ontario Ministry of Natural Resources and Forestry
Marisol Sepulveda, Purdue University
Nicholas Johnson, USGS
Mark Christie, Purdue University

Abstract:

Chemical control of pest species often imposes strong, predictable selection pressures on the target species, which can lead to rapid evolution of resistance. In this study, we investigate the evolutionary response of invasive sea lamprey (Petromyzon marinus) in the Great Lakes to the lampricide 3-trifluoromethyl-4-nitrophenol (TFM), which has been used to control population abundance for over 60 years. Despite high gene flow (lack of natal philopatry) and wide use of TFM over time and space, physiological evidence of resistance has yet to be identified. To determine whether invasive sea lamprey are in the early stages of resistance evolution to TFM, we exposed 8,611 larval sea lamprey to operational TFM concentrations and sequenced the genomes of individuals that survived the shortest and longest period of time. We identified 18 large genomic regions across different chromosomes with SNPs strongly associated with survival time in TFM.

Among the 748 annotated genes within these regions, we identified genes with functions directly related to TFM's mode of action, such as detoxification, mitochondrial function, oxidative stress response, and energy metabolism. One compelling outlier occurs on chromosome 2 is a cluster of UDP-glucuronosyltransferase (UGT) genes, which are essential for detoxification. These findings indicate that incipient adaptive responses to a mitochondrial toxicant are evolving in a wild vertebrate population. Furthermore, given that sea lampreys lack natal philopatry, our work also emphasizes the importance and urgency of integrating evolutionary principles into invasive species management.

12:15 PM - 12:30 PM

From Nests to Shells: Macroevolution of Hierarchical Defenses in Birds

David Ocampo, Princeton University

Abstract:

Reproductive success in birds depends on a hierarchy of protective traits, from constructed nests to the microscopic structure of the eggshell. While nests buffer embryos from environmental pressures, the eggshell—particularly its outermost cuticle—provides the final line of defense against microbial invasion, desiccation, and mechanical stress. Despite this functional continuum, the evolution of nest architecture and eggshell traits have largely been studied in isolation. Here, I integrate macroevolutionary patterns of nest construction with the evolution of eggshell cuticle diversity to test whether shifts in nesting strategies reshape selection on eggshell defenses. Focusing on tyrant flycatchers and allies (Tyrannida), I compiled a comprehensive database of nest architectures across environmental gradients, drawing from literature, museum collections, and fieldwork across the Americas. Using phylogenetic comparative methods, I quantified transition rates among nest types and identified ecological correlates of nest diversification. I then expanded this framework across other clades by characterizing eggshell cuticle structure in ~500 species spanning 128 families and 38 orders, combining field-collected material with Scanning Electron Microscopy analyses at the Smithsonian National Museum of Natural History. Across lineages, ground nests in humid environments tend to retain more robust cuticles, whereas elevated nests are associated with reduced or absent cuticles, consistent with shifts in microbial risk and gas exchange demands. By linking extended phenotypes (nests) with intrinsic reproductive traits (eggshell structure), I aim to test how multi-layered defenses coevolve to mediate environmental interactions and drive ecological diversification across birds.

Genomics I

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM
Development of genomic tools to study lagomorph population genetics, ecology, and conservation in Pennsylvania

Sarah Emel, Indiana University of Pennsylvania

Abstract:

Pennsylvania is at the species' range boundary for Appalachian cottontails (Sylvilagus obscurus) and snowshoe hares (Lepus americanus). Both lagomorphs are species of greatest conservation need in Pennsylvania. Sylvilagus obscurus and L. americanus populations face multiple conservation challenges, including anthropocentric landscape alteration, vulnerability to isolation inherent to the high elevation forests with dense understory, winters with variable duration of snow cover, and possible hybridization of S. obscurus with sympatric eastern cottontails (Sylvilagus floridanus). We used lagomorph fecal and tissue samples collected in Pennsylvania between 2020 and 2023 to determine species identification via mitochondrial DNA barcoding and to assess genotypic variation through the development of a Genotyping-by-Thousands (GTseq) SNP panel. DNA barcoding of fecal samples identified 436 S. obscurus localities across ten counties and 135 L. americanus localities across eight counties, which served as the basis for species distribution and landscape resistance modeling. PCA, Structure analysis, and genetic distances obtained from fecal and tissue GTseq data reflect genetic divergence between S. obscurus in the southwest and northcentral regions of the state, as well as cryptic genetic structure among individuals within the northcentral region. Future research is needed to determine whether this divergence is due to historical vicariance, contemporary dispersal barriers, or local adaptation, and additional management attention may be warranted to conserve this unique genetic lineage. Furthermore, PCA and Structure analyses provided no evidence of hybridization between S. obscurus and S. floridanus in our sampling localities, although continued monitoring is necessary to rule out this conservation concern.

11:30 AM - 11:45 AM
The genomics of convergent evolution in trap-jaw ants

Gaurav Agavekar, Okinawa Institute of Science and Technology Graduate University
Yoshihiko Suzuki, Okinawa Institute of Science and Technology
Miyuki Suenaga, Okinawa Institute of Science and Technology Graduate University
Douglas Booher, University of Georgia
Alexandre Casadei Ferreira, Biodiversity and Biocomplexity Unit
Po-Wei Hsu, University of Tokyo
Tainara Jory, Universidade Federal do Parana
Miguel Pachego-Leiva, University of Costa Rica

Leonardo Tozetto, Okinawa Institute of Science and Technology Graduate University
Chung-Chi Lin, National Changhua University of Education
Rajendhran Rajakumar, University of Ottawa
Adrian Pinto-Tomas, University of Costa Rica
Michael Hiller, Senckenberg Nature Research
Eugene Myers, Okinawa Institute of Science and Technology Graduate University
Evan Economo, University of Maryland

11:45 AM - 12:00 PM

Temporal regulatory landscapes of brain development are shaped by social context in bumble bees

Sarthok Rasique Rahman, Princeton University
Ian Traniello, Princeton University
Andrew Webb, Princeton University
Joanna Shoubaki, Harvard University
Anvita Chaudhary, Princeton University
Callum Kingwell, Princeton University
David Cardona, Princeton University
Eli Wyman, Princeton University
Sarah Kocher, Princeton University

Abstract:

In holometabolous insects, metamorphosis profoundly reorganizes the central nervous system, but the brain continues to develop throughout early adulthood. In bumble bees (Bombus impatiens), an early adult developmental window coincides with the first encounters of nestmates and integration into colony life, and social experience during this period impacts brain gene expression and morphology, as well as adult social behaviors. To characterize the molecular and regulatory dynamics of this sensitive developmental period, we generated paired brain gene expression (RNA-seq) and chromatin accessibility (ATAC-seq) data from worker bees raised either in groups or in isolation across six time points spanning early pupal development through 10 days post-eclosion. Our data reveal that epigenetic and transcriptional reorganization peaks at the pupal-to-adult transition, consistent with the massive reorganization that occurs during metamorphosis. However, following eclosion, chromatin landscapes are largely stable, but gene expression continues to shift with age and often in a social context-dependent manner. Transcription factor (TF) footprinting unmasks a hidden set of endocrine dynamics on this landscape: ecdysone-associated genes dominate pupal gene expression and decline rapidly following eclosion. At the same time, adult-specific regulatory modules, including those associated with juvenile hormone (JH), emerge progressively. Together, our findings suggest that there are distinct phases in the regulatory architecture of worker brain development: metamorphosis is associated with broad epigenetic and transcriptional reorganization, whereas post-eclosion development is regulated primarily by transcription factor expression dynamics superimposed on a largely stable chromatin landscape. These findings establish the molecular dynamics of early adult brain development in the eusocial bumble bee, paving the way for future comparative studies examining if and how developmental modules are shaped and co-opted to meet the demands of social life.

12:00 PM - 12:15 PM

Rapid evolution of genome size mediated by centromere expansion and contraction in Formica ants

Alan Brelsford, University of California
Shangzhe Zhang, University of California Riverside
Jennalyn Resendez, University of California Riverside
Zul Alam, University of California
Jessica Purcell, University of California Riverside

Abstract:

How and why does genome size evolve? We estimate centromere size in 1,800 Formica ants of over 100 species, by measuring the frequency of a centromere-associated satellite repeat in whole-genome sequence data. Species vary in satellite content from less than 3% to over 40% of the genome, with substantial changes in centromere proportion even between closely related species. Long-read genome assemblies show that the non-centromeric component of the genome has remained stable and largely collinear across the genus, while validating short-read-based estimates of centromere size and genome size variation. We trace the evolution of centromere size along the Formica phylogeny, identifying a ten-fold expansion of satellite DNA early in the diversification of the genus resulting in a 50% increase in genome size. We also identify several recent reductions in satellite content and genome size. Variation within and between species is correlated with climate, with larger genomes observed in colder climates, suggesting that genome size may be locally adapted.

12:15 PM - 12:30 PM

The coevolutionary dynamics of transposons and their hosts in Drosophila

Sarah Signor, North Dakota State University
Robert Kofler, Vetmedundi Vienna
Riccardo Pianezza, Vetmeduni Vienna
Almoro Scarpa, Vetmeduni Vienna
Sarah Saadain, Vetmeduni Vienna
Philipp Hummer, Vetmeduni Vienna
Prakash Narayanan, North Dakota State University
Shashank Pritam, North Dakota State University
Torsten Dikow, Smithsonian Museum of Natural History

Abstract:

Transposons are mobile pieces of DNA that replicate selfishly within animal genomes, and they are widespread across eukaryotic life. The co-evolution between transposons and their hosts is a major source of selective pressure. Hosts can suppress transposon movement, which in turn puts pressure on the transposon to resist host defenses or find a novel genome to invade. In Drosophila the advent of long read sequencing has allowed scientists an unprecedented ability to document the movement of transposons within and between genomes. We have found evidence of extensive

recent horizontal transfer in insect genomes, far beyond that expected given the known number of transposon families. In D. melanogaster alone there have been twelve transposon invasions in the last two hundred years, compared to an expected rate of about one every 100,000 years. We posit that because D.melanogaster is a humna commensal, this may be due to human introduction of dipterans to new territories and thus, new congeners. However, we have also found that the rate of TE invasion in other drosophilids is quite high, suggesting this phenomenon may be quite widespread. For example, we have evidence of a single TE transferring recently between species as many as 16 times. The implications of this genomic instability induced by anthropogenic changes to the environment is unknown, but is a potentially important selective factor on species genomes.

Molecular Evolution II

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Genome-wide alignments reveal turnover and retention of de novo genes in Brassicaceae

Adekola Owoyemi, Texas A&M University

Abstract:

De novo genes originate from previously noncoding DNA and represent a major source of lineage-specific genetic novelty. However, their study has been hampered by high false-positive rates and limited ability to identify reliable enablers substitutions. We developed a novel computational pipeline that minimizes undetected homology errors and annotation artifacts and rely on novel genome-wide multiple alignments generated with Progressive Cactus. We applied this framework to a comparative genomic analysis of 21 Brassicaceae species to investigate patterns of de novo gene emergence and retention. Focusing on Arabidopsis thaliana, we identified 958 candidate de novo genes, including approximately 839 de novo-like genes lacking detectable synteny and 305 A. thaliana-specific de novo genes supported by enabling mutations in syntenic noncoding regions. We also identified 141 older de novo genes shared across multiple species, constituting the first systematic set of retained de novo genes in plants. Our results indicate substantial turnover, consistent with other eukaryotes. Gene and protein features, including length, codon adaptation index, and intrinsic disorder, were similar between de novo and de novo-like genes, suggesting similar origination mechanisms and evolutionary trajectories. Older de novo genes exhibited similar features of young genes, indicating that de novo gene retention might be associated with characteristics present at birth. Unexpectedly, de novo genes encode significantly fewer transmembrane proteins than conserved genes, contrasting with yeast and human systems. Together, our study establishes a robust framework for investigating de novo gene evolution in plants and reveals lineage-specific evolutionary trajectories.

11:30 AM - 11:45 AM

Bacterial gene positioning is shaped by selection on both mean and growth-dependent expression

Ruiqi Yuan, University of Michigan

Abstract:

In bacteria with circular chromosomes, genes near the replication origin (oriC) are replicated earlier and consequently attain higher copy numbers than genes near the terminus (ter), particularly during rapid growth. Hence, mutations altering a gene's chromosomal position can affect its expression level and be subject to selection. Two non–mutually exclusive hypotheses regarding the target of this selection have been proposed. The mean expression hypothesis (MEH) posits that the target is a gene's average expression across environments, whereas the growth-dependent expression hypothesis (GEH) proposes that the target is the growth dependence of gene expression, quantified by the expression slope—the change in expression level per unit change in growth rate. To test these hypotheses and assess their relative support, we analyze eight multi-environment protein expression datasets from three bacterial species, as well as Escherichia coli promoter strengths measured in two environments. We observe a significant decrease in both mean expression and expression slope from oriC to ter, consistent with both MEH and GEH. In regression models predicting gene position, the relative contributions of the two hypotheses differ across species. However, even when combined, the two hypotheses explain only a small fraction of chromosomal gene positioning, in part because the replication-dose effect is incompletely offset by compensatory evolution of individual promoter strengths. We conclude that selection on both mean and growth-dependent expression shapes bacterial chromosomal gene positioning, but with modest effects.

11:45 AM - 12:00 PM

Global constraints do not explain evolutionary rate variation in anthocyanin and carotenoid loci

Zoe Hert, Indiana University
Leonie Moyle, Indiana University

Abstract:

While multiple different genetic changes can produce the same phenotype in principle, the number of genetic mechanisms observed in nature is often limited. But, why? One possibility is that genes differ in constraint: less constrained genes can accumulate more nonsynonymous variation so may be more likely to contribute to adaptation. Biosynthesis pathways are well-established models for quantifying these differences in selective constraint and assessing its contribution to adaptation. In plants, these analyses have largely focused on the anthocyanin pigment pathway, and its role in flower color evolution. However, both anthocyanins and carotenoids can contribute to color in important plant structures like flowers and fruits. Further, architectural differences between

anthocyanin and carotenoid biosynthesis pathways—including in pathway linearity and functional redundancy—suggest they may differ in patterns of selective constraint. Here, we quantify evolutionary rate variation among 73 anthocyanin or carotenoid pigmentation loci in 83 species from the nightshade genus Solanum, to jointly examine selective constraint across both pathways for the first time. We assess whether evolutionary constraint varies among genes within and between pathways, and whether this rate variation depends upon pathway position and functional (structural versus regulatory) class. In addition to global rates, we also quantify local (among-branch) rate heterogeneity as a measure of evolutionary constraint. With either metric of constraint, we detect rate variation among both anthocyanin and carotenoid genes, but little evidence that global genetic constraints consistently shape this molecular evolution. Instead, lineage-specific selective conditions are more explanatory of evolutionary rate variation in both pathways. Our integration of anthocyanin and carotenoid evolution across dozens of loci provides a new perspective into a classic question, and ultimately, will allow us to assess if and how constraint shapes the genetic mechanisms of repeated flower and fruit color evolution in this hyper-diverse plant group.

12:00 PM - 12:15 PM

Evolutionary history of the enigmatic Na+/H+ antiporter gene family across the phylum Arthropoda, with a special focus on the copepod Eurytemora affinis species complex

Patricia Zito, University of Wisconsin - Madison
Teresa Popp, The Ohio State University
Sean Schoville, University of Wisconsin-Madison
Carol Lee, University of Wisconsin

Abstract:

The Na+/H+ antiporter (NHA) gene family has been found to serve important functions for salt stress tolerance, water retention, and ion homeostasis in animals. Despite its physiological importance, no study has investigated its evolutionary history or patterns of molecular evolution in the phylum Arthropoda. Intriguingly, prior studies have found that NHA paralogs repeatedly show signatures of natural selection during independent saline-to-freshwater invasions by several sibling species of the copepod Eurytemora affinis species complex. To explore patterns of NHA gene family evolution in Arthropoda, we (1) reconstructed the first arthropod NHA phylogeny, (2) analyzed signatures of selection (dN/dS) across the phylogeny, (3) mapped amino acid sites with signatures of positive selection onto a predicted NHA7 protein model of E. carolleeae (Atlantic clade of E. affinis complex), and (4) localized NHA protein paralogs within the osmoregulatory swimming legs of E. carolleeae. We found that, unlike other cation exchanger families, NHA paralogs differentiated multiple independent times after the divergence of major arthropod lineages. Interestingly, paralogs NHA5, NHA6 and NHA7 of the E. affinis complex, which are top targets of selection in contemporary saline-to-freshwater invasions, also exhibited ancient signatures of selection. The single nucleotide polymorphism (SNP R283H), which had shown

signatures of selection during freshwater invasions by E. affinis complex populations, was mapped to an E. carolleeae NHA7 specific insertion between transmembrane segments 3 and 4 in the dimerization domain of the protein model. Finally, key paralogs NHA5 and NHA7 did not colocalize in expression within osmoregulatory organs, further suggesting that they have evolved different functions. This study uncovers a dynamic evolutionary history of the NHA family in Arthropoda and links SNPs under selection during contemporary habitat invasions to potential functional sites within the NHA protein.

12:15 PM - 12:30 PM

Repeated evolutionary turnover and the evolution of expression of skeletal muscle myosins in vertebrates

James Pease, The Ohio State University
Christina Harvey, Wake Forest University
Matthew Fuxjager, Brown University

Phylogenetic Comparative Methods I

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Phylogenetics, Trait Covariance Analysis, and the Evolution of Fin and Body Shape in the Surgeonfishes

Linnea Lungstrom, University of Chicago
Mireille Farjo, University of Chicago
Ryan Isdonas, University of Chicago
Andrew George, University of Chicago
Mark Westneat, University of Chicago

Abstract:

Insights into ecomorphology are enriched when investigating evolutionary correlations between ecologically and functionally important traits. However, tools currently available to model patterns of shape covariation limit researchers to either assume that trait covariances between taxa are independent of, or completely described by, their shared evolutionary history. Using a Pagel's λ adjustment to incorporate phylogenetic signal in trait covariance analysis, we aim to solve this long-standing problem in phylogenetic comparative methods and investigate ecological associations and evolutionary shape covariation in the ecologically and morphologically diverse case study of surgeonfishes (Acanthuridae). By revising acanthurid phylogenetic relationships and analyzing the geometric morphometrics of their body, head, and fins, we found that head and body shape were significantly associated with dietary ecotype. Surgeonfishes showed a significant

negative correlation between caudal fin and pectoral fin shape; high/low aspect ratio (AR) tails are associated with low/high AR pectoral fins, respectively, suggesting locomotor tradeoffs. With our novel approach to estimate the influence of phylogeny on trait covariances between taxa, we found that the caudal fin covaried with both the body and pectoral fin due to dietary and locomotor demands, respectively and exhibited the highest evolutionary variance along the primary axis of integration in all trait covariance comparisons.

11:30 AM - 11:45 AM

Do host material properties drive the evolution of parasitoid wasps' ovipositor buckling resistance?

Abby Weber, UIUC
Daniel Moen, University of California
Charles Roseman,
Philip Anderson, University of Illinois

Abstract:

Parasitoid wasps use an ovipositor to lay eggs in host insects whose exteriors are made of materials spanning from the soft membrane of caterpillars, to the intersegmental membrane of cockroaches, to the sclerotized cuticle of an adult beetle. It is presently unknown if this diversity in ovipositor morphology is a function of adaptation to the different material properties of host insects. Here, I ask the following question: Do host insect material properties influence the evolution of the ovipositor in the Braconid subfamily Euphorinae? Critical buckling force is the amount of force a column can withstand under compression before failure. We hypothesize that wasps who parasitize similar hosts have evolved similar critical buckling forces to complete a successful puncture during the oviposition event. To test this hypothesis, I calculated the critical buckling force for 30 species of wasps. I then fit a series of continuous phylogenetic comparative models exploring the relationship between critical buckling force and host insect using OUwie. The model support indicates the best fit is an Ornstein-Uhlenbeck model with multiple optima. This result indicates that host material properties may influence the evolution of ovipositor buckling resistance.

11:45 AM - 12:00 PM

How Reliable are Rate and Rate-shift Estimates in Multivariate Continuous Traits?

Izabel Salvi, Princeton University

Abstract:

Quantifying rates of morphological evolution is central to macroevolutionary inference as rate heterogeneity can reflect shifts in developmental, functional, or ecological regimes across clade history. In practice, these rates are frequently estimated from multivariate continuous traits derived from geometric morphometrics. Although widely used, the most common software frameworks for

estimating branch-specific rates and detecting rate shifts, ridge-regression approaches (e.g., RRphylo) and Bayesian methods (e.g., BayesTraits and RevBayes), have not been systematically benchmarked for multivariate continuous data. Here we benchmark BayesTraits, RevBayes, and RRphylo for inference of (i) branch-specific evolutionary rates and (ii) the placement of rate shifts across phylogenies of varying size. We jointly simulated phylogenetic time-trees and multivariate trait datasets consisting of 10 uncorrelated continuous characters. The trait value was the result of a multivariate Brownian motion process with variances changing across the tree. Using the true simulated trees as input, we estimated evolutionary rates for branches/nodes and inferred the locations of rate shifts. We repeated the analysis after subsampling the trees (25%, 50%, 100%) and the number of traits (5, 10). For both RevBayes and BayesTraits there is a positive correlation between simulated and inferred rates, with their ability to predict simulated rate values increasing as the tree size decreased, due to the analyses of larger trees frequently failing to converge. RRphylo showed stable behavior across tree sizes and number of traits, but overall correspondence between inferred and simulated rates was lower than for the Bayesian approaches. All methods performed better at approximating the locations of rate shifts than at recovering the magnitude of branch-specific rates. These results clarify the shortcomings of commonly used tools and provide practical guidance for selecting methods to study rate heterogeneity in multivariate continuous characters.

12:00 PM - 12:15 PM

Classifying patterns in comparative data using a neural network pipeline

Menna Jones, University of Chicago

Abstract:

An overarching goal of phylogenetic comparative biology is to identify the processes that generate morphological diversity across the tree of life. The standard approach fits a suite of statistical models to tip data, typically in a likelihood-based framework, and evaluates their support using likelihood ratio tests or information theoretic approaches such as Akaike weights.

Whilst this approach can provide reasonable estimates of evolutionary parameters, it is often difficult to discriminate between model classes. This problem arises in part from the assumptions of multivariate normality of tip data: because the likelihood of the tip data is conditional on the model's underlying covariance structure, there are finite ways to maximize likelihood whilst adhering to this assumption. For example, constraint and adaptation are very different evolutionary processes yet both reduce the similarity between species that is attributable to shared ancestry, which makes them challenging to discriminate based on likelihood alone.

Machine learning offers a promising alternative to classic model-fitting pipelines that can circumvent these issues. The applications of machine learning in Evolutionary Biology include modeling diversification dynamics and predicting ecological niches, however, it has received limited attention in the context of modeling trait evolution. Here, I introduce a neural network pipeline to predict generative models of trait evolution given a set of phylogenetic

summary statistics calculated from sets of simulated data. I conduct simulation studies to demonstrate its speed and efficacy across a range of tree sizes, generative models and parameters. I will demonstrate how the neural network approach succeeds in classifying generative models in scenarios where maximum likelihood methods struggle, such as when tree sizes are small and phylogenetic signal is low. Finally, I apply this pipeline in the context of anuran functional traits to evaluate the relative roles of adaptation and constraint in shaping trait evolution.

12:15 PM - 12:30 PM

Evolution of the Metazoan Protein Domain Repertoire Revealed by a Birth-Death-Gain Model

Yuting Xiao, Carnegie Mellon University
Maureen Stolzer, Carnegie Mellon University
Dannie Durand, Carnegie Mellon University

Abstract:

Reconstruction of the ancestral protein repertoire offers valuable insights into the tempo and mode of protein content evolution, but can be highly sensitive to model choice. Here, we apply a phylogenetic Birth-Death-Gain model to investigate the evolution of the metazoan protein domain repertoire. Domains, protein modules with distinct structure and function, represent the basic components of proteins. Given a species tree and protein domain family counts in present-day species, we estimated the most likely rates of family origination, duplication, and loss. Rates were allowed to vary across domain families and species lineages independently, revealing family-specific rates. Statistical hierarchical clustering of family-specific rates reveals groups of domains evolving in concert. Moreover, we observe a strong and significant association between family rate and family function. Interestingly, domain families with functions related to metazoan innovations, including immune response, cell adhesion, cell motility and tissue repair tend to have the fastest rates. Families involved in core cellular processes tend to evolve more slowly.

We further inferred the expected ancestral domain content and the history of family gains, losses, expansions, and contractions across species lineages. Our analysis reveals an ongoing process of domain family replacement and resizing, consistent with extensive remodeling of the protein domain repertoire. This contrasts with recent reports of widespread loss during metazoan evolution obtained with parsimony-based analyses. To investigate this discrepancy, we reanalyzed our dataset using Dollo parsimony. The number of losses inferred increased four-fold, suggesting that widespread loss may be a product of model choice and not an inherent property of metazoan protein evolution. Unlike Dollo parsimony, Birth-Death-Gain models do not seek to minimize homoplasy, permit parallel gains, losses, or reversals and allow multiple independent origins of the same family. This flexibility enables Birth–Death–Gain models to discover a level of genomic plasticity not revealed by more constrained models.

Population Genetics: Inferring Selection

06/21/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Differential evolutionary patterns of avian malaria immunity genes in three Hawaiian honeycreeper species

Carlos Campos, University of Louisiana at Lafayette
Kristina Paxton, Natural Resource Management
Carter Atkinson, U.S. Geological Survey Pacific Island Ecosystems Research Center
Robert Fleischer, Smithsonian National Zoo and Conservation Biology Institute
Loren Cassin Sackett, University of Louisiana at Lafayette

Abstract:

The Hawaiian honeycreepers (Carduelinae) are among the classical examples of adaptive radiation on island clusters. Human-mediated species introductions have contributed to the decline or extinction of nearly all of the more than 50 honeycreeper species. Perhaps the most devastating introduced species is the avian malaria pathogen, Plasmodium relictum, vectored by the introduced mosquito Culex quinquefasciatus. Avian malaria has caused severe population declines of many honeycreepers in recent decades, and most honeycreepers succumb to malaria infection. Although evidence of recently evolved immunity is emerging in a few species, immunity to malaria on the Hawaiian Islands is spatially variable – likely a function of variation in selective pressure from disease transmission due to heterogeneity in mosquito populations. The Hawai`i `amakihi (Chlorodrepanis virens) and `apapane (Himatione sanguinea) show evidence of variable malaria immunity, while the Maui `amakihi (C.v. wilsoni) has shown little evidence of immunity. Understanding the differential selection acting on putative malaria immunity genes of these species may illuminate the underlying processes that have shaped spatial patterns of immunity. We utilized WGS to quantify the degree of selection and evolutionary divergence in putative malaria immunity “Target” genes versus that of genomic background “Control” genes. We found no evidence of differential selection between Target and Control genes in both full-gene and spliced exon sequences for any species. However, our ability to detect differences may be overshadowed by demographic effects such as a recent historical bottleneck. A preliminary HKA test of outlier Target genes revealed that long-term balancing selection has maintained variation at immunity genes in C. virens and may have contributed to the evolution of tolerance for this species. Further testing is needed to quantify and confirm the degree which selection has acted on immune genes of each species and how adaptation may have been constrained by historical demography.

11:30 AM - 11:45 AM

A pipeline for rare variant detection in ancient genomes reveals preliminary evidence of elevated deleterious burden

Troy LaPolice, Pennsylvania State University
Anthony Kwong, Penn State University
Julien Mutton, Penn State University
Christian Huber, Pennsylvania State University

Abstract:

Ancient DNA (aDNA) provides a direct window into past evolutionary processes, yet most studies rely on SNP capture data and focus on common variants, limiting inference about rare, strongly deleterious mutations. Here, we present a reproducible, end-to-end pipeline optimized for high-coverage shotgun aDNA that enables direct calling, filtering, and functional annotation of rare coding variants while accounting for post-mortem damage and environmental contamination. Our framework integrates taxonomic filtering (Kraken2), aDNA-aware genotype likelihood estimation (snpAD), and stringent quality control to quantify loss-of-function (LoF) burden in ancient individuals.

Using 12 high-coverage ancient genomes spanning the Late Pleistocene and Holocene and modern samples from the 1000 Genomes Project, we test for relative enrichment of predicted loss-of-function (pLoF) variants using the rxy statistic, normalizing to synonymous sites to control for background differences in genetic variation and coverage. We detect a significant excess of pLoF variants in ancient individuals (rxy ~ 1.19), a pattern that persists when restricting analyses to transversions to mitigate damage-induced artifacts. Missense variants show weaker effects, and negative control site classes do not exhibit similar enrichment, supporting the specificity of the signal.

While based on a currently limited set of high-coverage ancient genomes, these results demonstrate that rare, potentially deleterious coding variants can be robustly identified in shotgun-sequenced aDNA and suggest elevated deleterious burden in ancient humans relative to present-day populations. As high-coverage ancient genomes continue to accumulate, this framework enables direct tests of how purifying selection and demographic history have shaped genetic load through time.

11:45 AM - 12:00 PM

Who wins and why? uncovering the genomic basis of resistance polymorphism in a snail–parasite system

Oluwaseun Adu, Oregon State University
Michael Blouin, Oregon State University
Stephanie Bollmann, Oregon State University
Javier Calvelo, Oregon State University

Abstract:

Schistosomiasis, a neglected tropical disease transmitted by freshwater snails, causes significant morbidity and mortality in endemic communities, particularly in sub-Saharan Africa. With the WHO targeting elimination by 2030, identifying snail genes controlling resistance to schistosome infection could offer novel strategies to break transmission cycles. Using a pooled-seq GWAS approach, we mapped genetic variation in the BgBAR population of Biomphalaria glabrata snail associated with resistance to the SmVEN population of Schistosoma mansoni parasite. Scanning for allele frequency differentiation between infected and uninfected snail populations via 10 kb sliding-window Fst analysis and Fisher's exact test, we identified a genomic region with a high Fst peak exceeding the null-hypothesis-generated mean. We validated this region using PCR markers on independently genotyped BgBAR populations. The identification of a previously unknown region on chromosome 16 in this study highlights the importance of examining specific host-parasite population combinations to uncover resistance-associated regions and advance our understanding of coevolutionary dynamics in host-parasite systems.

12:00 PM - 12:15 PM

Host-associated population genetics in a parasitoid wasp: An analysis of sequential divergence in the Pinus-Neodiprion-Perilampus neodiprioni system

Sarah White, The Ohio State University
Robin Bagley, The Ohio State University at Lima

Abstract:

In plant-feeding insects, host plant shifts frequently generate new insect species. Distinct host plants act as different environments, and divergent natural selection across plants creates barriers to gene flow, leading to new species via ecological speciation. Phytophagous insect diversification may cascade if newly diverged insects present niches for specialization of associates at other trophic levels. This process, called sequential divergence, may be responsible for high rates of parasitoid (lethal parasite) diversity in plant-insect-parasitoid systems. However, it is a severely understudied phenomenon, having only been investigated in a small number of systems and only identified thus far in systems with internally feeding insect hosts. To address this gap, we propose the Pinus (pine)-Neodiprion (sawfly)- Perilampus neodiprioni (parasitoid wasp) system as an ideal model for evaluating whether sequential divergence can occur in an externally feeding insect and

its parasitoids. Previous genetic and morphological studies have shown strong Pinus-associated divergence between and within species of Neodiprion. The parasitoid P. neodiprioni is found across these Neodiprion species, displaying ecological, morphological, and possible genetic variation consistent with undescribed differentiation, which may indicate sequential divergence. To evaluate a possible divergence cascade, we aimed to establish the population genetic structure of P. neodiprioni and consider if population differentiation is aligned with Neodiprion hosts, Pinus environments, or both. To do so, we selected 100 P. neodiprioni samples from a broad geographic, Neodiprion host, and Pinus environment range for low-coverage, whole genome sequencing. After obtaining the first P. neodiprioni genome and aligning sample sequences, we analyzed P. neodiprioni population structure. From this, we present novel descriptions of P. neodiprioni's genome and population genetics. Furthermore, we consider P. neodiprioni populations across Neodiprion host and Pinus environments, making recommendations for further assessments of sequential divergence in this system and others.

12:15 PM - 12:30 PM
Haplotype-based methods improve sweep detection in ancient admixed populations

Abigail Sequeira, Pennsylvania State University
Zachary Szpiech, Penn State University
Christian Huber, Pennsylvania State University

Abstract:

Admixture is well known for obscuring signals of selective sweeps, yet ancient DNA provides the opportunity to uncover historical selection events. Most methods rely on changes in allele frequencies or the site frequency spectrum (SFS) and haplotype-based methods have seen limited usage. Here, we investigate haplotype and SFS-based methods for detecting selective sweeps under a complex demographic model that reflects ancient and modern European history. To overcome the limitations of ancient data, we extend the haplotype-based likelihood framework, saltiLASSI, and use the truncated haplotype frequency spectrum and its spatial decay to detect selective sweeps in ancient populations without requiring phasing. Using forward-in-time simulations, we model selective sweeps of varying age in ancestral and admixed populations, two admixture pulses of different source population proportions, and selection schema. We compare our ability to detect sweeps in simulated and empirical data via saltiLASSI to a popular SFS-based approach, SweepFinder2. We find that saltiLASSI has higher power to detect sweeps in admixed populations compared to SweepFinder2, especially in the case of migration introducing the sweeping haplotype or if not enough time has passed for the selection signal to establish again. While both methods identified overlapping sweep regions in the empirical data, saltiLASSI detected additional regions containing genes known to be under selection that were not identified by SweepFinder2. These results showcase the ability of haplotype-based inference of selective sweeps in ancient data and how we can improve sweep detection in ancient DNA from admixed populations.

Adaptation and Ecology II

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Spatial heterogeneity drives phenotypic divergence and local adaptation in microbial populations

Chimaroke Onyeaghala, Clarkson University

2:45 PM - 3:00 PM

Why are there black birds in hot deserts?

Cody Porter, Hope College
Owen Harries, Hope College
Eric Riddell, University of North Carolina - Chapel Hill

Abstract:

Convergent evolution is often interpreted as evidence of adaptation, yet the mechanisms underlying repeated trait evolution are rarely tested directly. We combined solar heating experiments, feather reflectance spectra, and biophysical modelling to evaluate competing hypotheses for the repeated evolution of black plumage in birds inhabiting hot, arid deserts. Contrary to some biophysical predictions, we found no evidence that darker plumage reduces heat gain at the skin surface, indicating that black plumage does not function as a simple thermoregulatory shield. In comparative analyses of closely related species, darker plumage in the visible spectrum was associated with increased reflectance in the near-infrared in hot, arid environments. This pattern was absent in species with lighter visible plumage, consistent with compensatory evolution of near-infrared reflectance in black desert birds. Ongoing biophysical modeling is being used to quantify the thermoregulatory consequences of this compensatory mechanism. Together, our results help resolve a long-standing paradox of phenotypic convergence in desert birds and highlight the importance of integrating experimental and comparative approaches to test adaptive hypotheses.

3:00 PM - 3:15 PM
Predicting Fitness Consequences of Climate Change in Swedish eelgrass Zostera marina

Camille Rumberger, Northeastern University
Maru Bernal, University of Gothenburg
Marlene Jahnke, University of Gothenburg
Katie Lotterhos, Northeastern University Marine Science Center

Abstract:

As climate change increasingly threatens global biodiversity, species will have to adapt to cope with novel and extreme climates. To what extent specific populations will become maladapted, and how this maladaptation will impact fitness, has been the subject of heavy study over the past few decades. Responses to shifting climates are often dependent on genetic and environmental influences, giving rise to the development of genomic offset methods which aim to predict maladaptation following rapid environmental change. Several recent studies have sought to validate the fitness-offset relationship, but what kind of fitness change genomic offsets predict remains an open question. Here, we pair mesocosm experiments exposing populations of the eelgrass Zostera marina from along the Swedish coast to simulated climate change in order to quantify fitness loss in future climates. We then predict genomic offset to both current and future climates to determine whether offset better predicts fitness of multiple populations in a single environment or of a single population across multiple environments. We find that almost all individuals survive in current West coast conditions while those in future East coast conditions suffer nearly 100% mortality, indicating high vulnerability of eelgrass populations to climate change on Sweden's East coast. Genomic offsets predict survival of single populations across treatments, but are much less accurate when predicting survival of multiple populations in a single treatment. This suggests that genomic offsets should be applied with caution, if at all, for applications that aim to identify ideal populations for a given site, e.g. sourcing populations for restoration, and may be more suited to predicting maladaptation of individual populations across environments.

3:15 PM - 3:30 PM
Adaptation of weedy plants to organic agriculture

Robin Waterman, Michigan State University
Jeff Conner, Kellogg Biological Station

Abstract:

Weedy plants invading crop fields face a range of novel selection pressures. While the evolution of herbicide resistance in conventional fields has been well-studied, little is known about the evolution of weedy plants in organic fields. In this study, we reciprocally transplanted individuals of three common annual weed species sourced from regionally paired organic agricultural and non-agricultural environments into organic soy and old field plots. We used trait and fitness data from

these plants to evaluate evidence for adaptive evolution. For two of three species, plants sourced from organic fields had higher fitness in the organic plots, with no fitness tradeoff found in the old field plots. Evolved differences in traits between source environment types tended to be small with the notable exception of flowering time. We found evidence for earlier flowering among plants from agricultural environments in two species, but slower flowering in the third. Lastly, we used genotyping-by-sequencing data to evaluate levels of gene flow between plants found in organic fields and uncultivated environments. Overall, the results of this study suggest that weeds found in organic fields differ genetically from those in nearby uncultivated areas in ways that sometimes make them better-adapted to their environment and that changes in flowering time may promote weed success in agricultural fields.

3:30 PM - 3:45 PM
The osmoregulatory physiology facilitating juvenile alewife seaward migration

Emily Tarnawa, University of Denver
Jon Velotta, University of Denver

ASN Early Career Awards

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 3:00 PM
Evolution of thermal physiology in lizards across scale

Brooke Bodensteiner, University of Alabama

3:00 PM - 3:30 PM
Evolutionary games with clonal ants

TOMAS Kay, Rockefeller University

Comparative Biology III

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM
Non-random non-Lamarckian mutations increase fitness and variation: a simulation model based on Interaction-Based Evolution theory

Liudmyla Vasylenko, University of Haifa

Abstract:

Background. For nearly a century, mutations have been considered random with respect to fitness. Under this view, adaptive evolution results from natural selection acting on genetic variation that arises independently of its effect on the organism. Whether random mutation, natural selection, random genetic drift, recombination, migration, together with evo-devo considerations, are sufficient to account for biological complexity remains an open theoretical question.

More recently, the theory of Interaction-Based Evolution has been proposed, according to which mutations are neither random nor Lamarckian but rather are influenced by information accumulated in the genome over generations. This idea has been supported by several empirical studies, but no mathematical model of it as of yet has been proposed.

Methods. In this work, we compare random and non-random mutations through simulations of a finite population of constant size evolving across discrete generations, while incorporating an interaction between three basic elements of the evolutionary process: natural selection, mutation, and recombination. The phenotype is dependent in a complex manner on epistatic interactions between genes.

Results. The population mean fitness increases sharply during the evolutionary transient when mutations are nonrandom and non-Lamarckian, given that the population size and genome size are large enough. The mean fitness advantage of the population evolving under nonrandom mutation increases with population size and genome size. The distribution of fitness values is bell-shaped despite strong interactions between genes. Surprisingly, the rate of production of new heritable variation increases under changing conditions, in accord with Darwin's own observations from the Origin of Species, which have not received a straightforward explanation until now.

2:45 PM - 3:00 PM

Decoupled evolution of gas exchange and water loss in lungless salamanders

Nathalie Alomar, Yale University
Eric Riddell, University of North Carolina - Chapel Hill
Martha Muñoz, Yale University

Abstract:

Woodland salamanders (Plethodon) are a diverse radiation of lungless, terrestrial amphibians that rely entirely on cutaneous respiration, coupling gas exchange and water loss through a shared surface. This coupling may constrain phenotypic variation in these traits, potentially structuring variation along a shared physiological axis, or they may instead vary more independently among species. Here, we quantified metabolic rate, water loss rate, and the ratio between these traits across 30 Plethodon species and related these traits to elevational distributions, geographic range size, and climatic conditions across species' ranges. We also compared the relationship between gas exchange and water loss in Plethodon to that observed across a broader set of amphibian taxa.

Metabolic rate and water loss were not tightly correlated across Plethodon, despite a positive association across amphibians more broadly. Instead, physiological traits correlated with different aspects of species' elevational limits, range sizes, and climatic niches. Metabolic rate was most consistently associated with elevation and climate, with lower values observed in species occupying higher, cooler environments. Water loss alone showed weaker and less consistent environmental associations, but the transpiration ratio varied with elevational limits such that species extending into lower-elevation environments exhibited greater hydric efficiency. These patterns were also reflected in phylogenetic path analyses, which supported lower elevational limit as a mediator linking physiology to geographic range size. These results suggest that although cutaneous respiration imposes broad hydric costs across amphibians, Plethodon species do not show a single, shared pattern of physiological divergence between gas exchange and water loss.

3:00 PM - 3:15 PM

Eggs, Excretion, and Sperm: Does sex-specific functions generate sexual dimorphism in the Anuran cloaca?

Julia Soares Parreiras, Cornell University
Molly Womack, Cornell University

Abstract:

While facing distinct selective pressures related to water availability in terrestrial environments and the risk of egg desiccation, anurans have evolved the greatest reproductive diversity among tetrapods. Although the evolution of these diverse reproductive strategies is well documented, the variation in reproductive morphology that facilitates these successful adaptations remains largely unknown. The cloaca receives waste from the digestive and urinary systems and also serves as the final passage for gametes. Historically, the anuran cloaca has been described as a short, simple tube lacking significant sexual dimorphism, although comprehensive anatomical and histological studies supporting this characterization are limited. Because oviposition (egg laying) is a female-specific process, the female cloaca may have morphological specializations that facilitate egg passage, distinguishing it from the male cloaca within species. Conversely, an absence of cloacal sexual dimorphism may reflect selective pressures favoring the maintenance of a multifunctional organ that integrates shared urinary and digestive functions with a common pathway for both types of gametes. In this study, we investigated whether selective pressures associated with oviposition have shaped female cloacal morphology, resulting in sexual dimorphism—or not—in two anuran species, Rana sylvatica and Pseudacris crucifer. To assess sex- and species-level variation, we measured cloacal length and cloacal morphological traits associated with ovulation (e.g., epithelial thickness, degree of epithelial folding, and gland density and diversity) in both sexes and analyzed the data using generalized linear mixed models.

3:15 PM - 3:30 PM
Species-specific responses to ethanol drive divergence in the Drosophila gut microbiome

Nitin Bansal, University of Nebraska-Lincoln
Kristi Montooth, University of Nebraska-Lincoln
Ian Keesey, School of Biological Sciences

Abstract:

Host-associated microbiomes are shaped by environmental exposure and host-specific filtering, yet it remains unclear whether microbial responses to environmental stress are conserved across host species or instead reflect species-specific ecological and evolutionary histories. Here, we quantified how chronic ethanol exposure alters gut microbiome composition across eight Drosophila species spanning distinct ecological niches, including fermenting-fruit generalists and species associated with less fermented or chemically specialized substrates. Flies were reared under standardized laboratory conditions on identical diets with and without 2% ethanol, allowing us to isolate host-dependent microbial responses from environmental variation. For each species, we sampled adult males, females, and associated food microbiomes across replicate vials. Microbial communities were characterized using 16S rRNA gene sequencing, and community structure was analyzed using Bray–Curtis dissimilarities, principal coordinates analysis, and permutational multivariate analysis of variance (PERMANOVA). Host species strongly structured gut microbiome composition under control conditions (PERMANOVA, $R^2 = 0.62$, p Acetobacter and members of the Lactobacillus group, with both the direction and magnitude of change differing across host species. In contrast, ethanol produced only modest changes in environmental (food) microbial communities, while host-associated microbiomes remained distinct from the surrounding microbial pool, indicating selective assembly by the host. Together, these results demonstrate that microbiome responses to environmental stress are not conserved across hosts but instead reflect species-specific ecological and evolutionary context, highlighting host species identity as a primary determinant of microbiome assembly and suggesting that host–microbe interactions may evolve in response to ecological pressures such as dietary ethanol exposure.

3:30 PM - 3:45 PM
How snakes became long

Krista Koeller, University of Vermont

Abstract:

Snakes are a diverse lizard group known for their elongate, limbless body form. Though this group is well studied, it has been unclear whether they acheived their elongate body by lengthening their necks regions trunk regions, or both. In most vertebrates, the boundary between the neck and trunk regions of the body is defined by the position of the pectoral girdle. However, in species without pectoral girdles, such as snakes, the length of the neck can be difficult to determine. There are

characters that co-occur with the neck-trunk boundary in pentadactyl squamates that have been used as proxies in snakes, but these have led to dramatically different conclusions about neck length. Some studies have used certain neck-associated vertebral characteristics, hypapophyses, to define neck vertebrae, while others have used the position of vestigial shoulder elements. Still others have used the overall shapes of vertebrae as determined by a geometric morphometric analysis. To study the utility of each potential neck- trunk boundary marker in studying neck length in snakes, I used computed tomography scans of legless squamates from all major lineages and compared the positions of the above markers along the axial column. I found that in all groups showing a high degree of limb reduction, the neck-trunk boundary markers are dissociated. In most groups, the hypapophyses extend farther posterior than the pectoral girdle and the pectoral girdle itself is farther anterior than the ancestral condition. This suggests that the neck-trunk boundary is not one position. Each neck-trunk boundary-associated character must be an independent trait, patterned by a different developmental mechanism. These mechanisms become dissociated during the evolution of limblessness and must be coordinated in pentadactyl groups.

Evolutionary Ecology III

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

A new quantitative framework for local adaptation: pervasive trade-offs and widespread asymmetry

Arash Raeisbahrami, George Washington University

Abstract:

Local adaptation occurs when a population exhibits higher fitness in its native environment than foreign populations. While multiple mechanisms can lead to patterns of local adaptation, including general fitness advantages and fitness trade-offs, most studies have concentrated on the binary description of the absence/presence of fitness trade-offs instead of quantifying their relative contributions. Here, we introduce a new quantitative framework (CT) to partition the contribution of fitness trade-offs to local adaptation. Performing a meta-analysis on 496 reciprocal transplant experiments, we showed that fitness trade-offs significantly contribute to approximately 80% of local adaptation cases, and local adaptation is often asymmetric (65% of cases). Notably, the contribution of fitness trade-offs is significantly reduced in asymmetric systems (~ 0.45) than in symmetric ones (~1.08), emphasizing the need for the CT model to quantify their contribution in asymmetric cases. We further showed that the magnitude of local adaptation increases along the speciation continuum, while no significant differences were found across different animal dispersal modes and plant mating systems, which were used as proxies for degrees of gene flow. The relative contribution of fitness trade-offs remains high

along the speciation continuum (~0.70), and among different animal dispersal modes (~0.85) or plant mating systems (~0.55). These results establish our proposed CT framework as a powerful tool to evaluate the mechanisms underlying local adaptation.

2:45 PM - 3:00 PM
Floral nectar-dwelling Acinetobacter diversity in a temperate climate

Daphne Garcia, Cornell University
Vivianna Sanchez, Cornell University
Tory Hendry, Cornell University

Abstract:

Over 85% of the world's flowering plants depend on pollinators, and floral nectar microbiomes are a crucial component of the plant-microbe-pollinator tripartite symbiosis. Specifically, diverse members of the genus Acinetobacter specialize on floral nectar globally, where they can influence nectar chemistry, nutrient content, and pollinator foraging. In particular, nectar-specialist Acinetobacter can pseudogerminate pollen, a phenotype that releases pollen nutrients into nectar. However, work on nectar-dwelling Acinetobacter has largely focused on tropical and Mediterranean systems, while their evolutionary and population dynamics in seasonal climates remain understudied. We hypothesized that the lack of flowers during winter would introduce population bottlenecks and selective pressure for nectar Acinetobacter, leading to reduced genetic diversity, high rates of evolutionary divergence, or selection for distinct traits in seasonal locations.

We performed shotgun metagenomic sequencing on sampled floral microbiomes in central New York to characterize the genetic diversity of Acinetobacter in a seasonal climate. Species-level relative abundance revealed that only two species, A. pollinis and A. nectaris are found in New York. Phylogenetic analyses showed that temperate New York populations are genetically distinct from Californian clades, suggesting geographical divergence. Additionally, New York Acinetobacter contained several novel gene duplications of the genes encoding the enzymes pectin lyase and polygalacturonase, which are putatively involved in pollen pseudogermination, suggesting their potential ecological importance in temperate climates. Overall, this preliminary work supports the conclusions that New York hosts a reduced diversity of phylogenetically distinct nectar Acinetobacter compared to other climates, and provides one of the first insights into the diversity and evolution of nectar bacteria in seasonal ecosystems.

3:00 PM - 3:15 PM
Genetic tests for an eco-evolutionary feedback in a freshwater diaptomid copepod

Eric Prileson, Washington State University Vancouver

Abstract:

Strong trophic interactions are compelling candidates for when we might expect to uncover an eco-evolutionary dynamic, especially if they vary through fundamental evolutionary processes.The repeated ecological speciation of freshwater threespine stickleback Gasterosteus aculeatus in British Columbia and the impacts on their primary prey – the diaptomid copepod Skistodiaptomus oregonensis – provides an intriguing case study to test the relationship between eco-evolutionary dynamics and speciation. Here, I describe an ongoing project to test for an eco-evolutionary feedback in S. oregonensis from lakes with divergent predation regimes stemming from ecological speciation in stickleback. Currently, we are rearing copepods from these lakes in common garden experiments and assembling a reference genome that will allow us to directly test for genetic divergence of populations between lakes. We expect to find support for an eco-evolutionary feedback with significant phenotypic divergence in life history traits in copepods from species-pair lakes. Further, we anticipate population-level resequencing will show significant genetic distance between lake types and that genomic variation will be parallel, indicative of natural selection driving this variation. Finding an eco-evolutionary feedback in S. oregonensis will spur additional tests for how prey resource evolution might be a driving factor in stickleback character displacement that maintains ecological speciation. More broadly, this work with a diaptomid copepod addresses and provides resources for an extremely abundant, yet relatively understudied taxon with an outsized ecological impact.

3:15 PM - 3:30 PM
Mutant turtles: heat waves induce deleterious shell phenotypes

Fredric Janzen, Michigan State University
Gerardo Cordero, University of Valencia
Jose Bataller, VAERSA/Conselleria de Medio Ambiente
Tibisay Escalona, University of Porto
Matthieu Lassalle, TRAGSA/Conselleria de Medio Ambiente
Emily Dustman, Saint Louis University
Chad Dolan, Iowa Department of Natural Resources
James Lamer, Illinois Natural History Survey
John Tucker, Illinois Natural History Survey

Abstract:

Climate change is increasing the frequency of heat waves, not just overall environmental temperatures. Heat waves exert adverse impacts on populations, communities, and ecosystems of a variety of biota. In globally-imperiled turtles with temperature-dependent sex determination,

warmer temperatures should produce an excess of female offspring, potentially leading to long-term demographic collapse. But temperature spikes in turtle embryonic development could be problematic in more immediate ways. We find that heat waves during key periods of embryonic development substantially increase the frequency of shell scute abnormalities, using native and invasive slider turtles (Trachemys scripta) as a model. Anatomical assays confirm that a considerable fraction of these scute anomalies reflect underlying skeletal malformations. Quantitative genetic analysis of offspring from eggs incubated under thermally moderate conditions reveal a substantive heritable component to the presence/absence of abnormal scutes. In turn, large-scale field experiments link these abnormalities to reduced survival of neonates during the key life-stage of their journey from nest to water. Moreover, long-term fieldwork further detects that the frequency of turtles with scute anomalies declines with age, implying ongoing adverse impacts on survival through maturity and thereafter. Combining the heritability estimates with calculations of the strength of selection reveal minimal potential for microevolutionary response of this trait. In sum, an increase in environmentally-induced frequency of this deleterious trait should reduce population-level fitness, which constitutes an additional under-appreciated challenge for managing and conserving freshwater turtles in a rapidly changing world.

Genomics II

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Assessing the Impact of Continuous Traits on the Evolution of Discrete Traits: The Ancestral Condition Test.

Meghann McConnell, Texas A&M University
Heath Blackmon, Texas A&M University

Abstract:

Co-evolutionary relationships whereby the value of a continuous trait affects the evolution of a discrete trait remain challenging to study. Here we present the ancestral condition test, a new comparative method that evaluates whether a discrete trait tends to transition when a continuous trait has values more extreme than expected if both traits were evolving independently. This approach leverages ancestral state estimates of both the continuous and the discrete trait to test whether extreme values of the continuous trait appear to be associated with transitions in the discrete trait, and to assess statistical significance. We explore the robustness of our approach under a range of parameter values and patterns of trait evolution. We find that either a relatively strong contingency between the two traits or a large number of taxa is required to detect the underlying relationships reliably. Statistical power of the test is highest when the discrete trait

evolves with higher transition rates and species number on trees. In comparison to existing methods that can be used to explore similar hypotheses, we show that the ancestral condition test has both higher power and a lower false-positive rate. The types of questions that this approach allows us to test are common in evolutionary biology and, unlike existing methods, the ancestral condition test can be applied to account for the temporal order of transitions.

2:45 PM - 3:00 PM

Clustered Genomes, Partitioned Expression: How a Twig-Girdler Longhorn Beetle Organizes Its Host-Interface Gene Repertoire

Diego Souza, Field Museum of Natural History

Abstract:

Herbivorous insects have diversified through repeated interactions with host plants, yet the genomic organization and transcriptional deployment enabling host use across chemically defended plant lineages remain poorly characterized in many phytophagous groups. Twig-girdler longhorn beetles (Cerambycidae: Onciderini) present a distinctive system in which females girdle living branches prior to oviposition, converting chemically defended tissue into dead-wood substrate for larval development. We present a chromosome-scale genome assembly (474.7 Mb; N50 = 39.4 Mb; BUSCO = 99.4%) and multi-tissue, multi-stage transcriptomes for Oncideres impluviata, a Neotropical pest that exploits at least 21 host species across five plant families, including the tannin-rich introduced black-wattle (Acacia mearnsii). Telomeric and synteny evidence supports organization into 10 chromosomes, consistent with the conserved Lamiinae karyotype. Comparative analyses across 25 phytophagous beetle genomes reveal lineage-specific expansions in chemosensory (including a 40-gene Obp56d tandem cluster), neural signaling, detoxification, and digestive gene families, with GO enrichment confirming bias toward host-interface functions. Transcriptomic profiling shows these repertoires are deployed through stage- and tissue-structured programs: adults bear the primary transcriptomic burden of host assessment and chemical confrontation, chemosensory genes concentrate in antennae, and detoxification genes partition between antennae (odorant clearance) and thorax (systemic processing), with limited sex bias despite behavioral dimorphism in girdling. At the chromosomal level, over 170 tandem clusters show significant overrepresentation of differentially expressed genes, and seven multi-family superloci co-localize clusters from different gene families, suggesting coordinated deployment of complementary host-interface functions. These results link clustered genome architecture and regulatory partitioning to the ecological demands of broad host use and complex plant-manipulation behavior, providing a framework for understanding host breadth and host shifts in phytophagous beetles.

3:00 PM - 3:15 PM
Interspecific Limits, Diversification, and Biogeography History of the Obligatory Ant-Army Follower genus Gymnopithys (Aves: Thamnophilidae)

Juliana Damasceno, Louisiana State University

Abstract:

The genus Gymnopithys is widely distributed across the Neotropics, from Central America to Western and Eastern Amazonia, and comprises three species and 12 subspecies with contrasting plumage patterns, some of which hybridize in the Rio Negro headwaters. Understanding the diversification history, hybridization, and species boundaries in this group will provide insights into the processes driving Neotropical bird evolution. We hypothesize that Gymnopithys diversified in allopatry, followed by dispersal and secondary contact, with hybridization occurring where biogeographic barriers are weaker. To investigate phylogenetic relationships and hybridization, we sequenced whole genomes for 106 Gymnopithys individuals across their geographic range and conducted population structure and phylogenetic analyses. Our results indicate that G. bicolor and G. leucaspis are more related to each other than to G. rufigula. We also found signs of admixture in samples from southeastern Colombia, likely indicating a hybrid zone. Although these findings corroborate our initial hypothesis and align with relationships found in recent studies of Gymnopithys, they reveal a unique biogeographic pattern with paraphyletic Amazonian populations. We also found population structure within each lineage, which is currently under investigation. This study will clarify an uncommon biogeographic pattern and determine whether observed hybrid phenotypes result from isolated introgression events or a stable hybrid zone.

Co-authors' contributions: Andre Moncrieff, Camila Ribas, and Gregory Thom. AM: bioinformatics; CR: conceptualization, data curation, sampling loan; GT: conceptualization, data curation, methodology, and review.

3:15 PM - 3:30 PM
Genome-wide Comparisons Support the Hybrid Origin of Papilio appalachiensis

Alejandra Camargo, Boston University
Hannah Aichelman, Boston University
Tianzhu Xiong, Cornell University
Sean Mullen, Boston University

Abstract:

Papilio appalachiensis is named for its restricted distribution in the Appalachian Mountains. This swallowtail butterfly was originally described as a hybrid species derived from P. canadensis and P. glaucus, two closely related species in eastern North America. Evidence for its hybrid origin initially came from mixed morphological and ecological traits. Subsequent genetic studies found that six Z-linked genes in P. appalachiensis were more similar to P. canadensis, while a mitochondrial gene,

used as a proxy for maternal inheritance, was more similar to P. glaucus. These findings suggested inheritance of the Z chromosome from P. canadensis and the W chromosome from P. glaucus. However, genome-scale evidence for this hybrid origin has been limited. Here, we present the first chromosome-level reference genomes for P. canadensis, P. glaucus, and P. appalachiensis, assembled de novo from female specimens using PacBio HiFi long reads and Hi-C data. To infer evolutionary relationships, we reconstructed a maximum likelihood phylogeny using 98 ultra-conserved elements. This analysis recovered P. appalachiensis and P. canadensis as sister taxa (78% bootstrap support), with P. glaucus as their sister lineage. This pattern is consistent with partial shared ancestry and phylogenetic discordance expected under hybridization. We then performed an ABBA–BABA test using genome-wide SNPs and detected significant introgression from both P. canadensis and P. glaucus into P. appalachiensis. To further examine patterns of ancestry across the genome, we aligned all three genomes and reconstructed phylogenies across 50-kb sliding windows. Topology weighting analyses revealed that the P. appalachiensis–P. canadensis sister relationship predominates across most of the genome. However, discrete regions showed increased support for P. appalachiensis–P. glaucus cluster, indicating localized introgression. Together, these results provide strong genomic support for the hybrid origin of P. appalachiensis and establish a foundation for future evolutionary studies of this species complex.

3:30 PM - 3:45 PM
Geographic Predictors of Reticulate Evolution Across Deep Time in Toothy Skinks (Plestiodon)

Jon Hoffman, American Museum of Natural History / Michigan State University

Abstract:

Interspecific hybridization and introgression have been shown to be more widespread in vertebrates than traditionally considered. However, it remains unclear how the prevalence and magnitude of introgression correlate with different historical scenarios related to the geographic ranges of hybridizing taxa. Here, we integrate phylogenomic network inference with time-stratified historical biogeography to explicitly test how geographic range compatibility and dispersal connectivity influence introgression within the toothy skinks (genus: Plestiodon). Using whole-genome data from 57 individuals representing 37 species (73.6%), we inferred species relationships, estimated phylogenetic networks, and reconstructed ancestral ranges under alternative dispersal hypotheses. We identified six reticulation events spanning the Late Miocene through the Pleistocene, including five instances of asymmetric introgression and one consistent with homoploid hybrid speciation for P. fasciatus. Then, we derived quantitative, node-informed geographic predictors of introgression magnitude (γ), including range overlap, range adjacency, and connectivity via dispersal between donor and recipient lineages. We find that introgression occurred primarily among closely related lineages historically occurring in adjacent regions, consistent with hybridization along shifting parapatric boundaries rather than strict, long-term sympatry. Parapatric geographic situations were positively associated with γ, whereas direct overlap showed no relationship and dispersal-weighted connectivity exhibited a model-

dependent effect. By linking phylogenomic estimates of introgression to explicit, time-stratified geographic models, this study demonstrates that reticulate evolution is likely structured by dynamic dispersal connectivity rather than static range overlap alone.

Molecular Evolution III

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Mutation, selection, and drift shape codon usage bias in Mimulus guttatus

Luis Javier Madrigal Roca, The University of Kansas
John Kelly, KU

Abstract:

Synonymous nucleotide variation, unusually high in Mimulus guttatus, is shaped by two forces that are often treated as separable: direct selection on codon usage (translational efficiency) and indirect selection at linked sites. We integrated recently developed genomic and transcriptomic resources with polymorphism data from 187 inbred lines from Iron Mountain, Oregon, to disentangle these effects. Combining a mechanistic model (ROC-SEMPPR) with population-genetic inference from Wright's two-allele mutation–selection–drift equation, we estimated gene-specific selection coefficients (S = 4Nes) across the genome. Most genes are weakly selected for codon usage (roughly 76% fall in the range 0 1). Unlike the A/U-ending preferences reported for Rosid plants, M. guttatus, an Asterid, favors predominantly C-ending codons (74% of preferred codons), a pattern not explained by tRNA gene copy number and instead reflecting lineage-specific mutational and translational dynamics.

Levels of variation within genes reveal a strong imprint of linked selection. Nonsynonymous polymorphism declines in genes under strong purifying selection and as intragenic recombination falls; synonymous polymorphism generally tracks this decline through background selection. Counterintuitively, however, codon usage selection has a net positive effect on synonymous diversity at 4-fold degenerate sites. Because mutational pressure toward unpreferred bases is strong, intermediate-strength selection inflates heterozygosity (the McVean–Charlesworth "diversity hump"), and much of the genome sits on its upslope. Preferred-codon frequency also depends on position, peaking near codon 50, consistent with a translational ramp superimposed on an intragenic recombination gradient. Together, these results connect mechanistic models of codon evolution to observable patterns of sequence variation, showing that translational selection achieves localized victories against a pervasive mutational headwind.

2:45 PM - 3:00 PM
Variation in antifungal resistance in a forest yeast species

Miranda McKibben, University of Georgia

Abstract:

Antifungal resistance in clinical yeast species is a growing problem, and many studies have focused on how yeast strains develop antifungal resistance in clinical settings. Little research has been done to explore whether antifungal resistance could arise in natural environments. This study includes a population genomic analysis of 277 genomes (including 90 new sequences) from natural North American and European populations of the forest yeast Saccharomyces paradoxus, a yeast that lives on trees and soil and is not associated with humans. Surprisingly, a sliding window scan of natural genomic variation within this species has revealed an unusually large number of mutations in the FKS1 gene; a gene known to confer antifungal resistance to echinocandin class antifungals. While there have been many studies on the effects of FKS1 mutations, mutations in this gene have not been studied in S. paradoxus because echinocandin exposure in forest habitats would be unexpected. Antifungal susceptibility testing found differences in the FKS1 alleles correlate with strain response to several echinocandin drugs, revealing variation in innate antifungal resistance in some S. paradoxus strains taken from Europe and North America, but not others. It is unclear if this variation is a result of selective pressure due to environmental antifungal exposure from an unknown source or if strains with different FKS1 alleles have an advantage under other conditions. These results suggest the importance of further research into antifungal resistance in natural environments.

3:00 PM - 3:15 PM
Structure-informed analyses of molecular evolution reveal patterns of selection hidden from linear sequence analyses

Brad Broyles, Purdue University
Qixin He, Purdue University

Abstract:

Molecular evolution is typically analyzed at the level of individual sites or linear sequence windows. However, selection pressures on protein-coding regions frequently target spatially organized features such as protein-protein interfaces, ligand-binding sites, and catalytic domains. This creates a fundamental mismatch between how genetic variation is measured and how protein function is organized. With accurate protein structure prediction now routine, we can begin to study molecular evolution in the three-dimensional context in which protein function emerges.

To address this mismatch, we formalize structure-informed evolutionary analysis through evo3D, an R package that links protein structure to underlying genetic diversity. By extracting subsets of multiple sequence alignments corresponding to spatially defined regions, evo3D introduces spatial

haplotypes as an analytic unit for measuring genetic variation within structurally coherent neighborhoods. The full workflow is implemented in a single function call requiring only sequence alignments and a structure model.

Using two viral protein complexes, we show that spatial analysis reveals patterns of selection that are hidden from linear sequence-based approaches. In hepatitis C virus, we scan the E1/E2 protein complex surface with antibody-binding-site sized windows and identify conserved patches that are not detected using linear sequence windows. In the Chikungunya virus E1/E2 protein complex, we directly isolate the host receptor binding interface as a spatial haplotype spanning four structural chains (two E1 and two E2), revealing strong conservation within the interface and elevated balancing selection in surrounding surface regions, indicating spatial partitioning of functional constraint and immune driven variation.

These results demonstrate that a structure-informed perspective is not merely complementary but essential for revealing spatially organized patterns of selection across protein structures. evo3D automates the genetic to structural mapping, generalizes from monomers to protein complexes, and we anticipate its wide application in molecular evolution studies.

3:15 PM - 3:30 PM
Antibiotic Effects on the Rates and Effect Sizes of Spontaneous Mutations

Wei-Chin Ho, University of Texas at Tyler

Abstract:

When organisms encounter a new environment, a higher rate and larger effects of beneficial mutations facilitate the adaptive process, while a higher rate and larger effects of deleterious mutations drive the populational extinction. Therefore, the knowledge of mutational rates and effect-size distributions is critical for understanding and forecasting the fate of organisms in changing environments. Moreover, these mutational features may be altered when environmental changes shift the cellular physiology. Identifying the machineries underlying these context-dependent changes help expedite the desired or impede the unwanted adaptation. To address these questions, Escherichia coli in sub-inhibitory concentrations of antibiotics was used as a model system. Particularly, mutation accumulated (MA) lines with continuously strong population bottlenecks were used, as all non-lethal mutations are retained with less biases. The fitness assay of MA lines was performed by comparison of growth curves in a microplate reader with the ancestral wild-type on the same plate. As a result, the mutations accumulated in the presence of norfloxacin show more deleterious effects, independent from the elevated mutation rates. The altered distribution of fitness effects is a result of altered mutational spectrum and not merely the change of fitness effects of the same mutations in the stressful environment. Additional experiments reveal that the fitness effects of the same set of accumulated mutations change in the presence of streptomycin but not ampicillin. To sum up, these results reveal genetic-environmental interaction of fitness effects and suggest the diverse modes of evolutionary responses to different antibiotic treatment.

3:30 PM - 3:45 PM
Evolution of Weed Herbicide Resistance and Population Genetics Across North Carolina Field Stations

Nikolai Hay, North Carolina State University

Phylogenetic Methods Development I

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM
Estimating Gene Duplication and Loss Rates Using Machine Learning

Caden Noonan, Mississippi State University
Megan Smith, Mississippi State University

2:45 PM - 3:00 PM
Ancestral state reconstruction with discrete characters using deep learning

Anna Nagel, Washington University in St. Louis
Michael Landis, Washington University in St. Louis

Abstract:

Ancestral state reconstruction is a classical problem of broad relevance in phylogenetics. There are both maximum likelihood and Bayesian methods for ancestral state reconstruction for many models including Markov and SSE models for discrete characters.However, many factors that are thought to biologically relevant give models without a tractable likelihood, leaving us largely unable to investigate their biological importance.The rapid advancement of deep learning offers a potential alternative to likelihood-based inference of ancestral states, especially for models with intractable likelihoods. We extend the phylogenetic deep learning software phyddle to allow for ancestral state reconstruction. We evaluate phyddle performance for a variety of models and tree sizes and compare to Bayesian inference when possible.For simple models and small trees, the performance approaches the performance of Bayesian inference, but the performance degrades for larger trees. While phyddle still performs well on average for more complex models, such as speciation and extinction models, the estimates differ more from Bayesian inference in comparison with simpler models. Lastly, we use phyddle to infer ancestral states in two empirical datasets, one of the ancestral ranges of a subclade of the genus Liolaemus and ancestral locations for sequences from the 2014 Sierra Leone Ebola virus disease outbreak.

3:00 PM - 3:15 PM

Toward reference-agnostic phylogenomics from heterogeneous sequencing data

Nan Yao, Yale University
Anri Chomentowska, Yale University
Pauline Raimondeau, Yale University
Peregrine Todd,
Alison Carranza, Yale University
erika edwards, yale university

Abstract:

On theoretical grounds, what matters for phylogenetic resolution is that the data carry signal reflecting the history of lineage divergence, ideally evolving in a clock-like manner, not that they derive from predefined loci. This opens the possibility that the most informative phylogenetic signal emerges, at least in part, from the data themselves, without reference genomes or annotations that are costly and often unavailable for non-model species. We developed an alignment-free framework, phyloWeld, that extracts phylogenetic signal directly from raw sequencing reads. It readily accommodates heterogeneous data types, including genome skimming, RAD-seq, target capture, and transcriptomes. The framework can optionally interface with reference genomes to understand the relationship between phylogenetic signal and genomic regions at a fine scale, but does not depend on them. We hope this approach can lower the barrier to broader phylogenomic synthesis by reviving and integrating legacy datasets.

3:15 PM - 3:30 PM

Not too hot, not too cold: developing an adaptive cooling schedule for PICL (Phylogenetic Inference using Composite Likelihood)

Shelby Moshier, The Ohio State University
Laura Kubatko, The Ohio State University

Population Genetics Theory and Methods

06/21/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Borrowing signal across populations: domain adaptation for small sample population genomics

Niko Zuppas, The Ohio State University
Bryan Carstens, The Ohio State University

2:45 PM - 3:00 PM
Epistasis as a balancing mechanism in changing environments

Adina Ataran, University of California Davis

Abstract:

Balanced polymorphism is a fundamental yet elusive phenomenon in population biology, with profound implications for evolution in changing environments. Recent theory proposed that epistasis may promote balanced polymorphism in temporally varying environments, albeit under a restrictive model of phenotypic plasticity or infinite population settings. It remains unclear if epistasis could foster balanced polymorphism in finite populations. We explore the effects of reinforcing, diminishing, and sign interactions on levels of genetic polymorphism at two selected loci in a population inhabiting temporally changing environments. First, we argue that at least one of the two interacting loci needs to experience sign interactions for epistasis to promote balanced polymorphism. Next, we show that selection needs to be strong for such polymorphism to be protected in finite populations. Finally, we demonstrate that reinforcing epistasis, combined with balancing effects of spatial heterogeneity in temporally varying environments, may enhance polymorphism in finite populations even in the absence of strong selection. The latter uncovers a new balancing mechanism that significantly broadens the conditions under which epistasis promotes polymorphism. Intuitions for the effect involve a combination of indirect negative frequency dependence and the reinforced effect of rare alleles under reinforcing epistasis. Therefore, reinforcing and strong sign epistasis, emerge as mechanisms of balancing selection in finite populations. We support our findings with analytical approximations and an extensive set of stochastic Monte Carlo simulations across a wide range of parameters in Write-Fisher finite populations. This research, therefore, comprehensively examines and highlights one of the underexplored mechanisms of balancing selection — epistasis.

3:00 PM - 3:15 PM
Patterns of ancestral polymorphism across amniotes

Fernando Torres, Johns Hopkins University
EJ Huang, Johns Hopkins Univesity
Gabriel Bever, Johns Hopkins University

Abstract:

There is a growing body of research detailing the effects of polymorphism throughout the evolutionary process. Yet, the persistence of polymorphism across deep time remains understudied. Under the multispecies coalescent model, incomplete lineage sorting (ILS) provides a record of the persistence of polymorphism at the genomic level and predicts that gene tree discordance resulting from ILS should decrease as time separating speciation events increases. Here, we use whole genomes to investigate ILS signals on two datasets comprising 1079 orthologous genes across 24 amniote species. These datasets span a wide range of branch lengths

and evolutionary depths, from recent Cenozoic divergences to deep splits that approach the Permian. We measure the discordance across quartets and test whether the observed gene tree conflicts are consistent with ILS expectations. We then evaluate the strength of the relationship between discordance frequency and branch length measured in absolute time. Our Results show most of the discordance in these datasets is consistent with ILS. Notably, we detect strong ILS signals in quartets with internal branches spanning up to ~40Ma, indicating that ancestral polymorphism can be retained and detected over extended periods of time, including intervals that comprise speciation events of extinct lineages.

3:15 PM - 3:30 PM
Detecting and ameliorating model violations with machine learning

Megan Smith, Mississippi State University

3:30 PM - 3:45 PM
A model of the joint evolution of mutation rates, spectra, and DFEs in asexual populations

Mete Yuksel, University of Toronto
Tenoch Morales, University of Western Ontario
Puneeth Deraje, University of Toronto
Marwa Tuffaha, Western University
Lindi Wahl, Western University

Abstract:

Mutation is the ultimate source of variation in natural populations, but varies dramatically across lineages and the tree of life. This variation is the consequence of the fact that mutation is not only an input to the evolutionary process, but a phenotype that itself evolves. In line with this thinking, understanding of the dynamics of “mutators” and “anti-mutators” (mutations that increase or decrease the mutation rate, respectively) has been of long-standing theoretical and empirical interest. Such modifiers of mutation rate, e.g., those affecting enzymes that are involved in DNA repair, are common in bacterial populations. In addition to the rate, these modifiers often affect the relative abundance of the various types of mutations (the mutation spectrum) and, as a result, the observed distribution of fitness effects (DFE). Using a mechanistic mathematical model, we explore the joint evolution of the genome-wide mutation rate, spectrum, and DFE in an asexual population. In our model, two types of modifiers — those affecting the functionality (gain and loss) of repair enzymes associated to various mutational signatures, as well as signature-specific mutation rates — arise and fix sequentially. We develop predictions for the long-term evolution of the rate, spectrum, and DFE and characterize patterns in the number of substitutions separating lineages.

Adaptation II

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

The evolution of gender: can we agree on an adaptive view?

Lixing Sun, Central Washington University

Abstract:

This talk advances an integrative, evolutionarily grounded framework for understanding gender as an adaptive biological construct. Drawing on comparative evidence across taxa, I argue that gender, defined broadly as a suite of behavioral, morphological, physiological, and neuroendocrine traits associated with reproductive strategies, functions as a flexible mechanism that enhances Darwinian fitness under diverse socioecological conditions. Far from being a purely social construct, gender exhibits deep biological roots shaped by natural selection, while remaining highly responsive to environmental variability.

Empirical examples illustrate this adaptive flexibility. In sex-role reversed species such as jacanas, females compete for mates while males assume primary parental care, reflecting ecological pressures that favor paternal investment. Similarly, in Neotrogla, females evolve intromittent organs and engage in prolonged copulation to extract nutritional resources from males, demonstrating how resource limitation can invert conventional reproductive roles. In mammals such as spotted hyenas, female masculinization arises through hormonal mechanisms that enhance competitive ability in food-limited environments. These cases reveal that gender variation is not anomalous, but a recurrent evolutionary outcome driven by ecological constraints and reproductive trade-offs.

Crucially, gender provides a more rapid and flexible alternative to sex change, which is often costly and developmentally constrained. By modulating traits such as behavior and hormone profiles, organisms can adjust reproductive strategies without undergoing radical (and often irreversible) transformations. This flexibility is especially pronounced in humans, where biological predispositions interact with cultural systems to produce extensive gender diversity.

I propose that an adaptive view of gender, grounded in evolutionary biology yet open to interdisciplinary dialogue, offers a common framework for reconciling biological and social perspectives. Recognizing gender as a dynamic, fitness-enhancing system may foster a more objective and inclusive understanding of biodiversity while aligning scientific inquiry with broader societal discourse.

4:30 PM - 4:45 PM

Grow, adapt, repeat: How long-term evolution shapes niche breadth in Halobacterium salinarum

Nahui Medina Chavez, University of Minnesota
Adaluz Canseco-Barbeyto, Universidad Nacional Autonoma de Mexico
Steph Varghese, University of Minnesota
Mike Travisano, University of Minnesota

Abstract:

Environmental conditions like salinity and nutrient availability strongly influence how microbes grow and survive. A key question is whether adapting to a single, stable environment limits how well microbial populations perform when conditions change, or whether they retain the ability to tolerate a range of environments. These patterns can be understood through changes in niche breadth, which describes how perfomance varies across environmental gradients. Experimental evolution offers a way to directly test how these develop over time. In this study, we investigated the growth dynamics, genomic change and niche breadth in Halobacterium salinarum populations that had already evolved for 150 serial transfers (~900 generations) in a constant, high salinity and nutrient rich environment. Whole genome sequencing showed the accumulation of SNP's (single nucleotide polymorphisms), including repeated changes in genes related to membrane fuction and multiple ISH elements. Mutation rates and the mix of shared unique mutations points to both parallel and independent evolutionary paths, with evidence for selective sweeps as well as clonal interference. To test trade-off, we exposed these populations into a poorer environment with lower salt concentrations and reduced nutrients. While all populations performed well in the environment they evolved in, many showed reduced growth under these new conditions. At the same time, some populations were less affected, suggesting differences in how broadly they can toletrate environmental change. Our results, show that long-term evolution in a constant environment can lead to similar genetic changes across populations, but different outcomes in how they respond to new conditions.

4:45 PM - 5:00 PM

Strain background influences the rate but not the genetic target of laboratory adaptation to a biotic stress in Escherichia coli

Owen Hale, Vanderbilt University
Sara Williams, Vanderbilt University
Megan Behringer, Vanderbilt University

Abstract:

Escherichia coli is the most common cause of urinary tract infections (UTIs), To colonize the bladder, it must contend with the preexisting urinary microbiota. This community is often dominated by Lactobacillus crispatus, a commensal bacterium associated with a lower risk for recurrent UTIs that can inhibit the growth of E. coli in vitro. Despite its likely protective function, L.

crispatus can be found in the bladders of patients with E. coli UTIs. To determine how E. coli may adapt to overcome inhibition by L. crispatus, we performed an adaptive laboratory evolution experiment in which populations of E. coli strains K-12 (non-pathogenic laboratory strain) and UTI89 (UTI isolate) were passaged in increasing concentrations of L. crispatus spent media for up to 450 generations. Interestingly, the K-12 populations evolved the ability to grow in the maximum tested spent media concentration more slowly and less frequently than the UTI89 populations. Every population, regardless of strain background, that evolved the ability to grow in the maximum tested spent media concentration acquired mutations in a single oxidative stress response regulator that were previously shown to enhance oxidative stress resistance. These results demonstrate that the rate of phenotypic adaptation to this biotic stress is contingent upon strain background, but the genetic targets of the adaptive mutations required to reach the maximum tested level of resistance do not.

5:00 PM - 5:15 PM

Two ways to survive thin air: experimental transcriptomics reveal contrasting physiological acclimation in high-altitude residents and elevational migrants

Prashant Ghimire, Kent State University
Nan Wang, School of Ecology and Nature Conservation
Sangeet Lamichhaney, Kent State University

Abstract:

High-altitude environments impose hypoxic conditions that challenge oxygen delivery and cellular homeostasis. Although long-term genetic adaptation in high-altitude residents has been widely documented in different species, including birds, the molecular mechanisms that enable birds to cope with short-term acute hypoxia remain less understood, particularly across species with diverse life-history strategies. In this study, we have used time-resolved transcriptomics from transplantation experiments to compare transcriptional responses to changes in altitude between a high-altitude endemic and an elevational migrant bird. First, we investigated transcriptional responses to moderate elevational shifts in the Tibetan Partridge (Perdix hodgsoniae), a high-altitude resident of the Sino-Himalayan region. Individuals captured at 4,000 m were maintained at transplantation facilities either at 4,400 m or transplanted downslope to 3,000 m, and blood transcriptomes were sampled over four weeks to quantify temporal changes in gene expression. Gene-expression patterns remained largely stable across elevations, with altitude-specific regulation enriched for endocytosis and mTOR signaling pathways, whereas the temporal response was mostly related to the adaptive immune response. We then conducted a controlled transplantation experiment in the elevational migrant Blue-fronted Redstart (Phoenicurus frontalis). Birds captured at 3,000 m were either maintained at their native elevation or translocated to 4,400 m, and blood transcriptomes were sampled over three weeks. High-altitude exposure triggered strong temporal remodeling of gene expression, with early responses dominated by upregulation of innate immune and interferon-mediated pathways that gradually stabilized over time. These results reveal contrasting molecular strategies for coping with hypoxia: stable transcriptional regulation in

high-altitude residents with adaptive responses and dynamic innate immune-mediated acclimation in elevational migrants. These findings highlight how life-history strategy shapes physiological responses to fluctuating oxygen availability in mountain environments.

5:15 PM - 5:30 PM
Muscle Cell-Specific Gene Regulation Underlying Adaptation to High Elevation in Deer Mice

Peter Nimlos, University of Denver
Jon Velotta, University of Denver

ASN Early Career Award & Dobzhansky Award Talks

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:45 PM
Pattern to Process: Exploring Plant Evolution Through Natural History and Genomics

Patrick McKenzie, Harvard University

4:45 PM - 5:15 PM
Infrared radiation is an ancient pollination signal

Wendy A. Valencia-Montoya, Harvard University

Abstract:

Color and scent are well-known pollinator cues. Some plants also produce heat, but its role remains unclear. Here, we report that plant-generated thermal infrared radiation serves as a pollination signal and describe the underlying mechanisms of heat production and infrared detection. mitochondrial adaptations heat plant reproductive structures in a circadian pattern, radiating infrared that is sufficient to attract beetle pollinators. beetle antennae contain infrared-activated neurons with thermosensitive ion channels that are structurally tuned to match host plant thermogenesis. comparative analyses revealed that infrared is among the earliest pollination signals, and indicate a deep-time transition from infrared-based to color-dominated signaling in flowering plants. Our findings uncover an ancient sensory modality shaping the early evolution of pollination, one of the world's most vital processes linking plants and animals.

Bioinformatics

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Panmap: Scalable alignment, genotyping, and phylogenetic placement on pangenomes at sample and read resolution

Alan Zhang, UC Santa Cruz
Alex Kramer, UC Santa Cruz
Russell Corbett-Detig, UC Santa Cruz

Abstract:

Graph-based pangenome methods face scalability challenges, requiring extensive memory and time for read alignment and variant calling, particularly for large microbial pangenomes containing thousands or millions of genomes. We developed Panmap, a tool that leverages phylogenetic structure to enable ultrafast k-mer-based phylogenetic placement at both sample and read resolution. Panmap uses reference pangenomes encoded as mutation-annotated phylopangenomic trees (PanMAN format) and generates a phylogenetically compressed k-mer index that stores only the differences between sequences along each branch, achieving up to 500-fold smaller size than alternatives and building in a fraction of the time. In single-sample mode, Panmap uses k-mer-based placement to identify the closest reference to the sample, then performs alignment using already-indexed k-mers and generates a consensus assembly. In metagenomic mode, Panmap scores each read against all nodes to place each read to its closest reference, identify likely haplotypes present, and estimate their relative proportions in the sample. We demonstrate Panmap's effectiveness for genome assembly of various viral species, such as RSV and SARS-CoV-2. We further demonstrate accurate abundance estimation of viral species in simulated data and accurate lineage abundance estimation in real wastewater data, rivaling and in some cases outperforming state-of-the-art alternatives. Finally, we built a vertebrate mitochondrial PanMAN and demonstrate fast and accurate phylogenetic placement of ancient eDNA onto the mitochondrial tree, using a competitive-mapping filtering strategy. Application to previously published data revealed clear assignment hotspots concordant with previous results, with reads clustering at their expected species nodes. Panmap provides a scalable and accurate framework for phylogenetically-anchored analysis across genomic, metagenomic, and paleogenomic applications.

4:30 PM - 4:45 PM

Species-rich and genomically diverse: comparative genomics reveals how fusions, fissions, and sex chromosomes have shaped beetle evolution.

Dwayne Tally, Indiana University

Abstract:

Beetles (Coleoptera), the most species-rich animal order, exhibit extensive diversity in karyotype, yet the extent to which their chromosomes retain deep ancestral structure remains unclear. Here, we analyzed 190 chromosome-level genome assemblies spanning 39 families and 16 superfamilies to characterize genome diversity, evaluate the conservation of ancestral linkage groups (Stevens elements), identify neo-sex chromosomes, and explore the role of repetitive elements in driving karyotypic change. Our results reveal that beetle genomes are highly diverse, varying substantially in genome size, chromosome number, and transposable element (TE) composition. Despite this diversity, Stevens elements appear conserved across much of the radiation, with several superfamilies maintaining strong chromosome synteny over more than 200 million years of evolution. In contrast, the leaf beetles (Chrysomelidae) have undergone frequent chromosomal fusions and fissions, elevated genome size variation, and reduced conservation of ancestral linkage group relationships. Using synteny-based approaches, we identified 37 species (approximately 19.5% of those examined) with patterns consistent with neo-sex chromosome formation through X-autosome fusion events. These putative fusions vary in complexity and are disproportionately clustered within lineages prone to chromosomal instability. Repeat content varies widely across beetles, though no consistent association between transposable element composition and rates of karyotypic change was detected at this phylogenetic scale. Together, these findings help establish beetles as a promising comparative system for uncovering the evolutionary forces that maintain and disrupt ancestral linkage groups and drive the formation of neo-sex chromosomes.

4:45 PM - 5:00 PM

High-resolution single-cell analyses reveal evolutionary constraints and evolvability of sexual circuits in Drosophila

Justin Walsh, Holy Family University
Ian Junker, University of Pennsylvania
Yu-Chieh Chen, Temple University
Yen-Chung Chen, New York University
Helena Gifford, University of Pennsylvania
Dawn Chen, University of Pennsylvania
Yun Ding, University of Pennsylvania

5:00 PM - 5:15 PM
The Secrets of the Mantidfly Genome

Ethan Grebler, University of Florida
Andrew Mongue, University of Florida

Abstract:

Though recent advances in sequencing technology have made the sequencing of non-model organisms more practical and efficient, barriers remain. In particular, cost and (especially for small invertebrates) available tissue can be limiting factors for modern genomic projects of non-model species. By pooling tissue from multiple, distantly related species into one Hi-C crosslinking reaction and sequencing library, we retrieve Hi-C data to assemble multiple genomes from a single Hi-C run, and lower both the input tissue required for species and the per-species cost of generating chromosome-level assemblies. Using this pooling technique, we assemble for the first time the chromosome-level genomes of several bagworm moths, presented elsewhere, and four mantidfly species (Neuroptera: Mantispidae): Dicromantispa interrupta, Leptomantispa pulchella, Plega dactylota and Zeugomantispa minuta. Mantidflies display several unique characteristics within Neuroptera, with the larvae of many species serving as parasitoids within the egg sacs of spiders and the adults possessing raptorial forelimbs for use in prey capture. Mantidflies are the sister group to the green lacewings (Neuroptera: Chrysopidae) and are additionally closely related to antlions (Neuroptera: Myrmeleontidae), with larval green lacewings as well as antlions employing venom during prey capture. With these newly generated assemblies, we explore venom protein evolution, genome structure rearrangement, and sex chromosome dynamics in a rare invertabrate system with recombination in the heterogametic sex. These results serve as a primer for future research into the content of the genome and venom profile of Mantispids as well as dynamics of sex chromosome evolution. More generally, this approach of pooled Hi-C sequencing can allow for cheaper genomes of small, uncommon species.

5:15 PM - 5:30 PM
Evolutionary rates provide genomic insights into convergent and lineage-specific evolution in carnivorous plants

Sukuan Liu, Sloan Lab | Colorado State University

Abstract:

Carnivorous plants (CPs) are striking examples of convergent evolution across ecological, morphological, and molecular scales, making them ideal systems for investigating genomic adaptation to extreme environments. While genomic studies have shown that gene family expansion and functional recruitment underlie key carnivorous traits, the effects of these transitions on rates of sequence evolution remain incompletely understood. Here, we present a comparative framework to examine evolutionary rate shifts across 30 carnivorous and non-carnivorous eudicots, analyzing over 12,000 gene families . Analyzing branch-lengths and

evolutionary rate covariation (ERC), we detect both lineage-specific and convergent acceleration in genes associated with stress response, stimulus signaling, and light perception. Accelerated genes often belong to expanded families and show relaxation of purifying selection pressure. Despite limited overlap in the specific genes showing convergent acceleration across carnivorous lineages, we find strong convergence at the functional level, with repeatedly accelerated genes involved in similar biological pathways, particularly light and hormone responses. ERC network analysis identifies a stress- and stimulus-responsive gene community with lineage-specific acceleration in Sarraceniaceae species and moderate acceleration in other CP lineages. Hub genes in this network are also co-expressed in a distantly related non-CP model system, suggesting repeated co-option of an ancestral regulatory module for carnivorous functions. Together, our results show that convergent genomic rate accelerations in CPs primarily involves functionally equivalent or similar but lineage-distinct genes, shaped by gene duplication, relaxed selection, and co-option of stress-response networks.

Evolutionary Ecology: Species Interactions

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM
Coevolution of species' range borders

Farshad Shirani, Emory University

Abstract:

Existing theory on how interspecific competition can form range limits assumes that dispersal is random—and it is this random dispersal that creates maladaptive core-to-edge gene flow that contributes to limit ranges. But dispersal is unlikely to be random for many organisms, and it is plausible that adaptive dispersal would promote species' range expansion and prevent formation of range limits. In this talk I present a comprehensive mathematical model of species' range coevolution that we have developed to answer this important question: can interspecific competition cause range limits when species disperse adaptively? Surprisingly, our numerical computations of the solutions of the model show that adaptive dispersal results in even sharper range borders, meaning that the formation of range limits by interspecific competition is robust to assumptions about individual dispersal.

4:30 PM - 4:45 PM

Mapping behavioral networks to understand fine-scale habitat partitioning linked to species persistence in Lake Tanganyikan cichlids

Jimena Golcher-Benavides, Hope College
Catherine Wagner, University of Wyoming

Abstract:

The exceptional diversity of cichlid fishes in the African Great Lakes represents a classic example of adaptive radiation in freshwater ecosystems. However, the mechanisms that enable such high levels of species coexistence in these systems remain partially understood. Behavioral biases (e.g., males directing aggression preferentially toward phenotypically similar rivals) may promote the persistence of novel types, even if these occur at relatively low frequencies. Although less studied than mate choice biases in the context of adaptive radiations, aggression biases may facilitate species coexistence, with or without additional competitive advantages. Here, we used remotely obtained underwater footage of cichlid fishes in their natural habitat, combined with an ecological network framework, to quantify individual interactions and describe the fine-scale behavioral ecology of the Lake Tanganyikan cichlid radiation. Specifically, we tested whether "aggressors" specialize in their intraspecific/interspecific targets along a depth gradient, which represents an inverse energy gradient in primary productivity, using 1) species-level specialization metrics (describing the exclusivity of interaction partners) and 2) network-level metrics (describing how interaction exclusivity varies among species). We further determined whether individual interaction exclusivity was predicted by interspecific trait similarity and quantified how the resulting patterns shift along the water depth gradient. Behavioral biases remains an overlooked behavioral mechanism promoting elevated cichlid species-persistence in the shallow rocky reefs of Lake Tanganyika.

4:45 PM - 5:00 PM

Microbes are the glue that hold together fig (and likely other) community dynamics

J'Bonae McDonald, The University of Missouri
Isabella Hall, University of Missouri
Jenna Naumann, University of Missouri
Gracie Rinderer, University of Missouri
Ally Whitson, University of Missouri
Pamela Brown, University of Missouri
Justin Van Goor, University of Missouri Columbia

Abstract:

Biological communities are not only shaped by and conventionally understood in the context of interacting eukaryotes but are also universally composed of and often dominated by less understood microbial associates. The crucial ecological and evolutionary roles that bacteria play

on eukaryotic dynamics is challenging to examine in most natural biological communities. However, the closed nature of the fig (Ficus spp.) microcosm, which houses numerous co-occurring and interacting eukaryotic and bacterial mutualists, commensals, and antagonists, allows us the opportunity to assess (and soon manipulate!) the role of individual associates on broader community dynamics (and across multiple species/communities concurrently). Preliminary observations of wild and cultivated figs in the USA, Central America, and Europe suggested that figs containing nematodes were routinely free of a detrimental fungal pathogen (Fusarium spp.). Further examination of Neotropical fig-nematode associates (Diplogastridae: Parasitodiplogaster) suggested that an endosymbiotic Serratia bacterium was the causal agent underlying this fungal mitigation. 16S metabarcoding of three fig communities in the USA and Mexico showed highly diverse bacterial communities thriving within figs but also revealed that Serratia bacteria were present in nearly all examined figs, even those lacking pollinating wasps or nematodes. Nematode-infested figs were further found to have significantly higher rates of Kosakonia bacteria association, leading us to hypothesize that an intestinal interaction between Serratia and Kosakonia facilitates not only fungal spore and hyphal degradation, but also allows for nematodes to break down chitinous wasp material. To test these hypotheses, we will perform a series of bacterial, nematode, and fungal interaction experiments using a variety of fig-associated bacteria, Fusarium species, and Diplogastrid nematodes (forthcoming as of March 2026). These results show not only the ubiquity/complexity of bacterial species in biological communities but also highlight the important and beneficial ecological role/s nematodes may demonstrate in acting as a bridge between microbial and eukaryotic community dynamics.

Genomics III

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Illuminating the mystery of thylacine extinction: a role for relaxed selection and gene loss

Buddhabhushan Salve, IISER BHOPAL

Abstract:

Gene loss shapes lineage-specific traits but is often overlooked in species survival. In this study, we investigate the role of ancestral gene loss using the extinction icon—thylacine (Thylacinus cynocephalus; also known as the Tasmanian tiger or Tasmanian wolf). The thylacine was the largest modern-day carnivorous marsupial and the sole surviving member of the genus Thylacinus and the family Thylacinidae until its extinction in modern times. While studies of neutral genetic variation indicate a population decline before extinction, the impact of thylacine-specific ancestral gene losses remains unexplored. The availability of a chromosomal-level genome of the extinct thylacine

offers a unique opportunity for such comparative studies. Here, we leverage palaeogenomic data to compare gene presence/absence patterns between the Tasmanian devil and thylacine. We discovered ancestral (between 13–1 million years ago) loss of SAMD9L, HSD17B13, CUZD1, and VWA7 due to multiple gene-inactivating mutations identified using a machine-learning-based tool, TOGA, corroborated by short-read sequencing and BLASTn searches in the thylacine ~200 Gb paleogenomic database. The timing of gene loss mirrors the thylacine's shift towards hypercarnivory and increased body size. Notably, the loss of SAMD9 correlates with a carnivorous diet. Our genome-wide analysis reveals olfactory receptor loss and relaxed selection, aligning with reduced olfactory lobes in the thylacine, indicating olfaction is not its primary hunting sense. Therefore, these gene losses, occurring alongside ecological shifts such as increased carnivory (which occurred after the Middle Miocene Climatic Transition (MMCT)), may have been beneficial in the distant past. However, it may have reduced its resilience to disease and environmental changes. The findings suggest that historical contingencies such as ancient genetic changes, not just recent human impacts, played a role in its demise. This pioneering approach can inform conservation strategies by revealing hidden genetic vulnerabilities in both extinct and endangered species.

4:30 PM - 4:45 PM

Neurogenomic correlates of speciation by reinforcement in Upland chorus frogs (Pseudacris feriarum)

Carlie Ochoa, Florida State University
Alan Lemmon, Florida State University
Emily Lemmon, Florida State University

Abstract:

How transcriptomic variation drives speciation remains a key open question in evolutionary biology. One powerful approach is to compare gene expression profiles across brain regions in individuals or populations to uncover how transcriptomic differences contribute to behavioral divergence and reproductive isolation. Here, we leverage natural variation in the Upland chorus frog (Pseudacris feriarum) to identify patterns of synaptic transmission gene expression that may underlie incipient speciation. The focal species has evolved novel male advertisement calls and corresponding female preferences in populations sympatric with the closely related P. nigrita, driven by reinforcing selection. Recent neurophysiological studies suggest that changes in auditory midbrain neurons contribute to these behavioral shifts. We hypothesized that transcriptomic variation in the auditory midbrain would mirror these behavioral changes, with genes involved in synaptic transmission being enriched among differentially expressed genes. To test this, we collected auditory midbrain tissue of male and female P. feriarum from two allopatric populations (behaviorally similar) and three sympatric populations (behaviorally distinct) and performed bulk RNA-seq. Our results reveal extensive transcriptomic variation across the five populations, with one sympatric population exhibiting particularly striking divergence in gene expression. Surprisingly, transcriptomic patterns did not align with behavioral divergence: the two allopatric populations form distinct clusters,

despite their behavioral similarity, while two of the three sympatric populations showed largely overlapping expression profiles, despite clear differences in behavior and neurophysiology. In addition, candidate synaptic transmission genes were significantly depleted—rather than enriched—in several pairwise population comparisons. These findings suggest that behavioral evolution in this system may arise more from diffuse, transcriptome-wide shifts or coordinated pathway-level changes than from alterations in a few key synaptic genes. Overall, our study highlights the complex role of transcriptomic variation in shaping divergent behavioral phenotypes during speciation, providing new insight into the genomic basis of reinforcement in a classic vertebrate system.

4:45 PM - 5:00 PM

A tale of snowy and fiery bumble bees: Repeated cis-regulatory structural variation underlies convergent mimicry

Tunc Dabak, The Pennsylvania State University
Heather Hines, Pennsylvania State University

Abstract:

Müllerian mimicry in bumble bees (Bombus spp.) has generated striking color pattern convergence across geographically and phylogenetically distinct lineages. This presents an opportune system for understanding whether similar mutational pathways are used to generate adaptive convergent phenotypes. Here, we apply genome-wide sequencing in species that are part of two regional mimicry systems to reveal whether common genetic mechanisms underlie these convergent phenotypes. The snowy bumble bee, Bombus niveatus, transitions from ancestral yellow to derived white coloration to adhere to an Anatolian mimicry pattern. GWAS of these color forms revealed a tandem duplication, followed by subsequent sequence modification in one copy, in the cis-regulatory region of the homeobox gene BarH to be responsible for this color shift. This duplication may alter local regulatory architecture by selectively increasing transcription factor binding site availability. In the fiery-tailed bumble bees (Pyrobombus), we studied three North American species that transition between black and red abdominal coloration as a result of mimicry, finding this color shift is driven by independent variation in a narrow locus near the Hox gene Abdominal-B (Abd-B) for all three species. Each species utilizes indel variation in this regulatory region, and in one species, Bombus flavifrons, a tandem duplication with subsequent modification in one copy is implicated, similar to the type of modification in B. niveatus. Altogether, these systems reveal there are hotspots repeatedly targeted to drive convergence and that structural variation in cis-regulatory regions of key developmental genes is the most common means to generate these phenotypes.

5:00 PM - 5:15 PM
Population genomics of venom genes in speckled rattlesnakes

Dylan Highland, University of Virginia
Keaka Farleigh, University of Virginia
Megan Alderman, University of Virginia
Blair Perry, Michigan State University
Samuel Hirst, University of South Florida
Mark Margres, University of South Florida
Matthew Holding, University of Michigan
Drew Schield, University of Virginia

Abstract:

Understanding the evolution of complex, ecologically-relevant traits is key to linking patterns of selection to organismal fitness. Such traits may exhibit substantial inter- and intraspecific variation in their expressed phenotypes and underlying genetic basis. In rattlesnakes (genus Crotalus spp.), venom is thought to be under intense selection pressure for effective prey acquisition, yet the specific ways that selection affects venom genetic diversity are often unclear. We address this using a population genomic dataset for speckled rattlesnakes to identify how venom has been variably shaped by forms of natural selection. Across both shallow and deep timescales, major venom gene families show elevated genetic diversity that is shared across species, consistent with the effects of long-term balancing selection. Other loci, such as highly expressed PLA2 genes, show signals of recent directional selection, indicating heterogeneous selective pressures acting on different components of the venom phenotype. Because introgression can also increase genetic diversity, we compare patterns of divergence, allele sharing, and haplotype structure to distinguish adaptive introgression from ancestral polymorphism. Preliminary results suggest that both processes contribute to the maintenance of venom variation, with different toxin families showing distinct evolutionary histories. Together, these analyses support that venom genetic diversity is variably shaped by long-term balancing selection and adaptive introgression, suggesting that the maintenance of genetic diversity enables better exploitation of a diverse prey.

5:15 PM - 5:30 PM
Genomic signatures of repeated evolution of parental care in darters

Gabrielle Welsh, University of Chicago
Rachel Moran, University of Chicago

Abstract:

A major question in evolutionary biology is whether certain genes are more likely than others to contribute to adaptive change, and if so, what commonalities exist among those genes. This is especially intriguing for complex traits, such as behaviors, that are often polygenic and involve integration across various neuro, endocrine, and motor pathways. Systems where the same behavioral phenotype has evolved repeatedly offer a powerful means to uncover the genetic basis

of complex behavioral traits and provide insight into the predictability of this evolutionary process. One common behavior that has evolved multiple times across vertebrate lineages and plays a fundamental role in offspring health is parental care (both maternal and paternal). This includes any behavior that increases the survival and fitness of an individual's offspring at a cost to the parent's fitness. Darters, a diverse group of North American freshwater fish, provide an ideal system for investigating the repeated evolution of parental care as male-only parental care has both independently evolved and been secondarily lost multiple times across lineages. We use whole genome resequencing and population genomic approaches to identify genes under positive selection in species from lineages that evolved paternal care and test for relaxed selection in these same genes in species that experienced an evolutionary loss of care. snRNA-seq analyses on the hypothalamic preoptic area of the brain (a region associated with parental care) in males from care-giving vs no-care species to provide insight into the neural circuits involved in the evolution of paternal care. These combined approaches provide a comprehensive and novel insight into the biology of paternal care, the genetic basis of complex traits, and the predictability of the evolutionary process.

Phylogenetic Methods Development II

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Eliminating the population size parameter in species tree estimation

Dhruv Arora, The Ohio State University
Laura Kubatko, The Ohio State University

4:30 PM - 4:45 PM

Using geodesic tree distances to estimate Bayesian phylogenetic information content

Analisa Milkey, UConn Ecology & Evolutionary Biology
Paul Lewis, Ecol. and Evol. Biol. Dept.

Abstract:

Phylogenetic information content is important in determining whether biological questions are answerable with existing data. Previous Bayesian measures of phylogenetic information content do not scale to large numbers of taxa. We introduce a novel, scalable Bayesian measure of phylogenetic information based on geodesic distances in treespace. This measure compares variance of a sample of trees from the posterior distribution to variance of a sample of trees from the prior distribution. We also use geodesic distances to estimate dissonance, or information conflict, among posterior samples from different data sets. Dissonance is important in interpreting

results of a phylogenetic analysis. We test our methods on simulated and empirical data sets to illustrate the practicality of these measures.

4:45 PM - 5:00 PM
Model Misspecification in Molecular Phylogenetic Reconstruction

Rei Doko, Michigan State University
Kevin Liu, Michigan State University

Abstract:

Phylogenetic reconstruction using molecular sequence data is a multi-step process. Going from raw genomic sequence data to a phylogeny involves a number of methods, each carrying its own modeling assumptions. We explore simulated and empirical datasets to quantify the impact of estimation under models that violate common modeling assumptions, such as uniformity of substitution rates, correctness of multiple sequence alignments, unbiased and unchanging processes of substitution, as well as measure the performance of methods and techniques for addressing these issues.

5:00 PM - 5:15 PM
When trees disagree: How gene tree discordance skews branch lengths and evolutionary rates

Olivia Frary, University of Rochester
Mark Hibbins, University of Rochester

Abstract:

Variation in evolutionary rates reflects fundamental processes such as selection. Consequently, correctly interpreting variation in substitution and trait evolutionary rates is crucial to current tests of adaptive evolution. Branch lengths are often used to approximate substitution rates, so errors in branch length estimation directly bias evolutionary inference. Gene tree discordance, a widespread biological phenomenon, strongly influences this bias. This discordance arises from both incomplete lineage sorting (ILS) and introgression, yet these processes differ fundamentally: ILS generates stochastic variation in gene histories, whereas introgression produces non-random, directional gene flow across lineages. When gene trees disagree, the distribution of mutations across branches becomes harder to resolve with standard approaches on a single species phylogeny, increasing errors in species tree branch lengths. The baseline contributions of ILS and introgression to this error across divergence times and effective population sizes have not been formally characterized. Building on multispecies coalescent theory, we derive equations that predict biases in terminal branch lengths as the degree of discordance due to both ILS and introgression changes. We then simulate how branch length estimates are impacted by ILS and introgression. This work provides a quantitative foundation for understanding how discordance affects evolutionary rate inference and offers a path toward improving inference accuracy.

5:15 PM - 5:30 PM

Evaluating the accuracy of the stratigraphic-range fossilized birth-death process to estimate the phylogeny of extinct and living Canidae

Bruno do Rosario Petrucci, Iowa State University
Graham Slater, University of Chicago
Sejal Sharma, Iowa State University
Ugnė Stolz, ETH Zurich
Matheus Januario, University of Michigan
Tracy Heath, Iowa State University

Abstract:

Integrating fossil evidence into phylogenetic inference is essential for robust divergence-time estimation. Combined-evidence methods yield accurate estimates of dated phylogenies by providing coherent priors that jointly model species diversification and fossil sampling. However, these methods assume each fossil sample is an independent taxonomic unit, an assumption often violated by paleontological datasets. The stratigraphic-range fossilized birth-death (SRFBD) process was introduced to account for the structure of fossil data. This model accommodates paleontological taxonomy by considering fossil occurrences as stratigraphic ranges, and allowing for budding speciation. The SRFBD model can provide a more appropriate statistical framework for phylogenetic inference of groups with multiple fossil specimens per species. Canidae (dogs, foxes, jackals) is an ideal clade for application of the SRFBD model, since both the extant diversity and fossil record are well-sampled. Estimating a robust canid phylogeny incorporating extinct species can provide biologists the opportunity to assess complex macroevolutionary processes using historical information. I will present a simulation study examining parameter estimates (including topology, divergence times, and diversification rates) under the SRFBD process and an FBD model that considers fossils as individual specimens. With an understanding of these models and their limitations, I will apply the SRFBD model to infer the most taxonomically comprehensive phylogeny of Canidae to date. This will allow us to examine long-standing hypotheses in canid systematics, including some (e.g., direct ancestry) that are unavailable when using other models. This project will not only deepen our understanding of the evolutionary history of Canidae, but reveal the strengths and limitations of cutting-edge methods for combined-evidence analysis. Explicit testing of these models empowers researchers to select the tools that better fit their data and questions. This will increase the accessibility of complex methods in paleo-phylogenetics, allowing for further exploration of the deep history of the tree of life.

Population Genetics

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Developing a SLiM model to accurately assess patterns of coalescence in selfing tetraploids with double reduction

Justin Conover, Donald Danforth Plant Science Center
Shelly Gaynor, University of Florida
John Wakeley, Harvard University

Abstract:

For some species, in particular many plants, polyploidy and the capacity for self-fertilization are important determinants of genetic variation and evolution. Additionally, in some polyploids with tetrasomic inheritance patterns, the phenomenon of double reduction, in which two sister chromatids can migrate to the same gamete, can create similar patterns of inbreeding depression as selfing, but preferentially affect chromosomal regions that are sufficiently distant from the centromere. Integrating both selfing and double reduction into population genetic inference methods has proven challenging, and no simulation tools currently exist to model double reduction in a multi-locus framework. Here, we develop a SLiM script that can accurately model these complicated recombination dynamics, including in partial selfing populations. Additionally, we develop an analytical model of genetic ancestries of samples, conditional on the genealogical relationships or the pedigree of the population. We describe patterns of identity by descent among individuals which depend on their genealogical ancestries in the relatively recent past, and verify that these patterns are matched in our SLiMulations. We also describe patterns of coalescence among genetic lineages in the deeper past, and use this aspect of the model to predict the distribution of allele frequencies at single-nucleotide polymorphisms across the genomes of the sampled individuals. In total, our work lays the theoretical foundation to explore the chromosomal distributions and rates of double reduction in empirical populations, and provide a valuable resource to further explore the effects of double reduction on patterns of genetic variation through simulation approaches.

4:30 PM - 4:45 PM

Inferring selective sweeps from pooled long-read sequencing data

Skyler Berardi, Princeton University

Abstract:

Measuring the mode and targets of selection across populations of many species is central to uncovering general properties of adaptation in nature. However, generating population genomic data that are well-powered to detect recent selection (i.e., hard and soft sweeps) on multi-species

scales is both cost- and time-intensive. While current methods for pooled short-read sequencing allow for cost-effective sweep inference, these data lack important haplotype information. To overcome this barrier to scalability, we are developing a novel pipeline to infer sweeps from pooled long-read sequencing data, and we are starting by testing our pipeline in the model fly Drosophila melanogaster. We long-read sequenced a large pool of D. melanogaster (one female from each of 75 lines) to ~300× coverage at a read N50 of 22 kbp, providing reads that span our target inference window size of ~10 kbp. Library preparation and sequencing (Oxford Nanopore Technologies) were completed for under $500, comparable to short-read pooled sequencing. To infer selective sweeps from this dataset, we are utilizing deep learning methods that have been shown to mitigate potential issues associated with sequencing errors, uneven sampling, and demographic misspecification. Specifically, we are applying a domain-adaptive neural network (DANN) to detect known D. melanogaster sweeps, and we are testing the sensitivity and robustness of our DANN to simulated variation in read quality. We anticipate that our novel pipeline will improve the scalability of selective sweep inference in Drosophilidae, and our methodology can be adapted for broad use across many study systems.

4:45 PM - 5:00 PM

Positive Selection Predicts Patterns of Adaptive Introgression in an Early-Stage Hybrid Zone

Ziqi Xie, Portland State University
Mitch Cruzan, Portland State University

Abstract:

Introgressive hybridization has long been hypothesized to be an evolutionary stimulus for lineages to obtain adaptive genomic elements, but the lack of ongoing adaptive introgression events observed in nature limits our understanding of this process. Adaptive introgression is also difficult to characterize as most hybrid zones are relatively old and adaptive traits have stabilized. As a result, most hybrid zone theories emphasize selection against hybrids in regions where selection and dispersal are already in equilibrium. An exception is the Fisher-KPP traveling wave model, which describes the velocity of introgression of adaptive alleles in response to varying strengths of selection. In this study, we apply Fisher's model to understand patterns of ongoing introgression in a buttercup hybrid zone between a wider-range species, Ranunculus occidentalis, and a range-limited species, Ranunculus austro-oreganus. Using reduced-representation genomic markers and geographical cline analysis, we confirmed that this early-stage hybrid zone was a rare occurrence of active adaptive introgression. Common garden fitness measurements confirmed that many of the putatively adaptively introgressing loci were associated with intrinsic survival benefits. Fitness-associated adaptively introgressing loci with additive dominance demonstrated a positive association between selection and beneficial allele movement (cline displacement), as predicted by Fisher. However, contrary to Fisher's other prediction of stronger selection leading to narrower clines, we observed a lack of association between selection and cline width, suggesting a pattern of allele surfing in the introgressed endemic populations. This study is the first to verify the positive

fitness effects of genomic regions undergoing active adaptive introgression identified through cline analysis and is among the few real-world demonstrations of Fisher-KPP in the genetics of natural populations.

5:00 PM - 5:15 PM
Gene Flow and Recent Lineage Colonization Constraint Genetic Differentiation Despite Local Adaptation

Dylan Padilla, Yale University
David Skelly, Yale University

Abstract:

Demographic processes such as colonization to new environments and gene flow fundamentally shape the genomic landscape, either facilitating or constraining the efficiency of selection by altering the balance between genetic diversity and adaptive responses. Although theoretical predictions suggest that the efficacy of selection is dictated by a species' demographic history, empirical studies often overlook these constraints, yielding misleading observations. In this study, we present the first functional genome annotation for the wood frog Lithobates sylvaticus, providing a critical genomic resource for understanding the adaptive capacity of the species. Based on the annotation, we examined the potential for selection to drive genomic and phenotypic divergence among populations distributed across vernal ponds in Northeastern Connecticut, USA. A genotype-environment association analysis revealed that the frequency of two outlier loci (Col16a1 and Rab28) spikes in response to a relatively low canopy cover and high elevation of a specific pond. We also found that selection has driven a remarkable disparity in embryonic development among populations of wood frog at a rate exceeding that of neutral genetic drift. This genomic signature of selection together with a remarkable phenotypic differentiation suggests that natural selection overcomes the power of genetic drift, even in a landscape characterized by a recent colonization and significant connectivity between populations. Our work helps us understand how the wood frog's widespread success is underpinned by robust adaptive variation at a microgeographic scale.

5:15 PM - 5:30 PM
Population genomics of giant kelp in the eastern Pacific

Meaghan Clark, University of California
Malin Pinsky, University of California Santa Cruz
Filipe Alberto, University of Wisconsin Milwaukee

Quantitative genetics

06/21/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Genotype, rather than environment, explains variance in gene expression among clones of Daphnia pulex

Allison Nalesnik, Purdue University
Nathan Backenstose, Purdue University
Margaret Bui, Purdue University
Ilinca Ciubotariu, Johns Hopkins Bloomberg School of Public Health
Catherine Searle, Purdue University
Mark Christie, Purdue University

Abstract:

A central question in biology is the extent to which phenotypic variation is shaped by genetic differences, environmental conditions, or their interaction. The field of quantitative genetics provides a rigorous framework for addressing this question by partitioning phenotypic variance into genetic (VG), environmental (VE), and genotype-by-environment interaction (VGxE) components. Here, we extend this framework to include gene expression as a unified molecular phenotype and apply it to six distinct clones of Daphnia pulex exposed to four environmental conditions: 20 °C (control) and 25 °C (experimental) for 96 hr and 168 hrs. To assess how transcriptome-wide variation in gene expression measures of variance compare across different biological contexts, we partitioned variation in gene expression into noise (variation among identical genotypes in the same environment), VG, VE, and VGxE across four gene sets defined by expression level (high vs. low) and genes differentially expressed in terms of temperature and genotype-by-environment interaction. Across all gene sets, noise accounted for the largest proportion of variance (mean 53–69%), with the remaining variance partitioned among VG (mean 14–26%), followed by VG×E (mean 8–13%) and VE (mean 2–14%). Notably, the relative contributions of these components varied among gene sets, indicating that the drivers of gene expression variation depend on regulatory contexts. These results demonstrate that the classical quantitative genetic framework can be effectively applied at the gene expression level and both genotypes and their associated noise play dominant roles in shaping transcriptome-wide variation in gene expression. This work is key to not only understanding the regulation and evolution of gene expression, but also for understanding the role of genetics and the environment more broadly.

4:30 PM - 4:45 PM

The role of sexual selection, size, and morphological integration in the evolution of sexual dimorphism in simiiform primates

Lucas Camacho, University of São Paulo - Brazil

Abstract:

Sexual dimorphism is a widespread phenomenon in nature and can arise from multiple evolutionary processes. One of the most extensively studied drivers of sexual dimorphism is sexual selection, in which mate choice and direct competition among individuals alter reproductive success within populations. Simian monkeys exhibit substantial variation in both the magnitude of sexual dimorphism and the intensity of sexual competition. In addition, species vary in average size and in the degree of morphological integration, defined as stronger correlations among traits that share functional or developmental pathways than among traits that do not. Integrated traits form complexes known as modules, which can influence evolutionary responses to selection either by imposing constraints due to trait correlations or by increasing evolvability through coordinated changes in sets of traits. Here, we disentangle the effects of multiple components of sexual selection, average species size, and patterns of morphological integration to evaluate their roles in shaping sexual dimorphism. We combine a behavioral database, linear cranial measurements of simian monkeys, and phylogenetic comparative methods, including phylogenetic generalized least squares (PGLS) and Ornstein–Uhlenbeck (OU) models. Our results indicate that sexual selection variables show inconsistent associations with the magnitude and directionality of sexual dimorphism across models. In contrast, average species size and morphological integration exhibit a strong and consistent relationship with sexual dimorphism. OU model comparisons strongly support models including integration over models including size and sexual selection predictors, suggesting that this factor better explains macroevolutionary patterns of dimorphism. Overall, our findings indicate that, at broad phylogenetic scales, covariance structure and possible size play a more central role in shaping sexual dimorphism than behavioral proxies of sexual selection.

4:45 PM - 5:00 PM

Shared optima, divergent histories: How demography and selection shape polygenic trait architecture

Pro Manna, Clemson University
Shyamalika Gopalan, Clemson University

Abstract:

As populations expand into new environments, they often experience complex, non-equilibrium demographic processes - such as bottlenecks, gene flow, and population expansion - that reshape patterns of genetic diversity, including at loci underlying complex traits. At the same time, expansions often coincide with shifts in phenotypic optima, which create novel selective pressures that drive polygenic adaptation. In this context, fundamental assumptions of many traditional

population genetics methods are violated, making them ill-suited to disentangling the joint effects of demography and selection on complex trait architecture. To address this gap, we use forward-time simulations implemented in SLiM 5 to model the evolution of a polygenic trait in two recently diverged populations, varying both selection regime (stabilizing vs. directional) and demographic history (constant size vs. founder bottleneck followed by expansion). This framework allows us to track the full set of causal variants through time and to decompose additive genetic variance across the allele frequency spectrum under different evolutionary scenarios. We find that stabilizing selection concentrates additive variance in rare, large-effect alleles, whereas directional selection redistributes variance to intermediate and common small-effect alleles, particularly in populations retaining higher ancestral diversity. Following population divergence, additive variance becomes increasingly dominated by population-specific variants that accumulate independently within each lineage. As a consequence, differences in evolutionary history limit how well genetic predictions generalize across populations, even when populations evolve toward the same phenotypic optimum. This limitation not only reflects allele frequency divergence at shared variants but also a progressive shift in genetic architecture, as private variants account for an increasing fraction of additive genetic variance. Our results provide a simulation-based null model for detecting loci under polygenic adaptation by establishing a baseline expectation against which empirical data can be evaluated, and clarifying the relative contributions of demography and selection in shaping trait architecture.

5:00 PM - 5:15 PM

Testing variational constraints on adaptive trajectories in the stickleback fossil record

Reuben Ng, Loyola University Chicago
Kjetil Lysne Voje, Natural History Museum
Jacopo Cerasoni, Loyola University Chicago
Michael Bell, University of California Museum of Paleontology
Yoel Stuart, Loyola University Chicago

Abstract:

Evolutionary divergence among lineages tends to align with major axes of genetic (co)variation, indicating that evolutionary trajectories are constrained by genetic architecture during adaptation. However, this conclusion may be misleading if selection regularly reorients axes of covariance to align with evolutionary divergence. Without independent information on either the ancestral state of genetic (co)variances or the position of an adaptive optimum, it is difficult to assess the polarity of this relationship. The fossil record of the Miocene stickleback Gasterosteus doryssus from western Nevada provides an uncommon opportunity to test these alternative hypotheses (at the phenotypic level). A highly resolved fossil time series documents the microevolution of both population-level patterns of trait (co)variation and of trait means themselves as they approach observed adaptive optima over the course of about 16,000 years. These data permit a detailed examination of the microevolutionary persistence of the structure and extent of

covariation between traits, and provide a rare opportunity to test hypotheses about the influence of that covariation on phenotypic evolution across an adaptive landscape and toward an adaptive optimum.

5:15 PM - 5:30 PM

Non-linear variation in responsiveness to atrazine exposure in Drosophila melanogaster potentially due to endocrine disruption of the ecdysone biosynthesis pathway

Emily Yarbrough, Binghamton University
Anthony Fiumera, SUNY Binghamton

Abstract:

Despite suspected endocrine-disruption (ED) and other known detrimental effects on non-target organisms, atrazine remains a commonly used herbicide in the United States. Our lab has shown that atrazine exposure affects numerous fitness traits in Drosophila melanogaster, including development rate, body size, longevity, and male reproduction. Interestingly, a single genotype (ORE-R) displays a nonlinear response to an atrazine gradient, with exposure to intermediate concentrations causing the largest change in development time. The presence of this nonmonotonic response is not an uncommon phenomenon when studying ED chemicals, and my work aims to elucidate the genetic mechanisms driving these responses, as well as whether those mechanisms are sex specific. We measured development time of 130 homozygous D. melanogaster DGRP lines across an atrazine gradient (0ppm, 2ppm, and 20ppm). On average, exposure to the 2ppm concentration accelerated development, while exposure to 20ppm delayed development. There was, however, a significant genotype by environment by sex interaction, indicating that males and females from the different genotypes are responding differently to the stressor gradient. I then performed genome-wide association studies to identify polymorphisms associated with responsiveness across the atrazine gradient within and between the sexes. 11 genes associated in females, 61 in males, and 14 when comparing the sexes. Gene ontology enrichment and network analyses suggest variation in pathways regulating the synthesis of ecdysone, the primary developmental molting hormone, are responsible for the changes in development time after atrazine exposure. We are currently investigating potential sex-biased effects of genetic variation and atrazine exposure on nutrient acquisition and utilization pathways involved in ecdysone synthesis in hopes of gaining a better understanding of sex-specific behavior across gradients of exposure to an environmental stressor.

SSE Presidential Plenary

06/22/26: 8:00 AM - 9:15 AM

8:00 AM - 9:00 AM

Lessons from Weeds: Persistence and Resistance in the Anthropocene

Regina Baucom, University of Michigan

Abstract:

Weedy plants have vexed humans since the origins of agriculture, with tools for their suppression ranging from the ancient hoe to a modern, multi-billion dollar pesticide industry. Along with the annoyances they bring as "plants that do not belong," they have served as powerful model systems in evolutionary biology, long noted for their persistence through plasticity, rapid life-history shifts, and adaptation under intense selection. At the same time, "weed" is a cultural label–historically used as a pejorative for women, girls, and other marginalized identities, and more recently reclaimed as a symbol of resilience.

In this talk, I center four questions: What is a weed? What have we learned about evolution from weeds? Which traits allow weeds to persist? And what lessons can weeds teach us about persistence and resistance? I suggest that weeds are best understood as human commensals that exploit disturbance. Beyond rapid adaptation to human-mediated selection, weeds have revealed how mating systems evolve, how gene flow, hybridization, and polyploidy shape adaptive potential, and how phenotypic plasticity, G×E interactions, and genomic architecture structure evolutionary responses. Finally, because weeds symbolize resilience, defiance, and survival in marginal spaces, their persistence traits offer powerful allegories for sustaining persistence and resistance during uncertain and stressful times.

Behavior I

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Distributed neural computation and the evolution of the first brains

Vikram Chandra, Harvard University

Abstract:

The origin of brains in the Precambrian was a milestone in animal history: enabling predatory behavior and new lifestyles. Brains likely evolved from diffuse nerve nets, but we do not know what

the first brains looked like or how they were organized. Acoel worms, the likely sister lineage to all other animals with brains, offer a unique window into this transition.

Here, we develop the acoel worm Hofstenia miamia as a new neuroscience model, and we study its brain and behavior. We find that Hofstenia has a unique ‘diffuse brain’: a subepidermal network of dense neuropil tiled with clusters of sensory cells, with virtually no anatomical internal regionalization or stereotypy. Every brain is different in shape and changes over time, suggesting that the same circuits cannot be in the same relative positions across animals. Through analyses of kinematics, postural dynamics, and goal-directed hunting behavior, we find that behavior is robust to large, arbitrary amputations of brain regions, suggesting that most regions can perform most computations. More brain tissue improves performance on challenging tasks, but no specific region is required. Studying the distribution of neural cell-type markers, we find that all neural cell types lack regionalization. Together, this suggests that Hofstenia's brain is composed of tiles of computationally-pluripotent neural ensembles that interact, with coherent behavior emerging from their collective activity.

Our findings suggest a plausible trajectory for nervous system evolution in which early brains may have arisen through the condensation of diffuse nerve nets into unregionalized brains. These nascent brains likely then evolved elaborations: dense connectivity, new neural morphology and circuit motifs - coalescing in new behavioral affordances. Regionalized, stereotyped circuits likely evolved later, bringing forth the ground plan that enabled expansions into a diversity of bilaterian brains and a corresponding range of complex behavioral repertoires.

9:45 AM - 10:00 AM
Maybe she’s born with it, maybe it’s (not) her genes: behavioral individuality in a clonal fish

Jay Gallagher, UC Davis
Ammon Perkes, University of California Davis
Chia-chen Chang, National University in Singapore
Emma Chirila, University of California Davis
Karen Kacevas, University of California Davis
Aditya Bhaskara, University of California Davis
Kate Laskowski, University of California

Abstract:

Understanding where behavioral individuality comes from is a fundamental question in biology. The long-standing assumption is that these consistent behavioral differences among individuals arise through a combination of among-individual variation in genes and developmental environments. However, recent work has shown that even when minimizing such variation, individuality persists, questioning their obligatory role in generating individuality. Here, we used a unique animal system—the Amazon molly—to study the role of the most commonly proposed factor: genetic variation. Amazon mollies are a naturally clonal fish arising from a single hybridization event ~100,000 years ago between two sexual species: the Atlantic and Sailfin mollies. Amazons live in sympatry and

share ecologies with their two parental species, making the only notable difference between them their amount of genetic variation among individuals. This provides an ideal opportunity to test the role of genetic variation in generating individuality. We tracked ecologically relevant behaviors of Amazon, Atlantic, and Sailfin mollies, reared in standardized conditions, continuously from birth for four weeks, to compare how high and low amounts of among-individual genetic variation shape individuality. If individuality depends on genetic variation, the sexual species should show greater among-individual differences than clonal Amazons. If not, individuality must be arising through other mechanisms. Surprisingly, individuality did not differ between sexual and clonal species, either in magnitude or temporal onset over development, indicating that it was generated by something other than genetic or environmental variation among individuals. Amazons may have unique means of generating individuality (e.g., solely from maternal effects), and/or individuality may be much less dependent on among-individual genetic variation than we previously thought. This unexpected result challenges age-old assumptions about what makes individuals unique.

10:00 AM - 10:15 AM
Variation in territorial defense related to life-history trade-offs between current and future reproduction in larder hoarding North American red squirrels (Tamiasciurus hudsonicus)

Gladiana Spitz, University of Colorado

10:15 AM - 10:30 AM
Medusoid swimming in Muusoctopus robustus

J. McMichael, Auburn University at Montgomery

Abstract:

Medusoid or ‘arm’ swimming is a mode of locomotion by benthic octopuses, notable for the oscillatory opening and closing of all 8 arms in near tandem. This movement's effective propulsion and freedom of directionality using hydrostatic limbs are targets of high interest in soft robotics. Arm swimming has been modeled and simulated, but has seen very little formal analysis, especially for animals in their natural environment. Exploration of the ‘Octopus Garden’ near Davidson Seamount in Monterey Bay, California (USA) using a remotely operated vehicle has yielded over 10 minutes of arm swimming footage by 7 Muusoctopus robustus individuals. We evaluated and measured individual arm motions throughout 64 recovery (opening) and 60 power (closing) strokes of arm swimming. Our results indicate that the motion of the overall stroke involves three highly conserved bends in each arm, with consistent bend angle and relative location as the stroke progresses. These bends’ angles and locations were measured and reconstructed to approximate the motion of octopus arms throughout arm swimming. Our results demonstrate that despite octopuses’ notoriety for having a near-infinite degree of freedom, they restrict movements

to specific elements of their muscular hydrostat during arm swimming, possibly using motion primitives to simplify neurological control.

10:30 AM - 10:45 AM

Evolutionary Dynamics of Mucosal Immunity: Comparative Antimicrobial Activity Across Etheostoma Lineages with Variation in Parental Care

India Wesley-Cardwell, University of Chicago

Abstract:

Integrating ecological, evolutionary, and immunological perspectives provides a robust framework for understanding the selective pressures shaping behavioral diversity. Darters (Percidae: Etheostoma) represent a species-rich group of North American freshwater fishes characterized by significant morphological variation and a wide array of life-history strategies, including male nest guarding and parental care behaviors.Previous research indicates that male darter mucus may shield eggs from pathogens, yet the specific mechanisms of this protection remain unknown. This study characterizes the antimicrobial activity of darter epidermal mucus to explore how mucosal immunity can evolve alongside diverging social and reproductive behaviors.

We hypothesize that variation in antimicrobial composition reflects distinct evolutionary pressures associated with the transition from no care to nest guarding with care. To test this, we utilized a disc diffusion assay to screen for antimicrobial activity against a broad spectrum of microbial agents. Mucus samples from multiple Etheostoma species with and without paternal care were pooled by demographic (males, females, and juveniles) and applied to inoculated media to measure zones of inhibition. Preliminary results serve as a foundational step in characterizing the innate immune defenses of these fishes, with a specific focus on identifying potent antimicrobial activity in reproductive males.

The next phase of this research involves molecular profiling and the classification of integral peptide components to understand the biochemical basis of these immune responses. By bridging the gap between behavioral ecology and immunoengineering, this project clarifies how mucosal defenses evolve alongside complex life-history traits in freshwater teleosts.

Ecological Genetics I

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Distinct signatures of methylation associated with independently evolved populations of Mexican cavefish

Kaya Harper, Texas A&M University
Heath Blackmon, Texas A&M University

Abstract:

DNA methylation is a proposed mediator of acute and evolutionary-derived phenotypic plasticity in response to environmental change. Wide-spread epigenetic modifications have been documented in closely related teleost fish raising the possibility that changes in DNA methylation support adaptation to novel environments. The Mexican cavefish, Astyanax mexicanus have adapted food-sparse environments that lack daily fluctuations in temperature and light. Changes in methylation contribute to eye-loss in cave populations, but the broader methylation changes have not been investigated. Here, we combine whole-genome bisulfite sequencing (WGBS) and RNA-seq to quantify DNA methylation and transcriptional variation across three tissues (liver, muscle, brain) river-dwelling surface fish and two independently evolved populations of cavefish across fed and starved conditions. We found that genome-wide CpG methylation levels were largely stable across feeding states, suggesting that differences in transcriptional regulation, but not methylation, underlie acute responses to changes in feeding state. Conversely, methylation profiles diverged strongly among populations and across all tissues. Differentially methylated genes (DMGs) were as significant between cavefish populations as they were between cave and surface, supporting the notion that independent epigenetic mechanisms contribute to convergent evolution of diverse traits in cavefish. Together, these results support a model in which DNA methylation contributes to persistent, population-specific regulatory states associated with evolutionary divergence in Astyanax.

9:45 AM - 10:00 AM

An investigation of reproductive success in the eastern oyster to evaluate restoration frameworks

Anna Eaton, Northeastern University
Katie Lotterhos, Northeastern University Marine Science Center

Abstract:

Anthropogenic effects degrade ecosystems globally, igniting conservation projects that aim to maximize genetic diversity in order to restore ecosystem productivity. However, there are different methods to doing so and theory suggests these correlate to different outcomes, with strategies not

always working in practice. In niche partitioning, genetic diversity fosters productivity by limiting competition within populations. Differential success states genetic diversity increases the chance that individuals in a population will survive disturbances and maintain productivity. We investigate reproductive success in two Crassostrea virginica populations enhanced for genetic diversity via different methods. Results provide insight on ecological mechanisms in restoration projects.

10:00 AM - 10:15 AM
Mapping the genetic basis of heterosis in natural populations of A. thaliana

Juan Diego Rojas-Gutierrez, Purdue University

Abstract:

The study of genetic variation contributing to the differentiation among natural populations is a central focus in evolutionary biology. While natural selection remains the primary driver of adaptation, the intricate interplay with genetic drift introduces a layer of complexity. The potential of genetic drift to fix partially deleterious recessive alleles, thereby diminishing the efficacy of selection, raises concerns about population extinction. Crosses between individuals of different populations result in heterozygosity for these deleterious alleles and may exhibit heterosis, defined as the increase in fitness of F1 relative to the mean of the parents. However, the genetic basis of heterosis remains unclear specially on natural populations. We first asked whether heterosis arises solely from the masking of partially deleterious alleles (dominance). To test this, we examined the association between genomic load and heterosis using previously reported heterosis estimates from line crosses among 15 natural Arabidopsis thaliana populations from Fennoscandia. We found no association between genomic load and heterosis, suggesting that dominance complementation alone does not explain the observed patterns. We then investigated which specific loci contribute to heterosis by performing a genome-wide association study (GWAS). This analysis identified 67 SNPs associated with heterosis, spanning diverse functional categories. These results indicate that heterosis in natural populations is likely multigenic and that it cannot be explained solely by dominance complementation.

10:15 AM - 10:30 AM
Host genome as a driver for nitrogen fixation variability in moss microbiomes among high-latitude ecosystems

Alexander Horvath, University of Florida
Chathurani Ranathunge, FYR Bio
Bryndan Durham,
Stuart McDaniel, University of Florida

10:30 AM - 10:45 AM

Functional tests of immune gene divergence between closely related Drosophila species

Camila Beraldo, University of Kansas
Mariaelena Nabors, University of Kansas
Kistie Patch, University of Kansas
Rob Unckless, University of Kansas

Abstract:

Infectious diseases impose strong selective pressures on host populations and are a major driver of evolutionary divergence between species. Consistent with this, immune genes are among the fastest-evolving genes in the genome. Despite this pattern, the genetic basis of species-level differences in immune defence remains poorly understood, as relatively few studies have functionally tested how divergence at specific immune loci contributes to variation in resistance among closely related species. Here, we investigate the functional consequences of immune gene divergence using two closely related species, Drosophila simulans and Drosophila mauritiana, which differ in their responses to bacterial infection. We focus on a duplicated antimicrobial peptide gene as a tractable system to test how gene copy number and sequence divergence contribute to immune function. Antimicrobial peptides are central components of insect innate immunity and provide a powerful framework for experimentally dissecting immune divergence. To do so, we use CRISPR/Cas9 genome editing to systematically replace individual copies of this immune gene in both species with fluorescent markers (DsRed or GFP). Each native copy is deleted and replaced via site-specific integration, allowing precise control over genetic background and direct functional comparisons among gene copies between species. Ongoing work focuses on establishing all engineered lines in a homozygous state. Future experiments will assess immune function by infecting males from each line with a bacterial pathogen and quantifying survival outcomes. Together, this approach will provide direct functional insight into how immune gene duplication and divergence contribute to the evolution of host defence.

Molecular Ecology I

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Rethink the urban sink: Urban cores maintain source populations of coyotes with robust genetic connectivity

SUMMER VANCE, UC Berkeley

Abstract:

Urbanization is a rapidly growing evolutionary force, with the prevailing assumption that human-dominated landscapes act as sinks for wildlife in nearby exurban source populations. However, many existing studies rely on simplified urban-rural binaries and low-resolution genetic and environmental data that obscure the inherently nuanced mechanisms of contemporary evolution. In addition, migration analyses are rarely used to quantitatively assess dispersal and source-sink dynamics. To address these gaps, we applied high-resolution RADseq data to a landscape genomics framework and recent gene flow analysis to investigate contemporary evolution in urban coyotes (Canis latrans) across the greater Los Angeles, CA, USA metropolitan area. Our analyses include fine-scale environmental, social-ecological, and historical landscape variables to rigorously assess how urban heterogeneity shapes intra-city evolutionary dynamics. Our results refute the conventional “urban sink” model; rather than acting as regional sinks, high-density urban habitats in this system function as source populations for nearby greenspaces. Dispersal analyses further demonstrated remarkable landscape permeability, with sufficient gene flow across five major highways, including one previously identified as a genetic barrier. While coyote populations occupied distinct environments with varying anthropogenic exposure, landscape genetic models revealed that genetic differentiation was significantly correlated only with geographic distance, and not environment or landscape resistance. Together, these results demonstrate that even the most developed urban centers can serve as well-connected, demographic sources. These findings have broad implications for urban conservation planning worldwide and underscore the need to rethink the role of the city in the survival and connectivity of wildlife.

9:45 AM - 10:00 AM

Urban Policies Become Evolutionary Forces Shaping Squirrel Genetic Diversity in St. Louis, Missouri

Elizabeth Carlen, Washington University in St. Louis

Abstract:

Urban landscapes are shaped by both ecological and social forces, yet how these interact to structure urban wildlife populations remains poorly understood. We examined the genetic structure of eastern gray squirrels (Sciurus carolinensis) in the St. Louis, Missouri, USA

metropolitan area to test whether genetic differentiation is driven by geographic distance alone, or a combination of geographic distance and major roads, environmental variation, socioeconomic factors, and/or the legacy of historic redlining policies. Using low-coverage whole genome sequencing, we found that habitat similarity and socioeconomic factors–not geographic distance–are the primary predictors of genetic connectivity. Additionally, we found that squirrels north of the Delmar Divide, a socioeconomic boundary separating predominantly Black and white neighborhoods, exhibited significantly lower genetic diversity than squirrels in the south, mirroring patterns of neighborhood disinvestment rooted in racially discriminatory policies. Multiple analytical approaches consistently detected these patterns, suggesting that socioeconomics and urban development have created cascading ecological consequences that extend to evolutionary processes in wildlife. These findings demonstrate that urban policy decisions carry measurable evolutionary consequences for non-human species.

10:00 AM - 10:15 AM

Demographic history and mating patterns in a secondary contact zone between divergent lineages of the Southern House Wren

Pablo Fracas, Museo Argentino de Ciencias Naturales "Bernardino Rivadavia" - CONICET
Agustín Casale, Museo Argentino de Ciencias Naturales in Buenos Aires
Elvira Canio, Universidad Nacional de Río Negro. CIT Río Negro UNRN - CONICET
Laura Barone, Museo Argentino de Ciencias Naturales - Bernardino Rivadavia
Romina Gallenti, Museo Argentino de Ciencias Naturales "Bernardino Rivadavia" - CONICET
Ramiro Arrieta, Instituto Argentino de Investigaciones de las Zonas Áridas (IADIZA)
Belen Bukowski, Museo Argentino de Ciencias Naturales
Pablo Lavinia, Universidad Nacional de Río Negro. CIT Río Negro UNRN - CONICET
Paulo Llambías, Instituto Argentino de Investigaciones de las Zonas Áridas (IADIZA)
Leonardo Campagna, Cornell University
Pablo Tubaro, Museo Argentino de Ciencias Naturales “Bernardino Rivadavia” (MACN–CONICET)
Dario Lijtmaer, Museo Argentino de Ciencias Naturales “Bernardino Rivadavia” (MACN–CONICET)

Abstract:

Widely distributed species with complex evolutionary histories offer ideal systems to explore the speciation process. In southern South America, the Southern House Wren (Troglodytes musculus) comprises two mitochondrial lineages (widespread lowland and Patagonian) that diverged during the Pleistocene and came into secondary contact in central Argentina. To resolve their fine-scale genomic relationships, demographic history and the fitness consequences for admixed individuals in the contact zone, we analyzed 264 samples across the region using a mitochondrial marker (COI) and 7281 nuclear SNPs (ddRADseq), while also evaluating the presence of reproductive barriers in 53 breeding pairs in a focal population of the central andes in Mendoza province, Argentina. Geographic distance and genetic divergence correlations account for a weak effect of isolation by distance, while combined with genomic clustering analysis they consistently support a robust division into two main lineages. Spatial clines reveal a narrow nuclear contact zone across central Argentina, contrasting with a much broader area of mitochondrial overlap. Introgression analyses indicate pervasive gene flow across the Southern Cone, though the southernmost Patagonian

populations remain highly divergent. Although global nuclear differentiation between allopatric populations is weak, divergence is driven by a few highly differentiated loci. Patterns of shared co-ancestry and relatedness reveal that Patagonian populations experienced prolonged isolation and that the central andes population is an advanced-generation admixed cluster with low inbreeding. Reproductive results support this as they show random mating and high mixed-lineage offspring viability, although a male-biased sex ratio is observed, consistent with Haldane's rule. Demographic models suggest that the central andes population originated from the Patagonian lineage under an isolation with migration scenario, currently receiving asymmetric introgression from the northern widespread lineage. Ultimately, while parental lineages experienced contrasting demographic histories, their postglacial contact forged a stable admixed population that sets the stage for future exploration of mitonuclear coevolution.

Especies ampliamente distribuidas con historias evolutivas complejas son sistemas ideales para explorar el proceso de especiación. Al sur de Sudamérica, la Ratona (Troglodytes musculus) comprende dos linajes mitocondriales (patagónico y de tierras bajas de amplia distribución) que divergieron en el Pleistoceno y entraron en contacto secundario en el centro de Argentina. Para resolver sus relaciones genómicas, historia demográfica y los efectos en la viabilidad de la descendencia de linaje mixto, analizamos 264 muestras con un marcador mitocondrial (COI) y 7281 SNPs nucleares (ddRADseq), evaluando barreras reproductivas en 53 parejas de una población focal de los andes centrales en Mendoza, Argentina. La correlación entre distancia geográfica y divergencia genética muestra un débil aislamiento por distancia, que combinada con agrupamiento genómico respalda una sólida división en dos linajes. Las clinas espaciales revelan una estrecha zona de contacto nuclear en el centro de Argentina, contrastando con un solapamiento mitocondrial mucho más amplio. Análisis de introgresión indican flujo génico generalizado en el Cono Sur, aunque las poblaciones patagónicas permanecen muy divergentes. Aunque la diferenciación nuclear alopátrica global es débil, la divergencia está impulsada por pocos loci altamente diferenciados. Patrones de co-ancestría y parentesco revelan que las poblaciones patagónicas experimentaron aislamiento prolongado y que Mendoza es una población panmíctica de generaciones avanzadas con baja endogamia. Los resultados reproductivos respaldan esto mostrando apareamiento aleatorio y alta viabilidad en la descendencia de linaje mixto, aunque esta presenta una proporción de sexos sesgada a machos, consistente con la regla de Haldane. Modelos demográficos sugieren que la población de Mendoza surgió del linaje patagónico bajo un escenario de aislamiento con migración, recibiendo actualmente introgresión asimétrica del linaje norteño de amplia distribución. Finalmente, aunque los linajes parentales experimentaron historias demográficas contrastantes, su contacto postglacial forjó una población mezclada estable que sienta las bases para explorar la coevolución mitonuclear.

10:15 AM - 10:30 AM

Genome-wide Molecular Data Reveal Complex Phylogeography of the Imperiled Venus Flytrap (Dionaea muscipula J. Ellis, Droceraceae)

Wenbin Zhou, UNC Chapel Hill

Abstract:

Venus flytrap (Dionaea muscipula) is an insectivorous plant that belongs to the monotypic genus Dionaea and is endemic to a small geographic range in North and South Carolina. Its unique morphology and natural history have intrigued biologists for decades, yet population dynamics and genetic structure has not been adequately characterized. Population decline, driven primarily by disruptive land conversion, fire suppression, and illegal harvesting/poaching underscores the urgency to define the genetic diversity in the present populations for informed conservation. We applied a genome-wide SNP dataset to analyze admixture and population structure, and used coalescent modeling to demonstrate that current Venus flytrap populations comprise four different ancestral gene pools, which mirror their geographic distribution that includes two from the coastal plain (i.e., Cape Fear Arch and Onslow Bight) and two from the Sandhills region (i.e., Fort Bragg). Our population dynamics model supports four lineages with the Onslow Bight lineage as the ancestor and the two Sandhills lineages derived from the Cape Fear Arch lineage independently at ~3 Mya and ~13 Mya, respectively, when sea levels reached their peak during climate optima. Bottleneck events occurred among all lineages, with two ancient ones in the Sandhills lineages and two more recent ones in the Coastal lineages, leading to the current genetic structure. The significant niche differences in temperature, precipitation, and soil properties between the Sandhills and Coastal regions corresponds with a significantly shorter peduncle length in Sandhills populations, indicating that these populations may have adapted to the higher temperatures and xeric Sandhills environment. The relative lack of admixture between the sympatric Sandhills populations suggests that recent events, perhaps anthropogenic in nature, contributed to the current population genetic structure.

10:30 AM - 10:45 AM

The genetics of inbreeding depression in a pedigreed wild population of Florida Scrub-Jays

Faye Romero, University of Rochester
Jeremy Summers, University of Rochester
James Schmidt, University of Rochester
Daniel Seidman, University of Rochester
Sahas Barve, Archbold Biological Station
John Fitzpatrick, Cornell Lab of Ornithology
Nancy Chen, University of California

Phylogenomics, Biogeography, and Systematics

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Phylogenomics of the Galápagos carpenter bee and the paleogeography of Galápagos

Graham McLaughlin, University of South Carolina
Brian Hollis, University of South Carolina
Veronica Baquero, University of South Carolina
Sophia Sudak, University of South Carolina

9:45 AM - 10:00 AM

When mountains split species: Hierarchical divergence in Platymantis ground frogs within a montane system

Kier Mitchel Pitogo, Department of Ecology and Evolutionary Biology & Biodiversity Institute
Faben Tesfazion, Department of Ecology and Evolutionary Biology & Biodiversity Institute
Aljohn Jay Saavedra, School of Graduate Studies
Rafe Brown, Biodiversity Institute and Department of Ecology and Evolutionary Biology

Abstract:

Classical speciation models emphasize geographic isolation, yet divergence can persist despite ongoing gene flow when driven by strong selection. We investigated a compelling case of advanced parapatric speciation in Platymantis ground frogs from Mindanao Island, Philippines. Integrating genomic (ddRAD), phenotypic, and bioacoustic data, we identified a morphologically and acoustically distinct low-elevation lineage (1400 masl) in southern Mindanao. Results reveal a pronounced decoupling between phenotypic/acoustic differentiation and genomic divergence. Although morphological and acoustic differences are highly discrete—particularly in advertisement call structure—both pairwise relative differentiation (FST) and absolute divergence (DA) remain relatively low. Despite this low genomic divergence, clustering analyses indicate that these parapatrically distributed lineages form genomically cohesive groups, each exhibiting independent divergence, demographic expansion, and a lack of detectable contemporary hybridization. These phylogenetic and population genomic patterns suggest that ecological selection along steep environmental gradients can promote reproductive isolation more rapidly than neutral genomic divergence accumulates. By capturing this transition, our findings highlight how adaptive divergence functions across ecological and evolutionary timescales to generate cryptic biodiversity. This research provides a rare empirical window into the early stages of vertebrate diversification on topographically complex oceanic islands, where selection may drive the emergence of new biodiversity patterns long before they are captured by neutral genetic distance alone.

10:00 AM - 10:15 AM

Impacts of worsening climate change on Joshua tree fruiting and flowering

Kirsten Zornado, California State University
Jeremy Yoder, California State University Northridge

10:15 AM - 10:30 AM

How climatic transitions influence immunogenomics in pit vipers.

Leroy Nuñez, Stony Brook University
Pascal Title, Stony Brook University

Abstract:

Adaptive radiation is often initiated by ecological opportunity, which is the availability of ecologically accessible resources that may be evolutionarily exploited. Ecological opportunity can be presented when a lineage colonizes a new area. When a lineage enters a new area, they are often exposed to novel pathogens, potentially creating a barrier to persistence and diversification in the new environment. Ecological opportunity through colonization is not limited to geographic dispersal, as transitions between climate zones, such as along elevational gradients, may similarly present new ecological niches. Therefore, ecological opportunities within a clade may be more numerous than simply looking at geographic dispersal may imply. Using pit vipers (Subfamily: Crotalinae) as a model, we conduct phylogenetic comparative methods to infer transitions between different climate affinities across the phylogeny to identify potential ecological opportunities. Furthermore, we harness pit viper genomes within a comparative framework to examine selection patterns of immune response genes in lineages that exploit these instances of ecological opportunity. Here, we clarify how immunogenomic evolution correlates with climatic transitions in pit vipers and provide a framework for integrating climate, geography, immunology, and genomics to better understand the underlying mechanisms that allow lineages to exploit ecological opportunity and diversify.

Plant Reproductive Biology

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Pollinator behavior and hybrid fitness shape reproductive isolation in two Virginia Silene species

Andrea Berardi, James Madison University

Abstract:

Understanding how floral traits contribute to reproductive isolation is central to understanding the plant speciation process. We investigate this process in two closely related species native to the eastern United States, Silene virginica and Silene caroliniana, which differ in floral color, morphology, and pollination syndrome. S. virginica produces dark red, long-tubed flowers with abundant nectar and is primarily visited by hummingbirds, whereas S. caroliniana has light pink, open flowers with concentrated nectar that attract bees and other diurnal pollinators. Despite these differences, both species are occasionally visited by butterflies and can hybridize in nature and in the greenhouse. We ask whether divergence in floral traits and pollinator visitation is enhanced in sympatry, consistent with character displacement, and whether these differences contribute to reproductive isolation. We additionally address hypotheses for why hybridization between S. virginica and S. caroliniana remains rare: (1) strong pollinator preferences limit interspecific pollen transfer, and/or (2) hybrids experience reduced fitness due to genetic incompatibilities. To test these hypotheses, we integrate field observations, herbarium specimen measurements, experimental crosses, and morphological and genetic analyses across multiple populations, including two naturally occurring hybrid zones in Virginia. We will quantify pollinator visitation across at least three populations per species and two hybrid populations, complemented by an experimental mixed-species array. Pollinator efficiency will be assessed through single-visit pollen deposition, pollen removal, and fruit set. In parallel, we will measure floral traits associated with pollinator attraction, including morphology, nectar rewards, and petal pigmentation. To place floral variation in a broader geographic context, we also quantify differences in floral morphology from herbarium specimens of both species collected in sympatry and allopatry. Together, these data will reveal how pollinator behavior, floral trait divergence, and postzygotic barriers interact to maintain species boundaries despite ongoing hybridization potential.

9:45 AM - 10:00 AM

Functional divergence of AGAMOUS paralogs in the cypress family (Cupressaceae)

Austin Nguyen, University of Kansas
Kelly Matsunaga, University of Kansas

Abstract:

Gene duplication acts as a source of evolutionary novelty by doubling genetic material on which evolution can act and has been associated with increased morphological diversity and phenotypic innovation. AGAMOUS (AG) genes are members of the MADS-box gene family that show conserved function in specifying reproductive organ identity in seed plants. While the function, expression, and evolution of these genes have been extensively studied in flowering plants, they remain understudied in conifers. Based on work in the families Pinaceae and Podocarpaceae, conifer AG genes are expressed in the seeds and associated seed-bearing organ (termed the ovuliferous scale) of the seed cone. However, prior work in Cupressaceae has shown there is little AG expression in the ovuliferous scale, suggesting that AG expression in Cupressaceae differs from the pattern observed in other conifers. Here, we report that AG genes underwent two duplication events prior to the split between Cupressaceae and its sister family, Taxaceae, over 200 million years ago. Further, we characterize the expression pattern for each resulting orthogroup (AG1, AG2, and AG3) in seed cones of three Cupressaceae species, Metasequoia glyptostroboides, Taxodium distichum, and Juniperus virginiana (subfamilies Sequoioideae, Taxodioideae, and Cupressoideae, respectively), using RNAscope-based in situ hybridization (ISH). The ISH assays reveal expression patterns consistent with subfunctionalization: AG1 specialized in seed development, AG2 in seed cone and seed coat development, and AG3 in ovuliferous scale development. More broadly, our results uncover convergent patterns of subfunctionalization between conifers and angiosperms and the developmental underpinnings of reproductive morphological diversity in Cupressaceae.

10:00 AM - 10:15 AM

Larger bees, larger flowers: size correlations and phenotypic selection on the flower morphology of Impatiens capensis in cities

Jérôme Burkiewicz, Université de Montréal (IRBV)
Simon Joly, Montreal Botanical Garden

Abstract:

Urbanization significantly impacts wildlife. Amidst various effects, it can lead to changes in pollinator diversity, abundance, and traits, which may influence floral evolution by selecting for floral traits better adapted to the local pollinator community. In a previous study, we observed that urban flowers of the spotted jewelweed (Impatiens capensis) were larger than the natural ones in the Montreal and Quebec regions. Despite important phenotypic plasticity in the field, this genetic divergence was significantly correlated with the size of its primary pollinator, bumblebees. In a follow-up study, we investigated whether urbanization affected the strength and direction of natural selection on flower morphology. Our results show that urbanization did not alter phenotypic selection, and larger flowers were favored by pollinators in all populations. The selection gradients were constant even though populations occupy different areas within the floral adaptive landscape. This research offers valuable insights into how plants involved in mutualistic relationships evolve in response to human-induced environmental changes.

10:15 AM - 10:30 AM

Integrating Developmental and Macroevolutionary Approaches Reveals a Staminodial Origin of All Alternisepalous Organs in Caryophyllaceae

John Schenk, Ohio University
Riley Rees, Indiana University
Andrea Appleton, Harvard University

Abstract:

The identity of sterile floral organs in second-whorl, alternisepalous positions within Caryophyllaceae remains contentious, having been described as staminodes, “petaloids”, or petals homologous with those of other Pentapetalae. Limited ingroup and outgroup sampling, floral developmental data, and inadequate phylogenetic comparative methods in previous studies have added to this uncertainty. Crucially, staminodes have not been analyzed as discrete characters, leaving their homology with other structures unresolved. We reconstructed a chronogram of 775 species using five fossil calibrations for Caryophyllaceae and outgroups. Floral traits of 613 species, including number and position of petal-like structures, staminodes, and stamens, were quantified. Stochastic character mapping estimated ancestral character states and transition rates. Literature reviews provided developmental data to characterize common floral forms, while transition models assessed patterns of floral development and evolution. Staminodes evolved at the root of an apetalous Caryophyllaceae and were maintained throughout the backbone, being lost multiple times and becoming petal-like, especially in the Plurcaryophyllaceae in which a second whorl of stamens evolved in the alternisepalous position through the splitting of the alternisepalous primordia. The Caryophyllaceae crown ancestor likely had a single whorl of antesepalous stamens alternating with an alternisepalous staminodial whorl. Caryophyllaceae flowers are apetalous: all alternisepalous sterile structures are staminodes. Those staminodes have subsequently undergone multiple instances of loss, reduction, and elaboration. Their evolutionary history parallels patterns in early angiosperm lineages, making Caryophyllaceae a valuable system for investigating the role of staminodes in floral function and diversification.

Reproductive Biology

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

The Reproductive Impact on Caenorhabditis Nematodes from Bacteria Isolated from the Caenorhabditis Microbiome

Kevun Willis, Univeristy of Virginia
Katja Kasimatis, University of Virginia

Abstract:

A key component to the environmental network is host-associated microbial communities, which have long been recognized as important in structuring ecological relationships and driving coevolution. Host-associated microbial communities within the gut have been extensively characterized and appear to have sex-specific effects. However, little is known about the reproductive microbiome and its relationship with fertility. Here we expand on the power of the Caenorhabditis nematode model system to quantify the effect of diverse bacteria on fertility, characterize putative uterine infections, and identify the underlying transcriptional network changes associated with reproductive infection. We compare our results across two species that differ in mating system, namely C. elegans self-fertilizing hermaphrodites and C. remanei gonochoristic females. First, we quantified the fertility response of C. elegans hermaphrodites and C. remanei mated females when exposed to 53 different bacterial strains for a two-hour egg laying window. These bacterial strains were previously isolated from the Caenorhabditis microbiome (i.e., Big Biome) and represent a more natural bacterial community than the Escheria coli lab control. We found a highly plastic fertility response ranging from a mean of 0.60 to 8.77 hatched larvae. Both C. elegans and C. remanei had a significantly decreased fertility on 13 bacterial strains, while 1 bacterial strain showed a significantly increased response. We next characterized changes in the reproductive physiology that are associated with changes in the fertility response, including: gonad morphology, gonad color, and embryo retention. These data suggest that a decreased fertility response is due in part to bacterial colonization of the gonad itself. To support this putative infection status, we are sequencing the transcriptomes of females before and after bacterial exposure to determine the transcriptional response. Through this work we develop a holistic definition of a reproductive tract infection and demonstrate the importance of considering the role of the microbiome during reproduction.

9:45 AM - 10:00 AM

Differential gene expression in a native tree species with environmental sex determination

Jennifer Blake-Mahmud, Hope College

Abstract:

Plant sex may be determined through genetic or environmental mechanisms. When plants get proximate cues to be male or female through chromosomes, this is considered genetic sex determination (GSD). When environmental factors such as light, stress, injury, or size, cue sex expression it is known as environmental sex determination (ESD). Historically, these pathways of sex determination have been investigated separately. Almost all research on ESD has been ecologically-based and has ignored the underlying genetics, while most GSD research has been conducted on sexually stable species. This dichotomy obscures the truth that both genes and environmental factors are involved in sex expression in plants. Here we examine sex-based and tissue-based gene expression to better understand the genetic underpinnings of environmental sex

determination. To investigate this, we used a sexually plastic species, Acer pensylvanicum. We collected flower and leaf samples from A. pensylvanicum, extracted and sequenced the RNA, and examined the transcriptome by comparing differentially expressed genes (DEGs) between tissues within a sex and between sexes using a single tissue type. We found the most DEGs between tissue types. As expected, sex-based DEGs were also numerous in floral tissue. Previous ecological work suggested we might see differences in genes related to stress, carbohydrates, and photosynthesis. These hypotheses were supported by GO term enrichment in relation to stress and carbohydrates, but no GO term enrichment was found for photosynthesis-related categories in sex-based comparisons. We also investigate transcriptomic differences over time in male and female flower buds. We predicted that DEGs would be minimal at early collections, matching forced flowering experimental work, with transcriptomic patterns diverging later in floral development. These results shed light on the genetic basis for ESD and differences in sex-based physiology in sexually plastic species.

10:00 AM - 10:15 AM

Genomics of reproductive seasonality and sperm competition in two populations of brown mouse lemur (Microcebus rufus).

Rebecca DeCamp, Rutgers University
Severine Raveloson, Rutgers University
Finoana Faliarivola, University of Antananarivo
Santatra Randrianarisoa, Mahaliana Labs
Patricia Wright, Stony Brook University
Rindra Rakotoarivony, University of Antananarivo
Christina Bergey, Rutgers University

Abstract:

Mouse lemurs (genus Microcebus) are small, nocturnal primates native to Madagascar. Due to the seasonal unpredictability and unique biogeography of Madagascar, mouse lemurs exhibit highly seasonal reproduction, with females often coming into estrus for one night a year. Males experience strictly seasonal spermatogenesis, as well as high amounts of sperm competition during their limited breeding season, two factors that are predicted to strongly drive the evolution of male fertility-related traits. Previous genomic analysis have revealed that sperm competition is a strong driver of selection in genes related to male fertility across the animal kingdom. Here, we test the hypothesis that reproductive seasonality and sperm competition have differentially driven rapid evolution in genes expressed in the testis between two brown mouse lemur (Microcebus rufus) populations living in and around Ranomafana National Park, Madagascar, that are assumed to be reproductively isolated by the Namarona River. We predicted the phenotypic consequence of genetic variants that are putatively fixed within each population. We then isolated the genetic variants that were predicted to have high or moderate consequences that were putatively fixed in one population or another, and performed a gene ontology enrichment analysis to understand which biological functions may be impacted. We found that genes with predicted high/moderate impact alleles that had fixed variants between the two populations were significantly more likely to

be involved in ciliary biology. Significant human pathogenesis terms included “coiled sperm flagella,” “abnormal respiratory system morphology,” and “absent sperm flagella.” Further investigation of individual genes prioritized high impact variants between the populations in genes such as CATSPER3 and DNAH7, genes that are imperative for sperm flagellum formation and function. These findings suggest biologically significant divergence in genes impacting axonemal/motile-cilia between these two populations, with potential contributions to reproductive isolation.

10:15 AM - 10:30 AM

Leaving X: How scale insects repeatedly evolved alternatives to chromosomal sex determination

Andrew Mongue, University of Florida

Abstract:

Reproduction is a core feature of life, which makes understanding the reproductive diversity of organisms a fundamental goal of evolutionary biology. It is still unclear why sex determination systems are faithfully conserved for hundreds of millions of years in some taxa but repeatedly turn over in others. A prime example is the true bugs, Hemiptera. The vast majority of families employ a conserved X sex chromosomal system, but in scale insects (Coccomorpha), sex determination systems are far more varied. Different families may retain X chromosomes, employ a rare form of haplodiploidy known as paternal genome elimination (PGE), or forgo sexual reproduction in favor of simultaneous hermaphroditism. While these systems have been known for decades, only recently has non-model genomics enabled their study with modern bioinformatic methods. We collected and sequenced representatives of rare, early-diverging scale insects to study genomic changes that coincide with transitions between sex determination systems. Using ancillary expression data, we also explored sex-biased gene expression in a subset of scale insects on both sides of one transition. In a newly updated molecular phylogeny, we recovered two independent losses of X chromosomal sex determination, once in the family Monophlebidae and a second time at the base of the families that employ PGE. In the former, genomic rearrangements begin before the X is lost and any previously X-linked orthologs have been absorbed into one of two massive, shuffled autosomes in the hermaphrodites. In the latter, the X chromosome itself is faithfully preserved in early diverging PGE taxa; it appears to have merely lost its sex determination function. We analyze ortholog conservation across these transitions and find few genes lost, with only one orthogroup lost in both transitions, and a number of orthogroups gained, suggesting these large transitions did not require large changes to the gene content of the X chromosome. Expression data suggests that extreme sexual dimorphism of gene expression predates sex determination turnover and may have helped enable it. Together these new observations illustrate the multiple routes to sex determination turnover, help refine hypotheses for its causes, and provide a wealth of new resources for the modern genomic study of scale insects.

10:30 AM - 10:45 AM
Genome-wide patterns of divergence are shaped by cytonuclear coevolution in Campanula americana

Karen Barnard-Kubow, James Madison University
Alfredo López-Caamal, James Madison University
Laura Galloway, University of Virginia
Molly Walker, James Madison University
Aaron Wisteria, James Madison University

SSE Symposium: Impacts of Genome Architecture on Polygenic Adaptation during Rapid Environmental Change - Chromosomal Rearrangements

06/22/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM
Chromosomal fusions linked to adaptive evolution in an invasive copepod species complex

Zhenyong Du, University of Wisconsin–Madison
Carol Lee, University of Wisconsin

Abstract:

Genome architecture evolution is a rapidly advancing field in evolutionary biology, fueled by the surge of new genomic data revealing unexpected patterns and mechanisms of adaptation. Chromosomal rearrangements are increasingly recognized as contributors to evolutionary adaptation, yet direct empirical evidence linking chromosomal evolution with response to selection remains scarce. This study investigates the role of chromosomal fusions in adaptive evolution within the copepod Eurytemora affinis species complex (Crustacea). Within this species complex, certain clades repeatedly give rise to invasive populations that cross habitat boundaries. High-quality chromosome-level genome assemblies from three clades revealed remarkable karyotypic evolution driven by up to eleven independent chromosomal fusion events within this species complex. The Atlantic clade (E. carolleeae), which is the most invasive, exhibited the fewest chromosomes (four) due to numerous fusion events. Comparative analyses between saline and freshwater populations of E. carolleeae uncovered significant enrichment of selection signatures at the chromosomal fusion sites, particularly at the centromeres, coinciding with regions of reduced recombination. At these fusion sites, collections of ion transport-related genes form potential "supergenes." These particular sets of ion transporter genes repeatedly show population genomic signatures of natural selection in both wild populations and laboratory selection lines during salinity transitions. This work provides novel empirical support for the hypothesis that

chromosomal fusions might facilitate adaptation by clustering coadapted alleles. This emphasizes the potential role of chromosomal variation in driving evolutionary novelty and speciation. This study represents a rare demonstration that genome architecture evolution might be directly associated with adaptation to environmental change.

9:45 AM - 10:15 AM

A cosmopolitan inversion captures the polygenic architecture underlying a foraging-survival trade-off in D. melanogaster.

Alan Bergland, University of Virginia

Abstract:

Inversions - large chromosome rearrangements that suppress recombination - are widespread and are implicated in speciation, sex-chromosome evolution, and adaptation. Across many taxa, inversions underly some of the most conspicuous phenotypic variation because the lack of recombination links together many fitness related variants. However, the role of inversions in controlling quantitative variation has been less explored. I will discuss our recent work examining how cosmopolitan inversions contribute to quantitative variation in Drosophila melanogaster and the seasonal and spatial patterns of frequency change of one inversion, In(2L)t. Using the Drosophila Genetics Reference Panel (DGRP), we show that inversions in general, and In(2L)t especially, contribute to quantitative genetic variation in dozens of traits and often explain upwards of 10% of phenotypic variation. This association has largely been overlooked in the literature because of the statistical mapping approaches commonly used for the DGRP. Our meta-analysis of DGRP data shows that In(2L)t strongly affects behavioral, stress tolerance, and life-history traits. We validated the association between In(2L)t and many of these traits using controlled crosses and show that these phenotypic associations tend to be insensitive to aspects of larval and adult temperature. We discover that In(2L)t may underly a fitness tradeoff between starvation tolerance and foraging, wherein the standard allele is a more active forager but is more sensitive to starvation than the inverted allele. This tradeoff is consistent with the seasonal fluctuations of In(2L)t that we observe in natural populations, where the inverted allele is found at higher frequencies in the spring and late fall/early winter but lower frequencies in the summer. Finally, I will discuss patterns of molecular evolution around the In(2L)t locus, and highlight potential candidate genes based on patterns of linkage between specific loci and the inversion breakpoints.

10:15 AM - 10:45 AM

Impacts of genome architecture on selection response during laboratory experimental evolution

Carol Lee, University of Wisconsin
Zhenyong Du, University of Wisconsin–Madison

Abstract:

Genome architecture could have profound impacts on the predictability of evolutionary pathways and genetic mechanisms underlying parallel evolution. However, this topic remains largely unexplored. Recently, populations of the copepod Eurytemora affinis species complex have invaded many freshwater habitats throughout the world. During these invasions, distinct clades (sibling species) with different chromosome number display remarkable parallel evolution, with the same loci (and SNPs) repeatedly under selection during salinity transitions. In laboratory evolution experiments, we imposed salinity decline for 10-20 generations on selection lines from clades with 15 chromosomes (E. affinis proper, ancestral state) and 4 chromosomes (E. carolleeae, fused state). In both clades, several ion transport-related genes were under selection. However, selection responses differed radically between selection lines from the two clades, with strong signals of positive epistasis among beneficial alleles in the 15-chromosome clade but selection on standing variation in the 4-chromosome clade. In the 15-chromosome genome, beneficial alleles are concentrated near the telomeres, where recombination and positive epistasis could bring them together within genomes. Consistent with these results, theoretical simulations showed that under strong positive epistasis, higher chromosome number can increase parallelism between replicate selection lines. In contrast, in the 4-chromosome genome, beneficial alleles are already linked near fusion sites (especially centromeres) where recombination is low, such that selection acts on balanced polymorphisms of large linkage groups. Our results illustrate that genome architecture has profound impacts on selection responses of populations.

(Funding: NSF IOS-2412790, DEB-2055356; Refs: Du et al. 2025, NatureComm.; Du et al. 2024, GPB; Stern&Lee, 2020, NatureEcol.Evol.; Stern et al. 2022, NatureComm.)

Behavior: Evolutionary Ecology

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Social decisions under pathogen risk: How stickleback respond to immune-activated neighbors

Sidney Ryan, The Ohio State University
Jennifer Hellmann, The Ohio State University

Abstract:

In social animals, detecting and responding to sick conspecifics is crucial for limiting the spread of pathogens across a population. Defenses against pathogens commonly involve two strategies: 1) behavioral avoidance of risky environments or individuals, and 2) anticipatory immune activation. Hosts can utilize one or both strategies, but the balance been behavioral avoidance and immune activation may depend on historical pathogen regimes in their environment, with populations under intense pathogen pressure expected to display stronger defenses than populations under weak pathogen pressure. We investigated this variation in juvenile threespine stickleback (Gasterosteus aculeatus) collected from two Alaskan populations that differ in their exposure to a common tapeworm parasite. In the lab, healthy focal fish were paired with a single conspecific injected with either an immune stimulant (LPS) or saline (sham control). After four days of exposure, we quantified focal behavior in a 10 minute assay, focusing on aggression, swimming, hiding, and time spent within one body length of the injected partner. We then collected spleens and livers from all fish to measure the expression of pro-inflammatory and regulatory immune genes. We predicted that focal fish from the population with high parasite prevalence would reduce time spent near their LPS-injected partner and increase antisocial behavior compared to those from low parasite populations. Further, we expected these individuals to more strongly upregulate the transcription of immune-related genes, potentially preparing their immune system for infection. This study will advance our understanding of the mechanisms by which hosts respond to sick conspecifics and whether those responses diverge across natural populations. Understanding these differences is essential for predicting how social behaviors and immune activity influence the spread of pathogens across landscapes.

11:30 AM - 11:45 AM
Behavioral differences among color morphs of the eastern gray squirrel

Rick Lehtinen, The College of Wooster
Lydia Crane, The College of Wooster

Abstract:

Color polymorphism is widespread in many lineages and has a long history of study in evolutionary biology. In the pre-molecular era, color polymorphisms were crucial systems to empirically examine the roles of such fundamental evolutionary mechanisms as genetic drift, and natural and sexual selection. However, despite their importance, behavioral comparisons among co-occurring color morphs have been less well characterized than other aspects of color polymorphism. Leveraging a large dataset of behavioral observations in a color polymorphic urban population of eastern gray squirrels (Sciurus carolinensis), we assessed behavioral differences among color morphs using data from 17 years of walking surveys. We found that while some behaviors occurred at similar frequencies in both color morphs (e.g., sprawl posture, nest repair activities, sources of mortality), other behaviors differed in frequency among morphs. For example, gray morph squirrels were more likely to use feeders, more likely to be observed in “tail-up” posture and more likely to

engage in chase, grooming and play behavior than melanistic morph individuals. On the other hand, melanistic morphs were more active later in the day and more likely to be observed with bald patches in their fur. Mating behavior was observed to be asymmetric among color morphs with same-morph copulations being significantly more common than copulations among morphs. In contrast, environmental conditions had little impact on the relative proportions of gray or melanistic morphs observed on surveys (e.g., cloud cover, precipitation, ambient temperature). These data suggest that many under-appreciated behavioral differences exist among the color morphs of this species and that these differences may have important influences on evolutionary outcomes.

11:45 AM - 12:00 PM

Thermal ecology predicts how lizards and tadpoles navigate rising temperatures

Saúl Domínguez-Guerrero, Yale University
Brooke Bodensteiner, University of Alabama
Miguel Tejedo, Estación Biológica de Doñana - CSIC
Mirco Solé, Universidade Estadual de Santa Cruz
Eduardo Schaefer, IIGHI - CONICET (Instituto de Investigaciones Geohistóricas - Consejo Nacional de Investigaciones Científicas y Técnicas) - CHACO - ARGENTINA
Martha Muñoz, Yale University

12:00 PM - 12:15 PM

Interplay Between Predator-Induced Plasticity and Evolutionary History on Courtship Behavior in Alaskan Threespined Stickleback

Michaela Rogers, The Ohio State University
Jennifer Hellmann, The Ohio State University

12:15 PM - 12:30 PM

Resource allocation, wing color, and mate attraction in a fritillary butterfly

Carol Boggs, University of South Carolina
Daniel Chappell, Air Force Research Lab
Chloe Keck, Univ. of South Carolina
Madison Mengel, Univ. of South Carolina
Erica Fleishman, Oregon State University
Daniel Speiser, University of South Carolina

Biogeography I

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Well-supported phylogenomic tree suggests an alternative interpretation of chameleon evolution and biogeography.

Meghan Forcellati, American Museum of Natural History
Alexander Salis, American Museum of Natural History
Roger Benson, University of Oxford
Christopher Raxworthy, American Museum of Natural History

Abstract:

Chamaeleonidae is a lizard family distributed in Africa, Asia, and Europe, with unique traits, including independently-rotating eyes, autopodial zygodactyly, ballistic projectile tongues, and extensive color change. However, phylogenetic relationships within the group are poorly resolved, limiting our ability to test central questions of their evolution and biogeography such as divergence times and their implications for how chameleon evolution has been structured by historical climatic events, chameleon geographic origins, and potential dispersal(s) across the Mozambique Channel, a >420 km stretch of primarily deep ocean water between Madagascar and Africa. Here, we sequence the largest phylogenomic dataset of chameleons to date (N >90 species, including multiple species or individuals within all genera and subgenera, enriched for ~5k loci). We use coalescent and Bayesian models, applying new fossil calibrations, to resolve the evolutionary relationships and divergence times, and then perform historical biogeographic and ancestral states reconstructions of Chamaeleonidae. Our results confirm the previously supported placement of Madagascar leaf chameleons and resolve previously uncertain chameleon relationships with strong support. However, they challenge many other aspects of chameleon evolution by recovering previously never-proposed relationships, and could thus suggest a novel hypothesis for chameleon historical biogeography. Finally, we hypothesize major evolutionary and biogeographic events for the group may have coincided with the end-Cretaceous mass extinction and the Paleocene-Eocene thermal maximum.

11:30 AM - 11:45 AM

Exploring patterns of cryptic speciation across forest birds in India using integrative taxonomy

Archita Sharma, Indian Institute of Science Education & Research Tirupati

Abstract:

In peninsular India (25° N - 8° N), landscape (valleys, rivers) and climatic barriers have impacted the distribution and diversity of birds, resulting in as many as 200 subspecies. This study uses

genomics, morphometrics, and acoustics to reassess the taxonomy of four species complexes with 11 subspecies found in peninsular India and Sri Lanka - Indian Blackbird (Turdus simillimus), Tawny-bellied Babbler (Dumetia hyperythra), Jungle Owlet (Glaucidium radiatum), and Indian Yellow-tit (Machlolophus aplonotus). We systematically collected field samples across peninsular India and Sri Lanka. We additionally obtained morphometric data from natural history museums and collated song data from citizen-science databases. For 64 samples, we extracted DNA from blood samples, sequenced low-coverage whole genomes, and harvested ~5000 UCEs. We performed a suite of phylogenomic analyses, species delimitation, population-structure assessment, and divergence-time estimation. For the four subspecies of Indian Blackbird, UCE and SNP data revealed three groups (nigropileus, kinnisii, and bourdilloni+simillimus). Dating analysis revealed that migratory subsp. nigropileus diverged earlier (~ 2.49 mya) from the non-migratory subsp. bourdilloni and simillimus, suggesting that sedentary populations of these two subspecies could have arisen as migratory dropouts. Similarly, we also find previously unknown (cryptic) and strongly geographically structured genetic diversity within the Indian Yellow-tit and the Jungle Owlet species complexes. Contrastingly, we find evidence of hybrid speciation in the Tawny-bellied Babbler. Most species descriptions of birds in India have relied on century-old morphology-based taxonomy. Our study addresses key gaps in avian cryptic diversity in a biogeographically unique region in South Asia using modern integrative taxonomic methods.

11:45 AM - 12:00 PM

Phylogenomics resolve the systematics and biogeography of the ant tribe Myrmicini and tribal relationships within the hyperdiverse ant subfamily Myrmicinae

Matthew Prebus, Arizona State University
Christian Rabeling, University of Hohenheim

Abstract:

Ants are a globally distributed and highly diverse group of eusocial animals, playing key ecological roles in most of the world's terrestrial ecosystems. Our understanding of the processes involved in the evolution of this diverse family is contingent upon our knowledge of the phylogeny of the ants. While relationships among most subfamilies have come into resolution recently, several of the tribal relationships within the hyperdiverse subfamily Myrmicinae persistently conflict between or within studies, mirroring the controversial relationships of the Leptanillinae and Martialinae to the remaining ant subfamilies. Another persistent issue of debate in ant phylogenetics is the timing of major evolutionary events as inferred via divergence dating. Here, we test the topology of the myrmicine tribes using genome scale data, inspect gene tree-species tree concordance, and use posterior predictive checks and tests of compositional heterogeneity to infer sequence characteristics which potentially introduce systematic bias in myrmicine tribal topology. Furthermore, we test the placement of the Baltic amber fossil †Manica andrannae by integrating phylogenomic and morphological data from nearly all species within the genus Manica, and a broad sampling of its sister genus Myrmica. Subsequently, we demonstrate the effect of fossil

placement on overall divergence times in the Myrmicinae. We then re-evaluate the historical biogeography of the Myrmicini and Pogonomyrmecini considering newly generated genetic data and insights from our phylogenomic results. We find that our current understanding of tribal topology in the Myrmicinae is strongly supported, but this topology is highly sensitive to compositional heterogeneity and gene-tree species-tree conflict. Our fossil placement analyses strongly suggest that †Manica andrannae is a stem Manica species, and analysis of this fossil in context of the Myrmicinae demonstrates that a single fossil calibration point can have broad-scale cascading effects on divergence dates within the entire subfamily. The results of our biogeographic reconstructions indicate a South American origin for the Pogonomyrmecini + Myrmicini. Additionally, our results suggest that the MRCA of Myrmicamay have inhabited the western Nearctic in the early Miocene prior to repeated dispersal across Beringia throughout the Miocene and Pliocene. The MRCA of Manica, on the other hand, was inferred to have a Holarctic range prior to vicariance during the Pliocene. Unexpectedly, we found strong support in the Pogonomyrmecini for three coordinated dispersal events from South to Central America during the early Miocene, which has been previously proposed as an early biotic interchange event prior to the more commonly accepted 3.5 Ma closure of the Isthmus of Panama.

12:00 PM - 12:15 PM

Dissecting biogeographic patterns of speciation in a group of North American freshwater fishes

Julia Wood, Yale University
Thomas Near, Yale University

12:15 PM - 12:30 PM

A time-integrated view of climate contiguity and its role in shaping species communities

Pascal Title, Stony Brook University

Conservation Biology I

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Spatial extinction forecasting over the next 100 years demonstrates profound phylogenetic diversity losses across Hispaniola in multiple taxa

Wilson Guillory, Temple University
Ann Raiho, Temple University
Emmy Spadaro, Temple University
S. Blair Hedges, Center for Biodiversity

Abstract:

Environmental degradation and climate change linked to human activities are already causing extinctions worldwide. The coarseness of tools like the IUCN Red List make it difficult to perform nuanced assessments of extinction risk for species across spatial and temporal scales, or to determine the landscape factors that may be driving extinctions. In this project, we examine species loss from an eco-evolutionary perspective by estimating declines in endemic species, phylogenetic, and functional diversity across Hispaniola, one of the most deforested islands in the world. We gathered spatial occurrence data, time-calibrated phylogenies, and functional trait data for all endemic amphibians, reptiles, birds, and butterflies on Hispaniola. Using a previously developed extinction forecasting method that incorporates both future climate data and primary forest cover, we forecast the area of habitat for each species over the next 100 years. We estimate that around one-half of Hispaniola's endemic amphibians, one-fourth of reptiles, one-fourth of birds, and one-third of butterflies will go extinct within the next century, increasing with climate change severity. Losses to phylogenetic and functional diversity are tied to both spreading urban development and primary forest loss. This study plainly demonstrates the imminent loss of both ecosystem functioning and evolutionary information accumulated over millions of years, should no further action be taken to preserve our planet's environments.

11:30 AM - 11:45 AM

Traits under selection during experimental case of genetic rescue in wild populations

Alexa Guerrera, Michigan State University Kellogg Biological Station

Abstract:

Evolutionary ecologists have long sought to understand the circumstances under which gene flow promotes rather than restricts adaptive evolution. In small, inbred populations, the restoration of gene flow has been used to increase population growth and enhance fitness – an outcome known as genetic rescue. Whether populations will experience genetic rescue depends on the

evolutionary mechanisms that allow beneficial immigrant alleles to establish and improve the fitness of recipient populations without constraining local adaptation. However, the selective mechanisms that determine how quickly and effectively immigrant alleles spread and lead to population recovery through genetic rescue remain poorly understood. Populations in which ecologically important traits are subject to negative frequency-dependent selection (NFDS) should hasten genetic rescue by favoring rare immigrant or hybrid alleles, thereby promoting introgression and maintaining genetic variation through time. We used a previously conducted mark-recapture experiment that documented genetic rescue in natural populations of Trinidadian guppies (Poecilia reticulata) to test whether NFDS was associated with immigrant and hybrid fitness in two replicate populations in Trinidad. We found compelling evidence that hybrid ancestry and NFDS, in the form of male color pattern rarity, contributed to male success and aided in genetic rescue. The magnitude of this effect varied between the populations, potentially reflecting differences in ecological and demographic contexts. Our results emphasize the importance of NFDS in predicting beneficial responses to assisted gene flow.

11:45 AM - 12:00 PM

Between- and within-population genetic dynamics reveal conservation challenges for the rare plant Ribes echinellum

Zoe Diaz-Martin, Spelman College
Phoenix King, Spelman College
Joseph Stockert, Atlanta Botanical Garden
Lauren Eserman-Campbell, Atlanta Botanical Garden
Emily Coffey, Atlanta Botanical Garden
Loy Xingwen, Atlanta Botanical Garden

Abstract:

Understanding how genetic diversity is distributed within and between populations of rare species is critical for developing effective conservation strategies. The Miccosukee gooseberry (Ribes echinellum), a federally threatened shrub restricted to two known populations in South Carolina and Florida, faces ongoing ecological pressures and extremely limited regeneration. We used double-digest RAD sequencing to generate genome-wide SNP datasets to evaluate patterns of genetic diversity, structure, and reproduction across its range. The two populations are genetically distinct, with similar levels of genetic diversity and high numbers of private alleles, indicating that neither served as the source of the other. Within populations, we detected moderate levels of heterozygosity, no inbreeding, moderate clonality, background relatedness, and no isolation by distance despite small effective population sizes. These patterns likely reflect historical connectivity and past reliance on sexual reproduction, but contemporary recruitment occurs almost exclusively via clonal stolons and appears limited by ecological rather than intrinsic genetic factors. We caution that a demographic time lag may be maintaining genetic diversity in the short term, but low regeneration poses a long-term risk to evolutionary potential. To safeguard this species, conservation strategies should prioritize capturing unique alleles through ex situ collections, protecting and managing both populations, and carefully evaluating gene flow

interventions in light of potential local adaptation. These findings provide a rare case study of a clonally reproducing, range-restricted species where historical processes have preserved diversity, but contemporary demographic constraints threaten future adaptive capacity—insights that can inform management of other rare plants facing similar challenges.

12:00 PM - 12:15 PM

Effects of inter- and intra-population translocations on an endangered woodpecker population

Alexander Lewanski, Michigan State University

12:15 PM - 12:30 PM

Translocations for genetic rescue of an inbred coastal population of Florida Scrub-Jays

Sarah Fitzpatrick, Kellogg Biological Station
Michigan State University,
Tyler Linderoth, W.K. Kellogg Biological Station
Nancy Chen, University of California
Tram Nguyen, Cornell University
Andrew Clark, Cornell University
Karl Miller, Florida Fish and Wildlife Conservation Commission
Hannah Miller, Michigan State University
John Fitzpatrick, Cornell Lab of Ornithology

Disease

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Leveraging experimental evolution to extract predictive collateral drug response signatures in Ewings Sarcoma

Kristi Lin-Rahardja, Cleveland Clinic
Ethan Canavan, University of Pittsburgh
Jacob Scott, Cleveland Clinic

Abstract:

Therapeutic options for patients with relapsed or refractory Ewings sarcoma (EWS) remain limited. Collateral sensitivity, where resistance to one drug confers sensitivity to another, could be leveraged to optimize chemotherapy for EWS. Gene expression signatures that predict collateral sensitivity states can be used to guide treatment selection in an evolution-informed manner.

To generate such biomarkers, we experimentally evolved resistance to first-line EWS chemotherapy in independent replicates of an EWS cell line, all originating from the same ancestor population. Throughout, we measured collateral responses across a panel of anticancer drugs and quantified transcriptomic changes. Collateral drug responses varied across replicate evolutionary trajectories, but convergent states of collateral sensitivity emerged across different replicates at different times. By associating these convergent phenotypes with gene expression patterns, we derived a library of predictive signatures for numerous drugs. These signatures accurately distinguished states of collaterally sensitivity from states of collateral resistance within our dataset, irrespective of a replicate's evolutionary history.

Our findings demonstrate that gene expression signatures can predict collateral sensitivity in EWS, providing a foundation for personalized therapeutic strategies. This approach also establishes a generalizable workflow for developing predictive biomarkers to guide chemotherapy selection in patients with rare diseases that lack reliable second-line chemotherapy regimens.

11:30 AM - 11:45 AM

Raccoon population structure and rabies detection patterns in Alabama suggest a mismatch between host connectivity and disease dynamics

Andrea Miranda Paez, Auburn University

Abstract:

Understanding how host, environmental, and epidemiological features influence disease dynamics is critical for effective wildlife management. The raccoon rabies virus remains endemic across much of the eastern United States, including Alabama, where spatial variation in reported cases raises questions about the processes shaping disease patterns. In this study, we integrated population genomics, spatial analyses, and rabies surveillance data to evaluate whether host genetic structure or alternative processes better explain spatial heterogeneity in raccoon rabies incidence across Alabama. We analyzed genome-wide SNP data from 238 raccoons sampled across 38 counties. Genetic analyses supported a highly connected population at the county and statewide scale. Patterns of genetic variation were consistent with weak isolation by distance and localized genetic similarity, but without meaningful barriers to gene flow. In contrast, reported rabies cases from 2009–2025 exhibited significant spatial clustering, with distinct regions of elevated and reduced detections across the state. Landscape composition and proximity to oral rabies vaccination zones did not significantly explain variation in rabies burden. The mismatch between high host connectivity and spatially structured disease patterns suggests that rabies heterogeneity in Alabama is not driven by host population subdivision at this scale. Instead, observed patterns may be more consistent with localized epidemiological processes. These findings highlight the importance of integrating genetic and epidemiological data to better understand wildlife disease systems and suggest that management strategies focusing on transmission hotspots may be more effective than those based on assumptions of host population structure.

11:45 AM - 12:00 PM

From healthy brain to cancer cells: Understanding the origins of glioblastoma through the lens of Darwinian evolution

Jhan Salazar Salazar, Mayo Clinic
Sean McHugh, Washington University in St. Louis
Michael Landis, Washington University in St. Louis
Maria Gonzalez, Mayo Clinic
Hugo Guerrero Cazares, Mayo Clinic

Abstract:

Since Darwin, evolutionary biologists have sought to understand how traits evolve across lineages and have developed several tools to address questions regarding how lineages, species, and populations have evolved through time. In recent years, the use of evolutionary statistical methods to study cancer evolution has grown. These approaches remain limited to a few tumor types (e.g., blood and lung cancer), but the rapid growth of sequencing technologies and large-scale datasets has created new opportunities to address evolutionary questions across cancer types that have been understudied (e.g., brain tumors). Researchers are now using whole-genome, exome, single-cell, spatial, and multi-omic data to reconstruct tumor evolutionary histories, test adaptive hypotheses, and in a few cases, quantify rates and modes of evolution within tumors and between tumor types. However, there is not yet a consolidated framework for which evolutionary analyses are most appropriate to study cancer evolution, nor accessible guidance on how to implement these approaches in cancer datasets. We synthesize evolutionary statistical methods currently used in brain cancer research and propose additional approaches for future studies. We identify more than 30 evolutionary tools developed to study trait evolution, diversification, and lineage dynamics in biological systems, of which only one has been applied to brain cancer. We argue that adapting these methods offers a powerful opportunity to investigate cancer stem cell dynamics and tumor progression in glioblastoma and other understudied cancers. By bridging evolutionary biology and cancer genomics, this work provides a roadmap for expanding the evolutionary toolkit used to study tumor evolution and for generating testable hypotheses about malignant transformation, including state-dependent speciation and extinction methods.

12:00 PM - 12:15 PM

Phage Therapy and Global Health Equity: The Role of Ecology and Evolutionary Biology

Jordan Lewis, The University of South Carolina
Paul Turner, Yale University
Ben Chan, Yale University
Gerard Vong, Emory University

Abstract:

Despite progress in controlling microbial infections, the global burden of pathogenic bacteria remains high. Moreover, the spread of antibiotic- resistant bacteria has increased and is likely to continue. Consequently, recent research has focused on alternative antibiotics to slow the spread of resistance and improve patient outcomes. One promising approach is phage therapy, which uses lytic viruses of bacteria to treat bacterial infections. However, an underexplored potential benefit is its capacity to enhance health outcomes across the socioeconomic spectrum and improve healthcare equity. In our recent publication, we draw on the history of phage therapy, recent clinical successes, and advancements in research to argue that phage therapy is well-suited to advance health and healthcare equity. This is because it offers a greater potential to increase access and reduce the disadvantages faced by lower socioeconomic groups relative to traditional antibiotics. Based on these points, we proposed research objectives that aim to achieve these scientific and ethical goals. In this talk, we address the role that evolutionary biologists and ecologists can play in this work, and the research realms within these fields that can help advance health equity and our general understanding of phage biology.

See the manuscript here: www.annualreviews.org/content/journals/10.1146/annurev-virology-092623-110310

Molecular Ecology II

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

The contemporary Pacific gray whale (Eschrichtius robustus) gene pool includes ancestry from a potential ghost population: inferences from population genomics

Natalie Allen, Purdue University
Anna Brüniche-Olsen, University of Copenhagen
Jong Yoon Jeon, Purdue University
Andrew Mularo, Kellogg Biological Station
John Bickham, Texas A&M University
Jorge Urban, Universidad Autonoma de Baja California Sur
J. Andrew DeWoody, Purdue University

Abstract:

Local extirpations and extreme bottlenecks can deplete genetic variation and obscure population dynamics, especially in highly mobile species. The gray whale (Eschrichtius robustus) undertakes some of the longest known migrations among mammals, and conventional wisdom acknowledges two stocks (eastern and western gray whales) in the Pacific. Commercial whaling depleted both stocks, and while the Eastern North Pacific (ENP) stock has rebounded, the western stock was

feared extirpated. In the post-whaling era, the origin of a small summer aggregation near Sakhalin Island, Russia (which we refer to as the Western North Pacific (WNP) stock) is unclear; this group may include descendants from the original western stock, founders from the eastern stock, or some combination of the two. To clarify the genetic affinities of WNP gray whales, we generated whole genome resequencing data for 74 individuals sampled from both geographic regions to assess their origins. Surprisingly, WNP whales are more genetically varied than ENP whales according to principal components and admixture analyses. We present evidence that this structure is due to mixed ancestry in WNP, with admixture occurring between historical eastern and western stocks. Genomic signals based on both single nucleotide polymorphisms and on copy number variants indicate that despite mixed ancestry, the influx of eastern gene flow has largely homogenized genomic diversity across the Pacific. These findings highlight the ability of whole-genome data to help resolve questions of extirpation and to clarify complex gene flow dynamics in highly mobile species.

11:30 AM - 11:45 AM
Genomic and ecological investigation of rusty crayfish invasion

Jesse Wallace, The Ohio State University
Bryan Carstens, The Ohio State University
Marymegan Daly, The Ohio State University

11:45 AM - 12:00 PM
Seasonal migration, latitude, and the maintenance of genetic diversity

Ben Winger, University of Michigan Museum of Zoology
Teresa Pegan, University of Michigan

Abstract:

Genetic diversity shapes evolutionary potential and long-term persistence, yet explaining why co-distributed species differ in diversity remains challenging because distinct processes can produce similar genomic signatures. Life history traits, historical demography, and environmental factors have all been implicated but remain difficult to disentangle. Seasonal migratory species offer a unique opportunity to test competing hypotheses owing to migratory species' occupancy of different regions at different times of the year. Using approximately 1,700 low-coverage whole genomes from 35 co-distributed boreal-breeding bird species varying in migration distance and wintering location, we identify a strong positive relationship between migration distance and nuclear genetic diversity. Long-distance migrants wintering in tropical regions experience higher annual survival compared to short-distance migrants exposed to harsh temperate winters. We propose that this demographic stability buffers long-distance migrants against genetic diversity loss through reduced extinction-recolonization dynamics. These findings are consistent with a latitudinal gradient in genetic diversity, but specifically highlight the non-breeding geographic range

in migratory species as a critical but underappreciated driver of population genetic evolution along this gradient.

12:00 PM - 12:15 PM

Reconstructing the mating system of Santa Cruz Galapagos giant tortoises

Carolyn Jessop, University of British Columbia
Emily Donovan, Center for Wildlife Sustainability Research
Evelyn L Jensen, Newcastle University
Ainoa Nieto, St. Louis Zoo Insititue for Conservation Medicine
Patrick Moldowan, Charles Darwin Foundation
Sharon Deem, St. Louis Zoo Institute for Conservation Medicine
Guillaume Bastille-Rousseau, Department of Zoology
Stephen Blake, St. Louis Zoo Institute for Conservation Medicine
Michael Russello, University of British Columbia Okanagan

Abstract:

Mating systems influence the behavioral and eco-evolutionary processes of a species, so understanding a species mating system can inform conservation strategies. The two species of Galapagos giant tortoise on Santa Cruz Island (Chelonoidis donfaustoi and C. porteri) are keystone species in their respective habitats. To assist in conservation efforts, more knowledge of their mating systems in wild populations is necessary, including if multiple paternity is present. To enable investigation of reproductive behavior in Santa Cruz giant tortoises, we developed a genotyping in thousands by sequencing (GT-seq) panel that can identify species and individuals and estimate relatedness. Given the conservation status of these species, we designed and optimized the panel to genotype minimally invasive cloacal swab samples. The developed panel includes 325 SNPs; 38 targeted for species identification and 287 for individual identification and relatedness estimation. Genotypic data collected from 220 samples from 42 nests and attending mothers were used to reconstruct the mating system, support nesting data, and determine the presence of multiple paternity within the population. In total, 5 of the 14 females sampled had nests with different fathers in the same nesting season. Four of these females had nests in which two fathers contributed, indicating multiple paternity. Overall, the findings of this research contribute to existing literature on Galapagos giant tortoise mating systems, which can help inform future management decisions within the system.

Phylogenomics I

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Phylogenomics of East African Acacia trees: evolution of stress response in the savanna ecosystem

Anri Chomentowska, The Ohio State University
Ellen Weinheimer, Yale University
Joseph Charboneau, University of Michigan
Arjun Potter, Wake Forest University
Stephen Smith, University of Michigan
Nicholas Kortessis, Wake Forest University
T. Michael Anderson, Wake Forest University
James Pease, The Ohio State University

Abstract:

Acacia trees are among the most ecologically significant organisms in savanna ecosystems. In East African savannas, these trees are exposed to periodic fires and droughts, and the diversity in strategy by which different Acacia species deal with such environmental stressors is of great interest. However, the evolutionary dynamics among these tree species are poorly understood, due in part to previously limited genomic resources. As part of a collaborative multi-national and -institutional project, we sequenced the genome of 12 Acacia tree species (genera Vachellia and Senegalia) that inhabit the Serengeti National Park. By assembling a haplotype-resolved, chromosome-level genome of one the focal species, V. tortilis, we could confidently map short-read sequences from all 12 species with varied ploidies. Using homologous loci across the genomes, we inferred the phylogenetic relationships among Vachellia and Senegalia in the Serengeti. We also investigated patterns of genomic admixture among these often co-occurring species. Furthermore, we integrated previously collected eco-physiological and RNA-Seq data with our phylogenomic results to examine how drought response has evolved across this lineage. Notably, the reactiveness to drought has both increased (in Senegalia) and decreased (in Vachellia) over evolutionary time, with substantial variation in physiological responses to sustained drought conditions among species. We further hope to include physiological and transcriptomic responses to additional environmental variables, with the goal to integrate genomic inference and field measurements to better characterize the evolutionary history of this closely related group of trees.

11:30 AM - 11:45 AM

Widespread Hybridization in Neotropical Cichlids is Predicted by Shared Ecology

Shannon Whitney, Texas State University
Matthew McGee, Monash University
Samuel Borstein, Texas State University

Abstract:

Understanding the generators of biodiversity has been a central theme in biological studies. While once thought of as an evolutionary dead end, hybridization is now seen as a potential promoter of biodiversity that facilitates gene flow and generates variation among functional traits. Hybridization has been shown to play a key role in the adaptive radiation of African Great Lake cichlid fishes. However, the role of hybridization in the evolutionary history of the older Neotropical heroine cichlids (Tribe: Heroini) has received significantly less attention. Here, we leverage a publicly available RADseq dataset to investigate patterns of hybridization across heroine cichlids. Using 355,117 SNPs from 104 species, we reconstructed the evolutionary history for heroines using maximum likelihood and multispecies coalescent frameworks, the latter of which are specifically designed to handle gene flow and incomplete lineage sorting. We calculated Patterson's D-statistic to detect signals of hybridization between species and used a Bayesian regression to test if shared ecological traits predict increased signals of hybridization. While the maximum likelihood phylogeny yielded high bootstrap support, low site concordance factors and discordant topologies revealed substantial underlying genomic discordance. Our results show that hybridization is widespread both within and between the major heroine clades. Furthermore, we find that non-tree like evolution can be predicted by shared ecological traits among taxa. Our study reveals that hybridization is a non-random process that has played an important role in the evolutionary history of heroine cichlids.

11:45 AM - 12:00 PM
Eusocial origins in the sea: phylogenomic insights from sponge-dwelling snapping shrimps

Solomon Chak, Denison University
Phillip Barden, New Jersey Institute of Technology
Kristin Hultgren, Seattle University

Abstract:

Eusociality is a conspicuous and ecologically impactful behavioral syndrome that has arisen at least 19 times in animals. Sponge-dwelling snapping shrimps in the genus Synalpheus are the only known aquatic animals to have evolved eusociality, characterized by group living, cooperation, and reproductive division of labor. Remarkedly, based on Synalpheus collected from the West Atlantic alone, nearly one fourth of all known eusocial origins across the animal kingdom occur in this lineage. However, Synalpheus shrimps are distributed worldwide and include several putatively eusocial species outside the West Atlantic, suggesting additional independent origins of eusociality. Here, we constructed a global phylogeny of the genus Synalpheus to clarify the number and placement of independent eusocial origins in this genus. We obtained DNA samples from museum collections and new field expeditions and performed target-capture sequencing using a combined Anchored Hybrid Enrichment (AHE) probes and Ultra Conserved Elements (UCE) probe set designed for decapods. The resulting phylogenomic trees recovered previously recognized

eusocial origins in the West Atlantic clades and uncovered additional eusocial transitions that are geographically dispersed. This global phylogeny provides a framework for comparative analyses to test for genomic and morphological changes associated with eusocial transitions in the sea.

12:00 PM - 12:15 PM
Using genome-wide data to decipher the relationships in the Rosyface Shiner, (Notropis rubellus) species group in Arkansas

Brian Okwiri, Arkansas State University
Andrew Sweet, Arkansas State University
Brook Fluker, Arkansas State University

Abstract:

In the wake of accelerated extinction rates and growing threats to biodiversity, it is becoming increasingly important to accurately estimate biodiversity and put in place proper conservation measures. Such efforts are especially necessary for groups with unresolved evolutionary relationships and undescribed biodiversity. One such group is the Rosyface Shiner (Notropis rubellus) species group that is native to eastern North America and consists of allopatric fish clades with complex divergence patterns. Previous systematic reexaminations of this species group, based on allozyme and mitochondrial markers, resulted in the recovery of seven distinct allopatric clades. Four of these clades are currently recognized species and three have yet to be described and elevated to species. Arkansas is home to three clades of this species group: Notropis percobromus, Notropis suttkusi, and Notropis percobromus 'Clade F', the latter being an undescribed clade that is restricted to the Ouachita River drainage. Here we employ ddRAD data to reexamine the phylogeny of the N. rubellus species group clades found in Arkansas. We also present additional analysis exploring the species boundaries, population structuring and genomics, demographic analyses, and divergence time analyses of these clades. Our findings will contribute evidence to support N. percobromus 'Clade F' as a distinct species and to provide population genomic information that will be important for conservation decisions for these species within Arkansas.

12:15 PM - 12:30 PM
Rapid evolution of synteny associated with multiple origins of dioecy and XY sex determination

Mark Hibbins, University of Rochester
Cassandre Pyne, University of Toronto
Stephen Wright, Department of EEB

Abstract:

Chromosomal rearrangements can be major drivers of evolutionary innovation, shaping processes including local adaptation, speciation, and sex chromosome evolution. Synteny, the conservation of the physical co-localization of protein coding genes across species, can provide valuable

information on histories of rearrangement. However, statistical approaches that enable insights to be obtained from multispecies synteny datasets are still in their infancy. Here, we present a novel framework for the application of phylogenetic comparative methods to multispecies synteny datasets, implemented in open-source R package SynPhyMe. Our approach is based on recording adjacencies, binary characters that indicate if two syntenic blocks are physically adjacent on a chromosome, and mapping them as species characters on a phylogeny. We apply this approach to Rumex, a clade of flowering plants that exhibits rapid karyotypic evolution, including multiple origins of XY sex determination from hermaphroditic ancestors. Leveraging new genome assemblies, we find evidence for accelerated chromosomal rearrangement associated with evolutionary transitions to dioecy, illustrating how explicit phylogenetic hypothesis testing can generate new insights into adaptive hypotheses for chromosomal evolution.

Plants and Pollinators

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Cytonuclear incompatibility driven by disruption of coadapted plastid-nuclear translation

Alfredo López-Caamal, James Madison University
Ava Wehr, James Madison University
Laura Galloway, University of Virginia
Karen Barnard-Kubow, James Madison University

11:30 AM - 11:45 AM

Prairie fire increases plant pollination despite no change in pollinator visitation or fidelity

Jennifer Ison, The College of Wooster

Abstract:

In historically fire-dependent ecosystems, fire typically stimulates and synchronizes flowering, which can increase annual reproductive fitness. Multiple ecological processes could explain these beneficial effects of fire on seed production, including greater pollinator abundance and visitation, altered pollinator foraging behavior, or enhanced mating opportunities. However, very few empirical studies have directly evaluated these alternative explanations for greater post-fire reproductive fitness. We experimentally investigated the effects of fire on pollination of Echinacea angustifolia (Asteraceae) across 36 remnant prairie sites in western Minnesota (USA). Consistent with previous work, experimental burns enhanced seed set when E. angustifolia populations were sufficiently

large. However, we found no evidence that experimental burns are associated with increased pollinator visitation or changes in bee foraging behavior. We hypothesize that the influence of fire on mating opportunities, particularly the S-allele diversity of potential mates, plays an important role in improved post-fire annual reproductive fitness in E. angustifolia populations, as well as other plant species within historically fire-dependent ecosystems.

11:45 AM - 12:00 PM
Updates on a xeric model for the evolution of obligate apomixis

Amanda Grusz, University of Minnesota Duluth / Smithsonian Institution

---

SSE Symposium: Impacts of Genome Architecture on Polygenic Adaptation during Rapid Environmental Change - Plant Polyploidy & Plasticity

06/22/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM
Genome duplication and the evolution of ecological novelty

Kyle David, Vanderbilt University

11:30 AM - 12:00 PM
Four is better than two? Polygenic adaptation in polyploids in response to changing external and cellular environments

Justin Conover, Donald Danforth Plant Science Center

Abstract:

Whole genome duplication (polyploidy) is a macromutational change to the genomic architecture of an individual. Polyploidy is especially common in crops and other flowering plants, and occurs with less frequency in some animal clades, including fishes, amphibians, and insects. While multiple studies have found associations between polyploidy and rapid adaptation to novel environments or niche expansions, the precise causes of these associations remain largely unclear. Although there is a rich history of evolutionary and physiological consequences of polyploidy (for example, the ability to rewire gene regulatory networks, or the masking effect of polyploidy on segregating deleterious mutations), our understanding how these genomic changes

influence patterns of polygenic adaptation is incomplete. Additionally, there is a growing recognition that the transition from diploid to polyploid can per se create additional selective pressures requiring polygenic adaptation, including the need for exclusive bivalent chromosome pairing during meiosis. When bivalency is not strictly enforced, multiple chromosomes can pair together (forming multivalents), altering the segregation patterns of alleles from one generation to the next, and oftentimes creating additional variation in genetic architectures (e.g. homoeologous exchanges). While predicted to be a severe selective pressure to overcome, the difficulty in estimating how quickly polyploids can overcome these meiotic challenges to the polyploid genetic architecture lies, in part, to the underdevelopment of population genetic theory for polyploids relative to diploids, particular for polyploids that regularly form multivalents. Here, I will present a brief overview of the various internal and external selective pressures that arise when transitioning from a diploid to polyploid genomic architecture, and demonstrate how properties of quadrivalent formation (e.g. double reduction, homoeologous exchanges) may be a prerequisite for overcoming the initial selective barriers that polyploids may face early in establishment.

12:00 PM - 12:30 PM

Spatial heterogeneity in varying environments reverses selection for recombination and promotes gene clustering

Davorka Gulisija, University of New Mexico

Abstract:

Recombination is a fundamental biological process that enhances the genetic diversity and adaptive potential of populations by generating novel allele combinations. Temporally varying selection favors recombination, but how spatial heterogeneity reshapes its evolution in finite populations remains unknown. We employ Monte Carlo simulations to investigate how spatial heterogeneity impacts the evolution of recombination rates between two selected loci within a finite subdivided meta-population. Our findings reveal that spatial heterogeneity can significantly alter the evolutionary trajectories of recombination. Contrary to previous models, our results demonstrate that spatial heterogeneity can reverse the evolution of recombination, favoring the clustering of genes instead. This clustering preserves advantageous gene combinations under spatially heterogeneous selective pressures, thereby enhancing genetic diversity, a precursor to rapid adaptation. These findings have implications for understanding the mechanisms underlying the evolution of genetic architecture and its impacts on adaptation in rapidly changing environments.

Behavior II

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

FISH in fish: optimizing three-dimensional sample processing and machine learning for comparative analysis and novel brain atlas generation in a non-model system

Adheeta Dongre, University Of Chicago

Abstract:

In the study of evolution, brain structure and region of interest mapping are invaluable tools for the understanding of behavior and brain activity. Processing techniques for brain tissues are well-characterized and tested for model organisms; often with uniform and predictable morphology, documented developmental stages, and well-annotated references. However, non-model systems lack this depth of resource.

Darters (Etheostoma spp.) are a diverse clade of freshwater fishes. Closely related species in this clade have independently lost or gained traits, making these fishes a powerful system for studying speciation and the mechanisms of behavior in evolution. In the process of more comprehensively understanding the mechanisms behind this differentiation in behavior and neural activity, the novel application of more precise tissue processing tools and techniques enables us to map regions of interest in the brain, including areas of activation and their receptor makeup.

One of the most well-characterized three-dimensional tissue imaging pipelines is iDISCO. The iDISCO process involves the permeabilization and clearing of large tissue, which enables the tagging of signal molecules in three-dimensional space. In this work, we optimized tagging in situ using fluorescent probes (HCR-FISH via Molecular Instruments).

In order to effectively analyze signal molecules spatially in the darter brain, it was necessary to map the boundaries of each anatomical brain region. Using the ANTsX pipeline, we constructed a template darter brain by averaging together individuals, employing both probabilistic tissue segmentation and machine learning. This template brain was then mapped to a preexisting atlas to be further refined.

This darter brain atlas can then be used to process three-dimensional images of brains that have undergone the iDISCO pipeline to quantify HCR-FISH signal in a given region of interest. This allows for efficient and automated comparative analysis of the location and quantity of signal molecules between closely related darter species.

2:45 PM - 3:00 PM

- *Brain transcriptional patterns following behavioral cross-sexual transfer in a biparental cichlid*

Andrew Anderson, University of Minnesota
Suzy Renn, Reed College

Abstract:

Julidochromis transcriptus, a biparental cichlid, forms pairs where the male is typically larger than the female and there are distinct roles for each partner. In situations where the female is larger than the male, she plastically takes on the behaviors of male. Using the Ancestral Modulation Hypothesis framework, we predicted this cross-sexual transfer would recruit male-biased signaling pathways. We previously showed females increase circulating androgens and now we are investigating transcriptomic patterns in the brain. Overall transcriptomic patterns are matched by size of the individual and large females are recruiting regulatory genes suggesting females are using the male-biased expression patterns to generate these behaviors and are doing so by altering their own regulatory patterns. Further, we find large females alter gene expression associated with the gonadal hormone signaling pathway, with androgen receptors correlating with the observed behaviors. Interestingly, androgen receptors alpha and beta show different patterns based on the observed behavior indicating unique regulatory roles within the androgen signaling pathway.

3:00 PM - 3:15 PM

AI in Wildlife Monitoring: Climate-Driven Behavior in Boars, Lizards, and Ants

Ofir Levy, Tel Aviv University

Abstract:

Understanding how organisms respond to environmental variation is central to evolutionary biology, particularly in the context of behavioral adaptation and climate-driven selection. Artificial Intelligence (AI) is transforming ecological research by addressing one of the field's greatest challenges: extracting meaningful insights from massive datasets. Camera traps, for example, provide long-term, noninvasive wildlife monitoring but generate millions of images, most of them empty or irrelevant. AI enables efficient processing of these data, opening new opportunities to discover how animals respond to environmental conditions across broad spatial and temporal scales.

I will highlight three strategies we have developed and applied. First, we use general-purpose models for broad tasks such as animal detection and classification. By combining MegaDetector with species-specific classifiers, we analyzed wild boar activity and uncovered distinct schedules for adults versus mothers with offspring. Second, we build custom models for targeted questions. Our study on lizard thermoregulation trained a sun-versus-shade classifier that not only achieved high performance but also revealed that the AI relied on environmental cues (e.g., ground

brightness) rather than the animal itself—providing novel insight into model learning. Third, we tackle complex data such as time-lapse footage of desert ants. Here, we applied extensive pre-processing (stabilization, background subtraction, manual annotation) to enable successful training of object detection models.

Together, these approaches illustrate how we can leverage AI as a flexible toolkit to transform raw ecological data into targeted scientific knowledge, enabling new insights into the evolution of behavior and organismal responses to changing environments.

3:15 PM - 3:30 PM
Guppy cooperative anti-predator behavior is associated with gut microbiome diversity

Bronwyn Heather Bleakley, Stonehill College
Rachel Hirst, Stonehill College
Jessica Finn, Stonehill College
Matthew King, Stonehill College
Savannah Jeffrey, Stonehill College

3:30 PM - 3:45 PM
The genomics of cooperation and conflict in social amoebae

Elizabeth Ostrowski, University of Washington Bothell
Jennie Kuzdzal-Fick,
Cathleen Broersma, Massey University Auckland
Sean McFadyen,
Rafael Polo Prieto,
Fabiola Medina,
Murray Cox,

Abstract:

The complexity and sophistication of microbial behaviours has long been underappreciated, at least relative to those of large, charismatic macrofauna. However, it is increasingly recognized that microbes exist within societies, communicate and compete with their own and different species, and can have complex life cycles involving differentiation and division of labour.

In this talk, I will describe our large-scale genome sequencing project of Dictyostelium discoideum, a soilborne amoebae known for its rapid and dramatic transition to a multicellular state when starved. These organisms aggregate, communicate, and differentiate to form a multicellular fruiting body. Some cells die altruistically, forming a stalk that benefits the rest. Although Dictyostelium has long been an important model organism for cell and developmental biology, remarkably little is known about its basic ecology and evolution in nature.

We recently completed whole genome resequencing of a collection of more than 700 natural isolates, isolated from a variety of sites over space and time. Analyses of this dataset are being used to determine dispersal patterns, demography, the organism's microbiome, and the likelihood and frequency of a little understood sexual stage involving a dramatic act of cannibalism. Molecular evolution analyses allow us to identify which genes have experienced the strongest selection, and therefore what traits of the organism have been most essential to its survival. This work demonstrates how population genomics, combined with molecular evolution, is offering new insights into the secret lives of microbial eukaryotes.

Biogeography II

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Evolutionary Divergence of Octocorals in Oman and the Red Sea

Josie Nelson, Department of Evolution
Laura Macrina, Marine Science Program
Francesca Benzoni, Marine Science Program
Tullia Terraneo, Biological and Environmental Science and Engineering Division
Nicolas Oury, Biological and Environmental Science and Engineering Division
Giovanni Chimienti, Department of Biosciences
Fabio Marchese, Biological and Environmental Science and Engineering Division
James Reimer, Molecular Invertebrate Systematics and Ecology Laboratory
Federica Barreca, Biological and Environmental Science and Engineering Division
Silvia Vicario, Marine Science Program
Silvia Vimercati, SHAMS
Kaveh Samimi-Namin, Marine Evolution and Ecology Group
Catherine McFadden, Department of Biology

Abstract:

Octocorals, ecologically important marine invertebrates, are understudied in the Red Sea and the waters off the coast of Oman. These regions share some extreme environmental conditions, including high temperatures, high salinity, and vulnerability to low-oxygen stress. To establish a foundation for understanding octocoral diversity and biogeographic patterns in these regions, we conducted a molecular census of octocoral communities in Oman and the Saudi Arabian Red Sea. Octocorals were collected from shallow waters off the coast of Oman (n=540) and from shallow and deep waters along the entire length of the Saudi Arabian Red Sea (n=776). Octocoral diversity was assessed using a combination of DNA barcoding and ultraconserved elements to improve species delimitation and identify molecular operational taxonomic units (MOTUs). Our results show greater octocoral biodiversity in the Red Sea than in Oman, with 58 genera in 29 families recorded from the Red Sea versus 31 genera in 13 families from Oman. These communities were distinct,

with about two-thirds of the MOTUs in Oman absent in the Red Sea. These differences in species composition may reflect diverging evolutionary histories due to a combination of environmental and geographical factors, although they may also be related to unbalanced sampling efforts. Additionally, we found evidence for at least two genera and twelve species that are undescribed. Preliminary results of phylogenetic analyses revealed that within the same MOTU, octocorals from off the coast of Oman tended to have greater genetic diversity than those from the Red Sea, potentially reflecting the relative ages and histories of the respective bodies of water. These results highlight strong biogeographic structure and substantial undescribed diversity in octocoral communities of the Red Sea and Oman and provide an important baseline for future evolutionary and ecological comparisons.

2:45 PM - 3:00 PM
Drivers of species richness, occurrence, and speciation in island-endemic adaptive radiations

Kristen Martinet, University of Arizona
Cristian Roman Palacios, University of Arizona

3:00 PM - 3:15 PM
Bridging paradises: Squamate dispersal patterns support a complex emergence of the Isthmus of Panama

Matheus Pontes-Nogueira, Universidade Federal do ABC (UFABC)

Abstract:

The formation of the Isthmus of Panama represents one of the most consequential geological events in the history of Western Hemisphere biogeography, yet the precise timing of its emergence remains debated. The traditional “young Isthmus” hypothesis places final closure at approximately 2.8–3.5 million years ago (mya), while a growing body of geological and biological evidence suggests partial land connectivity as early as 13–15 mya. Here, we integrate molecular datasets, time-calibrated phylogenies, biogeographic model selection, and Biogeographical Stochastic Mapping to estimate the timing and directionality of intercontinental dispersal events across the Isthmus for eight American squamate genera. Our analyses estimated 41,663 dispersal events across 1000 stochastic maps, with the vast majority occurring within the last five million years, broadly consistent with a Pliocene land bridge closure. Contrary to classical expectations of asymmetric north-to-south exchange, we recovered more than twice as many south-to-north dispersals, likely reflecting the high squamate diversity accumulated during South America’s prolonged isolation and ecological opportunities generated by Miocene habitat restructuring in North America. Two genera (Micrurus and Marisora) exhibited dispersal events exclusively predating the 5 mya threshold, suggesting pre-Pliocene connectivity via proto-isthmian archipelagos or ephemeral land passages. Our results support a gradual, ecologically contingent

emergence of the Isthmus rather than a single discrete closure event, shaped by the interplay of intermittent physical connectivity, climatic filtering, and taxon-specific ecological tolerances.

3:15 PM - 3:30 PM
Diversification dynamics of chachalacas, guans and curassows (galliformes: cracidae)

Anupama Chandrasekhar, The University of Texas at Arlington

Abstract:

The Neotropics are one of the most biodiverse regions on Earth and provide a powerful setting for understanding how mountain building, drainage reorganization, and climate-driven habitat dynamics generate and maintain biological diversity. Birds have been a major model for studying diversification in this region, yet many avian groups still lack the dense phylogenetic and geographic sampling needed to evaluate diversification across an entire lineage. Sparse sampling can obscure dispersal events and bias ancestral-range reconstructions, limiting our ability to link diversification patterns to landscape history.

Cracidae (chachalacas, guans, and curassows) is an ideal system for testing hypotheses about Neotropical diversification. The family includes 57 species distributed from Mexico to South America across Central American forests, the Andes, Amazonia, the Atlantic Forest, and seasonally dry regions. Many cracids are large-bodied birds with potentially limited dispersal ability, making them likely sensitive to changes in landscape connectivity. Despite their ecological importance and conservation status, including one species (Mitu mitu) extinct in the wild, there have been few comprehensive studies of their molecular systematics and macroevolution.

This study aims to examine how major Neotropical landscape changes have influenced dispersal and diversification across Cracidae. Using a densely sampled phylogenomic dataset of ultraconserved elements (UCEs), this study evaluates species and subspecies limits, reconstructs a species-level time-calibrated phylogeny, and tests alternative historical biogeographic hypotheses using Bayesian models. Together, these analyses will clarify the evolutionary history of Cracidae and improve understanding of how landscape change has shaped diversification across the Neotropics through time.

3:30 PM - 3:45 PM
Niche conservatism and evolution explain variation within the global organization of biogeographic regions

Maria Alejandra Hurtado Materon, Texas A&M University
Baltazar Gonzalez, Life and Environmental Sciences
Gabriel M. Martin, Centro de Investigación Esquel de Montaña y Estepa Patagónica (CIEMEP)
A. Lawing, Texas A&M

Abstract:

Global biogeographic regionalization provides a framework for understanding how evolutionary processes structure biodiversity across space. The number and placement of proposed biogeographic regions can vary depending on taxa and methods, yet a consistent core-to-transition gradient emerges. In this gradient, core areas share biodiversity attributes (e.g., species richness, range size, and endemism), and transition zones act as permeable boundaries with greater dissimilarity. However, we lack a general understanding of the evolutionary processes that generate this structure. Species' ecological niches influence where lineages persist and how they diversify. Under niche conservatism, lineages retain ancestral environmental tolerances, whereas niche evolution allows shifts to novel environments. Although younger lineages tend to show faster ecological differentiation than older ones, it remains unclear whether variation in lineage age and niche overlap contributes to the emergence of core-to-transition biogeographic organization. Here, we test whether niche conservatism and evolution explain this pattern using 188 terrestrial carnivoran species across their global distribution. We quantified pairwise niche overlap from ecological niche models and identified evolutionary regions (evoregions) and their transition zones based on phylogenetic turnover. We found that biogeographic cores are composed of older lineages with greater niche overlap, whereas transition zones contain younger assemblages with more divergent niches. The relationship between niche overlap, lineage age, and position along the core-to-transition gradient varies across evoregions, as allowing group-specific intercepts and slopes improved model fit. A high proportion of variance ($R^2 = 0.94$) reflects differences among evoregions, while predictors captured a smaller but consistent proportion of within-region structure ($R^2 = 0.22$). These results suggest that niche conservatism in older lineages contributes to the persistence of regional cores, whereas niche evolution in younger lineages facilitates dispersal and establishment across environmental and biogeographic boundaries. Our study integrates niche and evolutionary theory to provide a mechanistic explanation for the spatial organization of biodiversity.

Conservation Biology II

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Comparative mutation load in the California Conservation Genomics Project

Anne Nakamoto, University of California
Erik Enbody, Department of Computational Biology
Russell Corbett-Detig, UC Santa Cruz

Abstract:

Earth's biodiversity has been generated through the evolution of genomic sequences. An understanding of the evolutionary history of these sequences can be used in the field of

conservation biology to identify threats to biodiversity, and respond with informed management decisions. While traditional conservation efforts have focused on the protection and recovery of individual species, a more holistic and forward-looking approach is to assess the population health of many species across the landscape, and identify regions in need of management attention. As part of the California Conservation Genomics Project (CCGP), we have built an extensive dataset containing species of conservation interest sampled across California, allowing a landscape genomics approach to conservation. Population health can be assessed using many metrics, such as genetic diversity, effective population size, homozygosity, inbreeding depression, and deleterious mutation load. Much attention and regulations have focused on genetic diversity, especially in efforts to rescue species of conservation concern. However, recent work suggests that the genetic burden imposed by deleterious mutations, along with the demographic history of a population, might be more relevant metrics to assess extinction risk. In this study, we identify deleterious genomic variants in CCGP species based on evolutionary constraint. We use this metric of deleterious variation, and thus genetic load, to investigate differences in load between species populations. By taking geographic location and phylogenetic relatedness into account, we also make broad comparisons of load across different species and the landscape. The understanding of population health we gain here can be used to inform management decisions for the conservation of California's biodiversity, and our workflow can be applied broadly to regions beyond California.

2:45 PM - 3:00 PM

Leveraging genomic data to inform genetic rescue and management of a critically endangered butterfly

Cinnamon Mittan-Moreau, North Carolina Zoo
David Pavlik, Kell
Tyler Linderoth, W.K. Kellogg Biological Station
Nicholas Haddad, Kellogg Biological Station - Michigan State University
Sarah Fitzpatrick, Kellogg Biological Station
Michigan State University,

Abstract:

The Mitchell's Satyr Butterfly (MSB) is a critically endangered butterfly with a disjunct range found in Michigan, Mississippi, Alabama, and Viriginia with an additional endangered subspecies, St. Francis Satyr (SFS), in North Carolina. Mitchell's Satyr faces extinction as small, fragmented populations struggle to adapt to increased climate variability and other threats. Genetic rescue, the increase in fitness caused by the introduction of new, genetic variation, could increase population health and resilience to these changes. Conservation stakeholders have considered translocating individuals from larger populations to smaller populations; however, management decisions have been stalled by the unresolved taxonomy of disjunct MSB populations and SFS. To address this, we collected non-lethal tissue samples from extant populations in every region of MSB and SFS to conduct whole-genome sequencing. In contrast with previous studies, we find that Mississippi and Alabama populations are more closely related to SFS than to MSB. Further, we find evidence of

inbreeding in Northern populations, despite large census sizes in some populations. We integrate these genomic findings with our previous work demonstrating successful breeding between Michigan and Mississippi populations to provide a framework for future augmentation and translocation strategies to promote genetic rescue. This is one of the first genomically informed interventions for an endangered insect, creating a road map for recovery plans for the many endangered species facing similar challenges.

3:00 PM - 3:15 PM

Linguistic ties between Caribbean islands predict introductions of Anolis

Paul Fenton, University of Texas at Arlington
Luke Frishkoff, University of Texas at Arlington

Abstract:

Why some species successfully invade some locations, but not others, is an ongoing biological question with consequences for conservation. Many studies have documented the role of species traits in biological invasions, yet species invasions are human-mediated, and far less scrutiny has been focused on the political and economic foundations influencing the patterns of invasion. The Caribbean is a highly biodiverse region where the sociocultural and economic landscape has been heavily impacted by the ramifications of colonialism. The languages of Caribbean nations are reflective of this history and act as a modern demarcation of former imperial influence. This investigation aimed to determine whether shared language between islands indicates economic ties influential to alien species introductions and promotes invasion success along former imperial boundaries.

Caribbean nations were assembled into 27 island regions, each of which use either Spanish, French, Dutch or English as an official language. Island regions were grouped into linguistic blocs where official languages served as proxies for sociocultural connections. Invasion success rates were measured by analysing pairwise combinations between the native ranges of 187 Anolis species and the 27 island regions. The effect of shared language and successful alien population establishment within these combinations was assessed via binomial GLMM, with spatial autocorrelation and species-level variation controlled via random effects.

Shared language between source and destination islands significantly increased the likelihood of invasion success. This effect was principally driven by English-speaking islands, which, when analysed individually, was the only language bloc with a significantly elevated rate of invasion. This indicates Caribbean economic ties linked with species introductions, while complex, are correlated with shared linguistic history. As globalisation and commerce increasingly links distant regions, these findings suggest investigating socio-historic bonds between nations may aid in deciphering the patterns of alien species introductions.

3:15 PM - 3:30 PM

Resolving the evolutionary history of bighorn sheep to inform future management: an answer to the California bighorn lineage question

Josh Jahner, New Mexico Tech
Thomas Parchman, University of Nevada - Reno
Marjorie Matocq, University of Nevada
Clinton Epps, Oregon State University

Abstract:

Although translocations can be effective for augmenting and restoring wild populations, they can disrupt native patterns of genetic structure, diversity, and local adaptation, thereby hampering conservation efforts. Managers must weigh potential costs and benefits of choosing well-differentiated donor individuals that could confer a boost to genetic diversity while avoiding outbreeding depression or ecological mismatch. This decision is more daunting when taxonomy is unclear or debated. For example, bighorn sheep (Ovis canadensis) populations in the United States that have been managed as the California lineage (part of the formerly recognized subspecies O. c. californiana) originate from serial translocations sourced from populations in British Columbia, resulting in reduced genetic diversity and elevated risk of inbreeding. After research on skull shape and RFLP analysis of mtDNA failed to find support for that subspecies, some jurisdictions treated the California lineage as part of the Rocky Mountain subspecies (O. c. canadensis) and mixed individuals in subsequent translocations, in part to increase genetic diversity of bottlenecked populations. Yet detailed genetic data addressing validity of those putative lineages were lacking. We reconstructed the genetic history of bighorn sheep by sampling the major putative subspecies or lineages, focusing on native (remnant) genetic variation, and generating high-throughput DNA sequencing data (~15,000-25,000 SNPs). Complementary phylogenetic and population genetic analyses supported the distinctiveness of four bighorn lineages at levels corresponding to subspecies. Our results confirm the genetic identity of the no longer putative California bighorn lineage, answering a question that puzzled geneticists and managers for decades. Moving forward, we recommend that managers 1) maintain the natural variation held in native populations by protecting them from intentional translocations or unintentional mixing with nearby populations; 2) prioritize within-lineage translocations for population augmentation or repatriation to previously occupied regions; and 3) cautiously consider any translocations that would lead to mixing of distinct evolutionary lineages.

3:30 PM - 3:45 PM

Evaluating potential targets of conservation: a case study of the Allen's (Selasphorus sasin) and rufous (S. rufus) hummingbird

Brian Myers, Eastern Oregon University
Payton Talbot, Eastern Oregon University
Dylan Parker, Eastern Oregon University
Andrew Baltensperger, Eastern Oregon University

Abstract:

Conservation efforts are needed now more than ever. Anthropogenic disturbance and habitat modification are reshaping species distributions, and in many cases, driving widespread declines in effective population size. However, conservation dollars are severely limited, prompting the need for prioritization of focal taxa for conservation efforts. Allen's (Selasphorus sasin) and rufous (S. rufus) hummingbird are thought to be experiencing widespread decline. Allen's hummingbird is currently listed as a "Red-Alert Tipping Point Species" by the "State of the Birds 2025" report, is currently listed by United States Fish and Wildlife Service (USFWS) as a Bird of Conservation Concern, and is estimated by Partners in Flight (PIF) to have experienced an 83% decline over the last 50 years. Rufous hummingbird is described on the same lists: rufous is an "Orange-Alert Tipping Point Species", is listed as a Bird of Conservation Concern (USFWS), and is estimated by PIF to have experienced a 60% decline over the last 50 years. Rufous hummingbird is also listed as "Near Threatened" by the International Union for Conservation of Nature. Much of the data underlying these designations comes from the annual North American Breeding Bird Survey, which has been criticized for its evaluation of hummingbird population trends (see Clark et al. 2017). Thus, a deeper evaluation of the conservation status of Allen's and rufous hummingbird is warranted. Here, we leveraged ecological niche modeling and demographic inference using whole-genome data to evaluate the hypothesis that Allen's and rufous hummingbird are in decline.

Molecular Ecology III

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Mitochondrial evolution fuels rapid environmental adaptation in house mice

Mal Ballinger, Cornell University

Abstract:

Mitochondria play a central role in linking cellular metabolism to environmental conditions, yet their contribution to rapid environmental adaptation remains poorly understood. House mice provide a powerful system to address this question because they have recently colonized and adapted to a wide range of climatic environments. Here, we use an integrative approach combining mitochondrial bioenergetic assays, liver RNA-seq, and mitochondrial DNA (mtDNA) analyses to investigate how mitochondrial function varies across climatic populations. We show that house mice from tropical environments exhibit greater mitochondrial respiratory capacity and ATP synthesis than mice from temperate environments. We further integrate mitochondrial physiology with gene expression and mtDNA copy number to link evolved differences in mitochondrial performance with genomic and regulatory variation. Together, these results suggest that

evolutionary changes in mitochondrial function may represent an important mechanism enabling rapid adaptation to novel environments.

2:45 PM - 3:00 PM

The population genomics of invasion: Founder effects, chromosomal inversions, and selective sweeps shape the rapid evolution of an invasive fish

Azwad Iqbal, Cornell University
Nina Therkildsen, Cornell University
Jennifer Grenier, Cornell University
Pavel Dimens, Cornell University
Paul Munn, Cornell University
Jacob Landis, Cornell University
Daniel Hasselman, AquaVeritas Research

Abstract:

Understanding the genetic dynamics of biological invasions can address key evolutionary questions and inform efforts to conserve native species. Invasions also serve as 'natural' experiments in rapid evolution, exposing species to novel environments and selective pressures. Here, we use whole-genome sequencing to study the rapid evolution of invasive American shad (Alosa sapidissima), a migratory fish native to the Atlantic coast of North America that was transplanted to the Pacific in the late 19th century. In the 150 years since, shad have spread across multiple Pacific rivers and now outnumber native salmon during annual migrations.

To identify genetic divergence and local adaptation, we sampled 395 individuals spanning the native and invasive ranges and generated phased whole-genome data using Haplotagging, a linked-read technology. Unlike standard short-read sequencing, Haplotagging preserves long-range haplotype information, enabling enhanced structural variant detection and robust phasing.

Combining summary statistics and demographic inference, we found that Pacific populations underwent a sharp reduction in effective population size immediately after introduction—a founder effect evident across genome-wide metrics and indicative of rapid diversity loss. Admixture and principal component analyses showed all Pacific populations to be significantly diverged from their Atlantic counterparts, forming distinct northern and southern clusters.

Using traditional summary statistics, haplotype-based selection scans, and the Ancestral Recombination Graph (ARG), we found strong evidence of local adaptation, including selective sweeps in genes contributing to life-history evolution, vision, olfaction, osmoregulation, and neural development in fishes. These candidates align with known life-history differences in invasive populations, including reproductive timing, maturation age, and growth curves. We also identified a large chromosomal inversion that segregates between rivers and by inland migration distance, suggesting an association with migratory capacity or willingness. Overall, despite strong founder effects, invasive American shad show clear signatures of rapid adaptation to novel environments.

3:00 PM - 3:15 PM

*Interpreting patterns of X chromosomal diversity in the coppery titi monkey (*Plecturocebus cupreus*)*

(John) Terbot, Arizona State University
Devangana Shah, Arizona State University
Vivak Soni, Arizona State University
Cyril Versoza, Arizona State University
Karen Bales, University of California
Susanne Pfeifer, Arizona State University
Jeffrey Jensen, Arizona State University

Abstract:

The unique properties of sex chromosomes in primates, such as the hemizygous status of the X chromosome in males, lead to the possibility of divergent evolutionary histories relative to autosomes. For example, the reduced recombination and increased germline cell divisions (and thereby mutation rates) in males — as well as the reduced effective population size relative to the autosomes — are all expected to have pronounced impacts on the population genetics of the X chromosome. In this study, we analyzed newly-generated polymorphism and divergence data from the X chromosome of the coppery titi monkey (Plecturocebus cupreus), a platyrrhine native to Brazil, in order to quantify differing population histories characterizing the X compared to the autosomes, infer male:female ratios, and identify sex-linked loci targeted by recent positive selection as well as long-term balancing selection.

3:15 PM - 3:30 PM

Population genomic perspectives on behavioral interference and divergence in rubyspot damselflies

Jonathan Drury, Durham University

3:30 PM - 3:45 PM

Population genomics of rock outcrop islands: early edaphic and late climatic drivers of phylogeographic breaks

Dexcem Pantinople, Mississippi State University
Nicholas Engle-Wrye, Mississippi State University
Carolina Siniscalchi, Mississippi State University
Ryan Folk, Mississippi State University

Abstract:

Despite their prevalence and importance in hosting rare and endemic species, there has been little focus on investigating and quantifying the forces that shape genetic diversity patterns in rock outcrop island systems. Specifically, population genomic analyses of rock outcrop flora in diverse

geoedaphic conditions and strong climatic gradients have largely been unimplemented. To explore the relative roles of soil and climate in driving population genetic structure in these systems, we investigated the genomic architecture in the Heuchera parviflora species complex, a group of wide-ranging perennial herbs endemic to the rocky outcrops of the eastern U.S. with diverse edaphic specialization and a highly disjunct distribution. Applying a population genomic approach using hundreds of low-copy nuclear loci coupled with model-based phylogeographic tools and edaphoclimatic datasets, we found deep genetic divergence that correlates with distinct edaphic conditions across the group and revealed a more recent genetic subclustering primarily associated with climate. Within taxa, results of our demographic history reconstruction further supported a subclustering origin consistent with major shifts in global temperature and precipitation during the Last Glacial Maximum and Mid-Holocene. Our work overall presents insights into the eco-evolutionary drivers of complex biogeographic patterns and highlights the relative importance of soil heterogeneity and climatic conditions in driving population genetic variation within naturally fragmented rock outcrop systems.

Paleobiology and Macroevolution

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Timing of two types of evolutionary novelty in a major animal radiation

Stewart Edie, National Museum of Natural History
David Jablonski, The University of Chicago

Abstract:

The early history of clades and their rebounds from mass extinctions are often viewed as times of opportunity. Whether through entry into novel habitats or regions, or through severe depletion of taxa at extinction events, these intervals are thought to promote the capture of anatomical novelties in both newly originating clades and surviving lineages. To test these dynamics, we evaluated the evolutionary timing of Type 1 novelties, involving novel character identities, and Type 2 novelties, involving extreme modifications of existing characters (both sensu G. Wagner 2014), among the ~3500 bivalve genera the Class has produced across its 520 million-year history. Contrary to expectations that novelties should cluster either early in the history of the clade (as part of the Cambrian Explosion and the subsequent Ordovician Biodiversification Event) or in rebounds following mass extinction, both types arose throughout bivalve evolution, although per-taxon rates decline through time. These results suggest that the origin of evolutionary novelty is neither simply an early-burst phenomenon nor a predictable consequence of ecological opportunity after global crises, but an ongoing feature of clade evolution.

2:45 PM - 3:00 PM

Morphological bottlenecks and phylogenetic restructuring following the end-Cretaceous mass extinction

James Mulqueeney, National Museum of Natural History
David Jablonski, The University of Chicago
Stewart Edie, National Museum of Natural History

Abstract:

The Cretaceous-Paleogene (K-Pg) mass extinction profoundly reorganized marine biodiversity, yet the extent to which extinction bottlenecks structure long-term diversification remains unresolved. Priority effects predict that clades with greater survivorship or earlier ecological occupation should dominate post-extinction radiation, whereas alternative frameworks emphasize retained morphological disparity as the primary enabler of diversification. We test these alternatives using marine bivalves, analyzing 1,213 genera across 85 families within an interval of the Late Cretaceous (Maastrichtian Stage), survivor assemblages, and the Recent. Shell morphology is quantified using geometric morphometrics to characterize both the magnitude and geometry of morphological bottlenecks, as well as the trajectories of post-extinction recovery. Neither the number nor the proportion of surviving genera within a family reliably predicts extant genus richness; families experiencing severe losses frequently attain present-day diversity comparable to those with high survivorship. Likewise, many of the most diverse extant families passed through pronounced contractions in morphospace, whereas some “dead-clade-walking” families retain broad morphospace occupation yet fail to diversify. At the class level, extinction appears approximately random with respect to morphospace, but family-level responses are highly heterogenous in both direction and magnitude. Notably, displacement within morphospace, rather than the severity of the contraction, emerges as a key predictor of taxonomic recovery, clades that lose taxa near the center of their pre-extinction morphospace and exhibit limited recovery of those morphologies tend to have lower present-day diversity. Comparisons with stochastic rebound simulations indicate that post-extinction expansions of morphospace are often more constrained than expected by chance, and phylogenetic analyses suggest that morphological replacement during the rebound is non-randomly distributed across the bivalve tree. Together, these results indicate that long-term diversification reflects interactions among the geometry of morphospace loss, its subsequent restructuring, and phylogenetic contingency, revealing a fundamental decoupling of morphological and taxonomic success following mass extinction.

3:00 PM - 3:15 PM

Differential filling of body-size-space through the Cambrian and Ordovician radiations

Mark Nikolic, Stanford University
Noel Heim, Tufts University
Pedro Monarrez, Virginia Tech
Jonathan Payne, Stanford University

Abstract:

Body size often gets overlooked in metazoan disparity studies in favour of more complex multidimensional trait spaces. This gap represents a missed opportunity as an animal's body size is one of its most fundamental and least abstract traits. It is also perhaps the most studied morphological trait, yet it has never been subject to broad-scale analysis of disparity through time. Here, we assessed the evolution of body-size through time in nine classes of marine invertebrates from their first appearances in the Cambrian and Ordovician radiations until the end of the Permian. We analysed the rate of expansion of the body-size-space and characterised its differential filling through time in each group, including across two mass extinction events. To do this, we utilised a dataset of biovolume and stratigraphic age information for >10,000 metazoan genera across the Paleozoic. Moreover, we jointly simulated body-size evolution on trees using parameters extracted from the diversification history for each class under several evolutionary scenarios to allow multiple-hypothesis testing. We find that for most - but not every - class, the rate of body-size-space expansion is highest, and the maximal range occurs, very early in the lineage's evolutionary history: indicative of an 'early burst'. However, the filling of the space generally lags behind, and the generating processes differ among clades. In general, mass extinctions tend to have little effect on total body-size disparity within a class, but they differ in the dynamics of replacement and successive diversification of subclades. We provide the first attempt to define, quantify and characterise the body-size-space in one of the most important intervals of time in the history of life. Early bursts of evolution in body-size appear to be common, but their dynamics differ in complex and nuanced ways among higher clades.

3:15 PM - 3:30 PM

Skyline intervals impact diversification rate estimates under the stratigraphic ranges fossilized birth-death model

Kate Truman, University of Canterbury
Bethany Allen, GFZ Helmholtz Centre for Geosciences
Ugnė Stolz, ETH Zurich
Alex Gavryushkin, University of Canterbury
Sasha Gavryushkina, Adelaide University

Abstract:

The fossilized birth-death process is a popular model for inferring phylogenies and diversification rates by utilizing both molecular and morphological data, as it can incorporate fossil samples which have descendants, known as sampled ancestors. By also including stratigraphic ranges in the model, we are able to explicitly specify when samples represent the same species which has continued through time. We consider the skyline variant of this model, under which diversification rates have piecewise-constant forms.

We implement and validate the skyline stratigraphic range fossilized birth-death model in the ssRanges package for the BEAST2 software. Under this model, we analyze a case study of crocodilians and eusuchians, for which the phylogenetic placement of the Thoracosaurus genus and Gavialidae family is disputed. We compare estimated diversification rates and inferred phylogenies produced under three contrasting sets of skyline intervals.

To compare phylogenies we consider clade supports and implement maximum clade credibility trees suitable for encapsulating stratigraphic ranges. Our results show that skyline analyzes can exhibit significant variation in estimated diversification rates which is not captured by constant diversification rates, such as high rates of fossil sampling near the present. The choice of interval boundaries is highly influential on diversification estimates for the same time period, with greater uncertainty when using shorter equal length intervals compared to the longer intervals chosen using chronostratigraphy. We find that while results agree that similarities between Thoracosaurus and Gavialidae are due to homoplasy, the classification of Eogavialis africanus as a eusuchian is disputed by two of our three analyzes, which place this species within Gavialidae.

3:30 PM - 3:45 PM
Exceptional disparity in brain shapes and ecological diversity in early snake evolution

Tiago Simões, Princeton University

Abstract:

Snakes are among the most diverse groups of vertebrates on Earth today, with over 4,200 extant species representing a third of squamate diversity. Their long evolutionary history (at least 160 million years) together with their highly modified body plan, have long sparked debate over their phylogenetic and ecological origins. Despite recent advances in phylogenetic methods and macroevolutionary tools, uncovering the origin of snakes remains challenging due to their poor fossil record and the profound anatomical transformations that accompanied their extant diversification. In this study, we address this long-standing problem in early snake evolution by combining two new major lines of evidence to understand the ecological drivers of specific phenotypes: bone microstructure and brain shape evolution using 3D geometric morphometrics. Both are highly accurate in predicting habitat preference in modern squamates, which here were used to predict the lifestyle of stem snakes. We applied these techniques to high-resolution micro-CT scans of extant and fossil snakes, including a new exceptionally preserved Cretaceous stem snake. The latter provided unprecedented details of cranial nerves, inner ear, and brain anatomy, enabling the most integrated reconstruction of stem snake neuroanatomy to date. Our results indicate that stem snakes had occupied a unique region of brain shape morphospace, distinct from each other and to all other squamates. This suggests substantial neuroanatomical disparity—and likely sensory functions—early on in snake evolution. Furthermore, both brain shape and bone microstructure converge on their predictions for habitat preference in stem snakes, including both fossorial and ground-dwelling lifestyles, indicating that key ecological transitions already occurred

by the Late Cretaceous in early snake evolution. Finally, stem snakes do not cluster close to the most recent common ancestor of crown snakes in shape and bone microanatomy morphospace, indicating these are not ideal proxies for understanding ancestral condition of modern snake radiations. Altogether, our findings indicate early snake evolution involved greater ecological and neuroanatomical diversity than previously thought.

Phylogenomics II

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Phylogenetic relationships among unionid mussels (Unionidae), and exploration of signal vs. noise from Anchored Hybrid Enrichment flanking regions

Ryan Garrick, U. Mississippi
Jamie Bucholz, Department of Natural Resources Science
Marlène Chiarello, Department of Biology
Garrett Hopper, School of Renewable Natural Resources
Colin Jackson, Department of Biology
Jeffrey Lozier, University of Alabama
Mark McCauley, U.S. Geological Survey
Irene Sánchez González, Odum School of Ecology
Stephanie Vaughn, University of Pittsburgh
Carla Atkinson, Department of Biological Sciences

Abstract:

Resolving phylogenetic relationships in freshwater mussels (Unionidae)—one of the most imperiled animal groups globally—is essential for informing taxonomy, conservation prioritization, and studies of diversification. Anchored Hybrid Enrichment (AHE) generates large multilocus datasets, yet the potential value of flanking regions (i.e., those adjacent to conserved probe targets) remains poorly understood. While these regions may provide additional phylogenetic signal due to higher variability, they may also introduce noise from alignment ambiguity and mutation saturation, particularly across deep divergences. Here, we aimed to (1) improve resolution of phylogenetic relationships within Unionidae through expanded taxon sampling, and (2) systematically evaluate trade-offs between phylogenetic signal and noise associated with inclusion of AHE flanking regions. We generated new AHE data for 100 specimens and combined these with published data to increase representation across this species-rich clade. Phylogenetic relationships were inferred using concatenation-based maximum likelihood and coalescent-based species tree methods. To assess flanking region effects, we constructed datasets with identical loci and taxa but varying proportions of flanking sequence relative to core regions. By progressively increasing the proportion of flanking sequence and quantitatively comparing resulting phylogenies, we evaluated how

dataset composition influences node support and inferred relationships. This work advances our understanding of relationships among members of Unionidae and provides a framework for evaluating best practices in AHE-based phylogenomics.

2:45 PM - 3:00 PM

Phylogenomics of the aquatic beetle genus Liocanthyrus Guignot (Coleoptera: Noteridae), a South American lotic specialist

Adry Gage, Louisiana State University
Jeremy Brown, Louisiana State University
Stephen Baca, Louisiana State University

Abstract:

Inland freshwater environments account for less than 1% of the Earth's total surface, yet little is known about insect biodiversity and evolution in these habitats. Liocanthydrus, a genus of aquatic beetles endemic to South America, is notable for being found exclusively in lotic (running freshwater) environments. Currently, 11 species of Liocanthydrus have been described based on morphology. However, the absence of a phylogenetic study of this genus raises concerns regarding the accuracy of morphological species delimitation in the group. Here, we take a phylogenomic approach to construct the first phylogenetic estimate of Liocanthydrus. We harvest approximately 3,100 ultraconserved elements (UCEs) via genome skimming from 30+ Liocanthydrus specimens collected across South America with a sampling emphasis on L. bicolor and L. clayae to examine species relatedness and geographic structure among populations. We recover a well-resolved phylogenetic estimate and discuss current species hypotheses, phylogeographic patterns, and implications for future research directions in light of these results.

3:00 PM - 3:15 PM

Phylogeography and population genomics of Amazonian bare-eyes (Aves: Thamnophilidae: Phlegopsis)

Luca Micheli, Louisiana State University

Abstract:

Recent phylogeographic research has challenged traditional views of Amazonian diversification by highlighting the pervasive role of gene flow, introgression, and reticulate evolution across riverine barriers. Rather than acting solely as static vicariant agents, Amazonian rivers are dynamic features that can both isolate and reconnect populations through processes such as headwater dispersal and river movements. Concurrently, genomic studies have demonstrated that differentiation is highly heterogeneous across the genome, shaped not only by demographic history but also intrinsic factors such as recombination rate and linked selection.

The ant-following genus Phlegopsis can be used as a model system to investigate the drivers of genomic differentiation across the Amazon basin. With a broad distribution across major

interfluves and well-documented population structure associated with major rivers, Phlegopsis also exhibits evidence of gene flow and mitonuclear discordance, making it ideal for addressing how the interplay of many genomic factors shapes diversification. We are addressing three key questions: 1) What processes are generating genomic differentiation across interfluves; 2) How genome architecture modulates signals of gene flow and selection; 3) How river dynamics contribute to phylogenetic discordance and mitochondrial capture events. To do so, we have integrated genome-wide summary statistics, phylogenetic reconstructions, and topology weighting across the genome.

Our results revealed strong population structure alongside localized admixture near river headwaters, as well as heterogeneous genomic landscapes where peaks in FST, dips in DXY, and π coincide with putative centromeric regions, suggesting an important role of genomic architecture in driving differentiation across interfluves. Moreover, topology weighting analysis has revealed that near these centromeric regions, the topology recovered by a separate mitogenome phylogenetic reconstruction was the most supported.

3:15 PM - 3:30 PM
Range-restricted relicts or ring species? The taxonomic riddle of Uroctonus (Scorpiones)

Jacob Gorneau, UC Berkeley
Damian Elias, University of California Berkeley
Rosemary Gillespie, University of California Berkeley
Lauren Esposito, Islands & Seas

Abstract:

Distinguishing the stepwise process of ring speciation from more relict processes is complex, as the patterns and distributions we observe today may be highly convergent, with differing underlying mechanisms. A common system for studying ring species dynamics is California, where Ensatina salamanders and other ring species in western North America have been extensively studied. The genus Uroctonus (Western forest scorpions), is found along the Cascade, Coast, and Sierra Nevada Ranges, in a distribution that quite closely mimics known ring species. Additionally, the group is a taxonomic enigma—Uroctonus as a genus has evaded conclusive family-level placement for over two decades despite repeated molecular and morphological analysis. Furthermore, the widely-distributed type species is rendered paraphyletic by its two congeners. With the goal of resolving species-level paraphyly, and identifying whether the group supports a ring species hypothesis, or relicts that have produced a ring species-like distribution, we examined the phylogeography of the group with low-coverage resequencing data. We collected from over 100 localities distributed across the range of this genus and supplemented these collections with museum specimens. For the type species, we assemble a high-coverage reference genome from PacBio HiFi and Omni-C reads. Consistent with recent work suggesting the genome diversity of scorpions is greater than previously known, our current estimate for this genome size is about 3.4 Gb. While the reference genome is still in progress, we examine the phylogeography of this species with both

ultraconserved elements (UCE) and mitochondrial genome data. Our results provide a rationale for a morphological revision of the genus, and provide insight suggesting this taxonomically complex genus is a case of nested relictualism, with the genus itself and the constituent species representing relicts. This work provides additional insight into disentangling convergent patterns from divergent processes.

3:30 PM - 3:45 PM
Patterns of speciation and lineage diversification in butterflyfishes

Konstantinos Andriotis, Yale University
Thomas Near, Yale University

Speciation I

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM
Major features of adaptive radiation in Yucatán pupfishes

Matthew Kustra, University of California

Abstract:

Understanding the sources of genetic variation and the stages of adaptive divergence of speciation remains a central problem in evolutionary biology. We used whole-genome resequencing of 123 individuals to compare the adaptive radiation of Cyprinodon pupfishes in Lake Chichancanab, Mexico, to an independent radiation of San Salvador Island (SSI) pupfishes in the Bahamas, and assess the repeatability of adaptive genetic architecture, sources of adaptive variation, and stages of selection. Despite rapid craniofacial divergence in both radiations, only two candidate genes (0.5%) were shared between Caribbean radiations. Although adaptive introgression played a major role in SSI, we found minimal evidence of adaptive introgression in Chichancanab, likely due to the geographic isolation of this inland lake. Instead, de novo mutations provided a substantial source of adaptive variation (30.6%) for the endemic zooplanktivore, 15 times higher than the endemic scale-eater on SSI. However, in parallel with SSI, we found strong evidence that adaptive divergence occurred in stages, first on regulatory and standing genetic variation, then on de novo and nonsynonymous mutations. Consistent with adaptive variants near opsin and spermatogenesis genes, functional categories unique to Chichancanab, we found greater visual acuity and divergent sperm morphology in lab-reared zooplanktivores relative to generalists using laboratory assays. Consistent with extensive adaptive de novo mutations in WNT10A and rapid diversification of tooth size in the zooplanktivore, we found that experimental inhibition of the Wnt pathway in generalists resulted in narrower oral teeth. We conclude that de novo mutations, not introgression, can drive rapid adaptive radiations in isolated environments.

2:45 PM - 3:00 PM
Comparative analysis of genomic attributes of speciation continuum in drosophilids

Mukta Joshi, Georgia Institute of Technology
Sean Anderson, Georgia Tech

Abstract:

Speciation frequently involves the accumulation of genetic incompatibilities that generate reproductive isolation. Both genic components (e.g., protein-coding genes, gene duplications, and mitonuclear interactions) and non-genic components (e.g., structural variation, transposable elements, and satellite DNA) are hypothesized to contribute to hybrid incompatibilities. But while the concept of a speciation continuum has become increasingly well defined, we still lack a clear understanding of the relative pace at which these components tend to accumulate. Such knowledge requires genomic sequencing and annotation across large numbers of related species – data that until recently did not exist.

In this study, we leverage genomic consortium data in drosophilids to investigate how divergence in genic and non-genic genomic features vary with the age of sister species pairs. We identify drosophilid sister species and rank them by relative divergence time. Using this ranking as a proxy for their position along the speciation continuum, we then quantified multiple genomic features, including coding sequence divergence, GC content, number of inversions, and transposable element accumulation, to assess support for their hypothesized roles in the speciation process.

Preliminary results show that while total coding density and overall genome-wide GC content show no clear correlation with relative age, features such as orthologous coding divergence and number and extent of inversions scale linearly with node depth. These findings provide insight into how different genomic features evolve across the speciation continuum and will help generate predictions about the relationship between these genomic features and reproductive isolation in other empirical systems.

3:00 PM - 3:15 PM
Functional tests of phenotype-genotype association in an Amazonian hybrid zone

Glaucia Del-Rio, University of Florida

Abstract:

When previously isolated species hybridize, their distinct evolutionary histories are put to the test. The fate of their defining traits hinges on the power of individual genes to cross species boundaries. Here, we document a case where the genetic innovation for a species-defining trait—the white throat of the antbird Rhegmatorhina hoffmannsi—is now sweeping through its sister species, R. berlepschi. We show this adaptive introgression is driven by a small but consequential change in

the cis-regulatory code of a single locus. Using whole-genome analysis, we pinpoint the innovation to a small number of nucleotide changes in a melanocyte-specific enhancer upstream of the melanin biosynthesis gene TYR. Enhancer reporter assays show that these substitutions disrupt TCF/LEF binding motifs, weaken LEF1 interaction, and reduce responsiveness to canonical Wnt signaling. This decrease in enhancer activity is consistent with the loss of pigmentation in the white throat phenotype. Strikingly, population genomics reveal this derived allele is now rapidly spreading through R. berlepschi populations via hybridization, its movement completely decoupled from the rest of the genomic landscape. Our findings show how a few regulatory mutations can gain their own evolutionary trajectory, charting a path of adaptation that redraws phenotypic boundaries and challenges the notion of species as impermeable genetic units.

3:15 PM - 3:30 PM

Depth-driven ecological speciation in the ciscoes of Lake Superior

Kristen Behrens, University of Michigan
Sarah Chang, University at Buffalo
Ann Ropp, USGS Great Lakes Science Center
Katie Anweiler, U.S. Geological Survey
J. Vinnie Siegel, USGS Great Lakes Science Center
Trevor Krabbenhoft, University at Buffalo
Amanda Ackiss, US Geological Survey

Abstract:

Diversification of species complexes is often driven by ecological factors and results in specialized niche adaptations. In fishes, one predominant and well-studied niche is depth which co-associates with both physiological and feeding niches. Lake Superior, the largest of the Laurentian Great Lakes, hosts a radiation of salmonid fishes known as ciscoes whose diversification is proposed to have been driven by adaptation to depth. In this study we utilize low coverage whole genome sequencing to characterize genomic differentiation between four confirmed extant Lake Superior ciscoes (Coregonus artedi; cisco, C. hoyi; bloater, C. kiyi; kiyi, and C. reighardi; shortnose), and two morphologically identified but taxonomically uncertain ciscoes (C. nigripinnis; blackfin, C. zenithicus; shortjaw). We find no evidence for either C. nigripinnis or C. zenithicus as genetically differentiated species, however we confirm the presence of a second population of C. artedi and clear support for recently rediscovered C. reighardi as a distinct species. Finally, we present several candidate genes likely involved in species-specific adaptation, predominantly in C. kiyi and C. reighardi, that support what is known about their respective niches. In particular, changes in C. kiyi to the ETS1-related gene may support this species' characteristic diel vertical migration. These results not only provide a snapshot of the current status of ciscoes in Lake Superior but also provide opportunities for further research to morphologically characterize species-specific adaptations.

3:30 PM - 3:45 PM

When Islands Collide: Divergence Predicts Outcomes of Secondary Contact During the Fusion of Sulawesi's Paleo-Archipelago

Ben Karin, UC Berkeley

Abstract:

Speciation often results from the accumulation of reproductive isolation associated with lineage divergence, but secondary contact between diverged lineages can reshape the trajectory of speciation and reveal its underlying processes. The Indonesian island of Sulawesi is a tectonically complex island formed by the fusion of many paleo-islands, resulting in replicated cases of secondary contact among once-isolated lineages. Unlike secondary contact on continents where hybridization often results from unpredictable range shifts, Sulawesi's fauna presents a replicated set of geologically constrained natural experiments to test how the magnitude of evolutionary divergence predicts outcomes of secondary contact and hybridization. Using thousands of genome-wide loci from Eutropis sun skinks spanning Wallace's Line on Sulawesi and Borneo, we reconstructed a reticulate evolutionary history shaped by overwater dispersal, isolation, island fusion, hybridization, and character displacement. We delimited five distinct species (three undescribed) and uncovered multiple ancient hybridization events following island fusion leading to distinct outcomes. These outcomes — speciation reversal, parapatry, and sympatry putatively through reproductive character displacement — were associated with increasing levels of prior divergence consistent with evolutionary theory. Sympatry, specifically, was preceded by substantial introgressive hybridization and body size divergence that likely confers reproductive incompatibility. Together, these results provide empirical support for divergence-dependent tipping points along the speciation continuum. The sun skink radiation also includes a rare instance of reverse colonization of Borneo across Wallace's Line that established a narrowly divergent species with a uniquely intermediate body size absent from Sulawesi.

SSE Symposium: Impacts of Genome Architecture on Polygenic Adaptation during Rapid Environmental Change - Large-Scale Comparative Genomics

06/22/26: 2:30 PM - 3:45 PM

2:30 PM - 3:00 PM

Population genomics and adaptive significance of structural variation across the songbird Tree of Life

Scott Edwards, Harvard University

3:00 PM - 3:30 PM

Why larger genomes aren't always AT-rich: The compensating role of chromosome number

Sean Chen, Taipei Medical University
Carol Lee, University of Wisconsin

Abstract:

Genome composition—the balance between GC and AT content—is a fundamental signature of molecular evolution. Across arthropods, a vast group including insects, spiders, and crustaceans, genomes are typically AT-rich, with notable exceptions such as ticks and barnacles. A longstanding expectation is that larger genomes, which accumulate AT-rich non-coding DNA, should show lower GC content. Surprisingly, we find no such relationship in arthropods. We resolve this paradox by identifying the compensatory role of GC-biased gene conversion (gBGC), a recombination-associated process that favors GC over AT. Specifically, we observe that species with more numerous, shorter chromosomes exhibit higher genome-wide GC content, consistent with elevated recombination rates and stronger gBGC. When chromosome number is accounted for as a proxy for gBGC intensity, the expected pattern re-emerges: larger genomes are indeed more AT-rich. Our results show that arthropod genome composition is shaped by a dynamic balance between mutation bias toward AT and recombination-driven forces that continually push genomes back toward GC.

Behavior: Sexual Selection

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Consequences of female bias for fitness-related traits in a mixed sexual/asexual species

Clare Mulcahy, University of Iowa
Aman Jajodia, Washington University in St. Louis
Morgan Anderson, University of Maine
Gwendolyn Gavin, University of Iowa
Seren Castellano, University of Iowa
Maurine Neiman, University of Iowa

Abstract:

Despite the many advantages of asexual reproduction, obligately sexual and asexual populations of the same species can and do coexist in nature. In these populations, female-biased conditions could increase the challenges faced by sexuals by increasing costs of sexual reproduction through

potential mate limitation among sexual females and increased variance in male reproductive success. While we know sex-ratio variation can be an important driver of behavior and reproductive outcomes, whether and how this variation affects the maintenance of sexual reproduction in these obligate sexual/asexual systems has yet to be characterized. The gonochoric New Zealand freshwater snail Potamopyrgus antipodarum is such a system, with wide across-population variation in the relative frequency of sex, and, thus, sex ratio. P. antipodarum males have been observed mating with sexual and asexual females at similar rates, raising questions about how female bias might affect mating behavior and fitness in this species. Here, we tested how sex ratio affects mating frequency and embryo production among sexual P. antipodarum. We kept snails in two experimental conditions, a female-biased condition (2 males, 8 females) and male-biased condition (6 males, 4 females), and recorded mating frequency. At the end of the experiment, we dissected females to count embryos. Male and female P. antipodarum both mated more frequently under male-biased conditions, suggesting plasticity in mating behavior based on sex ratio. Despite differences in mating frequency, embryo number was similar between groups, suggesting that sex ratio does not directly affect offspring number. These results raise the potential that female bias could lead to reduced mating frequency in P. antipodarum, with possible consequences for variance in male reproductive success or overall genetic diversity of offspring.

4:30 PM - 4:45 PM

Stable sexual selection and repeatable individual variation in song preference in the Pacific field cricket Teleogryllus oceanicus

Mingzi Xu, University of Minnesota

Abstract:

Choosiness, or how picky an individual is in mate choice, is key to both sexual selection and speciation. Yet how much variation there is in choosiness and how variation is partitioned among and within individuals remain largely unexplored. Using the Pacific field cricket Teleogryllus oceanicus, I quantify phenotypic variation in choosiness and investigate whether there is consistent individual variation in choosiness and whether choosiness for different song traits covary. Strikingly, I found that the overall shape and peak preference for one song trait remained similar to those reported in an earlier study from the same population more than a decade ago, providing evidence that directional sexual selection can be relatively stable over long time frames. Further, I found moderate levels of within-individual repeatability in choosiness for both song traits, suggesting a substantial level of individual variation in choosiness. Interestingly, choosiness for the two song traits positively covaries, indicating that there may exist overall choosier and more permissive females in song preference.

4:45 PM - 5:00 PM

Time to Shine: Two clocks drive courtship in bioluminescent ostracods to occur in darkness

Cheyenne McKinley, University of California

5:00 PM - 5:15 PM

Effect of Pesticides on Sexual Communication and Its Implications on Species Reproductive Barriers

Swastik Padhy, University of Minnesota
Mingzi Xu, University of Minnesota

Abstract:

Sexual communication involving male signals and female preferences, is crucial for maintaining the species reproductive barriers. However, these behaviors are highly labile to environmental perturbations like temperature, noise etc., which can disrupt the signal-preference coordination and potentially affect the species integrity. Anthropogenic activities, including the widespread usage of pesticides, may affect these behaviors even in non-target species. Many pesticides are neurotoxicants, so signals such as acoustic signals, which are under neuro-muscular control and coordination, could be affected by exposure. However, how these neurotoxicants affect sexual communication and the subsequent consequences on reproductive barriers remain poorly understood. Using field crickets, Gryllus rubens and its sister species, Gryllus texensis, which occur in sympatry and are pre-zygotically isolated from each other by their calling songs. I am measuring changes in male song traits and female preferences before and after pesticide exposure and evaluating the subsequent effects on the reproductive barrier. In this talk, I will primarily focus on how pesticide exposure affects male sexual signals in G. rubens and present preliminary data on changes in male calling song traits following pesticide exposure.

5:15 PM - 5:30 PM

Age-specific chemical cues and preference for them varies with age and sex in a mycophagous beetle

Clara O'Connor, University of Virginia
Lukas Westermann Salas, Biodiversity Institute
Vincent Formica, Swarthmore College
Chloe Lahondere, Virginia Tech
Edmund Brodie,

Abstract:

Partner choice forms the basis of all social behavior, as it determines what interactions are possible. Age is an important factor mediating social interaction, affecting a wide range of interactions from the outcome of within-sex competition and mate acquisition to the preference for social partners within a larger group, so nonrandom partner choice with respect to age may be expected. Mechanisms that allow discrimination of age are little known, though several taxa use chemical cues to communicate age. In this study, we asked whether male and female forked fungus beetles (Bolitotherus cornutus) of different ages show preference for different aged males based on chemical scent alone. We also sampled headspace volatiles of chemical cues from males of different ages to test for differences in chemical composition. Beetles were exposed to stimulus scents collected from older and younger males in 2-hour choice trials. Old females spent significantly more time with the scent of old males than the control, and they associated with the scent of young males significantly more than both the old males and the control. Young males showed a preference for the filter papers with any male scent. Chemically, cues from all ages are distinct. Our results indicate that some chemical cues vary with age, and such cues may be used to detect the age of conspecifics. This study also presents the novel finding that the differential preferences for chemical cues of individuals of different ages are themselves age dependent.

Coevolution and Mututalism

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Partner specificity in communities of legumes and their bacterial symbionts

Spencer Peterman, University of California
Lorena Torres-Martínez, St. Mary's College of Maryland
Alexandra Weisberg, Oregon State University
Jeff Chang, Oregon State University
Joel Sachs, University of California

4:30 PM - 4:45 PM
Comparative population genetic structure between Astragalus lentiginosus and its nitrogen-fixing rhizobia

Joshua Melnick, Loyola University Chicago
Mike Grillo, Loyola University Chicago

Abstract:

Coevolutionary interactions between hosts and symbionts are predicted to shape patterns of population genetic structure of each species and may ultimately contribute to diversification. While geographic distance is a well-established driver of population genetic differentiation, less is known on how host–symbiont interactions impact underlying genetic variation. In particular, for horizontally transmitted mutualisms, it is unclear whether host and symbiont population structures are aligned in ways that facilitate local adaptation or are decoupled potentially generating coevolutionary trait variation and phenotypic mismatch.

We examine this question in the legume Astragalus lentiginosus, the most taxonomically diverse species in the North American flora with over 40 taxonomic varieties, and nitrogen-fixing microbial symbionts termed rhizobia. Rhizobia can live in association with plants or be free living in the environment thus facing distinct selective pressures. We examined population genomic structure of 311 A. lentiginosus plants and 177 rhizobia.

We find that there are 11 distinct genetic clusters among host plants and 20 ANI groups of rhizobia from the genera Mesorhizobium and Allomesorhizobium, including several putatively novel lineages. Horizontal transfer of rhizobial symbiosis genes between distant clades appeared rare. Through RDA analysis we find that host genetic variation explains a greater amount of rhizobial genetic variation than geographic distance, indicating that host-associated differentiation is a primary driver of symbiont population structure. Comparative phylogenetic analysis revealed that host and symbionts had distinct evolutionary histories, however, several rare rhizobial lineages were restricted to specific host varieties and localized regions, suggesting fine-scale specialization. Together, these results reveal partial alignment between host and symbiont population structure which may promote local adaptation.

4:45 PM - 5:00 PM
Rapid shifts in microbial symbiosis of Hawaiian planthoppers

Christian Cabuslay, University of Hawai'i at Manoa
Rebecca Chong, University of Hawaii

Abstract:

Tightly integrated microbial partnerships are often cited as key factors in the evolution of animal hosts. While the effects of such relationships on host ecology are well-documented, the impact that host population dynamics can have on a symbiont community are poorly understood. Here, we

use a combination of 16S rRNA amplicon sequencing and metagenomics to examine shifts in symbioses among the highly fragmented populations of cave-adapted planthoppers from Hawai'i Island. Our results illustrate frequent taxonomic turnover in secondary symbionts between different populations, with a remarkable prevalence of taxa known to be reproductive manipulators. We conclude that host founder effects can rapidly reshape symbiont community structure, potentially reinforcing divergence between host populations. Future work will be aimed at understanding how different symbiotic relationships along the ancient-to-contemporary spectrum may contribute differentially to host diversification.

5:00 PM - 5:15 PM
One Symbiont, Two Symbiont: Red Symbiont, Green Symbiont: Searching for Shared Mechanisms of Symbiosis in Two Functionally Convergent Symbioses

Caleb Butler, Texas State University

5:15 PM - 5:30 PM
How Mutualism and Coevolution Affect Evolutionary Rescue

Christopher Carlson, University of Toronto
Megan Frederickson, University of Toronto
Matthew Osmond, University of Toronto

Abstract:

Mutualists are at risk of extinction from climate change and anthropogenic disturbance. Plants and pollinators face habitat destruction, corals and algae experience rising ocean temperatures, and over-hunting imperils seed dispersal mutualisms. Adaptive evolution is the ultimate mechanism that allows species to persist in a changing environment. However, it is unclear whether being mutualistic helps or hinders adaptive evolution in response to rapid environmental change.

We use a moving optimum quantitative-genetic modeling approach to investigate how being in a mutualism affects species' persistence in a changing environment. We consider a trait that is under selection from a changing environment that is genetically correlated with a trait that is under selection from a mutualistic partner. We examine the role of mutualism for adaptation and persistence and find that mutualisms can generate a selective push that increases abundance when the benefit from the push outweighs its demographic cost.

Next, we ask how mutualism affects the critical rate of environmental change, the minimum rate of environmental change necessary to drive a species extinct at equilibrium. We find that being in a mutualism provides a demographic benefit that allows mutualists to tolerate higher rates of environmental change than they would alone, especially when they have a partner that evolves rapidly or has a high intrinsic growth rate. When mutualists have perfectly correlated traits under biotic and abiotic selection and experience different rates of environmental change, the mutualism turns antagonistic and one species is driven to extinction at equilibrium. However, if the rate of

environmental change is the same for both species, or if mutualists' traits are imperfectly correlated, biotic selection can increase the critical rate of environmental change. Finally, we parameterize our model with data from a plant-pollinator mutualism and find that in this mutualism the demographic cost of biotic selection outweighs its benefit.

Conservation Biology III

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Genetic Diversity and Population Structure of the Black-Footed Cat: Insights into the Deadliest Predator

Victoria Grant, Stanford University

Abstract:

Black-footed cats (Felis nigripes) are one of Africa's least understood felines with the population dynamics and demographic history of this solitary species being not well-described. Reports of steady decline of present-day populations resulted in the IUCN Red List categorizing the species as vulnerable to extinction. However, the IUCN cited data deficiencies across the species range as a limitation in this categorization for black-footed cats. Here, we sequenced whole genomes of black-footed cats (N=44) from across their distribution in the first genomic study of free-roaming individuals. To do so, we incorporated whole genome sequences generated from modern biological samples and century-old museum specimens. We assembled a highly contiguous reference genome using a combination of PacBio HiFi reads and publicly available Hi-C data and investigated the demographic history, population structure, and genetic diversity of wild black-footed cats. We found evidence of historical effective population sizes estimated ~10,000, which is comparatively lower than other felid species. Consistent with historically moderate population sizes, we found that present-day genetic diversity genome-wide was low (&#8477? ≈ 0.0004). However, despite low genetic diversity, we find that black-footed cats do not appear to harbor long runs of homozygosity. Simulations suggest that the observed genetic diversity is consistent with their estimated historical population sizes. However, GONE results suggest recent population contraction, which could contribute to future genomic erosion. We also compared genomic data in individuals from across the range to evaluate patterns of population structure and found evidence of higher genetic similarity between individuals in closer geographic proximity. Together with analyses of population structure, we speculate that there may be greater connectivity between populations than previously assumed. Our study exemplifies the utility of genomics to provide insight into species population dynamics for better conservation management.

4:30 PM - 4:45 PM

Assessing the efficacy of translocations at purging deleterious variation in the imperiled Florida scrub jay

Andrew Mularo, Kellogg Biological Station

4:45 PM - 5:00 PM

Niche comparisons of closely related Texas crayfish lineages

Sarah Burgett, University of Texas at Tyler
Nathan Schubert, Sabine River Authority
Jared Dickson, Texas Parks and Wildlife
Jade McCarley, University of Texas at Tyler
Archis Grubh, Texas Parks and Wildlife Department
Lance Williams, UT Tyler
Marsha Williams, UT TYler
Joshua Banta, University of Texas at Tyler

Abstract:

Closely related organisms may retain similar ecological niches when geographically isolated in comparable environments or diverge when exposed to different environmental conditions. In sympatry, however, competition can reinforce divergence in resource use and environmental associations, driving niche differentiation. We examined these patterns in crayfish using ecological niche modeling. Our results indicate that niche relationships among closely related crayfish depend on geographic and ecological context. We found two lineages in geographic isolation that retain similar niches under comparable environmental conditions, and we found two others that exhibit divergence consistent with local environmental differences. And we found that two closely related species in sympatry show niche differentiation consistent with competition promoting ecological divergence. These findings suggest that both environmental variation and species interactions play important roles in shaping ecological niches and geographic distributions. More broadly, this work demonstrates that integrating biogeographic context with ecological niche modeling can improve our understanding of diversification and the processes that structure species distributions.

5:00 PM - 5:15 PM

Genomic insights into the divergence and conservation of Sotalia dolphins

Mariana Nery, University of Campinas

5:15 PM - 5:30 PM

Genomic Assessment of a Tusk Reintroduction Effort in Addo Elephant National Park, South Africa

Madison Lichak, Princeton University
Shane Campbell-Staton, Princeton University

Abstract:

Many African elephant (Loxodonta africana) populations have experienced a recent rise in the prevalence of "tusklessness," a congenital trait often associated with periods of intensive hunting or poaching. Because tusks are important for foraging, defense and other behaviors, increasing the number of tusked individuals in a population may become a management goal following population stabilization. Achieving this goal requires a population-specific understanding of the evolutionary genomics of tusklessness. To that end, we examined a case study in managed gene flow: the 2002 introduction of bull elephants from Kruger National Park, South Africa, into Addo Elephant National Park, in an attempt to reintroduce tusks in the Addo elephant population. Addo underwent a drastic hunting-related reduction in the early 20th century and, at the time of introduction, over 90% of female elephants in Addo were tuskless. Using a long-term observational dataset of births in Addo and whole-genome sequencing data of tissue samples collected from more than 75 Kruger and Addo elephants, we 1) quantified the impacts of the pre-introduction hunting-induced bottleneck on genetic diversity and heterozygosity, 2) determined inheritance patterns for tusk status in Addo, and 3) investigated the genetic underpinnings of tusklessness in Addo. Combined, this work helps assess the effectiveness of a past reintroduction effort and provides a framework to guide future management strategies.

Ecological Genetics II

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

"Sisters but not twins": Parallel local adaptation in generalist insect herbivore sister taxa

Billie Maguire, University of Massachusetts Boston
Mayra Vidal, University of Massachusetts Boston
Brook Moyers, University of Massachusetts Boston
Gina Wimp, Georgetown University
Shannon Murphy, University of Denver
Mattheau Comerford, UMass Boston
Mariana Abarca, Georgetown University

Abstract:

Insect herbivores are one of the most speciose groups of animals. The vast majority are specialized onto just one or a few host plant families, but a minority (~10%) are generalized and feed on more than three plant families. What is the genetic basis of host plant adaptation? For specialists, adaptation to the same host plant can occur at the same loci in parallel across species. For generalists the genetic basis of adaptation is likely more polygenic. Generalists occupy more places in the landscape than specialists and likely encounter diverse mosaics of selective pressures across their ranges. We do not know if generalists reuse genetic loci in parallel in the process of adaptation in the same way specialists can. Here we present results from a whole genome resequencing study of the highly generalized Hyphantria cunea (fall webworm, Lepridotera:Erebidae), a tractable study system of two morphologically and genetically distinct biotypes that are sympatric across eastern North America and do not interbreed in nature. We resequened 272 genomes of both biotypes at medium coverage from five sympatric sites from Florida to Maine to Missouri. Both biotypes do not show admixture in the wild, are differentiated across sites, and show signs of recent demographic expansion. On a local scale, loci under divergent selection between sites are shared between biotypes much more often than expected by chance. On a global scale, Tajima's D values are highly correlated between biotypes, especially at extreme values of the distribution. These patterns suggest that the two biotypes of H. cunea show parallel local adaptation to similar environments and that this adaptation involves the same loci among biotypes. Our findings highlight a common genetic basis of adaptation in independently evolving taxa, even in multidimensional environments with complex selective pressures. Our results are particularly interesting in the context of generalist insect herbivores, for which the genetic basis of adaptive traits is theoretically more complex and plastic.

4:30 PM - 4:45 PM

Newly arisen indel governs a leaf shape polymorphism in the Ivy Leaf Morning Glory (Ipomoea hederacea)

Amanda Peake, University of Toronto
Emily Glasgow, University of Toronto
Claire Abbasi, University of Toronto
Yunchen Gong, University of Toronto
Lauren Whitt, HudsonAlpha Institute for Biotechnology
Mellissa Williams, HudsonAlpha Institute for Biotechnology
Jane Grimwood, HudsonAlpha
Alex Harkess, HudsonAlpha Institute for Biotechnology
John Stinchcombe, University of Toronto

Abstract:

Leaf shape varies widely across plant taxa and has repeatedly been shown to affect ecophysiology, interspecific interactions, and fitness. We used population genomics, genome wide association studies (GWAS), and comparative genomics to determine the genetic basis and evolutionary history of an uncharacterized Mendelian leaf shape polymorphism in Ipomoea hederacea. To do so, we assembled a reference genome and generated whole genome sequencing for 123 individuals from

55 populations across the species North American range. There is a well-documented latitudinal leaf shape cline in I. hederacea where lobed genotypes are more common in the northern populations and entire-shaped genotypes in southern populations. Both ADMIXTURE and PCA results indicate an absence of neutral population structure, suggesting the leaf shape cline is due to selection. We conducted a GWAS and calculated coverage differences between leaf shapes to identify a 117 kb indel that perfectly co-segregates with leaf shape. Syntenic orthologs for genes on the indel were present in five other Ipomoea species with various leaf shapes, indicating the deletion is newly arisen in I. hederacea despite similar leaf shape phenotypes in the other species. Even though the indel perfectly co-segregates with the lobed phenotype, none of the genes on the indel are obvious leaf shape candidates. We posit that the 117 kb indel is affecting expression of genes involved in the auxin biosynthesis pathway found within the GWAS peak region. Additionally some genes on the indel may explain other phenotypic traits that are associated with leaf shape in I. hederacea such as herbivory preference, pathogen resistance, microbial community, and stomatal conductance in the field. More broadly, our results illustrate how a range of leaf shape phenotypes can be produced by distinct genetic mechanisms even in closely related species.

4:45 PM - 5:00 PM
Landscape genomics of a widespread Puerto Rican anole (Anolis cristatellus)

Pooneh Kalhori, UC Berkeley

5:00 PM - 5:15 PM
The desert thorn apple (Datura discolor) genome reveals the evolution of a lineage-specific immune-receptor network

Jay Goldberg, Arizona State University

Abstract:

The desert thorn apple (Solanales: Solanaceae: Datura discolor) is an herbabceous annual native to arid regions of North America. By generating a chromosome-scale genome assembly for this species and comparating it to those of other nightshades (family Solanaceae), we uncovered a remarkable contraction of of the Solanaceae-specific NRC immune receptor network. This finding sets the stage for research into the eco-evolutionary processes governing the immune systems of wild plants.

5:15 PM - 5:30 PM
Linking a genomic locus for leaf shape phenotypic plasticity to natural selection in the wild

Jill Love, Tulane University
Kathleen Ferris, Tulane University

Abstract:

Phenotypic plasticity is known as a mechanism that enables organisms to persist in heterogeneous environments, yet whether natural selection acts directly on the genetic basis of plastic responses remains poorly understood. While loci associated with plastic traits have been identified in a range of systems, empirical evidence linking these loci to selection in natural populations is rare, limiting our understanding of how plasticity evolves. Here, we integrate quantitative trait locus (QTL) mapping with field-based population genomics to test whether genomic regions underlying phenotypic plasticity also exhibit signatures of selection in nature. Using a recombinant inbred line population of Mimulus laciniatus, we identified a single moderate-effect locus associated with variation in leaf shape plasticity. We then leverage pooled whole-genome resequencing of pre- and post-selection populations from a reciprocal transplant experiment across an elevational gradient to quantify allele frequency shifts following one generation of field selection. The plasticity QTL overlaps a region of elevated genomic differentiation in a high-elevation site, and this overlap is significantly greater than expected under random genomic placement. Together with prior evidence that plasticity in this system influences fitness across environments, these results provide strong evidence that loci underlying plastic responses can experience allele frequency change under natural selection. More broadly, our findings demonstrate that the genetic basis of phenotypic plasticity can be directly linked to evolutionary dynamics in natural populations, offering empirical support for a central prediction of evolutionary theory regarding the evolution of phenotypic plasticity.

Macroevolution

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Are the phenotypic extremes ecological generalists? Testing Liem's paradox in a macroevolutionary framework

Samuel Borstein, Texas State University
Matthew McGee, Monash University

Abstract:

Morphological form is traditionally thought to be tightly linked to ecological form and function. However, species that exhibit specialized phenotypes do not always behave as ecological specialists, a phenomenon known as Liem’s paradox. While previous studies have explored this paradox through theoretical modeling or narrow taxonomic comparisons, few have explicitly tested it in a macroevolutionary framework. Here, we investigate Liem’s paradox in cichlid fishes, a model system for testing evolutionary and ecological hypotheses. Cichlids are a species-rich family of

freshwater fishes that exhibit high levels of both morphological disparity and trophic ecological diversity. Cichlids have undergone several independent adaptive radiations, in which adaptive diversification occurs along both morphological and trophic ecological axes. By combining a comprehensive trophic eco-morphological dataset with a large dietary dataset of cichlids, we explicitly test for mismatches between phenotypic specialization and trophic specialization in a phylogenetic comparative framework. Our results suggest that cichlids largely diversify along a body depth and elongation axis, as has been found in many other families of fishes. We find mixed signals when testing the relationship between phenotypic disparity and trophic ecological breadth in cichlids. We discuss potential drivers of discrepancies between perceived morphological specialization and trophic ecological specialization through the lens of preadaptation, structural versatility, resource abundance, and seasonal opportunism. Our results provide valuable insights into the evolution of morphology and ecology and the potential for mismatches between them, especially in rapidly diverging clades undergoing adaptive diversification.

4:30 PM - 4:45 PM
Hyoid Morphology and the Evolution of Vocal Learning in Birds

EJ Huang, Johns Hopkins Univesity
Amy Balanoff, Johns Hopkins University
Molly Ma, Johns Hopkins University

4:45 PM - 5:00 PM
Body size, functional ecology, and phylogeny: Analyses across Class Bivalvia

Amanda Doyle, University of Chicago

Abstract:

Though undoubtedly important in affecting an organism's relationship with its environment, the precise relationship between body size and the functional ecological categorizations used by paleontologists remains unclear. Is body size another functional axis upon which taxa might differentiate from otherwise functionally similar taxa, or does function determine size? Functionally diverse and spanning four orders of magnitude in size, the bivalves are an excellent clade with which to test this question. Using a family-level phylogeny for the entire Class Bivalvia, I analyzed the relationship between dissimilarity in functional ecology and dissimilarity in body size for all possible pairs of bivalve families, also accounting for their divergence times as a possible interaction. Although bivalve species show significant relationships between body size and each of their modes of fixation, attachment, and substrate, functionally similar families often showed significant contrasts in size distributions, indicating that function only partially determines size. Suspension feeding, exhibited by over two-thirds of all extant bivalves, covers nearly the entire spectrum of bivalve body sizes, indicating that it does not impose a limit on size at either end. Clearly, body size is partially determined but function, but it leaves room for functionally similar families — particularly the most closely related — to diverge from one another.

5:00 PM - 5:15 PM

Trait-dependent protracted speciation: from population divergence to species diversity

Guilherme Azevedo, Cornell University
Marshal Hedin, San Diego State University
Jenny Blair, Blair Wildlife Consulting

Abstract:

Understanding how traits and environments shape diversification is a central goal of evolutionary biology. Models linking trait evolution to speciation and extinction, such as State-Dependent Speciation and Extinction (SSE) frameworks, have advanced this field, but typically neglect microevolutionary processes underlying diversification. Protracted speciation birth-death models bridge micro- and macroevolution by treating speciation as an extended anagenetic process, yet trait-dependent extensions remain underdeveloped. Here, we present Traderpros (Trait-Dependent Rates Protracted Speciation model with hidden states), a novel Bayesian framework using data-augmented MCMC that integrates phenotypic and genetic information to model how organismal traits influence population formation, extinction, and speciation completion rates. We apply Traderpros to two spider genera with troglomorphic traits (Cicurina and Nesticus) using ultraconserved elements (UCEs) and COI data to estimate phylogenetic relationships and divergence times at the population level. We tested whether (1) troglomorphism is evolutionarily irreversible; (2) troglomorphic traits increase population fragmentation and extinction; (3) troglomorphism reduces speciation completion rates; and (4) troglomorphic populations exhibit lower evolvability. Using novel diversification descriptors derived from model parameters, we further evaluated population persistence in the context of the ephemeral speciation hypothesis. Simulation studies assessed model performance. Our results shed light on the role of cave-associated traits in driving diversification within karst ecosystems, biologically diverse yet threatened habitats of global conservation importance. By connecting trait-dependent diversification with the ephemeral speciation model, Traderpros enables robust tests of micro-macroevolutionary hypotheses such as evolutionary dead-ends, and ephemeral speciation, offering a powerful tool for studying diversification in highly fragmented systems under anthropogenic pressure.

5:15 PM - 5:30 PM

Mutualistic microbes drive niche expansion yet constrain diversification

Eleanor Hay, Univeristy of Miami
Rosana Zenil-Ferguson, University of Kentucky
Michelle Afkhami, University of Miami
Christopher Searcy, Univeristy of Miami

Abstract:

Mutualistic interactions are widely hypothesized to expand ecological niches and promote diversification, yet evidence for this relationship at macroevolutionary scales remains limited. Here, we investigate how fungal seed endophytes (Epichloë) influence niche breadth and diversification across over 100 species of the globally-distributed grass genus Poa. Combining global-scale climate, environmental, phylogenetic, and symbiosis data, we constructed species distribution models for suites of symbiotic and non-symbiotic plant species, then used a range of phylogenetic comparative methods to assess the influence of these symbionts on niche breadth, niche breadth evolution, and diversification. Endophyte-positive species had ~1.4 times broader primary niche axes (most often associated with temperature tolerances), ~2.5 times larger geographic ranges, and >30 times faster rates of niche breadth evolution than non-symbiotic species. Endophytic plants also had significantly drier climate centroids, consistent with endophyte-mediated drought tolerance, while simultaneously showing constraints along specific niche dimensions. Despite pronounced niche expansion, hidden state speciation and extinction models revealed two modes of diversification: endophytes decrease diversification rates in young lineages, and have a neutral effect in older lineages. Together, our results demonstrate that mutualists can enhance ecological flexibility while simultaneously constraining macroevolutionary outcomes, revealing a decoupling of niche expansion and diversification, and highlighting the complex role of symbiosis in shaping host evolutionary trajectories.

Parallelism and Convergence I

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Genetic basis of adaptation to nitrogen limitation differs between constant and fluctuating environments.

Genevieve O'Bryon, Loyola University Chicago

Abstract:

Fitness tradeoffs between environments are often predicted to occur during adaptation. However, many experimental tests have failed to find evidence of such tradeoffs. Elemental limitation, including nitrogen-limitation and carbon-limitation, is widely experienced by organisms in diverse environments, but tradeoffs to adaptation under limitation by different elements have not been well characterized. To test the prevalence of tradeoffs under elemental limitation, we evolved Escherichia coli under constant and fluctuating carbon and nitrogen limitation for 12 weeks. Our results showed that tradeoffs between carbon and nitrogen limitation were rare. In fact, all populations evolved under nitrogen limitation also had improved fitness in carbon limitation. All but one population evolved under carbon limitation showed neutral or improved fitness under nitrogen limitation, and all populations evolved under the fluctuation treatments improved in both environments. We found a high degree of parallel evolution under nitrogen limitation, especially in two genes in the ammonium

assimilation regulatory pathway, glnK and glnL, which were mutated in 22 of the 24 populations that experienced nitrogen limitation. Interestingly, glnL mutations were observed more often under constant nitrogen limitation, while glnK mutations were observed more often in populations that experienced fluctuations between carbon and nitrogen limitation,
suggesting that adaptation to nitrogen limitation proceeded differently in constant and fluctuating environments. Mutations in glnL conferred higher fitness in nitrogen limitation than glnK mutations, but fitness did not differ under carbon limitation. Despite having lower
fitness, glnK mutations occurred more often than glnL mutations in populations
evolved under a fluctuating environment, possibly due to epistatic interactions with other beneficial mutations.

4:30 PM - 4:45 PM

Two Serpentine Mimulus guttatus populations reveal parallel and non-parallel genomic evolution despite shared adaptive phenotypes

Whitney Murchison-Kastner, Tulane University
Kathleen Ferris, Tulane University

Abstract:

Leaf shape and flowering time differ significantly among serpentine-adapted populations of Mimulus guttatus, with some populations being polymorphic for highly lobed leaves and also displaying strikingly early flowering time. These shared traits are thought to be the result of adaptation to their rocky serpentine soils. Despite having similar phenotypes, analysis of pooled whole-genome sequencing of two populations of serpentine-adapted M. guttatus revealed moderate genome-wide differentiation, with some significant outlier peaks indicating strong genetic differentiation at some SNPs, providing evidence for local adaptation. G-statistic results comparing lobed and unlobed pools within each population revealed only three shared genes, with the majority of genes differing that are under selection for leaf lobing and flowering time, providing evidence for local adaptation and both parallel and non-parallel genomic evolution. We also found evidence for genome-wide skew toward negative Tajima's D in one serpentine population, which may suggest an excess of rare variants, perhaps due to stronger recent directional selection or demographic expansion.

4:45 PM - 5:00 PM

Determining genetic mechanisms behind the repeated evolution of cave traits in the Mexican tetra (Astyanax mexicanus)

Maya Enriquez, University of Minnesota Twin Cities
Stefan Choy, Lehigh University
Johanna Kowalko, Lehigh University
Suzanne McGaugh, University of Minnesota

Abstract:

The Mexican tetra fish, Astyanax mexicanus, is a unique model for evolution being that there exist two phenotypes: the surface phenotype which lives in surface rivers, and the cave phenotype which lives in completely dark underground freshwater caves. Cave fish exhibit troglomorphic traits such as eye loss, increased sensitivity in sensory modalities besides vision, and behaviors such as significantly reduced sleep compared to surface fish. Genetic reconstruction suggests cavefish developed from ancestral surface fish that colonized cave environments, but the genetic architecture underlying these drastic changes in phenotypes are unknown. Additionally, these reconstructions indicate that several independent colonizations of cave environments occurred. It is not known whether cave traits appeared through similar or divergent mechanisms across these cave populations.The purpose of this study is to characterize the parallel evolutionary trajectory of complex cave traits across three different cave populations. We are using quantitative trait locus (QTL) mapping to determine the genetic architecture of three complex traits in cave A.mexicanus: sleep reduction, increased neuromast density, and the interaction between starvation and sleep length. For one surface and three cave populations (Pachón, Molino and Tinaja) we used behavior tracking software to estimate sleep over 24 hours at two different time points and under different feeding regimes to examine the plasticity of sleep response in response to nutrient availability. After recording sleep, we additionally quantified the number of neuromasts within a facial anatomical region (suborbital 3) associated with increased sensitivity and response to vibration across all four fish. At the conclusion of the experiment, fin clips were taken from each fish that went through the pipeline and sequenced in order to conduct QTL analysis. Preliminary results suggest that neuromast quantity may be correlated with sleep in some populations and not others, suggesting a different genetic basis and evidence for parallel evolution.

5:00 PM - 5:15 PM
A new spin on old glands: evolution of diverse silk-spinning mechanisms in amphipods

Siena McKim, University of California

Abstract:

The ability to transform liquid silk into solid cylindrical threads is restricted to arthropods and has evolved convergently more than 30 times. Despite this repeated evolution, the origin of silk-spinning glands and the morphological mechanisms underlying silk transformation remain poorly understood outside of model systems. Two amphipod groups, Corophiida and Ampeliscidae, produce marine silk from their legs to construct feeding structures and protective domiciles. Although these groups are historically hypothesized to have evolved silk production convergently, this has not been tested with comparative glandular and phylogenetic data. Understanding whether silk production in amphipods is convergent or derived from shared ancestral glandular systems is critical for identifying how complex secretory structures evolve and are modified across animals. We investigated silk glands and extrusion morphology in both groups using light microscopy, confocal laser microscopy, scanning electron microscopy, and phylogenetic comparative analyses. Internal and external morphology of silk-spinning and non-silk-spinning legs were examined across

35 Corophiida species, 8 Ampeliscidae species, and 10 outgroup taxa. Both groups possess a two-gland system in silk-spinning legs, but differ in silk extrusion morphology, particularly in pore and duct structures at the distal leg tip. We found diverse extrusion morphologies in both lineages, with variation in duct architecture associated with differences in silk use and function. One gland type is also present in non-silk-spinning outgroups, suggesting an ancestral origin. Ancestral state reconstruction and correlated evolution analyses indicate that silk-specific glands in both lineages evolved from homologous ancestral gland types, followed by independent evolution of extrusion morphologies. We propose a revised evolutionary scenario in which silk production arises through co-option of ancestral glandular systems coupled with convergent innovations in silk extrusion morphology. This work highlights diverse evolutionary solutions for silk production and expands our understanding of how complex secretory systems repeatedly evolve and diversify in arthropods.

5:15 PM - 5:30 PM

Adaptive molecular convergence is pervasive across deep time and largely decoupled from phenotypic convergence

Cory Berger, University of California
Sam Abrams, University of California
Todd Oakley, University of California

Abstract:

Understanding the extent to which evolution is repeatable is a foundational goal of evolutionary biology, but the causes and frequency of molecular convergence across deep timescales are unclear. Often, biologists seek to infer the genetic basis of repeatedly-evolved traits using genome scans for signatures of selection. These approaches implicitly assume that molecular convergence between taxa is primarily driven by known phenotypic adaptations or ecological regimes, but genome-wide patterns of convergence may instead be influenced by diverse, unobserved ecological factors. Distinguishing between these possibilities requires understanding how frequently adaptive molecular convergence occurs across genomes and timescales, and whether it is systematically associated with particular phenotypic adaptations. Here, we analyze patterns of adaptive molecular convergence (AMC), defined as excess convergent nonsynonymous substitutions consistent with positive selection, over deep time in Medusozoa (jellyfish and hydroids). AMC was pervasive over more than 600 My of evolution, consistently exceeding mathematical null expectations based on random overlap even between distantly related species. Surprsingly, lineages sharing repeatedly evolved phenotypes (eyes, medusa loss, and upright colonies) did not exhibit elevated molecular convergence relative to other comparisons. Our results suggest that AMC is more common between distant lineages than generally appreciated, and is broadly shaped by diverse lineage-specific selection pressures rather than by phylogeny or a small number of obvious phentoypes.

Speciation II

06/22/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

The Freeway Hypothesis: Habitat Shifts, Range Expansions and the Origins of Species

Andrew Lupinski, University of Notre Dame
jeffrey feder, University of Notre Dame
Noah Barkoff, University of Notre Dame

Abstract:

Speciation is the fundamental process responsible for generating biodiversity. The buildup of reproductive isolation (RI) typically evolves via ecological speciation (adaptation to alternate habitats) or mutation-order (geographic) speciation. While traditional studies of speciation view these as strict alternatives, I hypothesize that the interaction between ecology and geography accentuates speciation. Using the Rhagoletis species complex of fruit flies, I test the “Freeway Hypothesis”, which proposes that shifts to geographically widespread host plants “freeway hosts” trigger range expansions, catalyzing subsequent bursts of both ecological and allopatric speciation. This study employed a Bayesian phylogenetic approach, overlaying host range data with phylogenetic reconstructions to determine if historical shifts to "freeway" hosts facilitated greater chances for subsequent radiation events of both modes of speciation. The results suggest that shifting to geographically expansive hosts allows phytophagous insects to escape evolutionary cul-de-sacs, enabling repeated, cyclic divergence. This research connects microevolutionary processes to macroevolutionary patterns, explaining why lineages capable of this interplay are significantly more speciose than those restricted by niche conservation. This study provides a novel opportunity to deepen our understanding of the processes responsible for the immense diversity of life.

4:30 PM - 4:45 PM

Desiccation Resistance and Ecological Speciation in Rhagoletis

Noah Barkoff, University of Notre Dame
jeffrey feder, University of Notre Dame
Andrew Lupinski, University of Notre Dame

4:45 PM - 5:00 PM

Speciation in parasites of oak gall wasps often correlates with shifts into new tree habitats, tree organs, or gall morphospace.

Guerin Brown, University of Iowa

Abstract:

Host shifts to new plants can drive speciation for plant-feeding insects, but how commonly do host shifts also drive diversification for the parasites of those same insects? Oak gall wasps induce galls on oak trees and shifts to novel tree hosts and new tree organs have been implicated as drivers of oak gall wasp speciation. Gall wasps are themselves attacked by many insect parasites, which must find their hosts on the correct tree species and organ, but which also must navigate the morphologically variable galls with which they interact. Thus, we ask whether host shifts to new trees, organs, or gall morphologies correlate with gall parasite diversification. We delimit species and infer phylogenies for two genera of gall parasites, Synergus and Ceroptres, reared from a variety of North American oak galls. We find that most species were reared from galls induced by just one gall wasp species, and no parasite species was reared from galls of more than four species. Most divergence events correlate with shifts to non-ancestral galls. These shifts often involved changes in tree habitat, gall location, and gall morphology. Host shifts are thus implicated in driving diversification for both oak gall wasps and their associates.

5:00 PM - 5:15 PM
Taxonomy and the broken bridge between micro- and macroevolution

Sean Anderson, Georgia Tech
Sonal Singhal, California State University

Abstract:

Speciation occupies the nexus between micro- and macroevolution. As a process of microevolutionary divergence among populations that ultimately yields new species (the units of interest in macroevolutionary research), speciation bridges the two scales of inquiry. It is thus all the more puzzling that in recent years, empirical tests for associations between population-level processes and macro-scale speciation rates have repeatedly yielded negative results. Most efforts to explain this broken bridge have focused on biological phenomena like the ephemerality of incipient species. Here I present and evaluate an alternative explanation, the ‘unit discordance hypothesis’, which holds that empirical tests have failed due to a technical problem that arises from the dependence of the macro-scale metrics on taxonomy. In most recent studies, speciation rates are estimated from phylogenies comprising taxonomic species. Two obstacles arise from this scenario, apart from issues like oversplitting and cryptic taxa: (1) most currently described species were delineated using metrics like diagnostic trait differences that the micro-scale variables are not designed to predict, and (2) more generally, a dependence on taxonomy lengthens the chain of causality between the variables we actually measure. I show quantitatively how and when existing relationships can be obscured by signal attenuation within the chain’s hidden links. I finally compare theoretical results to empirical relationships in global bird datasets to assess whether unit discordance is a plausible explanation for a recent spate of negative results. I stress that the unit discordance hypothesis is not a critique of any taxonomic practice, nor are the recent negative results a problem for taxonomists to solve; the onus is rather on researchers interested in micro-

macro connections to recognize the inherent dependence of their tests on taxonomic decisions and to adjust those tests accordingly.

SSB Presidential Plenary

06/23/26: 8:00 AM - 9:15 AM

-

Insect Evolution

Jessica Ware, Ware Lab

Abstract:

Winged insects evolved over 400 million years ago. Among the earliest flying insects were the Odonata, dragonflies and damselflies. Using various tools we have begun to understand the tree of life of odonates, and the evolution of their flight and reproductive strategies. This work was done through collaboration, and I will discuss this work while also discussing how collaboration is vital to the future of systematics.

Development

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Morphological marvels: Evolutionary origins and developmental repatterning of the treehopper helmet

Savanna Brown, University of Connecticut
Elizabeth Jockusch, University of Connecticut

Abstract:

Understanding the molecular mechanisms underlying the evolution of novel traits remains a central pursuit in evolutionary biology. As the most diverse animal phylum, arthropods provide an exceptional opportunity to examine the mechanisms underlying evolutionary innovation. Treehoppers (Hemiptera: Membracidae) exemplify this with their elaborate pronotal helmets, a morphological novelty unique to the lineage. Previous work showed that in the treehopper Entylia carinata, the developing helmet is transcriptionally more similar to the wings than to its serial homologue, the mesonotum, supporting the hypothesis that the helmet evolved through co-option

of the wing-patterning network (Fisher et al. 2020). This study builds on this finding by testing a central prediction of this hypothesis: that the helmet's wing-like transcriptional signature is evolutionarily concordant with the origin of the helmet itself. Additionally, it investigates when in development this wing-like signature emerges. To address these questions, we used RNA-sequencing data from serially homologous tissue sets across two developmental stages in three treehopper species and two hemipteran outgroups. Leveraging both species-specific and shared cross-species frameworks, we used hierarchical clustering and probabilistic classification methods to assess the transcriptional similarity of the helmet with other body regions. Together, these analyses showed that the helmet and wings share a conserved transcriptional signature restricted to the treehopper lineage, supporting the wing co-option hypothesis. They also revealed that the wing-like signature of the helmet emerges specifically during the final nymphal instar, coinciding with the developmental stage in which both the helmet and wings undergo epithelial bilayering. This finding aligns with the increasingly supported idea that the canonical wing-patterning network plays a more versatile role in development than its name suggests, functioning more broadly in patterning bilayered epithelial structures. This study illustrates the power of comparative, transcriptome-wide approaches for investigating the origins of evolutionary novelty in non-model organisms without requiring a priori candidate genes.

9:45 AM - 10:00 AM
Larval growth rate divergence distinguishes sympatric Danaus species with different migratory behaviors.

G Harrison, University of Michigan
EEB,
Delbert Green, University of Michigan

Abstract:

Monarch (Danaus plexippus) and Queen (Danaus gilippus) butterflies are sympatric across much of the southern United States but differ markedly in life history and related adult traits. We conducted a common-garden experiment to determine if Queens exhibit comparable plasticity to environmental cues experienced in higher latitudes (low photoperiod, reduced temperatures). We reared Monarchs and Queens under controlled summer-like and fall-like conditions and measured a battery of phenotypes, including larval growth rate, pupation and eclosion timing, adult morphology, and reproductive capacity. Both species showed strong environmental plasticity of pre-adult growth and development and less plasticity in adult phenotypes. Environmental modulation of timing and rate of developmental progression was species-specific. Monarchs grow larger (as measured by structural size) than queens in both environments through increased growth rate rather than differences in larval duration. Species differences in structural size emerge at different times depending on environment where fall-reared monarchs are larger than queens beginning in the fourth instar, but summer-reared monarchs are larger only in the final (fifth) instar. Consistent with larval growth differences, monarchs emerged as larger adults, with greater mass and longer forewings. Female monarchs show greatly increased reproductive capacity compared to

queens in both environments as well. Earlier onset of structural size divergence between species in fall, coupled with fall-specific divergences in pupation and eclosion timing, indicates that seasonal cues modulate specific metamorphic scheduling in monarchs, potentially reflecting adaptive shifts linked to migration. These results suggest that shifts in the environmental plasticity of larval developmental timing and scaling can be a target of evolutionary change to generate divergent morphologies and life histories of sympatric congeners.

10:00 AM - 10:15 AM

Genetic and developmental origins of extreme craniofacial evolution in pupfishes

M. Fernanda Palominos, University of California
Christopher Martin, University of California

Abstract:

How does evolution produce dramatic craniofacial innovation on ecological timescales? I address this question using an adaptive radiation of Cyprinodon pupfishes, a vertebrate system that exhibits one of the fastest known rates of craniofacial evolution. On San Salvador Island, Bahamas, pupfishes have evolved strikingly divergent jaw morphologies associated with specialized diets, including molluscivory and scale-eating, within the last 10,000 years. Thus, this radiation offers a unique opportunity to connect naturally evolved genomic variation with the developmental mechanisms that generate rapid morphological change.

I combine comparative genomics, tissue-specific transcriptomics, and high-resolution imaging across embryonic, larval, and post-larval development to identify how genomic variation reshapes craniofacial morphogenesis. Transcriptomic comparisons of craniofacial and caudal tissues across six species at hatching, the earliest stage of detectable morphological divergence, reveal large sets of genes differentially expressed specifically in the craniofacial region of trophic specialists. Intersecting these craniofacial-specific expression profiles with genomic regions under selection highlights candidate genes, including pycr3, atp8a1, and wdr31, that have not previously been implicated in craniofacial divergence and show both differential expression and regulatory-region variation.

Furthermore, I have identified craniofacial-specific alternative splicing events in the scale-eating pupfish that are present in jaw tissue but absent from tail tissue, revealing a previously unrecognized post-transcriptional layer of regulatory divergence shaping jaw morphology. I have also established CRISPR-based genome editing in this system, opening the door to direct functional tests of candidate variants in a naturally evolved vertebrate model.

Together, this work links genomic and regulatory variation to the developmental origins of extreme craniofacial diversity and provides a broader framework for understanding how evolution modifies developmental programs to produce morphological novelty.

10:15 AM - 10:30 AM

Redundant and Singular Regulatory Elements Underlie the Rapidly Evolving Drosophila Pigmentation Trait

Thomas Williams, University of Dayton

10:30 AM - 10:45 AM

Development's evolutionary hourglass and the architecture of complex biological systems

Steven Frank, University of California

Abstract:

Mid-stage embryos of different species look more alike than either early embryos or adults. The narrow middle waist often corresponds to setting the basic body plan. For example, most vertebrate species share neural tube, somites, and pharyngeal arches at this mid-embryonic stage.

Recent molecular data reinforce the hourglass pattern in animals. Among related species, gene expression converges in mid-development and diverges early and late.

Hourglass patterns in gene expression have also been observed in flowering plants. Such molecular convergence across kingdoms hints at deep organizational principles underlying complex multicellularity.

The puzzle is why a middle developmental stage should be so conserved, given the observed diversity of starting and ending forms. Classical explanations invoked modularity, canalization, or pleiotropy. But none provided a compelling explanation for why the middle should be special.

I propose that mid-embryogenesis is conserved because it is when embryos must translate between different types of biological information. Early development lays down raw materials and axes; late development executes fine-grained organogenesis. In between, embryos must bridge from physical dimensions of geometry, timing, and topology to genetic programs of fates and identities.

The bridging mechanisms are the protocol waists. They form standardized, narrow interfaces that convert one domain into another. Because protocol waists are single points of cross-domain communication, they are both deeply conserved and intrinsically fragile. Fragility concentrates at the waist because there is no alternate path around a broken translator.

The same logicdomain translation producing conserved interfacesmay underlie the hierarchical architecture of behavioral control systems and the layered organization of immune regulation, suggesting a general principle behind the structure of complex biological systems.

Ecological Genetics III

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

MHC II heterozygosity, marine heatwaves and mother's age drive offspring viability in wild dolphins

Oliver Manlik, United Arab Emirates University
Jannet Mann, Department of Biology and Department of Psychology
Michael Krützen, Department of Evolutionary Anthropology
Vivienne Foroughirad, Department of Marine Biology
Molly McEntee, Department of Biology and Department of Psychology
Georgeos Hardo, Biology Department
Kopps Anna, Independent Consultant
Simon Allen, School of Biological Sciences
Celine Frère, Faculty of Science
Richard Connor, Institute of Environment and Department of Biological Sciences
Lars Bejder, Marine Mammal Research Program
William (Bill) Sherwin, EERC

Abstract:

Natural selection drives evolution by favoring advantageous genetic variants, resulting in an accumulation of beneficial fitness traits in populations over generations. However, direct evidence linking parental genetic variation to offspring fitness in long-lived species is rare. In this study we investigated the potential effect of major histocompatibility complex class II (MHC-II DQB) variation on offspring viability (calf survival) of a natural population of bottlenose dolphins (Tursiops aduncus). Using a generalized linear mixed model (GLMM) we also explored other potential drivers or mediators of calf survival, including neutral genetic diversity, the age of the mothers and sociability, as well as marine heatwaves. Our multi-decadal study (1984-2022) revealed that MHC-heterozygosity for the peptide-binding region of MHC DQB—crucial for the adaptive immune response—was a strong predictor of offspring viability. MHC-heterozygous mothers did not produce more offspring, but their offspring were about twice as likely to survive. Also, the mother's age and a 2011 marine heatwave were associated with offspring viability. Calves born to females that remained reproductively active into old age were more likely to survive, while the heatwave contributed to reducing offspring viability. In contrast, neutral genetic diversity was unrelated to fitness. Interestingly, MHC-heterozygous females were more successful but less sociable mothers, possibly prioritizing investment in offspring over social bonds. This is in contrast to other social mammals that rely on sociability to mediate fitness. This study offers the first empirical evidence that MHC-diversity confers a fitness advantage across generations in long-lived mammals, a finding consistent with theorized but rarely tested expectations for MHC-dependent mate choice.

9:45 AM - 10:00 AM

Evolution after whole-genome duplication (WGD), more than WGD per se, drives phenotypic and transcriptomic divergence in the autopolyploid perennial herb Biscutella laevigata

Sandra Grünig, The University of British Columbia

Abstract:

Whole-genome duplication (WGD) is a major driver of plant speciation and often hypothesized to promote rapid adaptation to new or changing environmental conditions. However, the extent to which WGD per se fosters phenotypic and transcriptional novelties, and the relative contribution of WGD-induced changes vs post-WGD evolution to trait differentiation between cytotypes remains poorly understood as few studies replayed the tape of evolution using a full set of cytotypes. Here, we investigated the phenotypic and transcriptomic consequences of WGD and subsequent evolution in the Biscutella laevigata diploid–autotetraploid complex by comparing replicated diploid, synthetic autotetraploids, and natural autotetraploids (originated some 24 000 to 7,000 generations ago) under moderate daily temperature fluctuations (stable) vs. daily heat stress (changing) conditions. WGD led to reduced specific leaf area and slower rosette growth but had no significant effect on biomass. Post-WGD evolution acted in contrasting directions on WGD-induced changes, either reverting traits to diploid-like values or maintaining them in natural autotetraploids. Overall, WGD induced a decrease in fitness that was mitigated by post-WGD evolution, resulting in natural autotetraploids with similar or higher fitness under changing conditions than diploids. While the genetic background modulates the effects of WGD, cytotype-level transcriptomic analyses revealed no immediate effects of WGD under stable conditions, although heat stress induced different responses across cytotypes. Altogether, our results highlight a complex interplay between immediate WGD-induced and subsequent evolution at the phenotypic and transcriptomic levels, supporting a predominant role of post-WGD evolution in the differentiation of current cytotypes and the adaptive evolution of autotetraploids of B. laevigata.

10:00 AM - 10:15 AM

Detoxification genes may contribute to host shifts in pine sawflies

Alaine Hippee, University of Kentucky
Jakeb Watts, University of Kentucky
Ashleigh Glover, University of Kentucky
Kayleigh Dobson, University of Kentucky
Serena Limberg, University of Kentucky
Pruthviraj Mali, Max Planck Institute for Chemical Ecology
Axel Schmidt, Max Planck Institute for Chemical Ecology
Jonathan Gershenzon, Max Planck Institute for Chemical Ecology
Catherine Linnen, University of Kentucky

10:15 AM - 10:30 AM
Do species' responses to deep-time climate change predict their fate under anthropogenic warming?

Gbolahan Reis, Utah State University
Zachariah Gompert, Utah State University

Evolutionary Theory I

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM
The paradox of the organism

J. Arvid Ågren, Cleveland Clinic
Manus Patten, Georgetown University

9:45 AM - 10:00 AM
AI recapitulates evolution, and we can study it: Using mathematical parallels between quantitative genetics and AI model training to study high-dimensional evolution in silico

Russell Dinnage, University of Alberta

Abstract:

One of the most consequential results in modern AI – that models pretrained on broad data adapt to novel tasks far more efficiently than those trained from scratch – recapitulates a pattern evolutionary biologists have studied for decades under names like exaptation, ecological fitting, and evolvability. Yet these fields develop theory in near-complete isolation. I argue this neglect is costly in both directions, and demonstrate that the parallel between the fields is mathematically robust, not merely metaphorical. The multivariate breeder's equation with genetic drift is formally equivalent to the primary AI training method Stochastic Gradient Descent (SGD), mapping additive genetic variance to learning rate, effective population size to minibatch size, and fitness surface curvature to the training loss Hessian. Results from machine learning theory can then be imported directly: the Ornstein-Uhlenbeck models now ubiquitous in phylogenetic comparative methods are rigorously derivable as the continuous-time limit of the discrete stochastic breeder's equation (through its equivalence with SGD), providing a formal microevolutionary foundation that has been missing from comparative methods. I then demonstrate that this correspondence is experimentally productive. Using PhenoVision, a computer vision system for plant phenology, I vary the "evolutionary history" (pretraining regime) while holding the "selective environment" (downstream

task) constant – counterfactual experiments impossible in biological evolution but routine in AI. Models pretrained on a domain-relevant task outperform both generic pretrained models and models trained from scratch. Analysing the training dynamics, I decompose the contribution of evolutionary history into three components with direct biological analogues: ecological fitting (initial performance without any adaptation), short-term evolvability (rate of adaptive improvement), and long-term evolvability (quality of the best reachable outcome). I argue that evolutionary biology and machine learning would benefit from recognising that they are developing convergent theory for the same fundamental problem: how deep evolutionary history shapes future adaptation.

10:00 AM - 10:15 AM
Chromosome-scale recombination landscapes govern de novo gene evolution in humans.

Matthew Marano, Texas A&M University

Abstract:

De novo gene birth is increasingly recognized as a major source of evolutionary novelty, yet the forces shaping the emergence and persistence of de novo genes remain poorly understood. It has been proposed that many young de novo genes are slightly deleterious and therefore more likely to persist in genomic regions where genetic drift is strong, such as low-recombination regions associated with reduced effective population size (Ne). Here, we tested this hypothesis using the GENCODE catalog of 7,264 human small open reading frames (sORFs) encoding microproteins, of which more than 4,000 evolved de novo. We focused on the two most prevalent sORF categories containing substantial numbers of both de novo and non-de novo cases: long noncoding ORFs (lncORFs) and upstream ORFs (uORFs). After controlling for chromosome size, GC content, and gene density, we found that de novo lncORFs preferentially accumulate on long, low-recombination chromosomes, whereas de novo uORFs are relatively enriched on short, high-recombination chromosomes. Notably, chromosomes 4, 13, and 18, which combine low recombination with low gene density, harbor disproportionately high ratios of de novo to non-de novo lncORFs. Furthermore, we observed a similar enrichment of de novo lncORFs, but not uORFs, in the X-linked recombination desert recently described in mammals. Together, these findings support the hypothesis that many de novo lncORFs represent slightly deleterious novel genes that persist preferentially under conditions of reduced selective efficiency. Our results reveal how chromosome-scale variation in recombination and linked selection shapes the evolutionary trajectories of emergent coding sequences in the human genome.

10:15 AM - 10:30 AM
Evolution of functional domain within pleiotropic genes involved in immunity and development

Danial Asgari, Vanderbilt

Abstract:

Immune genes are expected to evolve rapidly due to host–pathogen arms races. However, many immune genes have been shown to evolve more slowly, partly because they also function in other pathways such as development (i.e., are pleiotropic). In addition, not all parts of a protein are expected to evolve at the same rate. Functional domains might be more conserved to faithfully carry out their function. On the other hand, functional domains may evolve more rapidly. For example, domains of immune proteins that directly interact with pathogens are often subject to stronger selective pressures and may therefore exhibit elevated rates of evolution. Here, using six species of Drosophila, we examine the rate of evolution of functional domains within pleiotropic genes (involved in immunity and development) and compare the results to genes involved solely in either immunity or development. We found that functional domains evolve more slowly (lower dN/dS) than whole proteins in pleiotropic and developmental genes, whereas in non-pleiotropic immune genes, domain and protein evolution rates are similar. The same pattern was observed when using radical versus conservative amino acid changes instead of dN/dS. Using these two metrics (dN/dS and radical vs. conservative changes), we show that, for some immune proteins (e.g., those involved in signaling), a faster rate of change in functional domains does not necessarily indicate substantial functional change. Calculation of the proportion of adaptive changes (α) showed that pleiotropic genes have a higher α than both developmental and non-pleiotropic immune genes. Overall, our findings show how pleiotropy and domain-specific constraints influence the evolution of immune genes, providing insight into how pleiotropy shapes selection at the level of protein domains versus whole proteins.

10:30 AM - 10:45 AM

Distinct evolutionary processes, identical tip patterns, and their mapping in SSE models

Albert Soewongsono, Washington University in St. Louis
Michael Landis, Washington University in St. Louis

Abstract:

Biologists often wish to explain why one trait is more common than its alternatives among species in a clade: is it due to asymmetries in diversification or character evolution processes? State-dependent speciation–extinction (SSE) models provide a flexible framework for jointly modeling such processes. Here, we derive mathematical results that define functional relationships (``rulesets") among rate parameters, establish a mapping between rulesets and evolutionary scenarios, and characterize how these scenarios give rise to different long-term tip-state distributions. In particular, we show that multiple evolutionary scenarios can produce identical stationary distributions of tip-state frequencies. Performing inference on simulated data from extant-only trees, we find that not all scenarios are equally favored for explaining datasets constructed solely from extant species. This bias arises from the interplay between mixing rates, elapsed time, and the conditioning inherent in tree likelihoods. As a proof of concept, we apply our

framework to the BiSSE model across multiple Squamate clades and conduct a literature survey of BiSSE applications to other empirical datasets. We show that, to some extent, the preference for certain scenarios observed in simulations is also reflected in analyses of empirical trees. This study provides a theoretical ground to directly link data-generating process and observed tip-state patterns under an SSE framework.

Macroevolution and Phylogenetic Comparative Methods

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Biogeographic differentiation but recurrent ecological outcomes in a global radiation of cockle clams

Ava Ghezelayagh, The University of Chicago
Stewart Edie, National Museum of Natural History
Rüdiger Bieler, The Field Museum
David Černý, LMU Munich
Nick Crouch, The University of Chicago
Sean Keogh, National Museum of Natural History
Lisa Kirkendale, Western Australian Museum
Kaustuv Roy, University of California San Diego
Ellen Strong, National Museum of Natural History
Jan Johan ter Poorten, The Field Museum of Natural History
David Jablonski, The University of Chicago

Abstract:

We built the most comprehensive species-level phylogeny to date for a bivalve family, using it to test how geography, body size, and bathymetric distribution are structured within the globally distributed family of cockles (Cardiidae). Sampling spans 200 of the 297 extant species and all but one of 53 living genera, providing a broad comparative framework for testing the relationships among phylogeny and biogeography, and how biogeographic partitioning influences the subsequent evolution of organismal traits. We find that regional cardiid distributions are primarily partitioned among deep splits corresponding to morphologically distinct subfamilies, indicating strong phylogenetic structure to their global distribution, while body size and bathymetric distributions recur among regions. Together, these patterns suggest that although large radiations can be geographically structured and accompanied by general differences in body form, key ecological variables such as body size and depth can nonetheless converge in their frequency distributions across lineages.

9:45 AM - 10:00 AM
A diversity-dependent model of discrete character evolution

Miriam Ahmad-Gawel, University of Chicago
Richard Ree, The Field Museum

Abstract:

Where closely related species co-occur, divergent traits may evolve to reduce heterospecific gene flow or competition for shared resources. If the selective pressure for divergence increases with the number of co-occurring species, the rate of trait evolution should exhibit diversity-dependence. Phylogenetic models of diversity dependence have been developed for continuous trait evolution and lineage diversification, but not for discrete traits. Here, I present a model of discrete character evolution, where the rate of transition between character states is a function of the number of co-occurring taxa through time, and inferences are marginalized over uncertainty in biogeographic history. I explore different parameterizations of the model, highlighting the challenges of identifying and measuring different diversity-dependent relationships (e.g., linear versus saturating) on phylogenies of extant species.

10:00 AM - 10:15 AM
Macroevolution of snake body size and vertebral count

Jessica Tingle, Brown University

Abstract:

A common refrain in vertebrate evolution has been the repeated evolution of taxa with elongate, limb-reduced body plans. Of the highly elongate vertebrate clades, snakes have not only achieved the greatest taxonomic diversity, with >4,000 species in 31 families, representing ~12% of all terrestrial vertebrates, but also extraordinary functional and ecological diversity. Snakes have particularly high interspecific variation in both body length and vertebral count, ranging from ~0.1–10 m with ~100–440 trunk vertebrae, indicating a high degree of evolutionary lability in both traits. Given the importance of the vertebral column and associated musculature for most snake behaviors, dramatic interspecific differences in vertebral count almost certainly have functional importance. To study the evolution of body length and vertebral count with respect to habitat and each other, used phylogenetic comparative methods to analyze a dataset compiled from the literature for ~2,000 snake species from 27 families. I found strong evidence for associations among these traits, which likely result from a combination of developmental mechanisms and selection related to functional demands in different habitats. These results suggest future experiments to untangle the causes and consequences of vertebral count variation within and among species, which will help us more deeply understand anatomical and functional diversity of an extreme vertebrate body plan.

10:15 AM - 10:30 AM

The Tempo and Mode of Body Size Evolution in Whip Spiders: Disentangling Climatic and Habitat Drivers

Paulo Martins, University of Notre Dame
Gabriela Galvão, Universidade Federal Rural de Pernambuco
Diogo Provete, Federal Univ Mato Grosso do Sul
Thiago Gonçalves-Souza, University of Michigan
Gustavo de Miranda, Sam Noble Oklahoma Museum of Natural History

Abstract:

Background and Objectives The arachnid order Amblypygi (whip spiders) originated over 330 million years ago and exhibits a remarkably conserved body plan despite its widespread global distribution and the occupation of highly heterogeneous environments. While adaptive radiations frequently accelerate phenotypic evolution when lineages colonize novel habitats or climatic niches, whip spiders present a fascinating evolutionary paradox characterized by prolonged morphological stasis. Within this dynamic, overall body size represents a fundamental trait that modulates crucial aspects of organismal ecology, including metabolic rates, fecundity, mobility, and life-history strategies. However, the specific macroevolutionary mechanisms and ecological drivers maintaining this stasis have rarely been explored under an explicit phylogenetic framework. This study investigates the evolutionary trajectory of body size in Charontidae, the most speciose family of whip spiders. We aimed to disentangle the relative contributions of macroclimatic gradients, pure spatial variation, habitat-specific selective pressures, and shared evolutionary history to test whether their phenotypic conservatism results from genetic constraints, stabilizing selection, or a generalist adaptive strategy.

Methods We compiled linear morphometric data, using carapace length as a proxy for body size, from females of 69 species across three charontid genera. Species were systematically categorized by their primary ecological habitat: strictly cave dwellers (hypogean), occasional cave dwellers (troglophile), or surface dwellers (epigean). We extracted macro- and microclimatic variables from geographical coordinates that represent annual temperature and precipitation. Using the most comprehensive, total-evidence phylogeny available for the group, we applied Bayesian Phylogenetic Generalized Linear Mixed-effects Models to test the effects of climate and habitat on body size, while controlling for spatial autocorrelation. Furthermore, we quantified phylogenetic signal using Blomberg's K, tested for differences in rate among habitats, and compared the relative fit of alternative macroevolutionary models: Brownian Motion (BM), Early Burst, BM with trend, and Ornstein-Uhlenbeck via MCMC.

Results Our models explained 21% of the variance in whip spider body size, which was due to habitat, with a negligible effect of climate and space. Hypogean species exhibited an average size increase of 0.55 mm compared to epigean species. Body size was negatively related with mean annual temperatures (decreasing by 0.05 mm per unit increase) and slightly positively related with annual precipitation and precipitation seasonality. We found a moderate phylogenetic signal for

body size (K = 0.6188). Evolutionary rates for body size did not differ among habitat types. We found strong support for a BM model accompanied by a positive directional trend, indicating a gradual, continuous increase in body size over the evolutionary history of the family.

Conclusion The macroevolutionary dynamics of body size in charontid whip spiders reflect a complex interplay between environmental filtering and deep evolutionary trends. The observed inverse relationship between body size and mean annual temperature aligns with Bergmann's rule, likely driven by the accelerated maturation rates of ectotherms in warmer climates. The evolutionary trajectory of increasing body size through time supports Cope-Depéret's rule, suggesting that larger sizes may consistently confer advantages in prey capture, survival, or metabolic efficiency across environments. Rather than undergoing rapid morphological divergence during speciation, our findings suggest that whip spiders employ a highly conservative "jack-of-all-trades" bet-hedging strategy. By maintaining a broadly conserved, gradually expanding body size with stable evolutionary rates across all habitats, these ancient arachnids were able to occupy diverse ecological niches without undergoing phenotypic changes, which avoided evolutionary dead ends associated with extreme specialization.

10:30 AM - 10:45 AM

Application of Fisher information to phylogenetic birth-death models illuminates unexpected statistical behavior with implications for parameter estimation

Michael May, Utah State University

Abstract:

Phylogenetic birth-death models are well known to suffer from a range of statistical pathologies, from severe errors in parameter estimation to more fundamental issues like nonidentifiability. While significant progress has been made in characterizing these problems, we lack a general framework for quantifying how much information phylogenetic trees contain about the parameters of birth-death models. Fisher information is a natural framework for quantifying statistical information, providing insight into parameter identifiability and establishing theoretical lower bounds on the precision of estimators. In this talk, I discuss both the theoretical foundations and practical applications of Fisher information for phylogenetic birth–death models. I show that parameter estimates are subject to extreme (sometimes infinite) error even as trees grow infinitely large. These results clarify the origins of well-known pathologies and demonstrate that Fisher information provides a coherent framework for understanding the fundamental limits of inference for phylogenetic birth–death models.

Mutation

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM
OOPS: estimating the rate of mutation using a single parent-offspring pair

Trang Nguyen, University Indiana
Matthew Hahn, Indiana University

Abstract:

Accurate estimation of de novo mutation (DNM) rates is essential for studying mutational mechanisms. Existing pedigree approaches require that both parents be sequenced, which limits their applicability in real-world settings where only one parent may be available. Here, we introduce OOPS (Only One Parent Sequencing), a framework for detecting DNMs using

sequencing data from only one parent. OOPS combines short-read data from the available parent with both short-read and low-coverage long-read data from the offspring to reconstruct extended haplotype blocks in the child, which are then compared to the parent's genotype to identify candidate mutations. We evaluate OOPS using a high-resolution, multigenerational human pedigree that has been sequenced with both long- and short-reads. The use of this pedigree allows us to compare results from OOPS to results achieved when using both parents. We show that OOPS achieves comparable accuracy to trio-based pipelines

in detecting DNMs and estimates mutation rates correctly, using either male or female parents alone. By removing the requirement for complete pedigree sequencing, OOPS expands the scope of mutation rate estimation to a wide range of settings, including non-model organisms and incomplete pedigrees.

9:45 AM - 10:00 AM
Mutation accumulation in a hybrid parthenogenetic vertebrate

Zoë Müller, University of Texas at Arlington
Matthew Fujita, University of Texas at Arlington

Abstract:

Asexual lineages are thought to experience elevated extinction rates compared to sexual species, yet direct evidence for the underlying genetic causes remains scarce. Muller’s ratchet predicts that the absence of recombination in asexual organisms facilitates the accumulation of deleterious mutations, thereby reducing long-term fitness. Here, we test this hypothesis in the hybrid-origin, parthenogenetic whiptail lizard Aspidoscelis tesselatus by integrating short-read RNA-seq and long-read IsoSeq data from both asexual and the parental sexual species. We reconstructed phased transcripts for A. tesselatus to quantify mutation accumulation relative to

the parental species. Comparative analyses revealed elevated ω ratios in both parental genomic complements (subgenomes) of the parthenogenetic lineage, consistent with accelerated accumulation of nonsynonymous mutations. Structural variant analyses identified multiple indels in expressed transcripts predicted to disrupt protein domains. Functional annotation indicates that genes affected by both single-nucleotide and structural variants are enriched for roles in chromatin organization, apoptosis regulation, and transcriptional control. While both parental subgenomes showed similar evolutionary patterns, the maternal complement exhibited more structural and missense mutations than the paternal complement. Together, these results provide evidence that mutations accumulate in asexual A. tesselatus and impact genes involved in key cellular functions, supporting theoretical predictions that Muller’s ratchet may contribute to mutation accumulation in asexual lineages.

10:00 AM - 10:15 AM
A high-throughput base-resolution approach to estimating mutation rates at a target locus

Ben Kerr, University of Washington

Abstract:

Mutation is a core evolutionary process and the ultimate source of biological diversity. A key property of this process is the rate at which mutations arise. Methods to estimate mutation rates have a long history in biology. Common experimental approaches measure the emergence of a selectable phenotype, effectively collapsing all underlying mutational pathways into a single metric. Here, we combine the Luria–Delbrück fluctuation test with deep sequencing to quantify mutation rates at a target locus with base-level resolution, thereby disaggregating different mutational routes. As a proof of concept for this new method (Mut-SIFT-Seq), we examine rifampicin resistance in Escherichia coli, which is primarily driven by mutations in the rpoB locus. Our estimates are reproducible and consistent with prior work. We further integrate a parallel high-throughput assay of mutant fitness with methods to estimate lineage extinction, allowing us to correct for common sources of bias in mutation rate inference. Finally, we highlight applications of this approach, including (i) identifying the role of low-level resistance mutations in facilitating high-level resistance and evolutionary rescue, and (ii) quantifying how local sequence context influences mutation rates at specific sites.

10:15 AM - 10:30 AM
New insights on the evolution of the mutation rate and spectrum in nematodes using Caenorhabditis briggsae mutation accumulation lines

Md Monjurul Islam Rifat, University of Florida

10:30 AM - 10:45 AM

Characterizing mutation rate and variation in sexual and asexual freshwater snails

Srivarshini Sarvanakumar, University of Iowa
Maurine Neiman, University of Iowa
Curt Lively, Indiana University
Joel Sharbrough, The University of California
Stephen Wright, Department of EEB

Abstract:

Theory predicts that reproductive mode shapes the evolution of genome-wide mutation rates through its effects on linkage disequilibrium (LD) and indirect selection on mutator alleles. As such, asexual lineages are expected to evolve lower mutation rates than sexual lineages. Here we address this expectation in the New Zealand freshwater snail Potamopyrgus antipodarum, which is characterized by frequent coexistence between obligately sexual and obligately asexual individuals in nature. We find that sexual individuals harbor more unique mutations per haploid genome than asexual individuals. We also find that there is a higher variation in mutation rate across sexual individuals than in their asexual counterparts. These differences are accompanied by distinctly lower mutation rates in sexual male than in female sexual snails. Altogether, these data are consistent with expectations under stronger indirect selection on asexual lineages. We now plan a comparison of a much larger set of sexual and asexual P. antipodarum, to give a broader assessment of theoretical predictions involving mutation rate evolution in closely related sexual and asexual lineages.

Speciation and Reproductive Isolation

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Apparent Reinforcement: Reproductive Communities and Indirect Effects on Patterns of Premating Isolation

jeffrey feder, University of Notre Dame
Andrew Lupinski, University of Notre Dame
Daniel Bruzzese, University of Notre Dame
Noah Barkoff, University of Notre Dame

9:45 AM - 10:00 AM

Evidence for asymmetry in female-mediated assortative mating between two populations of Microtus californicus

Harrison Lin, University of California - Riverside
Miles Johnstone, University of Caliifornia Riverside
Polly Campbell, University of California Riverside

Abstract:

Understanding the nature of reproductive barriers between incipient species is integral to the study of speciation. The California vole (Microtus californicus) is a rodent endemic to the west coast of North America that diverged into two genetically distinct lineages (northern and southern) around 50,000 years ago. The two lineages appear to be reproductively isolated in the present day with no hybrids found in wild populations. This suggests that behavioral barriers are important in this case of rapid speciation. We performed a behavioral assay to determine whether females from northern and southern lineages preferentially interact with males from the same lineage as themselves. For each assay, the female was allowed to roam freely in a rectangular apparatus with a northern male tethered at one end and a southern male tethered at the other. Videos were scored for both positive and negative male-directed behaviors. We found evidence for a preference for males from the same lineage in northern females but not in southern females. Specifically, northern females (n=16) sniffed the anal-genital regions of northern males significantly more than they did southern males whereas male lineage had no effect on the behavior of southern females (n=13). Asymmetry in reproductive barriers is common in diverging populations in secondary contact. In the California vole, F1 male sterility in reciprocal lab crosses is more severe when a northern female is the mother. The fact that this asymmetry in hybrid male sterility is recapitulated in our behavioral data suggests that females from the lineage that experiences a higher cost to inter-lineage mating are more discriminating.

10:00 AM - 10:15 AM

Evolution of Reproductive Isolation in the Hawaiian Red Alga Amansia glomerata

Lauric Reynes, University of Hawaii
James Fumo, University of Hawai‘i
Alison Sherwood, University of Hawaii

Abstract:

Speciation in marine environments is inherently complex, and the mechanisms underlying the evolution of reproductive isolation remain a fundamental yet understudied challenge in macroalgae. This study examines two genetically divergent lineages of the marine red alga Amansia glomerata around the island of O‘ahu, Hawai‘i, to understand processes leading to speciation in this system. We tested the hypothesis that strong reproductive isolation has shaped the genomic

landscape through divergence during extended periods of allopatry. Using genome sequencing (ddRAD), fine-scale spatial transects, and demographic inference, we characterized lineage spatial structure and patterns of genomic divergence. Results showed that the two lineages remained strongly differentiated across the genome, even where they were spatially intermixed across extensive areas of sympatry. Demographic analyses supported a scenario of allopatric divergence followed by secondary contact, likely driven by Pleistocene sea-level fluctuations. The absence of recombinant hybrids, along with numerous loci that act as barriers to gene flow, was consistent with the development of strong postzygotic isolation. However, signatures of introgression across a subset of loci showed that gene flow during secondary contact was geographically structured and heterogeneous across the genome. While our results support allopatric divergence and intrinsic reproductive barriers, the role of ecological differentiation remains to be explored. Overall, this study offers pioneering insights into the genomics of speciation in Hawaiian seaweeds and underscores their potential as a model system for marine speciation.

10:15 AM - 10:30 AM

Evolution of genome-wide barriers to gene flow during complex speciation in rattlesnakes

Keaka Farleigh, University of Virginia
Dylan Highland, University of Virginia
Megan Alderman, University of Virginia
Yannick Francioli, University of Texas at Arlington
Samuel Hirst, University of South Florida
Ellie Faber, University of Virginia
Blair Perry, Michigan State University
Matthew Holding, University of Michigan
Gamaliel Castañeda-Gaytán, Universidad Juárez del Estado de Durango
Miguel Borja, Universidad Juárez del Estado de Durango
Hector Franz-Chávez, Herp.MX
Christopher Parkinson, Clemson University
Jason Strickland, University of South Alabama
Mark Margres, University of South Florida
Stephen Mackessy, UNIVERSITY OF NORTHERN COLORADO
Jesse Meik, Tarleton State University
Todd Castoe, University of Texas at Arlington
Drew Schield, University of Virginia

Abstract:

Speciation with gene flow presents a central paradox: how do genome-wide barriers to gene flow accumulate when recombination disrupts associations among loci under selection? Theory predicts that interactions between recombination, selection, and genome structure shape barriers to gene flow. Yet, empirical studies have identified conflicting patterns, suggesting that these determinants vary across the speciation continuum. We sought to address theoretical predictions by comparing genomic landscapes of introgression across rattlesnake lineages spanning a continuum of divergence. We assembled a chromosome-level reference genome for the

Southwestern Speckled Rattlesnake (Crotalus pyrrhus). We then used whole-genome sequencing data from 181 samples from two species complexes with evidence of gene flow following secondary contact to characterize genomic landscapes of introgression. We found that reproductive isolation is highly polygenic and that its determinants vary across the speciation continuum. Early in divergence, selection against gene flow occurs at few large-effect loci, as indicated by lower introgression in high-recombination regions. As divergence continues, linked selection becomes the predominant force opposing introgression, leading to a positive relationship between recombination and introgression, which is expected to arise from non-random association of polygenic barrier effects. This pattern results in introgression landscapes becoming more strongly correlated between more divergent species pairs because barrier effects accumulate in the same genomic regions. The Z chromosome, in particular, harbors a disproportionate number of barrier loci, supporting a major role in reproductive isolation. Altogether, these findings demonstrate how recombination, selection, and genome organization interact to influence speciation with gene flow across the speciation continuum.

10:30 AM - 10:45 AM

Host-shifts may be a common diver of speciation in North American oak gall wasps

MaKella Steffensen, University of Iowa

Abstract:

When populations of the same parasitic insect species use different hosts, divergent ecological selection can result in reproductive isolation and divergence. Speciation driven by host shifts has been studied in Rhagoletis, goldenrod gall flies, and some agricultural pests, but are these exceptions or representatives of a common theme? A signal indicative of speciation by host shifting is host-associated differentiation (HAD), wherein genetic differences accrue between populations using different hosts. Here, we test for HAD in 11 different species of oak gall wasps, which have more that 700 species in North America alone. Partnering with a network of citizen scientists, we gathered collections from across the U.S., focusing on species previously recorded to use multiple host oak species. We extracted DNA, sequenced mtCOI, and assessed for preliminary signals of HAD. For the species Andricus quercuspetiolicola which uses 11 different host oak species, we also sequenced hundreds of loci via an ultraconserved elements (UCEs) approach. The resulting A. quercuspetiolicola phylogeny shows clear distinct clades based on host tree use which is consistent with speciation by host-shifting. Preliminary mtCOI gene trees show this same pattern for all other target gall wasp species. In oak gall wasps at least, host shifting-may be a common driver of new species.

Species Interactions and Coevolution

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Divergence in symbiont transmission across closely related insect hosts

Kayla Stoy, Florida State University

Abstract:

Evolutionary theory predicts that pairwise specialization between host and symbiont underpin the long-term maintenance of cooperation in symbiosis. When hosts interact with a single symbiont lineage across many generations, they have more opportunities to exert strong control over symbiont evolution. Yet, many symbioses appear highly generalized such that hosts associate with multiple genetically distinct symbionts, and the same symbiont lineages are detected across multiple host species. Detecting patterns of specialization using approaches that rely on single-strain inoculations in lab-based settings may limit the power to detect cryptic patterns of specialization occurring on important traits in ecologically relevant environments. To overcome this limitation, we tested for patterns of symbiotic divergence across insect-bacterial symbioses in semi-natural mesocosm environments. Specifically, we compared mechanisms of Caballeronia zhejiangensis transmission and acquisition across two closely related and geographically overlapping insect species: Anasa tristis and Anasa andresii. Consistent with prior work, we find that A. tristis insects exhibit fecal transmission and symbiont searching behavior. Our study further demonstrates that in the absence of adults, juvenile A. tristis can acquire their bacterial symbiont from the soil. However, when adults are present, fecal transmission becomes the primary mechanism of symbiont acquisition for A. tristis juveniles, even in environments inundated environmental bacteria (up to 2x107 cells/gram of soil). In contrast, despite a shared reliance on Caballeronia symbionts, A. andresii adults do not conduct fecal transmission and juveniles do not exhibit symbiont searching behavior. When exposed to A. tristis feces, A. andresii shows only low levels of symbiont acquisition (~10% infection), suggestion transmission primarily occurs through the environment. Overall, these results reveal divergent transmission strategies across closely related insect hosts and suggest niche partitioning within this symbiosis, which could ultimately shape differential patterns of selection and specialization.

9:45 AM - 10:00 AM

Investigating the common genomic denominator of algal endosymbionts of ciliates with synthetic biology

Joseph Kelly, University of Denver
Niklas Futterknecht, Universität Konstanz
Mina Eberlein, Max Planck Institute for Chemical Ecology
Sven Ernst, University of Konstanz
Fiona Savory, University of Oxford

Masa Zuber, University of Konstanz
Annette Sommershof, University of Konstanz
Andreas Marquardt, University of Konstanz
Lutz Becks, University of Konstanz

Abstract:

Secondary intracellular endosymbiosis, where a unicellular eukaryote is engulfed by and maintained inside another, distantly-related eukaryotic cell entails shifts in the selective pressures of both participants and can shape their evolutionary trajectories. The establishment of secondary endosymbiotic associations is predisposed between some clades, such as Ciliophora and Chlorophyta, in which the ciliate hosts maintain chlorophyte algal symbionts from which they reap photosynthetic byproducts to supplement their carbon budget. These two phyla present an ideal system for the study of the evolution of secondary endosymbiosis as this phenotype has been derived multiple times independently in both, thus allowing for broad-scale phylogenetic comparisons. However, until recently, our understanding of the patterns of genome evolution underlying this phenotype has been focused on the ciliates, owing largely to a paucity in genomic resources and reverse genetic techniques in the algae. To fill this gap in knowledge, we performed a comparative genomic study of multiple algal symbionts of ciliates against non-symbiotic, free-living algal strains. We discovered that symbiotic algal genomes are distinguished from non-symbiotic genomes in that they possess multiple, transcriptionally active paralogs of CHL27, a gene involved in chlorophyll biosynthesis. To investigate the impact of this gene family expansion on the association of the algae with the ciliate host, we developed a transformation pipeline to simulate the expansion of this gene family by synthetically introducing additional CHL27 copies into the nuclear genome of Micractinium tetrahymenae, the algal symbiont of the ciliate Tetrahymena utriculariae. We then collected comparative proteomic data of the algal strains bearing synthetically duplicated CHL27 copies, and metatranscriptomic and metaproteomic data of T. utriculariae inoculated with the transgenic algal strains to test whether the duplication of this symbiont gene family influences the hosts' physiology.

10:00 AM - 10:15 AM
The kinship projection equation: a framework to study the evolution of kin-mediated social behaviour

Christophe Coste, NINA

Abstract:

Demography shapes kinship: processes such as survival, fertility, and dispersal determine how individuals in a population are related to one another. Kinship, in turn, feeds back on population dynamics, ultimately affecting both demography and evolutionary potential. This occurs through genetic (e.g. inbreeding) and behavioural mechanisms, including cooperative breeding, competition at the nest, and kin selection. Understanding this feedback between demography and kinship is therefore central to the evolution of kin-mediated social behaviour. Yet we currently lack

general and tractable tools to predict how kinship structures respond to demographic change, especially in variable environments. Here, I introduce a general projection framework for kinship networks in structured populations. Its central result, the kinship projection equation, tracks through time the expected number of relatives—at arbitrary genealogical depth—of individuals in the population. Because this equation mirrors classical demographic models, it allows kinship dynamics to be analysed using the full toolkit of structured population theory. I show how this framework can be used to study the emergence and evolution of kin-mediated behaviours, such as cooperative breeding or intergenerational transfers, by linking demographic rates, kinship structure, and fitness. This provides a new framework for predicting how social traits evolve under various environmental conditions and for studying the coevolution of demography and kin-selection.

10:15 AM - 10:30 AM

Genomic contingence beneath ecological convergence: the tempo and mode of gene loss in parasitic bilaterians

Alexander Clarke, Yale University
Lilla Bozek, Dartmouth College
Abayomi Babalola, Dartmouth College
Łukasz Wyrożemski, The Arctic University Museum of Norway
Vanessa Paynter, The Arctic University Museum of Norway
Jakob Vinther, University of Bristol
Alexander Donath, Centre for Molecular Biodiversity Research (zmb)
Jørgen Olesen, Natural History Museum of Denmark
Henrik Glenner, University of Bergen
Mark McPeek, Dartmouth College
Terence Farrell, Stetson University
Robert Fitak, University of Central Florida
Pedro Martinez, Universitat de Barcelona
ICREA (Institut Català de Recerca i Estudis Avancats),
Bastian Fromm, The Arctic University Museum of Norway
Kevin Peterson, Dartmouth College

Abstract:

Parasitism has independently evolved hundreds of times among bilaterian animals. Nonetheless, parasites have explored a relatively limited range of ecologies, and they display frequent convergence in morphological, physiological, behavioral, and life-history traits. Although gene loss in parasitic species is well-documented, it is not known if gene loss converges along the same ecological lines as other traits. To test for convergent patterns of gene loss, we characterized the housekeeping, regulatory, and DNA-repair complements of 48 bilaterian species, including 20 parasites belonging to six different phyla. Using a wide array of robust statistical methods, we found that the six canonical parasitic strategies (parasitoidism, castration, direct transmission, trophic transmission, vector transmission, and micropredation) do not display characteristic tempos or modes of gene loss. Further, we found that parasites typically do not display a different pattern of gene loss from their close free-living relatives, indicating that the accelerated tempos and unusual modes of loss previously observed in some species arose before parasitism. Therefore, the

convergent ecological strategies and adaptations that have independently appeared in distantly related parasitic lineages overlie contingent gene losses which largely reflect their phylogenetic histories. These results have important implications for how ecologists and evolutionary biologists should model the acquisition of parasitism, especially regarding the long-held assumption that reversion from a parasitic to a free-living state is impossible.

10:30 AM - 10:45 AM

Should I stay or should I go? Dispersal as a strategy to avoid parasites

Mandy (Amanda) Gibson, University of Virginia
Louis Bubrig, University of Virginia

Abstract:

Hosts experience strong selection to avoid being parasitized. Dispersal may offer a solution: hosts could avoid parasitism by leaving sites where parasites are present. This long-standing hypothesis proposes that dispersal behavior, a central life history trait, evolves as part of hosts' repertoire of parasite defenses. Dispersal, however, carries substantial costs. It is not clear whether the benefits of parasite avoidance outweigh the costs associated with dispersal. We tested the potential for parasites to select for increased dispersal propensity by measuring the costs and benefits of dispersal in experimental populations of the nematode Caenorhabditis elegans and its natural microsporidian parasite Nematocida parisii. We find that parasites can reverse the optimal dispersal strategy: in the absence of parasites, hosts achieve highest relative fitness by dispersing as late as possible. In the presence of parasites, hosts achieve highest relative fitness by dispersing as early as possible, when infection risk is relatively low. This result is sensitive to the fitness consequences of infection, with more resistant hosts showing no benefit from dispersing early. We conclude that parasites do have the potential to impose strong selection on dispersal, and the balance of costs and benefits may contribute to the maintenance of variation in dispersal behavior.

SSB Symposium: Genetic Diversity in Ecological Communities: A new biodiversity pattern that unifies ecological and evolutionary timescales I

06/23/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Resolution of emergent patterns in community genetics with environmental DNA

Taylor Ely, University of Hawai'i at Mānoa

Abstract:

Understanding how natural populations are connected, how far organisms disperse, and where barriers to exchange lie relies heavily on genetic data. When these patterns are compared across taxa, we gain the clearest picture of which population differences actually reflect underlying biological processes rather than statistical noise. Yet, studying these patterns across many species traditionally requires capture and sampling of tissue from many individuals. Environmental DNA (eDNA) offers a powerful alternative by capturing genetic information from entire communities in a single sample, but its utility for estimating haplotype frequencies and population genetic structure remains uncertain. Here, we evaluate the accuracy of eDNA-derived mitochondrial diversity and differentiation across 18 Hawaiian marine vertebrates by directly comparing estimates from seawater samples to those from traditional individual-based tissue sampling. eDNA consistently recovered dominant haplotypes at their relative frequencies, and measures of sequence diversity were significantly correlated between methods. However, population structure metrics were only weakly correlated at this spatial scale, because eDNA more frequently returned positive values of ΦST than tissue-based methods. While there were some limitations in frequency-based inference of population structure, eDNA successfully converted complex mixed samples into accurate estimates of haplotype frequencies. Thus, enabling comparative genetic analyses across entire marine communities in the North Central Pacific to reveal broad patterns of connectivity.

9:45 AM - 10:00 AM

Beyond taxonomy: quantifying biodiversity directly from eDNA sequences

Zihui Wang, University of British Columbia

Abstract:

Environmental DNA (eDNA) metabarcoding has become a central tool in biodiversity science, yet most eDNA analyses are still based on conventional diversity frameworks built around taxonomic or operational units. This typically requires sequences to be clustered into ASVs or OTUs and assigned to taxa, potentially discarding substantial molecular variation encoded in sequence composition.

Here, we present a conceptual and computational framework for quantifying biodiversity directly from raw DNA sequences, bypassing limitations of sequence clustering and taxonomic annotation. We first introduce sequence-informed diversity metrics based on sequence distance and k-mer complexity. We then explore how eDNA sequences can be transformed into two-dimensional images, and embedded into high-dimensional vectors using pretrained DNA language models, enabling the extraction of diversity information through images-based and vector-based analysis.

Using Earth Microbiome Project data, we show that sequence-based approaches capture complementary dimensions of diversity that are not fully reflected by conventional taxonomic- or operational unit-based measures. We further show that sequence-based metrics are less sensitive to study-specific variation and better preserve ecological signals in cross-study synthesis. Finally, we demonstrate that image and vector representations of eDNA can be used to train machine-learning classifiers with high accuracy.

Together, this study highlights community-level molecular variation in eDNA as a previously underrecognized component of biodiversity. More broadly, this sequence-based analytical framework opens new opportunities to link community DNA features to biodiversity monitoring and eco-evolutionary inference.

10:00 AM - 10:15 AM
Metaphylogeography of Lake Tanganyika cichlid diversity revealed by eDNA metabarcoding

Kara Andres, Illinois State University
Peter McIntyre, Cornell University
Catherine Wagner, University of Wyoming
Jose Andres, Cornell University
Jared Freedman, Cornell University
Kristy Deiner, SimplexDNA

Abstract:

Environmental DNA (eDNA) metabarcoding provides a powerful approach for assessing aquatic biodiversity, yet its ability to simultaneously characterize inter- and intra-specific genetic variation in diverse assemblages remains underexplored. We used eDNA sampling along the eastern shore of Lake Tanganyika to investigate phylogeographic patterns among cichlid fishes and evaluate how historical biogeographic barriers shape genetic and species diversity in one of the world's most biodiverse freshwater ecosystems. Across sampled sites, we recovered 689 distinct mitochondrial ND2 haplotypes, including haplotypes matching reference mitogenomes from 115 cichlid species spanning all major lineages. Species richness varied among sites, reflecting spatial turnover in cichlid assemblages.

The detection of haplotypes in many species enabled phylogeographic analyses of 65 species. Most exhibited either panmixia across the study area or strong regional differentiation between the Kigoma and Mahale regions, suggesting barriers to dispersal and/or broad geographic isolation by distance for many lineages. Fine-scale isolation by distance was uncommon, possibly reflecting the limited resolution of short mitochondrial sequences. These findings demonstrate that eDNA metabarcoding can simultaneously detect species distributions and population genetic structure across diverse taxa, highlighting its utility for comparative metaphylogeographic analyses of historical environmental change, dispersal barriers, and genetic connectivity.

10:15 AM - 10:45 AM
Models and Machine learning tools for studying community genetic diversity

Isaac Overcast, Columbia University
Deren Eaton, Columbia University

Abstract:

Community genetic diversity (CGD) is a new biodiversity variable that sits at the nexus of ecology and evolution. We can fruitfully study this pattern with classical tools from community ecology or population genetics, but to do so leaves new biodiversity insight on the table. I will demonstrate how new eco-evolutionary models (MESS) and AI tools (MEADOW) can be applied to regional-scale genetic sequence data and remotely sensed environmental variables to infer underlying biodiversity processes. I will also highlight how the same approach generalizes across systems, from plant and animal communities to microbiomes, where high-throughput sequencing produces similarly rich, high-dimensional data.

MESS (Massive Eco-evolutionary Synthesis Simulations) is a simulation framework that integrates community ecological, macroevolutionary and population genetic processes to model biodiversity across scales of organization. The model jointly predicts species abundances, phylogenetic/functional diversity, and community-wide genetic diversity, enabling direct assessment of ecological and evolutionary processes that generate CGD patterns. Within a simulation-based machine learning approach, MESS can be used to test hypotheses about community assembly and estimate underlying demographic and ecological parameters from community-scale genetic data. MESS is the first model of any kind that predicts CGD patterns, providing a starting point for developing community genetic diversity as a novel biodiversity pattern.

MEADOW (Multispecies Estimation of Dispersal on netWorks), a machine learning framework for learning landscape connectivity from multispecies genetic data. MEADOW models landscapes as graphs in which nodes represent sampling locations and edges encode potential pathways for dispersal. The model learns edge weights (genetic connectivity) directly from sequence data by integrating both geographic distance and environmental features. A key feature of MEADOW is its ability to decompose connectivity into shared and species-specific components. A shared model captures general features of the landscape that influence dispersal across taxa, while species-specific components allow for deviations reflecting ecological or evolutionary differences among

species. This hierarchical structure enables the model to leverage information across species while still capturing biologically meaningful variation, providing a scalable approach to community-level inference.

Ultimately, the objective of this work is to develop predictive models that utilize machine learning to integrate transdisciplinary computational models with multidimensional biodiversity data, with the goal of transforming our understanding of how biodiversity will respond in our ever changing world.

Ecology I

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Jack of All Trades Master of None? Does generalization preclude ecological success across an adaptive radiation of Anolis lizards?

Taylor Wright-Poteet, The University of Texas at Arlington
Edita Folfas, University of Texas at Arlington
Zachary Lange, University of Texas at Arlington
Gavia Lertzman-Lepofsky, University of Toronto
Alexander Murray, John Carroll University
Dan Nicholson, University of Texas Arlington
Luke Mahler, University of Toronto
Luke Frishkoff, University of Texas at Arlington

Abstract:

The mechanisms that give rise to the ecological and evolutionary success of some species but not others are debated among ecologists. Several hypotheses, namely the “Jack of All Trades Master of None” and the “Generalist Success Hypothesis”, attempt to explain patterns of resource use and its relationship with ecological success. Both hypotheses hinge on the degree of specialization exhibited by species. Per the Jack of All Trades hypothesis, species specializing on a subset of resources can mitigate competitive pressures within a community by being the most effective resource extractor, thereby dominating that community. Conversely, the Generalist Success hypothesis predicts generalists to be more successful overall by using a wide variety of available resources, perhaps even some that no specialists use, thus avoiding competitive pressure, and dominating the community as a result. Here, we investigate the role that specialization plays in determining abundance patterns across Anolis communities spanning multiple evolutionarily independent regions—the islands of Jamaica, Hispaniola, and Puerto Rico. We conducted plot-based surveys across each island, and used mark-resight methods to estimate true abundance of all Anolis species encountered. We combine these abundance data with species’ niche characteristics (position and breadth) along perch height, perch diameter, and perch temperature axes—also gathered during plot surveys. In contrast to predictions of the Jack of All Trades

hypothesis, but in support of the Generalist Success hypothesis, we found that abundance positively correlates with perch diameter breadth. Additionally, species preferring low perch heights were more abundant than those using higher perch heights, suggesting that specific niche positions, in addition to niche breadth, matters. Together, our results not only buck longstanding claims about specialization and success by the Jack of All Trades hypothesis, but bolster the claim that species cannot specialize without costs to their overall success in a community.

11:30 AM - 11:45 AM
The bacterial diversity of Ficus petiolaris

J'Bonae McDonald, The University of Missouri
Justin Van Goor, University of Missouri Columbia

Abstract:

Figs (Ficus spp.) are a model system that contain a diverse number of micro-organisms. These microorganisms may introduce a plethora of bacteria into the system that interact with other organisms within the fig. One such micro-organism is the Parasitodiplogaster nematode, which is introduced via pollinating fig wasps. Parasitodiplogaster nematodes carry a bacterial Serratia endosymbiont in their intestinal cavity. This bacterium is hypothesized to aid in the consumption of pollinating fig wasps but may also incidentally mitigate a pathogenic fungus (Fusarium spp.). This fungus, which is also introduced into fig systems via pollinating fig wasps, is the causative agent for Fig Endosepsis, a problematic disease for the cultivated fig, Ficus carica.. Interestingly, we found that Serratia bacterium is present within unpollinated figs, suggesting that this bacterium is endogenous to figs and used secondarily by nematodes. Another bacterium found to be associated with Parasitodiplogaster nematodes is Kosakonia. In an attempt at understanding the role of bacterial endosymbionts within Parasitodiplogaster nematodes and the fig system, we first characterized the bacterial communities within multiple replicates of figs containing various eukaryotic community associates. 19 naive (unpollinated) figs, 25 pollinated figs, 26 figs containing Fusarium fungus (but no nematodes), and 26 figs containing Parasitodiplogaster nematodes (but no fungus) were used for 16S metabarcoding. We expect to see the bacteria Serratia present in all samples, as previous 16S Serratia PCR experiments showed ubiquitous association. We also expect to see the bacteria Kosakonia present in nematode samples only, as we believe this aids in the mitigation of the fungus Fusarium. Characterization of these endosymbionts will allow us to properly culture and replicate the natural mitigation of the fungus Fusarium, by observing interactions between all three organisms.

11:45 AM - 12:00 PM

Islands reveal eco-evolutionary drivers of extinction resistance across Australia's vertebrate biota

Matheus Januario, University of Michigan
Dan Rabosky, University of Michigan

Abstract:

Extinction is a fundamental component of biodiversity dynamics across nearly all spatial and temporal scales. Yet most of what we know about extinction comes from either ensemble-level fossil estimates spanning millions of years or short-term demographic responses to human disturbance over decades. However, we still know very little about how species and environments differ in their "natural" extinction propensity, especially at intermediate spatiotemporal scales. Here, I address this gap by leveraging natural patterns of extinction debt on landbridge islands formed thousands of years ago to infer area- and species-specific rates of extinction. By applying this approach to 323 of such islands and 470 species of land vertebrates across Australia, I uncover extensive spatial and biological variation in extinction rates across most of Australia's biomes and land vertebrate groups. Extinction propensity is not uniform across subclades of amphibians, squamate reptiles and mammals, but instead emerges from the interplay between ecological context (e.g., solar radiation availability) and clade-specific evolutionary histories (e.g., energetic demands in reptiles vs. mammals). Further unpacking this structure could be the key step that connects insights across taxa and spatiotemporal scales, kickstarting a comparative research program on the biology of extinction.

12:00 PM - 12:15 PM

Physiological limits and ecological success: a test of thermal specialization and generalization in the anthropocene

Tristan Herod, University of Texas at Arlington
Brooke Bodensteiner, Yale University
Edita Folfas, University of Texas at Arlington
Saúl Domínguez-Guerrero, Yale University
Zachary Lange, University of Texas at Arlington
Daniel Nicholson, University of Texas at Arlington
Martha Muñoz, Yale University
Luke Frishkoff, University of Texas at Arlington

Abstract:

Understanding how organismal traits scale up to shape species distributions and abundances is a central challenge in ecology and evolution, particularly under rapid anthropogenic change. Because temperature governs physiological performance in ectotherms, thermal traits are expected to play a key role in determining species ecological success (i.e., a species maximum abundance). Yet, direct tests linking thermal specialization and generalization to indicators of

ecological success across contrasting environments remain rare. Here, we integrate field estimates of species maximum abundances with laboratory-derived estimates of critical temperature maximums, critical temperature minimums, and the difference between the two critical temperatures as thermal tolerance breadth for 25 Anolis lizards across the islands of Jamaica, Hispaniola, and Puerto Rico. Species maximum abundances were estimated in both human-modified and natural locations spanning environmental and elevational gradients across all islands. Specifically, we tested whether thermal specialists are more abundant than generalists in natural habitats because lower thermal variability allows specialists to optimize their performance on the narrow band of temperatures they experience. However, thermal specialists will underperform thermal generalists in human modified environments where thermal variability is high, rendering thermal generalists more abundant. Using a combination of mark–resight models and phylogenetically informed comparative analyses, we show that the relationships between thermal tolerance breadth and abundance is context dependent but favors thermal specialization regardless of habitat type. Natural and modified habitats contained higher abundances of thermal specialists exhibiting narrow thermal tolerance breadths. By linking physiological limits to abundance estimates across environmental contexts, this study provides a mechanistic framework for forecasting species responses to climate and land-use change and underscores the need to integrate old theory with new predictions to better understand biodiversity dynamics in the Anthropocene.

12:15 PM - 12:30 PM
Ecological chaos in experimental bacterial populations

William McLaughlin, Vanderbilt University

Abstract:

Predicting the dynamics of ecological systems is a central challenge in biology. One factor that may limit predictability is ecological chaos. Theory has long suggested that even simple interactions can produce chaos, yet empirical demonstrations in living systems remain scarce. Here we show that chaos emerges naturally in a minimal microbial community exposed to feast–famine cycles. In a two-strain system of Escherichia coli, increasing the duration between resource replenishment reveals transitions from competitive exclusion to chaos, driven by asymmetric ecological interactions and periodic environmental forcing. Guided by these observations, we developed a dynamical systems framework grounded in empirical data that recapitulates the observed dynamics and predicts intermediate ecological states and transitions with striking accuracy. Experimental validation of these predictions by implementing the corresponding conditions successfully reproduces the full range of predicted dynamical regimes. Because feast–famine cycles and asymmetric interactions are widespread in nature, our findings provide a model for uncovering the ecological and evolutionary significance of chaos, opening new avenues to employ resource fluctuation and interaction strength to quantify, monitor, and manipulate complex ecosystem behavior previously understood as stochasticity.

Evolutionary Theory II

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Epistasis in evolutionary accumulation processes

Dmitry Biba, Cold Spring Harbor Laboratory

Abstract:

11:30 AM - 11:45 AM

Ecological dynamics and the evolution of cooperation on social networks

Brian Lerch, University of California Davis

Abstract:

It has long been recognized that the positive assortment of cooperators facilitates and stabilizes the evolution of cooperation. One context where this has been extensively studied using abstract mathematical models is the evolution of cooperation on social networks. While these models have been valuable for clarifying how patterns of social interactions can facilitate the evolution of cooperation, they make many simplifying assumptions that challenge their relevance for understanding social evolution in real populations. We develop a new model of the evolution of cooperation on social networks that includes network rewiring based on observed strategies, negative density-dependent social competition for a finite resource, and dynamic group size. We find that social network structure depends critically on individuals' social strategies, with cooperators giving rise to larger and more tightly connected networks than defectors. High birth rates strongly favor the evolution of cooperation, primarily because parents exploit their offspring as cooperators. We compare fixation probabilities from our ecologically explicit model to analogous models more in line with "standard" assumptions of fixed networks to explore how previous simplifying assumptions influence the evolution of cooperation on social networks. Broadly, our study helps to clarify the relevance of abstract theory on the evolution of cooperation on social networks with social evolution in real populations.

11:45 AM - 12:00 PM

Internal conflicts, ontogeny, and biological individuality

Martijn Schenkel, Wageningen University and Research

12:00 PM - 12:15 PM

Nucleotide and amino acid-level effects combine to shape the navigability of protein fitness landscapes

Bryan Gitschlag, Cold Spring Harbor Laboratory
Carlos Martí-Gómez, Cold Spring Harbor Laboratory
David McCandlish, Cold Spring Harbor Laboratory

12:15 PM - 12:30 PM

One model to rule them all: Combining genomes, phenotypes, geography, and environments for truly integrative species delimitation

Daniel Schönberger, University of Kentucky
R. Alexander Pyron, George Washington University
Julian Dupuis, University of Kentucky

Abstract:

Species delimitation remains a central and persistent challenge in evolutionary biology because boundaries among lineages often emerge across multiple, potentially discordant axes of divergence. However, most integrative approaches continue to analyze genetic, morphological, and environmental evidence separately, with conclusions drawn through post hoc comparison. Fully integrative species delimitation therefore remains uncommon, partly because it is difficult to construct models that jointly accommodate such heterogeneous data structures. Here, we present delim-SOM, an unsupervised machine-learning framework in R based on self-organizing maps that infers lineage boundaries from multimodal data within a single unified analysis. The delim-SOM framework integrates genomic, phenotypic, spatial, and environmental layers by projecting individuals onto a two-dimensional map and identifying clusters within the resulting joint space. It further assesses the stability of inferred clusters across replicate analyses, allowing discordance among data types and potential hybridization to be evaluated explicitly.

We demonstrate the utility of this framework using empirical study systems that differ in the geographic and evolutionary contexts in which lineage boundaries may arise. These examples allow us to evaluate whether delim-SOM avoids excessive population splitting and accommodates outcomes ranging from no inferred lineage subdivision (k = 1) to more complex, hierarchical structure. By quantifying the relative contributions of individual data layers and variables to delimitation outcomes, the framework identifies which ecological, geographic, and phenotypic features contribute most strongly to inferred patterns of divergence.

Finally, we evaluate the robustness of delim-SOM using a two-species simulation scenario involving recent divergence and secondary gene flow, conditions that commonly obscure species boundaries. These simulations allow us to assess how gene flow influences clustering outcomes

and to identify the point along a divergence continuum at which two clusters are inferred rather than one.

Overall, delim-SOM provides a step toward fully integrative species delimitation by enabling species discovery from multiple independent sources of evolutionary evidence within a single analytical framework, while also providing an explicit basis for evaluating layer concordance and cluster stability.

Experimental Evolution I

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

PrinTE: A Forward Simulation Framework for Studying the Role of Transposable Elements in Genome Expansion and Contraction

Christopher Benson, Ohio State University
Shujun Ou, The Ohio State University

Abstract:

Genome expansion and contraction are reportedly driven by transposable element (TE) activity, but the underlying dynamics remain enigmatic due to a lack of historical records tracing these changes. Here, we present PrinTE for versatile, forward-time simulation of whole-genome sequences with highly customizable transposon dynamics. Through simulations, we confirm that the distribution of TE sequence divergence reflects their historical insertion and deletion dynamics, which can be used to infer TE dynamic parameters through PrinTE simulations. We analyzed the pangenome of Pucciniomycotina, a subdivision of fungi containing myrtle rust (Austropuccinia psidii), which drastically expanded its genome size to 1018 Mb. Our analyses reveal that the best strategy for controlling genome size is to avoid the invasion of LTR retrotransposons (LTR-RTs). While illegitimate recombination (IR) is considered the most effective counteraction of LTR-RT invasions leaving only solo LTR remnants, we observed a strong positive correlation between solo:intact LTR ratio (strength of LTR-RT removal) and genome size (r = 0.65), and a near-linear correlation between solo LTR count and genome size (r = 0.98). This result suggests that IR alone may not effectively prevent genome obesity. Through simulation of Pucciniomycotina genomes, we proposed that A. psidii might experience a prolonged period of genome expansion followed by a short, potent, and likely ongoing period of contraction. PrinTE is freely available at https://github.com/cwb14/PrinTE.git.

11:30 AM - 11:45 AM

How sanctuary environments facilitate complex adaptation

Isaiah Jordan, Virginia Tech

11:45 AM - 12:00 PM
Evolutionary capacitance driven by Hsp90 during the de novo evolution of multicellularity

Dung Lac, Georgia Institute of Technology

Abstract:

The molecular chaperone Hsp90 is a classic example of an evolutionary capacitor, yet its role in shaping major evolutionary transitions remains poorly resolved. Here we use long-term experimental evolution in snowflake yeast to test how changes in Hsp90 expression influence the emergence of macroscopic multicellularity. In the Multicellularity Long-Term Evolution Experiment (MuLTEE), simple multicellular clusters evolved to become >20,000-fold larger through cellular elongation and physical entanglement, and this transition was repeatedly associated with convergent downregulation of Hsp90. To directly examine Hsp90's role, we performed an evolutionary replay experiment comparing a standard background to a strain overexpressing HSC82, the major yeast Hsp90 homolog. Although Hsc82 overexpression initially reduced fitness and cluster size, all five overexpression lineages convergently evolved macroscopic multicellularity within 100 transfers, considerably faster than in the original MuLTEE. Overexpression was subsequently lost, yet the macroscopic phenotype persisted, indicating that a transient proteostatic perturbation can durably redirect evolutionary outcomes. Genome sequencing revealed that transient Hsc82 overexpression reshaped the mutational landscape, consistent with Hsc82 buffering client mutations from purifying selection and enabling alternative adaptive routes. Persistent mutations in Hsc82-interacting genes, including STT4, synergized with elevated Hsc82 expression to increase cell and cluster size, while recurrent aneuploidy repeatedly arose and reverted, providing a reversible mechanism for tuning phenotypic state. Together, these results demonstrate that transient disruption of a central proteostatic regulator can accelerate a major evolutionary transition and open new evolutionary paths to macroscopic multicellularity.

12:00 PM - 12:15 PM

Selection and demographic variance shape fitness repeatability in a heterogeneous evolutionary experiment

Thomas Blankers, University of Amsterdam

Abstract:

The repeatability of evolution is fundamentally important for understanding the origin and diversification of life as well as for developing evolutionary forecasting tools. Repeatability is limited by stochasticity, which are defined as changes that are independent of genotypic fitness effects. Over short timescales, two main sources of stochasticity in evolutionary change are environmental stochasticity and demographic stochasticity. . Environmental stochasticity results from spatio-temporal changes in interactions with the abiotic and biotic environment and results in variation in the selective regime. Demographic stochasticity affects variation available to selection and the genetic background of selected variants and results from individual-level stochastic event. Quantifying the effect of these two sources of stochasticity and how they interact in driving fitness outcomes is crucially important for predicting contemporary evolutionary responses. To do so, five institutes replicated an evolutionary experiment exposing Caenorhabditis elegans to novel rearing conditions. Replication across the institutes led to variation in selective environments, including through divergent environmental microbiomes. Within institutes, demographic treatments that influence the potential for population-size dependent fluctuations in allele frequencies (drift) and genetic hitchhiking (draft) were included. We found high among-institute variation in fitness outcomes, which was partially explained by variation in microbiota. Whereas lab-specific effects explained most of the variance in mean fitness, the repeatability of fitness outcomes depended strongly on demographic heterogeneity. Specifically, population bottlenecks resulted in high among-replicate variation in fitness. When combined, environmental and demographic stochasticity additively reduced repeatability, underlining their additive importance in developing evolutionary forecasting tools. These results further highlight the importance of statistically integrating heterogeneity in experimental evolution to identify factors constraining outcome repeatability and study replicability.

12:15 PM - 12:30 PM

Cue reliability and the evolution of adaptive plasticity in maternal traits

Stephen Proulx, UC Santa Barbara
Henrique Teotonio, Ecole Normale Superieure

Abstract:

Disentangling the interplay between how environmental factors trigger development and create selection is central to understanding the adaptive evolution of phenotypic plasticity. Using experimental evolution in C elegans, we tested whether plasticity in maternally transmitted effects can evolve when a innocuous cue reliably predicts a stochastic fluctuating environment that

causes high offspring mortality. Populations exposed to reliable cues evolved adaptive maternal effects, enhancing offspring fitness through improved environmental sensing and resource provisioning. In contrast, unreliable cues led to maladaptive outcomes. Our results provide direct experimental evidence that cue reliability shapes the evolution of maternal effects, linking theoretical predictions with empirical proof of adaptation in variable environments.

Invasion Biology

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Salinity Tolerance and Osmoregulatory Strategies in an Invasive Mud Crab

Shelbie Cast, Texas A&M University
Heath Blackmon, Texas A&M University

Abstract:

The Harris mud crab, Rhithropanopeus harrisii, is one of the most successful brachyuran invaders worldwide. Native to brackish waters along the North American Atlantic coast, this species has expanded into multiple freshwater systems across Texas. Its ability to persist across a broad range of salinities raises important questions about the physiological mechanisms that allow it to maintain osmotic homeostasis. To investigate these mechanisms, crabs were collected from the shoreline of Lake Whitney, Texas, and acclimated to a range of salinities. Hemolymph was extracted and analyzed using an OsmoPro Multi Sample Micro Osmometer. Additional experiments examined hemolymph osmolality in molting individuals and survival across salinity treatments.

In non-molting crabs, hemolymph osmolality remained consistently higher than environmental osmolality across all salinities, indicating strong hyperosmoregulation, with a tendency toward osmoconformation at higher salinities. Molting crabs exhibited lower mean hemolymph osmolality across all salinities, suggesting that osmoregulatory capacity may be reduced during ecdysis. Survival was lowest at the most extreme salinities, although crabs in all treatments survived for at least 130 days. These results suggest that osmoregulatory flexibility contributes to the invasion success of R. harrisii, while physiological constraints during molting may limit the range of suitable environments.

11:30 AM - 11:45 AM

Genomic signatures of rapid invasion reveal multiple introduction pathways in the box tree moth

Sangeet Lamichhaney, Kent State University

Abstract:

Biological invasions provide powerful opportunities to study evolutionary processes such as founder effects, rapid demographic expansion, and adaptation to novel environments. The box tree moth (Cydalima perspectalis) is a rapidly spreading invasive species that has expanded across Europe and recently established in North America, causing widespread damage to ornamental and natural boxwood populations. Despite its rapid spread and increasing ecological and economic impacts, the invasion history and introduction pathways of this species remain poorly resolved, particularly in North America, where the invasion is still in its early stages.

We have used genome-wide SNP data to investigate the population genomic structure and invasion history of C. perspectalis across its native range in China and its invasive ranges in Europe and North America. Principal component analyses and population genomic comparisons reveal strong genetic differentiation between native and invasive populations, consistent with founder events during introduction. Within the invasive range, European and North American populations occupy a tightly clustered region of genomic space, suggesting a shared invasion history. However, finer-scale analyses reveal heterogeneity within North America, with some populations clustering more closely with European samples than with other North American populations, indicating the possibility of multiple introductions or secondary spread from Europe.

To further resolve invasion pathways, we have identified highly differentiated SNPs between candidate source populations and invasive lineages, providing a set of candidate diagnostic markers capable of distinguishing among invasion routes. These markers will form the basis of a reduced SNP panel for rapid assignment of newly detected populations to their likely geographic origin.

Together, our results highlight how genome-wide data can disentangle complex invasion histories and provide practical genomic tools for tracking invasive species spread. This work demonstrates the value of integrating population genomics with invasion biology to better understand the evolutionary dynamics underlying biological invasions and to support biosecurity and management efforts.

11:45 AM - 12:00 PM

Co-invasion and future spread of the brown widow spider and its egg sac parasitoid

Rilquer Mascarenhas, York College - CUNY
Jessica Garb, University of Massachusetts Lowell
Yael Lubin, Ben-Gurion University of the Negev
Michal Segoli, Ben-Gurion University of the Negev
Thembile Khoza, South African National Biodiversity Institute
Robin Lyle, Plant Protection Research Institute
Jerome Marie, Institut Louis Malardé
Monica Mowery, City University of New York

Abstract:

The brown widow spider, Latrodectus geometricus, is an invasive venomous spider that has recently spread throughout the world. The range of the spider is cosmopolitan and is predicted to expand under future climate change scenarios. We hypothesized that a common natural enemy of this spider, Philolema latrodecti, a parasitoid wasp that attacks widow spider egg sacs, has spread along with egg sacs of invading L. geometricus. We investigated the origin and route of spread of these species around the world through population genomics and then predicted spread in the invasive range under future climatic conditions using species distribution models. We constructed two ddRADseq datasets from worldwide sampling of the widow spider host L. geometricus and P. latrodecti to clarify the origin and spread of the spider and parasitoid. L. geometricus collected from South Africa showed high genetic diversity, suggesting that the species is native to that region. Furthermore, L. geometricus in South Africa were more likely to occur in natural habitats compared to the invasive range. Spiders from the U.S. were genetically clustered with spiders from northern South Africa, suggesting the route of invasion to the U.S. was likely from Johannesburg or Pretoria. Parasitoid wasp populations from the United States and Tahiti were very genetically-similar, suggesting a very recent invasion from the U.S. to Tahiti. Under future climate change scenarios, we found that the brown widow range will expand north across the southern and northeastern United States. Overall, we found patterns of genetic connectivity across large geographic distances, increased reliance on urban habitats in the invasive range, and predicted range expansion with climate change.

12:00 PM - 12:15 PM

Following the slime trail: tracing Arion invasions with genomics and species distribution modeling

Audrey Bales, Mississippi State University
Megan Smith, Mississippi State University

12:15 PM - 12:30 PM
Impact of dispersal and landscape structure on evolution of plastic generalist during expansions

Caitlin Miller, Virginia Tech

Macroevolution: Diversification

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM
Parallel decoupling of species richness and morphological complexity across latitude in marine bivalves

Sharon Zhou, Committee on Evolutionary Biology
David Jablonski, The University of Chicago
Stewart Edie, National Museum of Natural History
Katie Collins, The Natural History Museum

Abstract:

The latitudinal diversity gradient (LDG) is one of the most general patterns in biogeography, but it has been studied almost exclusively through the lens of species richness. Morphological complexity - a less well-understood yet equally fundamental biodiversity currency - is rarely quantified at scales suitable for macroevolutionary comparison, leaving open the question of whether phenotypic diversity tracks, lags, or diverges from taxonomic diversity across latitude. Here we develop a feature-explicit quantitative metric of bivalve shell ornamentation complexity that integrates multiple sculptural traits and their interactions to capture the developmental information encoded in shell morphology. We apply it to 705 West Atlantic and 2,046 West Pacific shelf bivalve species, from the Equator to the Arctic Ocean. Along both coastlines, species richness and mean complexity peak in the tropics, but their gradients sharply decouple at the tropical-temperate boundary. Richness begins its principal decline near 19 - 21°N, while mean complexity remains comparatively elevated roughly 8 - 9° further poleward, producing a decoupling interval in which complex morphologies persist even as taxonomic diversity collapses along both coastlines. This pattern is driven not by a simple shift toward intermediate forms, but by the restricted poleward ranges of highly complex species and the broader ranges of simpler ones. Cross-basin comparisons show that the same general pattern emerges despite different lineage composition: family-level complexity is only partly conserved between the two coastlines, and families achieve richness through different mixtures of ornament components rather than a single universal route to complexity. Ecological mode also contributes, with epifaunal taxa tending to retain higher complexity than infaunal groups. These parallel patterns reveal that species richness alone can

obscure how phenotypic diversity is distributed across space, and offer a generalizable framework for comparing morphological complexity across clades, environments, and biogeographic regions.

11:30 AM - 11:45 AM
Physiological constraints and geographical barriers dictated the diversification of bats

Gabriel Garcia, Universidade de São Paulo
Michael Landis, Washington University in St. Louis
Tiago Quental, Universidade de São Paulo

Abstract:

Explaining the uneven distribution of global biodiversity remains a central challenge in evolutionary biology. Powered flight enabled bats to achieve a cosmopolitan distribution, yet their richness remains disproportionately concentrated in the tropics, with distinct biotas between continents. Such a distribution could be tied to the physiological demands of flight, which generates excessive metabolic heat primarily radiated away by the highly vascularized wings. While essential for thermoregulation, the high dissipation efficiency of wing membranes may also put bats at hypothermia risk, especially in cold climates. This suggests that while high mobility facilitates dispersal, physiological and geographic constraints heavily influence where diversification can occur. In this study, we employed a spatially explicit analysis (TimeFIG) to quantify how abiotic features (climate and geography) shaped the diversification dynamics of bats. We hypothesized that dispersal is a main driver of diversification by promoting between-region speciation. Fundamentally, it should be limited by geographic distance, with a strong signal from thermal barriers associated with cold regions colonization. Extinction risk should increase at lower temperatures, whereas warmer, wetter areas should have higher speciation.

We used a dated molecular phylogeny with 840 tips alongside a set of paleoclimatic and paleogeographic reconstructions to model the effect of environmental features across eight zoogeographical regions (spanning Wallace's zoogeographical realms and plate tectonics). We first performed a model focused on geography to assess the impact of landmass connectivity, and later implemented a climate-space model (using the main five Köppen climatic zones) to specifically test the role of environmental constraints and niche restrictions.

Overall, most of the tested features lacked any noticeable effects. As expected, dispersal was frequent, having more significant feature effects than other base rates. Colonization success was indeed limited by physical distance and favored by landmass adjacency. Even though temperature itself had no effect on dispersal in the geographical model, climate collectively imposes the largest constraint by suppressing colonization events from tropical to extra-tropical regions (and vice-versa). Tropical regions exhibited lower extinction rates while climatically stable regions (South America, Tropical Africa, and Indomalaysia) recorded higher rates of speciation. Notably, geographic distance increased the probability of between-region speciation, whereas adjacency decreased the rate at which widespread species were split.

Different from the geographic model, the climatic-space model successfully captured the negative effect of temperature drops on the rate of dispersal, demonstrating that feature effects are maximized when climate is directly involved in defining geographical units. For instance, three features without an effect in the geographical model had a strong effect on the rate of extinction in the climatic model: precipitation, temperature, and relief heterogeneity. Most assessed features, though, still lacked a significant effect, with precipitation being the only feature with a detectable (but weak) effect on within-climate speciation. Curiously, like geographical adjacency, climatic adjacency decreased the rate of between-climate speciation, suggesting that tolerance to broad environmental conditions hinder climatic niche specialization.

Here, we show that a combination of geographic and environmental filters shaped bat diversification. Powered flight seems to increase the opportunities for between-region speciation through long-distance dispersal, while high connectivity suppresses the splitting of new species. Our results suggest the disproportionate concentration of bat richness in the tropics is maintained by a physiological constraint, revealing how basic aspects of organismal biology can have profound macroevolutionary implications that shape current patterns of species diversity. Most speciation events, though, happened within (not between) geographical regions, indicating that accounting for within-continent evolutionary pressures is necessary to fully explain diversification dynamics. Lastly, the fact that most of the features we tested had no detectable effect suggests that beyond creating new hypotheses, we might consider discarding effects by focusing on available biological knowledge of the system.

11:45 AM - 12:00 PM

Investigating habitat shift in Symphyotrichum subg. Virgulus: A three-way integration of morphology, ecological niche, and phylogenomics

Sushil Dahal, Mississippi State University
Ryan Folk, Mississippi State University

Abstract:

The radiation of species in a changing environment can be understood by investigating morphological evolution through time. Accomplishing a three-way overlay of phylogenetic, ecological, and morphological relationships among species allows the investigation of the radiation process and particularly disentangling phylogenetic niche conservatism (PNC) and rapid, convergent change, which often co-occur in clades in a complex matrix. Here, we investigated morphological and ecological disparification in Symphyotrichum subg. Virgulus (Symphyotrichum, Asteraceae) from a comparative perspective by integrating 13 morphometric characters and 36 environmental predictor variables capturing aspects of climate, soil, land cover, and topography, and a well-resolved phylogeny. Species were significantly different across morphological and environmental axes; both Pagel's λ and Blomberg's K revealed a lack of phylogenetic signal in overall morphological and environmental space, although individual morphologies and niche

attributes often showed strong signal. We further evaluated distinct habitat shifts by clustering quantitative niche descriptors into categorical habitat classifications. We found independent evolution of most of the examined morphological traits and environmental variables, and a complex and possibly discordant relationship of morphological aspects with niche shift and evolutionary history. Morphological evolution was more strongly shaped by habitat than phylogeny. Moreover, we found evidence for multiple major habitats shifts during the climatic volatility of the Pleistocene epoch, yet other species radiated in the ancestral habitat, possibly explaining discordant morphology-environment relationships. Further studies focusing on the role of biotic interactions in understanding the drivers of evolution in Symphyotrichum was carried out to complement the abiotic framework presented here. We recovered the significant role of floral scent in understanding the evolution of plant-pollinator interaction in Symphyotrichum.

12:00 PM - 12:15 PM
The Evolutionary Fate of Live Birth Depends on Where it Begins

Laura Alencar, Yale University
Gustavo Burin, University of Gothenburg
Saúl Domínguez-Guerrero, Yale University
Liam Revell, University of Massachusetts Boston
Fabio Machado, Oklahoma State University
Josef Uyeda, Virginia Tech
Harry Greene, University of Texas at Austin
Martha Muñoz, Yale University

12:15 PM - 12:30 PM
An Evolutionary Approach to the Dietary Preferences in Fruit-Eating Bats

Jorge Carballo Morales, Stony Brook University
Daniel Caetano, Towson University

Abstract:

Frugivory is a widespread diet among vertebrates and has enormous benefits for global ecosystems. In tropical regions around the world, fruit-eating bats (FEB) feed from more than 1,300 plant species and act as seed dispersers for most of them. Here, we used a novel evolutionary approach to test the predictions of a critical ecological hypothesis, the "core-plant-taxa hypothesis", which proposes that bat species exhibit selective behavior and dietary preferences that facilitate coexistence by reducing interspecific competition. We included both neotropical and paleotropical FEB (i.e., family Phyllostomidae and Pteropodidae, respectively), thereby conducting a worldwide macroevolutionary study of these bats. Our results show that dietary preference patterns in Neotropical FEB are associated with their evolutionary history. Confirming our prediction, we show that closely related bat species tend to have more similar diets—composed of closely related plant species—compared to the diets of more distantly related bats. Furthermore, we found that a strong preference for plants in the Moraceae and Urticaceae families within the

neotropical FEB is positively associated with their net diversification rate. On the other hand, the paleotropical FEB lack these associations. Our results support the evolutionary expectations of the core-plant-taxa hypothesis only for neotropical bats and suggest that, despite their ecological similarity as fruit-eaters and seed dispersers in tropical ecosystems, the diets of both bat clades are not influenced by the same evolutionary factors.

Sensory Systems

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Energetic costs of electrogenesis in a highly encephalized weakly electric fish

Ellen Urquhart, Washington University in St. Louis
Bruce Carlson, Washington University in St. Louis

Abstract:

Large relative brain size and sensory specializations are usually studied in the context of how they contribute to adaptive behaviors. However, less is known about the energetic costs of sensory specializations, which may lead to a key tradeoff for many organisms. Mormyrids, a group of African weakly electric fishes, possess unusually large brains and an electric organ which mediates active electrosensation. This combination of encephalization and active electrosense is unique to mormyrids, and while we know neural tissue is expensive, it is unknown if this specialized sensory system is also energetically costly to these fish. Here, we quantify how much energy is devoted to electric organ discharge (EOD) production in the mormyrid species Brienomyrus brachyistius. Using whole animal respirometry, we compared oxygen consumption rates between fish with intact and surgically silenced EOD production. Using previously published data, we calculated predicted ATP production per EOD generation for an electric organ of a given size. We predicted that intact fish would have higher oxygen consumption rates than silent fish, since electrogenesis has been estimated to be metabolically costly in another less encephalized electric fish group. However, we found no difference in oxygen consumption rates between intact and silent fish. We confirmed through additional experiments and analyses that restricting movement and potential inflammatory response caused by surgical silencing had no significant effects on oxygen consumption rate, and that intact fish consistently produced EODs in the respirometry chamber. Together, these results suggest metabolic rates in this species may be constrained and a fixed aspect of evolved physiology. Therefore, we conclude that silent B. brachyistius are reallocating their energy typically spent on EOD production to other functions, continuing to maintain this constrained metabolic rate.

11:30 AM - 11:45 AM
Morphological changes to marine bivalve eyes in the twilight zone

Jeanne Serb, Ohio State University
Jorge Audino, University of São Paulo
Rafael Mattiolo, University of São Paulo

11:45 AM - 12:00 PM
Rapid Divergence of Innate Sensory Perception in Monarch Butterflies

Darene Assadia, University of Michigan
Delbert Green, University of Michigan

Abstract:

The evolution of sensory systems is driven by natural selection acting on how organisms detect and respond to ecologically relevant cues. Sensory traits are expected to diverge when populations experience different environmental conditions, particularly when those conditions vary across spatial and temporal scales. Long-distance migration represents a powerful selective force that may shape sensory capacity: migratory animals must locate resources in unfamiliar, heterogeneous environments, whereas non-migratory (i.e. resident) animals often exploit stable habitats with consistent resources. The monarch butterfly system is an ideal model to test how migration shapes the evolution of sensory capacity, as it includes both migratory and resident populations that are distributed worldwide. Here, we compare innate sensory capacity among migratory eastern North American monarchs and resident populations from Costa Rica and Hawaii using a novel indoor flight arena. We show that innate sensory capacity differs among populations. Migratory monarchs exhibit increased attraction to a common nectar plant (Lantana camara) relative to both resident populations. The mechanistic basis underlying this behavioral divergence remains under investigation, with differences in sensory input (morphology) and integration (neural) being considered. These results suggest that innate sensory differences are genetically based and can evolve rapidly in this species.

12:00 PM - 12:15 PM
Comparative genomic analysis of chemosensory receptor genes in pteriomorphian bivalves

Sharmistha Goswami, The Ohio State University
Kyle McElroy, Ohio State University
Anna Ward, The Ohio State University
Jeanne Serb, Ohio State University

Abstract:

Background: Most marine invertebrates are characterized with a biphasic life cycle that transitions between a pelagic larval stage and a sessile benthic adult form. These planktonic larvae get

influenced by chemical and physical cues from the surrounding environment to settle and metamorphose into adult form. At this juncture, larvae face an extraordinary challenge: locating a suitable settlement habitat within a complex, dynamic, and often variable marine environment while going through a morphological transition as well. Chemoreception is fundamental for the settlement and survival of these larvae. Previous research has already depicted that chemical cues significantly influence substrate selection for the larvae as well as their fate in future. But chemosensory receptors are poorly studied among marine organisms like bivalves, which are an ecological and economically important mollusk class. Here, we targeted chemosensory G-protein coupled receptors (GPCRs) and ionotropic glutamate receptors (iGluRs) that detect chemical cues, neurotransmitters, etc.

Method: We used RNA-seq data for six pteriomorphian bivalves and conducted phylogenetically informed annotations to identify candidate receptors, followed by examining their expression across three larval stages (i.e., trochophore, veliger, pediveliger).

Result: ML phylogeny revealed that these putative chemosensory genes have expanded significantly in pteriomorphian bivalves.Larvae express all chemoreceptor genes in these bivalves across all three developmental stages, but many are highly expressed in the later larval stages. Notably, some clades include highly expressed orthologous genes from all species which reflect conservation.

Conclusion: Divergence of chemosensory genes indicates more evolutionary opportunities for these species to expand into new ecological niches. And the highly expressed conserved genes across these tested species suggest that these are fundamental for the survival across all the larval stages for these pteriomorphian bivalves.

12:15 PM - 12:30 PM
Evaluating the impacts of temperature perturbations on sexual communication and reproductive barriers

Lata Kalra, University of Minnesota
Mingzi Xu, University of Minnesota

Abstract:

The stability of sexual communication and reproductive barriers between species relies on a tight coupling between signal traits and preferences. Both traits and preferences can alter in a coupled manner in response to environmental perturbations like those in temperature. Studies on this so-called “temperature coupling” have primarily tested how signal traits alter over limited temperature ranges. Our understanding of how temperature perturbations shape preferences and whether, over certain ranges, they can disrupt the trait-preference coupling remains limited. Further, the implications of these temperature-induced alterations on the stability of reproductive barriers between closely related species remain largely unexplored. In this talk we present preliminary results on how temperature alterations impact signal traits in closely related crickets species G.

rubens and G. texensis. We discuss the potential implications of these findings on the strength of pre-zygotic reproductive barriers between the two species. Finally, we will discuss our plans for assessing how temperature perturbations influence female trait preferences and for quantifying the neurogenomic mechanisms underlying these temperature-induced alterations.

Sexual Selection and Recombination

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Quantifying fitness trade-offs in lifespan and fecundity between oviparous and viviparous nematodes

Lynsey Blevins, University of Virginia
Wystan Byers, University of Virginia
Katja Kasimatis, University of Virginia

Abstract:

A fitness trade-off exists between survival and reproduction in most species, such that greater reproductive success is often correlated with a shorter lifespan. This trade-off is especially prominent in females, as the metabolic costs of reproduction in this sex are higher, and there is often greater investment in parental care. However, the mode of reproduction – namely live-bearing (viviparous) or egg-bearing (oviparous) – also creates life-history trade-offs that have additional fitness implications. Here we aim to disentangle the costs of viviparous versus oviparous reproduction along with the impact on lifespan in a trio of Caenorhabditis nematode species: C. sp30 (oviparous), C. sp2 (ovoviviparous), and C. drosophilae (viviparous). We find that while distribution of reproductive effort differs across all three species, only C. sp2 has significantly lower fecundity. Surprisingly, C. sp30 and C. drosophilae do not differ in total fecundity despite having dramatically different modes of reproduction. Lifespans significantly varied in a species-specific manner with median lifespan being highest in C. sp30, indicating an effect of genetic background on lifespan. Interestingly, within each species there was little to no difference in median lifespan between virgin and mated females, suggesting that mating is less costly than previous studies suggest. While examining uterine composition, we find that all three species are capable of producing eggs regardless of reproductive method. We show that C. sp2 and C. drosophilae females contain a large proportion of late-stage eggs and, in the latter case, larval offspring in utero, indicating that increased egg retention is a precursor for live-birth. Together these results support a gradual transition to viviparity in the C. drosophilae supergroup rather than a causal mutation in the C. drosophilae lineage. Moreover, they suggest that viviparous reproduction in C. drosophilae does not represent a costly trade-off, but rather a potentially adaptive alternative state.

11:30 AM - 11:45 AM
Trying to solve the lek paradox in the house fly (Musca domestica)

Farnam Ghaemmaghami, University of Houston
Richard Meisel, University of Houston

Abstract:

How is male genetic variation maintained when females preferentially mate with some male genotypes? One proposed answer to this question is genotype-by-environment (GxE) interactions, where no single genotype is universally superior across environments. Another proposed answer is variation in female preference, such that different females prefer different male genotypes. Additionally, male genotypes may differ in their reproductive output as they age. The house fly (Musca domestica) is a well-suited system to evaluate these explanations for genetic variation in male reproductive traits because two male genotypes (YM and IIIM) differ in mating performance. Specifically, IIIM males outcompete YM males in mating assays because IIIM males have a shorter copulation latency. To determine the relative importance of GxE interactions, female variation, and male age on the maintenance of genetic variation in male reproductive behaviors, we performed non-competitive (one male to one female) and competitive (one IIIM male and one YM male to one female) mating assays using YM and IIIM males of multiple ages with different female strains. IIIM males attempted more matings regardless of competition level, female genotype or age, but mated faster than YM males only with females of their own strain and only performed more matings in non-competitive trials. IIIM males additionally performed more mating attempts toward female siblings of YM males, which could be explained by the increased copulation latency when presented with those females. However, female strain did not improve the mating success of YM males. We also did not observe evidence for genotype-by-age interactions on male mating success. We therefore only found mixed evidence for interactions or tradeoffs that could explain the maintenance of genetic variation for male mating success. To explain the maintenance of IIIM and YM males, other factors such as temperature should be investigated, as the genotypes are found in natural environments with contrasting temperatures.

11:45 AM - 12:00 PM
Transposable element proliferation on the Caenophidian W chromosome

Megan Alderman, University of Virginia
Keaka Farleigh, University of Virginia
Dylan Highland, University of Virginia
Blair Perry, Michigan State University
Drew Schield, University of Virginia

Abstract:

Caenophidan snakes exhibit ZW sex determination with female heterogamety. Because W-linked regions no longer experience sexual recombination, they are susceptible to mutation accumulation, including increased rates of genomic repeat proliferation due to transposable

element (TE) activity. Such TE proliferation may constitute sex-biased mutational load, with impacts on genome regulation, female fitness, and hybrid incompatibility. A previous study demonstrated that the Prairie Rattlesnake (Crotalus viridis) W chromosome is over 80% repetitive and houses a disproportionately large quantity of TEs, yet broader perspectives on TE proliferation in snakes are still needed. We address this gap in knowledge by studying female genomes sampled from across the broader Caenophidian clade, including high-quality genomes for representative species in the Colubridae, Elapidae, and Viperidae. We identified and annotated W-linked scaffolds in available genome assemblies, finding that W chromosomes are highly repeat-rich across all taxa, constituting genomic refugia for TEs potentially capable of self-replication. We also find dynamic evolution of distinct TE families on Caenophidian W chromosomes, with distinct expansions characteristic of the highly degenerated viperid W chromosome. We assessed the 'toxicity' of the W chromosome by quantifying the proportion of full-length LTR retrotransposons, LINEs, and DNA elements in females relative to males, then test for sex-biased dysregulation of TE silencing due to higher rates of TE expression in females. Our findings suggest that, while W-linked genes play important roles in female fitness, the W chromosome nonetheless acts as a key source of intragenomic conflict and may constitute a hotspot for postzygotic reproductive isolation between species.

12:00 PM - 12:15 PM
Sexual selection maintains ancient structural polymorphisms across natural populations

Judith Mank, University of British Columbia

Abstract:

Understanding the distribution, frequency, and long-term persistence of chromosomal structural variants (SVs) in natural populations, such as inversions, is key to understanding population evolution and adaptive processes. Structural variants often span multiple genes, are subject to strong selective pressures and can affect complex traits. Here, we used an unbiased method to identify SVs in three different Trinidadian rivers with paired high- and low-predation populations which differ in a wide range of morphological, behavioural and life-history traits. We identified 23 SVs, ranging in age from 1 to 6 million years, which are widespread across the genome and predate the colonization of each river. We find three SVs that are significantly associated with local adaptation syndromes in high- versus low-predation populations, however none are reciprocally fixed throughout all three replicate rivers. Additionally, we observe seven SVs maintained in all three rivers without evidence of local adaptation. Simulations reveal that the level of SV polymorphism that we observe is far greater than expected under a neutral model. We observed a significant overlap between polymorphic SVs and loci previously implicated in male ornament pattern variation in guppies, suggesting that negative frequency-dependent selection due to female preference for male pattern novelty might explain the maintenance of SV polymorphism. Overall, our results show the role of sexual selection in the long-term maintenance SV polymorphisms, and an interplay between sexual and natural selection in frequency dynamics.

12:15 PM - 12:30 PM
Do female preferences have different rules for within versus between species?

Roman Yukilevich, Union College

SSB Symposium: Genetic Diversity in Ecological Communities: A new biodiversity pattern that unifies ecological and evolutionary timescales II

06/23/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM
Ecological and evolutionary dynamics of the microbiome along the tract of the gut

Michael Wasney, UCLA
Leah Briscoe, UCLA
Richard Wolff, UCSD
Hans Ghezzi, UBC
Carolina Tropini, UBC
Nandita Garud, UCLA

Abstract:

While environmental gradients are known to result in heterogeneous distributions of bacterial species along the gastrointestinal tract, the spatial distribution of genetic diversity within these species remains poorly understood. Because bacterial genetic variants influence host traits like inflammation and metabolism, understanding their distribution is critical. Here, we analyze ~30 common gut commensals in germ-free mice colonized with the same healthy human stool. Unexpectedly, we find that while species composition varied significantly across gut regions, genetic diversity within species remained remarkably uniform. This uniformity is driven by similar strain frequencies along the gut lumen, indicating that genetically divergent strains can coexist without spatial segregation. Furthermore, ~60 evolutionary adaptations arising within the mice tend to sweep globally throughout the gut, showing little region-specificity. We observe similar dynamics in conventional mice and humans, suggesting that uniform bacterial genetic diversity is a conserved, robust feature of mammalian gut ecosystems.

11:30 AM - 11:45 AM

Bacterial evolution in a freshwater lake microbiome over two-decades

Robin Rohwer, The University of Texas at Austin
Katherine McMahon, University of Wisconsin-Madison
Brett Baker, The University of Texas at Austin

Abstract:

Contemporary microbial evolution has been observed in real-time in several famous long-term culturing experiments. However, bacteria in natural environments exist in complex interconnected communities with constantly shifting ecological drivers. To observe real-time evolution simultaneously across the full diversity of a microbiome, we collected a two-decade time series from a freshwater lake, sequenced 470 shotgun metagenomes, and assembled over 40,000 bacterial genomes. We took two approaches to observe bacterial evolution. First, we collapsed the genomes into 2,500 individual species and mapped metagenomic reads to each species. This allows us to infer evolutionary change through shifts in the single nucleotide variants (SNVs) present in the metagenomic reads on different sample dates. In the ~300 species with high enough abundance to observe SNVs over time, we found that 4/5 bacteria had recurring seasonal SNV profiles. This suggests that seasonal preferences differentiate sub-species bacterial strains, resulting in cyclical evolution. Additionally, 1/5 bacteria experienced long-term evolutionary shifts, and 1/10 experienced lasting change. Our second and most recent approach relies on the full set of 40,000 genomes and the fact we recovered some abundant species dozens or even hundreds of times from different samples. Based on whole-genome average nucleotide identities (ANI), we clustered highly similar genomes into species dendrograms using single-linkage clustering. We developed a technique to correlate population structure (each sub-species node) to the genomes' sample dates. This identified discrete time periods of evolutionary change, often resulting in strains at either end of the time series that would typically be considered different species (ANI < 95%). Our findings from comparing metagenomic reads and from comparing distinct genomes both suggest that evolution is commonplace in natural microbiomes. The high standing diversity and fluctuating conditions of natural ecosystems result in a dynamic where "microbial ecology" is just as likely as "microbial evolution."

11:45 AM - 12:00 PM

Climate, wildfire, and human modification shape multi-species genetic diversity across California

Anusha Bishop, University of California

12:00 PM - 12:15 PM

Linking broad scale remote sensing with community genetic diversity across a geological age gradient in the Hawaiian Islands

Rilquer Mascarenhas, York College - CUNY

Abstract:

The distribution of intraspecific genetic variation across species in a community contains valuable biological information reflecting both ecological and evolutionary processes responsible for its assembly. Many studies highlight how this distribution can be summarized as the Community Genetic Diversity (CGD) and how expected CGD values can be modeled while integrating processes across different scales of biodiversity to make inferences about the past, present and future of communities. A remaining challenge is to integrate the information on CGD metrics with rapid assessment technologies required for biodiversity monitoring. Here, we present how CGD is being used to monitor the resilience of communities to anthropogenic change using the model system of the Hawaiian Islands. This project integrates high-throughput arthropod biodiversity sequencing and remote sensing imagery to examine correlated shifts in characteristics of the community across two orthogonal gradients: a geological chronosequence in evolutionary time (from 0-5 million years) and a second gradient from native to heavily invaded forest habitats. Models of community assembly are used to infer the role of key processes (filtering, competition and neutrality) and provide estimates of the resilience of communities in the face of biotic change and the correlation of resilience with CGD. We then utilize Structural Equation Modeling to combine remote sensing imagery at scales ranging from regional to local to identify candidate parameters that reflect arthropod community dynamics in rapidly changing island forest systems. The outcomes of this investigation elucidate important proxies of CGD to be used for biodiversity monitoring, providing actionable solutions for measuring biodiversity health.

Ecology II

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Climate shapes spring ephemeral fitness directly and indirectly through phenology-mediated pathways

Clayton Hale, University of Georgia
Paul Frankson, University of Georgia
Jacqueline Mohan, University of Georgia
Megan DeMarche, University of Georgia

Abstract:

Climate change is resulting in substantial and well documented phenological shifts across taxa and around the world. Spring phenological events, such as leaf out and flowering, are particularly sensitive to warming and are shifting at a higher rate than later phenological events. No plant

functional group is as tightly tied to spring climate and phenology as spring ephemerals, which emerge, flower, and go dormant before overstory canopy closure in early spring. Although climate change is driving well documented shifts in spring ephemeral phenology, we still have little understanding to what extent climate influences on fitness are mediated by phenology. In this study, we ask whether warming alters vital rates directly and/or indirectly through phenological shifts. To address this question, we planted 360 individuals each of three species of spring ephemerals (Claytonia virginica, Erythronium americanum, and Uvularia grandiflora) into an established soil warming experiment with a moderate warming treatment (+1.5°C above ambient), a high warming treatment (+2.5°C above ambient), and a control. For three years (2023-2025), we monitored the timing of each plant's emergence and flowering as well as vital rates. We then constructed species specific piecewise structural equation models to untangle the direct and indirect impacts of warming and phenology on the vital rates of spring ephemerals. We found strong effects of climate on both phenology and fitness, including both direct and indirect effects that differed among species. For example, reproductive success is affected by climate directly as well as indirectly through shifts in flowering phenology in both C. virginica and U. grandiflora. In contrast, clonal reproduction in E. americanum is directly impacted by spring temperature alone and not by any metric of phenology. Our results show that the effects of climate change on spring ephemeral fitness must be accounted for both directly and indirectly through phenological shifts.

2:45 PM - 3:00 PM

Functional Ecology shapes the phylogenetic signal of Avian viromes

Luisa Maria Diele-Viegas, Michigan State University
Aida Giozza, Butantan Institute / Ohio University
Larissa Depa, UFBA
Larisse Depa, UFBA
Nick Fountain-Jones, University of Tasmania
Roderick Gagne, University of Pennsylvania
Simona Kraberger, Arizona State University
Christopher Kozakiewicz, Michigan State University

Abstract:

Birds are a major component of wildlife virome diversity, playing an important role in pathogen circulation across ecosystems due to their high ecological diversity, mobility, and broad habitat use. Despite growing interest in avian viromes, it remains unclear how host evolutionary history and ecological function jointly shape viral community structure across bird species. In particular, the extent to which phylogenetic relatedness influences viral diversity within different functional groups has not been explicitly tested at broad comparative scales. Here, we evaluate the phylogenetic signal of viral diversity across avian functional groups using a curated dataset of 126 wild bird-associated virome studies extracted from a large-scale systematic review of wildlife viromes. Bird hosts were classified into functional ecological groups based on traits such as diet, foraging behavior, habitat use, and mobility. Viral diversity metrics were standardized at the host level, and comparative phylogenetic methods were used to quantify the strength of phylogenetic signal within

and across functional groups. Our analyses test whether closely related bird species harbor more similar viral communities than expected by ecological similarity alone, and whether the strength of this evolutionary signal varies among functional groups. By integrating host phylogeny, ecological traits, and viral community data, we aim to understand how functional ecology can modulate evolutionary patterns in host-virus associations and advance predictive understanding of viral diversity across avian lineages.

3:00 PM - 3:15 PM
Multispecies niche overlap: moving beyond pairwise metrics to understand community-wide similarities in resource use

Cody Kent, Luther College
Scott Powell, George Washington University
Thomas Sherry, Tulane University

Abstract:

Measures of niche overlap – particularly in terms of resource use – are important tools in various ecological and evolutionary studies. A wide range of these overlap indices are used, but all are pairwise measures involving only two species. Yet, most communities are more complex, suggesting the potential value of measures that can be extended to the overlap among more than two species. Here we extend percent overlap to any number of potentially overlapping species and then partition the amount of overlap attributable only to any subset of species. We then apply this partitioned multispecies percent overlap metric to both simulated and empirical communities. Additionally, we provide recommendations on the use and extension of this metric for a variety of research goals across topics in both ecology and evolution – illustrating how this methodology may capture interactions and structure of niche space in ways that traditional, pairwise metrics overlook – such as identifying foraging guilds, measuring the degree of diffuse competition, or providing overall levels of niche overlaps within phylogenetic clades.

3:15 PM - 3:30 PM
Applying Modern Coexistence Theory to Cytotype Coexistence

Lacey Rzodkiewicz, University of Pittsburgh/Ashland University
Alba Rodriguez Parra,
Briante Najev, University of Pittsburgh
Tia-Lynn Ashman, University of Pittsburgh
Martin Turcotte, University of Pittsburgh

Abstract:

The Modern Coexistence Theory provides a robust framework in which to test hypotheses on coexistence. Despite repeated whole genome duplication throughout evolutionary history, it is unclear how resulting higher ploidy cytotypes are able to establish within diploid populations given the disadvantages of polyploidy (e.g., increased body size, metabolic constraints). Given the

challenges in explaining cytotype coexistence, we completed reciprocal biological invasions of ten genotypically distinct lineages of Spirodela polyrhiza duckweeds with three neotetraploid sublineages. We used the sensitivity approach based on invasion and monoculture growth rates to define niche differences and relative competitive ability of the diploid and tetraploid pairs. Given these values, we can then predict coexistence. Then, we consider the relationship between coexistence parameters and 1) key duckweed traits and 2) phylogenetic distance using Mantel frameworks. Additionally, we considered traits in a nonparametric framework to compare trait values between coexisting and non-coexisting pairs of diploid and tetraploid duckweeds.

3:30 PM - 3:45 PM
Ploidy Structures Phyllosphere But Not Rhizosphere Microbiomes Across Diverse Flowering Plants

Amanda Rawstern, University of Pittsburgh

Abstract:

Whole-genome duplication (polyploidy) and domestication are two of the most influential evolutionary drivers of plant diversification. Polyploids are often more robust to environmental change than their diploid counterparts, and plant-associated microbial communities may be an important but overlooked contributor. Whether polyploidy or domestication more strongly structures these microbial communities across phylogenetically distinct plant lineages remains largely unexplored. Using a globally compiled dataset of 87 studies spanning 156 angiosperm species, we tested whether polyploidy and domestication shaped phyllosphere and rhizosphere microbiome properties. We found that polyploidy consistently structured phyllosphere but not rhizosphere microbiome properties, with effects largely conserved across prokaryotic and fungal communities. Phyllosphere richness was driven by a ploidy × domestication interaction, with domesticated diploids harboring roughly 50% lower richness than all other groups, indicating that polyploidy may compensate for the richness reductions typically associated with domestication. Polyploids also exhibited significantly higher phyllosphere network modularity and 147% greater prokaryotic functional redundancy for abiotic stress mitigation functions. Differential abundance analysis further identified enrichment of phosphorus-cycling enzymes in polyploid phyllospheres, indicative of potential growth-promoting advantages. Taken together, the elevated richness, modularity, and functional redundancy of phyllosphere polyploid microbiomes collectively point to greater stability to fluctuating environments. In contrast, rhizosphere properties were driven primarily by geographic variables, suggesting rhizosphere responses to ploidy or domestication are likely plant or environment-specific rather than phylogenetically generalizable. These findings indicate that polyploidy shapes phyllosphere microbiome assembly in ways that may confer advantages to polyploid plants, with broader implications for understanding how plant genome evolution drives microbiome diversification.

Evolutionary Ecology: Genomics

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Explaining the mysterious evolution of short stamen loss in Arabidopsis thaliana: progress and challenges from genomic and growth chamber trait data

James Bingman, Michigan State University
Jeff Conner, Kellogg Biological Station
Ava Garrison, Michigan State University

2:45 PM - 3:00 PM

Global adaptation to climate change in the twilight zone revealed by shared signals of selection in mesopelagic lanternfishes

Bruna Cama, UC Berkeley

Abstract:

Rapid accumulation of greenhouse gases threatens humanity and global diversity. The oceans absorb 30% of anthropogenic carbon emissions annually, yet is vulnerable to rising global temperature and the rising concentration of CO2, which causes ocean acidification (OA). Adaptation to climate change by the biotic components of this sink has only been explored in a limited number of taxa, and rarely in the wild. Deep-sea lanternfishes (Myctophidae) are the most abundant vertebrates on the planet by biomass and the dominant vertebrate consumers in the mesopelagic “twilight” zone 200 – 1000m below sea level, thus major contributors to the global carbon cycle. However, it is unknown whether lanternfishes are adapting to rising ocean temperatures and OA. Here, we use whole-genome sequencing to investigate their demographic history and identify shared recent signals of selection across lanternfishes from multiple sites in the Atlantic and Pacific spanning three species/genera (Benthosema glaciale, Triphoturus mexicanus, and Diaphus theta). Across all species we found evidence of expansion from a historical population bottleneck possibly corresponding to the last glacial maximum, and effective population sizes of only 5 million, suggesting substantial reproductive skew and spatially restricted populations. We discovered 33 genes located near signals of selection across all taxa in both oceans. 81% of these appear related to adaptations to global warming and OA, including a heat-shock protein (HSP70) and genes active in skeletal development, calcium homeostasis, biomineralization, and circulatory system development. Of these, 14 genes are known to be involved in climate change responses from published experiments involving hypoxia, pH, and thermal stress. Additionally, we found significant enrichment in gene ontologies for otolith (ear stone) morphogenesis, in concordance with past findings that OA strongly affects otolith size in

fishes. This study provides a new approach for studying climate change adaptation at a global scale in an understudied ecosystem and taxon, and our results imply widespread shared adaptive responses of marine species to climate change.

3:00 PM - 3:15 PM
Genomic diversity and the domestication history of cotton (Gossypium hirsutum)

Weixuan Ning, Iowa State University

Abstract:

Gossypium hirsutum is the leading fiber crop globally, but its origin as a domesticated plant and patterns of diversity in the wild remain to be elucidated. Here we use extensive sampling of wild populations and comparative genome sequence data to illuminate the scope and patterning of wild cotton diversity across its native range. Analyses confirm the hypothesis that the Yucatán Peninsula (México) is the center of domestication, from which the original perennial forms and later modern annualized cultivars were derived. Population structure and phylogenomic analyses indicate that northwestern Yucatán harbors greater genetic diversity relative to smaller, geographically dispersed populations in northeastern Yucatán and the Caribbean basin. Genetic load and transposable element burden also are lowest in northwestern Yucatán relative to other regions, consistent with its greater diversity and reflecting the effects of historical genetic bottlenecks in other populations. Populations from Florida and elsewhere in the Caribbean basin maintain unique pockets of diversity. Analyses of selection suggest that cotton domestication entailed long-term accumulation of mutations with relatively minor phenotypic effects, as opposed to a more punctuated process involving major domestication genes. Our study quantifies the scope and scale of genomic diversity in wild cotton, the origin of the cultivated gene pool, and the likely ecological and anthropogenic processes that shaped extant diversity and modern geographic patterning.

3:15 PM - 3:30 PM
The genetic architecture of mimicry in Peruvian poison frogs of the genus Ranitomeya

Adam Stuckert, University of Houston
Andrew Rubio, University of Houston
Galina Aglyamova, University of Houston
Ashley Dye, University of Houston
Ammon Corl, University of California Berkeley
Rasmus Nielsen, University of California Berkeley & Natural History Museum of Denmark
Roberto Márquez, Virginia Tech
Rebecca (Becca) Tarvin, University of California Berkeley

Abstract:

Coloration is a critical aspect of phenotype in many animals, affecting a variety of evolutionary and physiological processes ranging from thermoregulation to predation and mate choice. In aposematic species, conspicuous coloration acts as a warning signal to predators that potential prey are defended. These aposematic signals are often learned by predators, and are under frequency-dependent selection. Many aposematic species have mimics, which may contribute to predator learned avoidance if the mimics are also defended. Here, we examine the mechanisms of color production in mimetic poison frogs in the genus Ranitomeya, seeking to understand if these species use the same genetic and biochemical mechanisms to produce coloration. In the lowlands and foothills of Peru, Ranitomeya imitator mimics several congeneric species, including a green-spotted morph and yellow-striped morph of R. variabilis. We sampled 274 Ranitomeya variabilis and Ranitomeya imitator from these two co-mimetic morphs. We collected phenotypic data on color and pattern, as well as genetic material. We then did whole genome resequencing to examine the genes and networks underlying the repeated, parallel evolution of striped to spotted frogs.

3:30 PM - 3:45 PM
Opsin loss in deep-sea glass scallops

Kyle McElroy, Ohio State University
Anna Ward, The Ohio State University
Jeanne Serb, Ohio State University

Abstract:

Light detection is a nearly ubiquitous feature of cellular life, with photoreceptive proteins found in all major organismal clades. Despite the importance of light to vision and myriad physiological functions, some animals have invaded and adapted to habitats of near-to-total darkness, including deep in the oceans. The bivalve family Propeamussiidae, also known as “glass scallops”, includes species found across a range of photic to aphotic marine environments. Like their sister family, the scallops (Pectinidae), glass scallops may have a sophisticated distributed visual system characterized by numerous eyes lining their mantle tissue, but in deep-sea species eyes are reduced or absent. To better understand the evolution of eye regression in glass scallops, we generated an anchored hybrid enrichment (AHE) sequencing dataset and developed a robust Pectinoidea phylogeny, the bivalve subfamily containing scallops and their kin. Additionally, we asked whether genes involved in light-detection would be present or absent in deep-seq species. So, we designed baits targeting opsins, which support photoreception for vision. As propeamussiid genomic and transcriptomic data was unavailable for bait design, we relied on scallop sequences, thus raising the question of whether an opsin sequence was absent from the genomes of these animals, or merely our data because of bait and target dissimilarity. We therefore additionally generated whole-genome sequence data from three species representing photic and aphotic habitats to compare our AHE results against. Our baits were generally successful in capturing partial opsin sequences where present and especially useful for analyzing the intronless opsins that are highly expressed in scallop eyes. We find that opsins have been pseudogenized or lost entirely in glass scallops from aphotic habitats, adding to our previous findings of total opsin loss in

some deep-sea lineages of molluscs, including gastropods and other bivalves, and connecting dramatic changes in habitat to organismal and genomic evolution.

Experimental Evolution II

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Deciphering phenotypic signatures in response to directional selection for multicellularity

Beatriz Baselga Cervera, University of Minnesota

Abstract:

Natural selection acts on phenotypes, which are often largely a product of the genotype. However, the role of phenotypic plasticity in the evolution of differentiation and developmental systems is receiving increasing emphasis. Concretely, within the major evolutionary transition from a single cell to multicellular organisms, the implications of unicellular plasticity in maintaining phenotypic diversity and the evolvability of alternative phenotypes have been overlooked. To address these questions, we investigate the phenotypic consequences following directional selection for increased size. We capitalized on the experimentally evolved Saccharomyces cerevisiae multicellular system to address: (i) how phenotypic heterogeneity can arise in isogenic populations of an experimentally evolved multicellular yeast under constant environments, and (ii) whether the carryover ancestral phenotypic plasticity informs multicellular responses to a change in environment. We characterize the phenotypic dynamics of various clonal ancestral and multicellular strains (both experimentally evolved and genetically constructed). Reappraisal of phenotypic variability can help understand the effect of multiple factors, their interaction, and thereby adaptive possibilities.

2:45 PM - 3:00 PM

Experimental evolution on loss of heterozygosity using engineered Saccharomyces cerevisiae

Yi-Hong Ke, University of Michigan
Michelle Orozco-Quime, University of Michigan
Josh Bauman, University of Michigan
Tamilie Carvalho, University of Michigan
Victor Garcia, University of Michigan
Grant Landry, University of Michigan
Shuhua Ge, University of Michigan
Anuj Kumar, University of Michigan
Timothy James, University of Michigan

Abstract:

Loss of heterozygosity (LOH) is a major contributor of genetic variation in natural populations and lab-evolved asexual diploids. However, its contribution to adaptation is uncertain, because the full spectrum of its fitness effects remains largely uncharacterized. To systematically investigate the distribution of fitness effects (DFE) of LOH, we engineered a diverse, barcoded library of heterozygous diploid Saccharomyces cerevisiae strains, each containing randomly induced LOH events. By employing competitive fitness assays and barcode sequencing (Bar-seq) across seven distinct environments, including various stressors from chemicals, temperature, and an in vivo host model, we quantified the fitness consequences of LOH events. Our results reveal that the DFE of LOH is predominantly neutral to deleterious, with a general trend of decreasing fitness correlated with larger cumulative lengths of LOH tracts. However, the fitness effects were variable and the fitness landscape was highly environment-dependent. While beneficial LOH events were rare and of small effect in standard rich media, they were common and conferred substantial fitness gains in novel or stressful conditions. A key finding was the prevalence of antagonistic pleiotropy, where over 75% of strains exhibited fitness trade-offs, gaining an advantage in one environment at the cost of fitness in others. The magnitude of these trade-offs was also found to correlate with longer LOH tracts. Additionally, we developped methods to estimate the rate of LOH accumulation and adaptability across lineages, enabling prediction of how LOH-mediated diversification shapes evolutionary trajectories in clonal diploid populations. Overall, this work demonstrates that LOH plays a dual role in evolution: while it often imposes a genetic burden, it also provides a powerful mechanism for rapid, environment-specific adaptation, driving specialization by trading general robustness for niche-specific advantages.

3:00 PM - 3:15 PM

Diverse genetic backgrounds confer variation in a transition to multicellularity

Jordan Sivigny, University of Minnesota

Abstract:

The degree to which evolutionary convergence and divergence predict outcomes of a transition to multicellularity remains an open question. In response to selection, the long diverged yeast species Saccharomyce cerevisiae and Kluyveromyce lactis have been observed to evolve multicellularity via convergent genetic mechanisms. Despite this convergence, it has also been observed that K. lactis differs from S. cerevisiae in its ability to evolve multiple distinct multicellular phenotypes in response to this selection. To further explore the degree of variation in multicellular evolution in this species, selection for multicellularity was performed on a pool of strains differing in genetic background and emergent multicellular phenotypes were tracked. Variation in tempo (when multicellular phenotypes appeared), multicellular phenotype evolved, and genetic mechanism conferring multicellularity was observed across strains indicating that evolutionary convergence in

the evolution of multicellularity may be highly dependent on the genetic background of the unicellular ancestor.

3:15 PM - 3:30 PM
Dose-dependent selection shapes the tempo and repeatability of resistance evolution

Mina Dinh, Cleveland Clinic
Kristi Lin-Rahardja, Cleveland Clinic
Joshua Nworie, Cleveland Clinic
Jinling Wu, Cleveland Clinic
Masahiro Hitomi, Cleveland Clinic
Jacob Scott, Cleveland Clinic

Abstract:

The tempo and repeatability of adaptation depend critically on the strength of selection, yet how varying selective pressures shape evolutionary trajectories remains incompletely understood in complex, multi-state systems such as cancer. Here, we investigate how osimertinib dose shapes resistance dynamics and trade-offs to second-line drugs in EGFR-mutated non-small cell lung cancer cells. We serially propagate evolutionary replicate populations under four conditions spanning a gradient of selection intensity, with longitudinal sampling to characterize growth dynamics, genomic and transcriptomic profiles, and shifts in drug response over time. To assess the pleiotropic consequences of adaptation, we perform longitudinal collateral sensitivity profiling using four FDA-approved anticancer agents.

We expect that all drug-exposed populations will evolve osimertinib resistance, but that the timing of resistance emergence will vary with dose. From a population genetics perspective, higher drug doses are expected to narrow the range of mutations that can confer resistance, potentially reducing competition among lineages and allowing resistance to emerge and fix more quickly than at lower doses, where multiple adaptive solutions may coexist. In contrast, intermediate doses may maintain greater standing heterogeneity and enable alternative adaptive trajectories. We further predict that phenotypic outcomes will be more similar among replicate populations within each dose condition than across conditions, reflecting dose-specific adaptive pathways rather than universal convergence across treatments. Finally, we will test whether dose-dependent evolutionary histories produce distinct or overlapping collateral sensitivity profiles across clinically relevant drugs.

Together, in this work, we use cancer as an experimentally tractable evolutionary system to interrogate how selection strength shapes the repeatability, tempo, and collateral structure of adaptive evolution.

3:30 PM - 3:45 PM

How mutation and recombination shape rapid adaptation: insights from a global Arabidopsis evolve & resequence experiment

Ruth Epstein, UC Berkeley

Abstract:

Genetic diversity is the ultimate fuel of evolutionary change. Mutations and meiotic recombination generate the majority of all genetic diversity, and although their molecular pathways have been studied in-depth, these studies have mostly occurred within laboratory settings, and within a single reference ecotype or variety. Unfortunately, the lack of studies investigating the dynamics of de novo mutation formation and recombination in natural environments and across diverse genotypes has created a gap in understanding of how these diversity generating processes will be modulated within diverse populations and by a changing climate. To bridge this gap, we used an unprecedented Evolve & Resequence (E&R) experiment in the primarily self-fertilizing plant, Arabidopsis thaliana, with a starting seed mix of 231 diverse genotypes, and sequenced over 760 progenies individually from generation three of the experiment, from five contrasting geographic locations to assess how mutation and recombination contribute to evolution over short time scales. First, we found evidence of multiple migrations of 1001G and/or local Arabidopsis ecotypes into the experiment, particularly in Germany, along with variable outcrossing rates across all sites. At some locations, up to 20% of offspring in generation 3 were outcrossed, demonstrating that even low outcrossing rates can rapidly generate genetic diversity over short time scales. In outcrossed individuals, the number of recombination events varied across chromosomes between locations, possibly due to selected ecotypes at each location having divergent recombination pathways. We also examined the distribution and types of de novo substitutions in multiple diverse ecotypes that comprised a large bulk of our sequenced progenies. Using ecotype-specific long-read assemblies, we found that genes and transposons surprisingly had similar substitution rates, reflecting the dual effect of their diverse genetic backgrounds and the complex selective pressures of natural environments. Overall, studying genetic diversity dynamics in natural environments will bring us closer to understanding how natural populations can adapt or persist under a changing climate.

Expression/Transcriptomics

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Rapid evolution of mouse saliva through regulatory rewiring and gene expansions

Luane Landau, University at Buffalo

Omer Gokcumen, University at Buffalo

Abstract:

Mammalian saliva plays essential roles in digestion, immunity, and host-microbiome interactions, yet its protein composition varies widely across species and sexes. This diversity makes saliva a powerful model to study evolution of gene expression. Here, we compared mouse and human salivary glands at the genomic, transcriptomic, and proteomic levels to understand how saliva composition evolves. We found that evolution of gene expression in mouse salivary glands is driven by rapid gene turnover and sexual dimorphism. In the submandibular and sublingual glands, 68% and 73% of expression from genes encoding secreted proteins derives from lineage-specific genes that lack one-to-one human orthologs. This contrasts the prevailing view that gene expression is largely conserved across tissues and highlights saliva as an unusually dynamic system of molecular evolution. Mouse submandibular gland shows striking sexual dimorphism, with 1537 tissue specific sex-biased genes, five times higher than in the liver, a classic model of sex-biased expression. These genes cluster in regions shaped by recent gene duplication, such as the kallikrein gene cluster, a mouse-specific expansion that accounts for ~16.4% of male-biased submandibular gland expression. Our analyses suggest that this bias arises through regulatory changes that are expanded by gene duplication, including the spread of a testosterone-associated regulatory motif and the expansion of a shared chromatin domain that promotes coordinated gene regulation. Our results describe a novel mechanism through which lineage-specific gene duplication and regulatory rewiring drive rapid, sex-specific evolution of the mammalian saliva.

2:45 PM - 3:00 PM

Segregating homeologous exchange in Coffee arabica has genome-wide impacts on gene regulatory networks.

Michael McKibben, Donald Danforth Plant Science Center
Joel Sharbrough, The University of California
Justin Conover, Donald Danforth Plant Science Center

Abstract:

Polyploid formation is often accompanied by interspecific hybridization, resulting in cells that contain two or more complete sets of chromosomes in the nucleus. The hybrid nature of these polyploids can create regulatory challenges, as cis and trans factors that have evolved independently for potentially millions of years are saltationally reunited in the same nucleus. These regulatory challenges can be further complicated by homoeologous exchanges (HEs)—crossover events that occur between duplicated chromosomes—in which the dosage of genes originating from each diploid progenitor can vary substantially. In Coffea arabica, all available reference genomes show evidence of one such HE on chromosome 7, and all show that the initial recombination breakpoint occurred at the same genomic position, approximately 1.2 Mb from the telomere. Here, we use RNA-seq data from over 400 C. arabica accessions and find that only ~1.2 Kb of the originally reported ~1,200 Kb region is fixed in the population, and the rest of HE

region is still segregating. To explore how this segregating HE influences gene co-expression networks, we conducted weighted gene co-expression network analysis (WGCNA) to compare changes in network connectivity within gene-regulatory modules. We find that two modules are enriched for genes affected by the HE - one module showed a significant decrease in between-subgenome expression correlations, while the other showed significant decreases in both within- and between-subgenome correlations. These large-scale shifts in co-expression were not limited to genes directly affected by the HE, but extended to other within-module genes on other chromosomes. These results demonstrate that HEs can have genome-wide regulatory consequences, and underscores the role HEs play in generating genomic and transcriptional novelty in polyploids that form through interspecific hybridization.

3:00 PM - 3:15 PM
Understanding a nascent endosymbiotic interaction between a ciliate and green algae using single nuclei transcriptome atlas

Israt Jahan, University of Oxford

3:15 PM - 3:30 PM
Evolution of Y-added genes in Microtus voles

Louise Heitzmann, University of California Riverside
Polly Campbell, University of California Riverside

Abstract:

The mammalian Y chromosome is highly degenerated and enriched in repetitive content, with only 1-3% of ancestral genes retained across species. Yet, the Y chromosome is also a site of gene gain and content regeneration. Y-added genes – acquired from the X chromosome or autosomes – are often found in high copy number and associated with male fertility, being mostly expressed in testes. However, we lack understanding of how these gene expression patterns evolve. Were these genes pre-adapted for male fertility or does testis-specific expression evolve after addition to the Y? Are multicopy added genes associated with specialization? We address these knowledge gaps in six closely related Microtus vole species for which we generated highly contiguous, fully annotated Y chromosome assemblies. We sequenced transcriptomes for 10 tissues per species and conducted comparative analyses of gene expression for Y-added genes and their parental copies. We show that, with the exception of one highly ampliconic gene shared across species (Spin2l), many Y-added genes are species-specific and exhibit expression patterns similar to those of their parental copies, with some genes being broadly expressed and others tissue-specific. Despite a positive correlation between gene copy number and tissue-specific expression, not all genes with high tissue specificity are testis-specific. Overall, these findings suggest that Y-added genes are not pre-adapted to testis function in Microtus voles and that, if Y-added genes acquire a testis-specific function, it evolves relatively slowly.

3:30 PM - 3:45 PM

Expression of Anthocyanin Pigments as a Response to Abiotic Soil Stressors in the California Native Plant Leptosiphon parviflorus

Weston Gonor, California Polytechnic State University
Magdalene Lo

Abstract:

Environmental stressors can often lead to fluctuating selection that maintains variation within populations and drives adaptation. In plants, anthocyanins, which are responsible for red, pink and blue colors, are often associated with protection against UV radiation, metabolic stress, and drought, suggesting their potential role in adaptation to harsh environments. Leptosiphon parviflorus Benth. (Polemoniaceae, variable linanthus) is an annual wildflower that exhibits a flower color polymorphism, with pink and white flowers co-occurring within populations. Despite this, variation in flower color prevalence has been seen across soil types. Harsh serpentine soils that are characterized by high magnesium and low water, tend to have a higher proportion of pink-flowered individuals.

To assess the role of anthocyanin pigments in response to abiotic soil stressors, Leptosiphon parviflorus was grown in a 2x2 factorial greenhouse experiment manipulating magnesium concentration and water availability across both flower color morphs. Expression of five genes relating to the anthocyanin biosynthesis pathway was quantified using qPCR for flower, leaf, and root tissue for each morph. In an adjacent study, fitness components were measured for each morph. Pink individuals exhibited higher expression of anthocyanin biosynthesis genes than white morphs with expression varying across tissues. However, white-flowered individuals had greater lifetime fitness regardless of soil treatment. These results suggest a potential fitness trade-off associated with anthocyanin production, which may contribute to the maintenance of flower color polymorphism across various environmental conditions.

Genomics IV

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Copy, Paste, Evolve: Dynamics of Multicopy Genes on the Y Chromosome

Swopnil Adhikari, UC Riverside
Polly Campbell, University of California Riverside

Abstract:

Although the mammlian Y chromosome is characterized by extensive degeneration, it has also acquired and amplified genes, many of which function in spermatogenesis. The mechanisms underlying the evolution of these Y-added multicopy gene families remain unclear. For example, we do not know whether Y-added multicopy gene families that are shared between closely related species retain orthologous copies inherited from a common ancestor or instead undergo independent lineage-specific amplification. To investigate this question, we analyzed two Y-linked multicopy gene families, Spin2l and Kmt5a, in seven closely related Microtus vole species. Copy number estimates for Spin2l varied by more than an order of magnitude across species, with close to 5,000 copies estimated for M. montanus and M. pennsylvanicus and fewer then 100 in M. ochrogaster and M. longicaudus. Kmt5a showed less extreme but still variable copy numbers across species. Phylogenetic analyses that included Y-linked Spin2l and Kmt5a copies recovered from non-Microtus rodents supported single ancestral retrotranspositions to the Y for both genes, with a longer tenure on the Y for Spin2l. Most Y-linked copies of Spin2l and all Y-linked copies of Kmt5a formed species-specific clades and gene trees largely recapitulated the species tree. This suggests that any signature of orthology among copies is erased by rapid, lineage-specific mutation and copy amplification/deletion. We also discovered Y-derived autosomal copies of Spin2l in all focal Microtus species. To our knowledge, this is the first case of a Y-added gene moving back to the genome shared by both sexes. The results of this study shed new light on one of the most rapidly evolving compartments of mammalian genomes, the Y chromosome.

2:45 PM - 3:00 PM
Sex chromosome turnover and mitonuclear conflict drive reproductive isolation

Rachel Moran, University of Chicago

Abstract:

Identifying the genetic basis of reproductive barriers is essential for understanding the origin and maintenance of biological diversity. While some hybrid incompatibilities evolve as incidental byproducts of divergence, theory predicts that sex chromosomes and cytoplasmic genomes can generate especially strong and repeatable barriers to gene flow through conflict, linkage, and constrained coadaptation. Yet tests of these predictions in natural systems with ongoing hybridization remain limited. Here, we combine whole-genome resequencing and experimental backcrosses in North American darter fishes to show rapid sex chromosome turnover. Across two hybrid zones involving closely related lineages, sex determination maps to different, nonhomologous chromosomes in the hybridizing partners, indicating two independent turnovers. Sex chromosomes show reduced introgression in hybrid zones and transmission distortion in hybrids. We also detect cytoplasmic-background–associated allele-frequency shifts concentrated on sex chromosomes and enriched near nuclear-encoded mitochondrial genes, consistent with cytonuclear selection contributing to postzygotic barriers. Finally, parental crosses and comparative genomic patterns support a recessive female-determining mutation underlying one turnover, providing a rare empirical example of a predicted but seldom observed route to sex

chromosome evolution. Together, these results implicate dynamic sex chromosomes and their linkage context as recurring features shaping hybrid genomes and reproductive isolation despite gene flow.

3:00 PM - 3:15 PM
Mitochondrial genome evolution in tinamous lice

Menglin Wang, Arkansas State University
Andrew Sweet, Arkansas State University

Abstract:

Mitochondrial genome fragmentation is an extremely unusual pattern in animal genome evolution, but its evolutionary consequences are still poorly understood. In some parasitic lice, the typical single-circulized mitochondrial genome is broken into several circular mini chromosomes. This makes lice an ideal system to study how genome structure may affect evolution at a molecular level. My current research focuses on lice from tinamous to test whether fragmented mitochondrial genomes are associated with the changes in AT content and codon usage bias. Using species-level mitochondrial genomic data with phylogenetic generalized least squares (PGLS) analyses, my results suggest that shared ancestry contributes to both the AT content and codon usage bias, and its effects may be stronger at the synonymous codon level than at the amino acid level. In the future, I hope to expand this research to a broader taxonomic scale in order to test whether these patterns are consistent across multiple louse lineages and fragmentation types. This broader approach will help provide new insight into the general principles linking genome structure and molecular evolution.

3:15 PM - 3:30 PM
Incorporating modes of phenotypic evolution into species delimitation of Psittacara parakeets

Julian Moulton, The American Museum of Natural History

Abstract:

Accurate species delimitation in morphologically conserved clades remains a persistent challenge in avian systematics. Psittacara parakeets, a clade of 22 Neotropical taxa, exemplify this challenge due to their conserved green plumage, overlapping ranges, and longstanding taxonomic controversies. We applied an integrative taxonomic framework combining whole-genome sequencing with comparative analyses of morphometric and plumage color variation to identify characters that reliably delimit taxa and to reconstruct evolutionary processes underlying phenotypic diversification across the genus. Genomic phylogenetic analyses recovered geographically structured major clades and deep divergence within the P. mitratus complex. Notably, P. m. hockingi and P. m. chlorogenys formed a strongly supported clade (~2.87 Ma divergence) distinct from remaining mitratus lineages, supporting hockingi as a distinct

evolutionary lineage rather than a juvenile variant or fully independent species. Morphometric traits showed strong phylogenetic signal (Pagel's λ = 0.986–1.000) and were better explained by Brownian motion models, consistent with gradual size divergence along phylogenetic lines. In contrast, plumage coloration exhibited weak phylogenetic signal and heterogeneous evolutionary dynamics across body regions, with Ornstein-Uhlenbeck models favored for most patches, particularly the throat and nape, suggesting stabilizing selection toward lineage-specific optima. Facial coloration showed the greatest intertaxa differentiation and likely functions in species recognition or social signaling. Together, these results demonstrate that morphology and plumage reflect distinct evolutionary processes in Psittacara. Morphometric traits track phylogenetic history and are unreliable for fine-scale delimitation, while facial plumage provides diagnostic signal at the species and subspecies level, particularly in sympatric populations. Integrating genomic and phenotypic data is essential for resolving species limits in morphologically conserved avian radiations.

3:30 PM - 3:45 PM
A Hemizygous Dichogamy Locus Reveals the Limitations of Single Reference Genomes

Joanna Rifkin, HudsonAlpha Institute for Biotechnology

Abstract:

Many complex traits, such as reproductive polymorphisms and Batesian pattern mimicry rings, depend on recombination-suppressed "supergenes" with complex genetic architecture. For example, a form of sequential hermaphroditism called dichogamy is common in flowering plants, which can promote outcrossing via temporally separating male and female flowering phases. In pecan, the two phenotypes (protogynous and protandrous) are determined by a single locus with two highly divergent alleles. The dominant G haplotype is roughly twice the length of the recessive g haplotype (445 kb and 220 kb, respectively), primarily due to elevated TE content. This structural complexity poses a challenge for traditional reference-based genotyping approaches: hemizygous sequences without appropriate reference regions are highly vulnerable to mapping bias, which can severely limit downstream inference. However, combining multiple reference haplotypes into a single pangenome graph structure allows for reliable typing of short and structural variants across this region, demonstrating the utility of graph structures to detect complex causal variants without requiring extensive a priori analyses to guide single-reference selection. Complex regions and presence-absence variation are increasingly appreciated as widespread and important in evolution, and therefore strategies to address these methodological challenges are essential to the future of the field.

Phylogenomics and Macroevolution

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Phylogeny and characterization of lipases in lipid-storing copepods

Maria Valadez Ingersoll, Woods Hole Oceanographic Institution
Sierra Brown, Woods Hole Oceanographic Institution
Ann Tarrant, Woods Hole Oceanographic Institution

Abstract:

Diapause is an adaptive state of low metabolic rate and developmental arrest that many taxa, from crustaceans and insects to embryonic mammal species, have evolved to survive adverse environmental conditions. Certain clades of copepods, large lipid-storing mesozooplankton, undergo developmentally-restricted diapause to survive extreme variations in food availability and other environmental challenges in their temperate and polar oceanic habitats. To prepare for diapause, these copepods store large volumes of lipids in specialized organs called oil sacs and are thus able to rely on these sequestered lipids while they overwinter at depth. Lipid-storing copepods use various lipases to break down lipids from different sources throughout their life cycle (i.e., food during active periods and stored lipid reserves during diapause). In vertebrates, the roles, tissues, and substrate specificities of different lipases have been characterized in high detail, including the evolutionary diversification of various lipases across clades (e.g., fish versus mammals). In copepods, and marine invertebrates in general, lipase characterization is significantly lacking, although lipid metabolism in these organisms has a critical impact on ecosystem and food web dynamics. Here, we have performed a phylogenetic analysis of lipases across 41 species of copepods, using neutral lipases from mammals, fish, and insects as reference. We have identified clades of copepod-specific lipases and additional putative copepod lipases belonging to the Pancreatic Lipase and the Carboxyl Ester Lipase clades. We have expressed and purified lipases from Calanus finmarchicus (a keystone lipid-storing copepod from the North Atlantic) and are currently working to determine the temperature and substrate specificities of these lipases. This work will have implications for our understanding of energy storage and consumption, especially in the context of development and diapause in marine invertebrates.

2:45 PM - 3:00 PM

Cytonuclear discordance in an island radiation: phylogenomic insights from Jamaican anoles

Inbar Maayan, Harvard University
Devon Main, University of Johannesburg
Alyssa Vanerelli, Rutgers University Camden
Scott Edwards, Harvard University
Jonathan Losos, Washington University

Anthony Geneva, Rutgers University

Abstract:

Adaptive radiations are the natural laboratories of evolutionary biology, allowing us to study how diversification unfolds. Their genomic histories, while richly informative about evolutionary processes and relationships, are often also marked by extensive conflict among loci, raising key questions: How should we interpret discordance between mitochondrial and nuclear phylogenies? What can discordance tell us about speciation dynamics, and to what extent do introgression and incomplete lineage sorting (ILS) shape relationships within clades as they radiate? And how can modern phylogenomic methods clarify relationships among species described long before genetic data became available? I use the Jamaican Anolis clade—the only monophyletic radiation among the classic Greater Antillean anole replicate radiations— to explore these questions and offer insights that can be applied more broadly. To elucidate the processes underlying previously reported cytonuclear discordance, we generated the most robust nuclear and mitochondrial phylogenies for the Jamaican clade to date, using the same samples for both trees. We recovered updated, well-supported relationships among all species and confirmed conflicting topologies: mitochondrial data render several species paraphyletic, whereas nuclear data recover them as monophyletic and infer different relationships among them. Our matched sampling revealed that the distinct intraspecific mitochondrial lineages also emerge as genetically distinct nuclear lineages, indicating repeatable evolutionary units despite topological discordance. To understand the underpinnings of this discordance, we reconstructed phylogenetic networks to capture reticulations in the clade's history, and assessed the relative contributions of introgression and ILS. Finally, we investigated the intraspecific lineage diversity identified above using an nDNA dataset of >700 samples. We found that species with distinct (and discordant) lineages exhibited elevated nucleotide diversity relative to others, and that those lineages are structured spatially across the landscape. Together, our findings help clarify the roles of non-treelike processes and highlight the value of understanding genomic diversity in adaptive radiations.

3:00 PM - 3:15 PM

Incomplete Lineage Sorting as a signature of selection across 15 million years of oak evolution

Kieran Althaus, University of Chicago
Andrew Hipp, The Morton Arboretum

Abstract:

How does natural selection, playing out across evolutionary timescales, affect the distribtion of variation across contemporary genomes? Understanding how these changes accrue over time, whether that be tens or millions of years, is of utmost importance in understanding the pace and mode of evolution. Information on past selection is commonly summarized with population genomic summary statistics, such as nucleotide diversity, and divergence. However, if the underlying geneology were known precisely, we could have direct access to the geneological

history (i.e. the coalescent history), from which these statistics were derived. Here, we use the signal of incomplete lineage sorting to reconstruct the history of selection during the radiation of Mexican oak trees. We infer the ancestral recombination graph (ARGs) under the multi-species coalescent to identify regions inflated for incomplete lineage sorting. By examining these patterns across multiple nodes in the phylogeny, we aim to identify common targets of selection that may have contributed to the diversification in this species rich clade.

3:15 PM - 3:30 PM
The Macroevolutionary Cost of a Physiological Innovation

Chase Brownstein, Yale University
Richard Harrington, Yale University
Julia Wood, Yale University
Laura Alencar, Yale University
Christine Thacker, Natural History Museum of Los Angeles County
Martha Muñoz, Yale University
Thomas Near, Yale University

Abstract:

Biological features that promote capitalization of novel resources can be fatal weaknesses when ecosystems suddenly change. Here, we examine the evolution of the swim bladder, which allows fishes to modify their position in the water column, using a phylogenomic analysis of >1300 species in a clade where swim bladder losses are concentrated. In the short term, swim bladder losses are associated with the origination of several iconic evolutionary radiations, especially in environments where this organ is costly or functionally prohibitive. Yet, losing the swim bladder has been a death knell during anoxic, warm period, including a bout of extreme global warming 56-45 million years ago. Our results show how rapid environmental change can dampen or reverse the effects of organismal biology on biodiversity accumulation.

3:30 PM - 3:45 PM
Mapping the Leopard's spots: Integrating genomic, ecological and landscape drivers of leopard (Panthera pardus) diversity and distribution

Danielle Del Castillo, Fordham University

Abstract:

As the most widely distributed felid, the leopard (Panthera pardus) serves as a model for understanding factors that shape diversity in wide-ranging carnivores. However, vast sampling gaps have historically obscured its phylogeographic structure. We assembled the most comprehensive genomic dataset to date (n=198), spanning the full range-extent of leopards, to investigate patterns of genomic variation. Mitochondrial genomes resolve seven Asian subspecies and three distinct African haplogroups. In contrast, nuclear genomes reveal weak structure and high levels of mito-nuclear discordance in Africa, likely driven by incomplete lineage sorting (ILS). Moreover, we

identify in Africa a Congo Basin diversity hotspot (Par II) and three sub-saharan lineages (Par I, II and III). Utilizing species distribution modeling (SDM) approaches, we demonstrate that African leopard lineages exhibit ecological niche partitioning, suggesting that environmental heterogeneity contributes to leopard distributional preferences and competitor avoidance. To identify the environmental basis for genomic variation, we employed Genome-Environment Association (GEA) tools (redundancy analyses, RDA). Within the PAR-II lineage, we identified candidate SNPs for local adaptation in genes linked to pigmentation (MITF) and sensory transduction (ANO2), as well as neuroprotective functions (MEIS3, WDR26). These signatures suggest that leopard genomes are tuned to specific landscapes and environmental architecture where camouflage and hunting performance may play important roles. By bridging the gap between landscape-level variables and molecular mechanisms, this work characterizes the evolutionary potential of a top predator facing a 70% historical range loss, providing a genomic baseline for both evolutionary theory and global conservation forensics.

Sexual Selection

06/23/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

The effects of urbanization on mating calls in the fall field cricket, Gryllus pennsylvanicus

Gracie Bellino, Case Western Reserve University
Ryan Martin, Case Western Reserve University

Abstract:

As cities continue to expand, understanding the impact of urbanization on animal behavior is critical. This study investigates how factors surrounding the urban environment influence the mating calls of the fall field cricket (Gryllus pennsylvanicus) in Cleveland, Ohio. Our project analyzed field recordings from six distinct sites, which displayed varying levels of urbanization, as measured by impervious surface area (ISA). We also collected data on the temperature, humidity, and ambient noise level for each recording, all of which are known to differ between urban and rural settings, and which are expected to impact cricket calling behavior. Our findings reveal that urban and rural crickets differ in some aspects of their mating call, and also that calls varied in relation to temperature. As warmer temperatures increase crickets' metabolic rates, they are known to chirp faster and higher-pitched. However, here we see that, at a given temperature, crickets in more urban sites displayed lower frequency chirps with more time between pulses and between chirps compared to their rural counterparts. This may indicate that urban males are more robust to changes in temperature due to regular exposure to the urban heat island. Alternatively, males are

chirping at lower pitches either due to inability to contribute increased effort or are doing so intentionally in response to urban noise.

2:45 PM - 3:00 PM
Age structure: an overlooked demographic factor shaping sexual selection

Vincent Formica, Swarthmore College
Butch Brodie, Mountain Lake Biological Station
Charlotte Charlotte Greene1, University of Virginia

Abstract:

As animals age, they exhibit well-documented changes in behavior and performance. As a result, populations that differ in age structure may present markedly different competitive environments. The ages of social partners thereby represent a dynamic social context that could have substantial impacts on how individual and group behaviors are expressed, and consequently on the targets and modes of natural selection. Other demographic factors, including density and operational sex ratio (OSR), are well known to influence spatial and temporal variation in selection across populations. Recent empirical work has examined how age structure influences population growth rate and density, as well as life-history evolution and social aging. However, how the age of social partners influences the landscape of selection is largely unexplored. Given the ubiquity of aging and the central role of social environments in behavior, we argue that the age structure of the population can be an important social determinant of variation in behavioral phenotypes and fitness. Here we review recent work supporting this hypothesis and highlight some of our own findings in forked fungus beetles (Bolitotherus cornutus) and discuss how age structure could provide a hidden link between ecology and social evolution.

3:00 PM - 3:15 PM
To Fight or to Sneak? Alternative Sex Ratios, Mating Tactics, and Male Morph Determination in Non-Pollinating Fig Wasps

Maya Killmade, University of Missouri- Columbia
Justin Van Goor, University of Missouri Columbia

Abstract:

Sex ratio theory predicts an evolutionarily stable 1:1 male: female ratio across obligately outcrossing panmictic populations. However, in species that experience local mate competition (LMC), such as haplodiploid pollinating fig wasps, mothers (foundresses) maximize their fitness by laying just enough sons to adequately mate with many daughters, resulting in a highly female-biased local sex ratio. Some non-pollinating fig wasps (NPFWs) present an additional layer of complexity: heteromorphic males. Such males present two distinct phenotypes- wingless ‘fighters’, who compete within the fig for mating opportunities, and winged ‘sneakers’, who can disperse from the fig to mate. There has been little investigation into the determination pathway of

fighters and sneakers. Thus, it remains a mystery whether foundresses can strategically distinguish between fighters and sneakers when ovipositing.

To address this, we first analyze the ratios of morphs to conditions of individual figs. Preliminary results indicate altered ratios under various conditions, suggesting strategic adjustments in morph ratios. With these results in mind, we then investigated morph determination systems. Genomic results indicate two potential pathways. From patterns in microbiome reads, a bacterial component to morph determination, as in Wolbachia pathways in Nasonia wasps, is feasible. Additionally, there may be chromosomal differences that allow females to choose morph type during fertilization, or that are altered post-translationally to alter phenotypes. By investigating the mechanisms and strategies behind alternative mating tactics, we can gain insight into their relationship to sexual selection and sex ratio theory.

3:15 PM - 3:30 PM
Linking pre- and postmating traits: acoustic communication and gonadal investment across treefrogs

Pedro Aguiar, Federal University of Juiz de Fora
Cynthia Prado, Pós-Graduação em Ecologia
Steafan Lüpold, University of Zurich
Renato Nali, Universidade Federal de Juiz de Fora

Abstract:

The intensity and direction of sexual selection may vary depending on mating systems. Under these conditions, sperm competition theory predicts trade-offs between pre- and postmating investment, whereas the phenotype-linked fertility hypothesis predicts positive covariation between these traits. In frogs, acoustic signaling plays a key role in shaping social and reproductive dynamics. We tested whether acoustic traits and gonadal investment show patterns consistent with these alternative predictions across 85 species of true treefrogs (Hylidae). Acoustic, morphological, and reproductive data were compiled from the literature, and phylogenetic generalized least squares (PGLS) models were used to test relationships between call traits and gonadosomatic index (GI), a measure of testes mass relative to body mass, controlling for body size and temperature when appropriate. To account for phylogenetic uncertainty, analyses were conducted across 100 trees. Temporal acoustic traits were associated with temperature, and spectral traits were strongly associated with body size, consistent with expected evolutionary patterns across species. Dominant frequency showed a strong and consistent negative relationship with GI (N = 65), which was maintained across 97 trees and remained independent of body size, indicating that species with lower-frequency calls, typically associated with larger body size and increased mating success, also exhibit greater gonadal investment. No other acoustic traits showed consistent associations. These results are consistent with the phenotype-linked fertility hypothesis and suggest that this mechanism may drive coevolution between dominant frequency and gonadal investment, indicating that acoustic signals may convey reliable information about male fertility at a macroevolutionary scale.

3:30 PM - 3:45 PM

The Role of Cuticular Hydrocarbons Within Male Laupala Mate Recognition and Choice

Gabriel Martinez-Amezaga, Shaw Lab
KERRY SHAW, Cornell University

Abstract:

Sexual isolation is a critical prezygotic barrier driving speciation, a process fundamental to the generation of biodiversity. Within insects, cuticular hydrocarbons (CHCs), a thin nonvolatile wax layer present on the cuticles of all insects, have been co-opted for the mediation of chemical communication in sexual behavior across many species, positioning them as a compelling candidate for the study of mechanisms driving sexual isolation. In this study, I investigated the role CHCs play in male mate recognition within Laupala, the most rapidly speciating arthropod genus, where sexual isolation is the likely principal driver of their speciation. Through a novel "painting" method which transfers conspecific female CHCs onto heterospecific antennae, I conducted a paired behavioral assay to observe differences in male L. kohalensis behavior when exposed to "painted" vs "unpainted" female L. kona antennae. Males exhibited significantly more pumping behavior, a key marker of sexual receptivity, and spent more cumulative time antennating when exposed to painted antennae in contrast to unpainted antennae. To validate the painting method, I conducted a gas chromatograph assay analyzing CHC profiles of painted L. kona antennae in comparison to unpainted L. kona antennae and L. kohalensis antennae possessing donor CHCs. A principal component analysis confirmed that CHC profiles were significantly altered and shifted toward donor profiles when treated with the novel painting method. In tandem, these results provide promising evidence for the role of CHCs within Laupala conspecific mate recognition, suggesting CHC-mediated communication may contribute to the strong sexual isolation of this rapidly speciating genus.

Evolutionary Ecology: Adaptation

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Evolution of nitrogen fixation related phenotypes in wild and cultivated maize

Keyvan Maleki, Ohio State University
Layne Connolly, Ohio State University
Nicola Lorenz, Ohio State University
Richard Dick, Ohio State University
Kristin Mercer, Ohio State University

4:30 PM - 4:45 PM

Patterns of selection on rice varieties grown under different environmental conditions in a common garden field experiment

Gabriella Quartuccia, Fordham University
Isaura Rosas-Reinhold, Center for Genomics & Systems Biology
Mignon Natividad, International Rice Research Institute
Yu-Chen Lin, Center for Genomics & Systems Biology
Isabel Bojanini, Center for Genomics & Systems Biology
Amelia Henry, International Rice Research Institute
Michael Purugganan, Center for Genomics and Systems Biology
Steven Franks, Fordham University

4:45 PM - 5:00 PM

Genomic predictability and evolutionary limits of adaptation in Arabidopsis thaliana

Laura Leventhal, Carnegie Institution for Science/ Stanford University
Megan Ruffley, Carnegie Institution for Science
Moises Exposito-Alonso, Howard Hughes Medical Institute

Abstract:

As climate shifts faster than populations can evolve, predicting the genomic limits of adaptation has become a central challenge in evolutionary biology. While accumulating genomic knowledge could be used to predict population extinction risk from maladaptive genetic composition, testing such predictive approaches in natural environments remains challenging. This work integrates two complementary approaches to test both the predictability and the limits of adaptation in Arabidopsis thaliana. First, leveraging the genomic resources of A. thaliana, we created experimental synthetic populations of similar genetic diversity but differing genetic composition by mixing 245 natural accessions that differed in the frequency of climate-associated alleles and the genomic burden of putatively deleterious mutations, and planted them in a multi-year, multi-level precipitation manipulated common garden. Population survival and growth were highly predictable from genomic composition: deleterious burden and climate maladaptive alleles synergistically reduced fitness under increased drought stress. These results demonstrate that standing genomic variation influences population persistence under climate stress. Second, in a meta-analytic framework, we combined fitness data of 1,600 unique A. thaliana accessions across 42 common gardens spanning broad climatic gradients and modeled thermal performance curves while allowing genotype-specific shifts in climatic optima. This global analysis reveals a mean thermal adaptation lag exceeding 1oC, indicating that accessions perform best at climates cooler than their home environment. Even an annual species capable of rapid turn over appears unable to fully track modern rates of warming. Together, these results show that while evolutionary outcomes can be forecast from genomic data, adaptation may be too slow to match contemporary climate change.

By linking controlled genomic experiments with broad meta-analysis, this work illuminates both the predictability and evolutionary limits of climate adaptation.

5:00 PM - 5:15 PM
Phenotypic responses to urbanization in squamate reptiles: Insights from a global meta-analysis

Tiberiu Sahlean, Institute of Biology Bucharest
Petronel Spaseni, Alexandru Ioan Cuza University of Iasi
Ryan Martin, Case Western Reserve University

5:15 PM - 5:30 PM
Rapid Divergence Along a Multidimensional Niche

Maria Kalambokidis, University of Minnesota
Nahui Medina Chavez, University of Minnesota
Caleb Smithberg, University of Minnesota
Mike Travisano, University of Minnesota

Abstract:

The abundance of life is shaped by the ability to grow, particularly in environments that are considered extremely harsh. Does the ability to grow under harsh conditions necessarily trade-off with growth in more benign environments, or does it depend upon evolutionary history? The scope and specificity for adaptation are reflected in niche breadth. A species' niche has been widely explored by measuring abundances across environments, with specialists and generalists distributed among a narrower or larger range of conditions, respectively. Experimental evolution studies provide a unique opportunity to investigate multidimensional niche evolution. We explored adaptation and niche breadth in two halophilic species which are highly convergent phenotypically yet distinct phylogenetically. We find significant divergence in niche breadth evolution among bacterial and archaeal lineages. Fitness tradeoffs rapidly emerge for bacterial populations, whereas fitness gains are observed for archaeal populations in novel environments, particularly for archaeal lineages selected in the poor environment. While the two species have a similar ancestral fitness in either environment, we find that their ancestral niche breadths are indicative of specialist and generalist strategies for bacterial and archaeal populations, respectively, underscoring how knowledge of a species' niche breadth may provide predictive power in anticipating its evolution.

Experimental Evolution III

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

The past as prologue: how evolutionary history shapes antibiotic resistance and informs treatment

Kyle Card, Cleveland Clinic

Abstract:

The global rise of antibiotic resistance poses a significant threat to public health. Accurately predicting how resistance evolves is a promising strategy for combating this problem. However, this goal is complicated when a lineage's prior history influences its future evolution. Our early work using experimental Escherichia coli populations established this principle, showing that genetic background can sometimes limit resistance and direct evolution along specific mutational pathways. Building on these findings, our recent work investigates the evolution of vancomycin resistance in the opportunistic pathogen Staphylococcus aureus. We discovered that resistance emerges via at least two distinct evolutionary pathways: one involving changes to cell wall metabolism and the other altering the global stress response. Critically, these distinct routes create different vulnerabilities, resulting in predictable but opposing collateral sensitivities to other antibiotics. By quantifying the probability of each outcome, we developed a framework for understanding how a pathogen's history shapes its susceptibility to future treatments. Ultimately, our work argues for a shift toward dynamic, evolutionarily-informed therapeutic strategies that anticipate microbial evolution to preserve the efficacy of our most crucial antibiotics.

4:30 PM - 4:45 PM

Outcrossing Limits Genomic Resilience by Retaining Structural Variants Under Mutagenic Stress

Rohit Kapila, Florida International university
Jasbelle Sosa, Florida International University
Janna Fierst, Florida International University

Abstract:

While classical theory predicts that outcrossing enhances the efficiency of selection by facilitating the purging of deleterious mutations, emerging empirical evidence suggests that this advantage may be context-dependent. Here, we investigate how mating system variation shapes genomic resilience under mutagenic stress using Caenorhabditis elegans as a model system. Leveraging genetically tractable fog-2 (obligate outcrossing) and xol-1 (male-deficient, effectively selfing) mutants, we combine experimental evolution, controlled mutagenesis, and whole-genome sequencing to quantify mutation accumulation and purging dynamics across reproductive modes.

Our preliminary results reveal that outcrossing populations can retain large structural variants (SVs) spanning megabase-scale genomic regions, which in turn harbor and shield numerous linked single nucleotide polymorphisms (SNPs) from purifying selection. In contrast, selfing populations exhibit more efficient purging of such variants, leading to reduced genomic burden under sustained stress. Integrating empirical data with forward-time simulations, we test the hypothesis that recombination, while beneficial in breaking linkage among weakly deleterious mutations, may paradoxically slow the removal of large-effect structural mutations under specific genomic and environmental conditions.

4:45 PM - 5:00 PM

Can induced mutations substitute for natural variation? Evaluating fast neutron mutagenesis as a tool for evolutionary ecology

Inam Jameel, University of Michigan
Regina Baucom, University of Michigan

Abstract:

Understanding the origins and maintenance of phenotypic variation is a central goal of evolutionary ecology, and identifying the drivers of ecologically relevant trait variation requires experimental populations that harbor sufficient variation. Critically, experimental populations should reflect the genotype-by-environment interactions present in realistic contexts, since plasticity can shape evolutionary trajectories. We examined whether populations derived from fast neutron mutagenesis capture biologically meaningful variation in comparison to natural populations generated from among-population crosses. Specifically, we compare F2 intercross and 30 Gy fast neutron mutant populations of the agricultural weed Ipomoea purpurea across varying watering regimes and herbicide exposure. By measuring a suite of traits related to flower size, foliar traits, mating system, and reproductive phenology, we ask whether these two experimental populations differ in the magnitude of trait variance, genetic variance among lines, phenotypic plasticity, and fitness consequences of trait variation. Our results suggest that fast neutron mutant populations recapitulate, and occasionally exceed, variation in ecologically relevant traits. While patterns of genetic variance differed between the populations, fast neutron mutagenesis generates lines that may harbor causal mutations for trait variation. This work demonstrates the value of mutagenesis as a complementary tool in evolutionary ecology.

5:00 PM - 5:15 PM

Epistatic mutations drive incidental antimicrobial sensitivity in Escherichia coli during adaptation to intermediate feast–famine cycles

Ashlynn Bruder, Vanderbilt University

Abstract:

Microbial populations experience fluctuations in resource limitation in nearly all environments, and adapting to navigate these fluctuations is key to their survival. Here, we identify the rapid evolution of antimicrobial susceptibility in populations of Escherichia coli within the first 300 days of experimental evolution under 10-day cycles of repeated feast and famine. Using longitudinal metagenomic sequencing of the evolving populations, we identified candidate parallel mutations in a gene encoding a primary outer membrane porin, ompF, and acrB, a gene involved in multidrug efflux. To investigate how these mutations might contribute to adaptation to recurring starvation, we reconstructed mutations in ompF and acrB, both individually and in combination. We assessed these mutants against their ancestor for competitive fitness, antimicrobial susceptibility, and growth on diverse carbon sources. Competitive fitness assays revealed effects consistent with positive epistasis between ompF and acrB after 1-day of culture, and reciprocal sign epistasis after 10-days. We confirm that these mutations contribute to the increased antimicrobial susceptibility latent phenotype observed across multiple classes of antimicrobials. And dissected the physiological effect of each mutation, confirming that while loss of AcrAB activity is beneficial during 1-day feast/famine, mutations in ompF serve a compensatory function to limit uptake of toxic metabolites during 10-day culture in the absence of acrB. Overall, we conclude that adaptation to fluctuating resources can lead to unexpected tradeoffs and that utilizing these approaches can identify the quantitative genetics underlying the emergence of latent phenotypes.

5:15 PM - 5:30 PM

Evolution of cell differentiation in long-term multicellularity evolution experiment

Sayantan Datta, Georgia Institute of Technology

Abstract:

The evolution of cell differentiation is a critical step in the transition to multicellularity, playing a central role in the evolution of increased organismal complexity. Because the ancestors of extant multicellular organisms are long extinct, understanding how differentiation originates in simple, homogeneous multicellular systems remains challenging. Using our Multicellularity Long Term Evolution Experiment (MuLTEE), in which snowflake yeast are selected for larger size, we demonstrate that two novel cell states evolved over 5,000 generations of laboratory evolution. Single-cell RNA sequencing revealed phenotypic heterogeneity in gene expression within the ancestral snowflake yeast, providing raw material for differentiation that was subsequently

reinforced and amplified. After 1,000 generations, the first novel state emerged, characterized by upregulation of cell-wall biogenesis genes that increase physical toughness. By 4,000 generations, a second novel state arose, marked by high expression of stress response genes underlying increased rates of apoptosis: a simple form of developmentally-regulated cell death that facilitates multicellular reproduction through the release of propagules from tough, entangled clusters. Our findings demonstrate that pre-existing phenotypic heterogeneity within nascent clonal multicellular organisms can give rise to distinct cell states, enabling rapid evolution of cell differentiation and providing insights into the early stages of this major evolutionary transition.

Floral Evolution

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM
Evolution of trait loss along altitudinal and latitudinal gradients

Ava Garrison, Michigan State University
Jeff Conner, Kellogg Biological Station
James Bingman, Michigan State University

Abstract:

The family Brassicaceae is home to over 4000 plant species, including important crop and weed species. A diagnostic trait that unites nearly all Brassicaceae plants is tetradynamy, or the possession four long medial stamens and two short lateral stamens. However, in the primarily selfing species Arabidopsis thaliana, short stamens are not useful for self-pollinating and are being lost. The loss of short stamens is incomplete and follows altitudinal and latitudinal clines, with populations at higher altitudes and latitudes retaining more short stamens and populations at low altitudes and latitudes losing them nearly completely. We present our results from reciprocal transplant experiments at altitudinal and latitudinal extremes to explore the roles of selection and pleiotropy on the loss (and retention) of short stamens.

4:30 PM - 4:45 PM
Differential regulation of PELAN in the petal lobe and corolla tube of Mimulus verbenaceus

Laurel Eddins, University of Connecticut
Amy LaFountain, University of Connecticut
Yaowu Yuan, University of Connecticut

Abstract:

Flower color is an important evolutionary trait which allows plants to attract specific pollinators. The hummingbird pollinated Mimulus verbenaceus produces a bright red flower through anthocyanin accumulation controlled by the R2R3-MYB transcription factor PELAN (PETAL LOBE ANTHOCYANIN). Given the temporal nature of its activation, PELAN is hypothesized to be regulated by upstream transcription factors involved in developmental processes, although precise regulators underlying its spatial and temporal expression remain unknown. During flower bud development, anthocyanin pigmentation is first displayed in the petal lobe and appears later in the corolla tube once the bud has reached approximately 15mm. CRISPR-Cas9 was used to generate stable M. verbenaceus transgenic lines with deletions in the PELAN promoter region. Multiple mutant lines display mature flowers with bright red petal lobes and yellow corolla tubes. Although previous work confirms that PELAN is responsible for the activation of structural anthocyanin genes in both the petal lobe and the corolla tube, this observation suggests that the regulation of petal lobe coloration is decoupled from that of the corolla tube. To ascertain the nature of this differential regulation, we analyzed regions of the promoter whose deletion generated the decoupled phenotype to identify the binding sites of important regulatory elements and performed RNA sequencing to determine differential expression of potential upstream regulators at four developmental milestones. The ultimate goal of this work is to determine the mechanisms dictating temporal and spatial regulation of floral coloration in M. verbenaceus and provide insights into the importance of cis-regulatory evolution in floral pigmentation.

4:45 PM - 5:00 PM
Flower color evolution in Penstemon

Haylee Coffman, University of Kansas

5:00 PM - 5:15 PM
Loci responsible for evolution of a hummingbird-adapted Penstemon species

Lena Hileman, University of Kansas
Aidan Short, University of South Carolina
Samson Acoca-Pidolle, University of Kansas
Solomon Scheiner, University of Kansas
John Kelly, KU
Carrie Wessinger, University of South Carolina

5:15 PM - 5:30 PM
Early responses to artificial selection on floral longevity

Rachel Spigler, Temple University

Geographic Variation

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Untangling potential drivers of adaptive thermal trait variation in a California salamander

Daniel Oliveira, University of California

Abstract:

Environmental change poses a significant risk for organisms facing increasing climatic extremes and variability. For dispersal-limited organisms, such as many salamander species, responses to climate change are limited to “in situ” mechanisms, including adaptation from standing genetic variation, phenotypic plasticity, or thermoregulatory behaviors. Here, I investigate patterns of local adaptation in thermal tolerance across the California distribution of the Ensatina salamander (Ensatina eschscholtzii). To identify potential drivers of intraspecific variation, I correlate thermal tolerance with historic and contemporary thermal and moisture regimes. I then use future climate projections to investigate parts of the distribution where existing physiological limits are likely to be exceeded by the end of the century. We find temperature variability, rather than mean or maximum temperatures, to be a stronger selective driver of thermal tolerance variation. Vulnerability to thermal extremes appears region-specific, suggesting microhabitat selection, plasticity, or behavioral mechanisms may play an important role in the persistence of certain populations. Ongoing work includes integrating genomic data to assess the extent of standing genetic variation in this species and identify genotype-environment associations, which will provide insight into how adaptive variation is structured under a distribution facing climate warming.

4:30 PM - 4:45 PM

Trait variation within and among provenances explains drought responses in plants from different climates of origin

Miranda Shetzer, Holden Arboretum

Abstract:

Climate change is altering drought regimes which can have major consequences on plant performance and evolutionary processes. Rhododendron minus is an evergreen shrub native to the Southeast United States, spanning different climates and elevations across latitudes. This region is predicted to experience increased drought intensity due to greater evaporative demand from raising temperatures. To advance the understanding of native plant drought responses, it is imperative to investigate sources of intraspecific variation. R. minus presents an interesting study system as plants from the northern region of the species range experience different potential selective factors like colder temperatures and exposure on montane rock outcrops compared to southern plants.

Although currently described as one species, it is debated whether the taxonomic status should be revisited with the possibility that R. minus represents two species. Previous studies indicate distinct physiology between plants from northern and southern provenances. To understand the genetic component of this variation, we implemented a clonal design using 6 provenances along the species range, with 2-3 genotypes per provenance. Clones were subjected to drought and well-watered conditions in a manipulative experiment designed to investigate within versus among provenance variation. Linear mixed-effects models with provenance, treatment, and their interaction as fixed effects and genotype as a random effect revealed no significant interaction between provenance and treatment for any trait examined. We did see a significant effect of treatment on water use traits, indicative of drought stress, but the lack of significant provenance X treatment interaction revealed that drought response was similar across provenances despite different climates of origin. Conversely, linear models investigating within provenance variation showed significant interactions between genotype and drought treatment for traits of certain provenances. If within-provenance variation is higher than among-provenance variation, then plasticity in some genotypes could help buffer plants of a particular location from changing environments.

4:45 PM - 5:00 PM

The macroevolutionary and macroecological drivers of thermal sex-ratio reaction norm variation

Caleb Krueger, W. K. Kellogg Biological Station
Marc Girondot, Ecology
Fredric Janzen, Michigan State University

Abstract:

For some species, gonadal sex determination relies on environmental cues and thus ought to match local conditions, which can be accomplished through changes in maternal behavior and / or the sex-ratio reaction norm. Here, we investigate the evolution of the latter at broad spatial and phylogenetic scales for turtle species with temperature-dependent sex determination (TSD). We find evidence that pivotal temperatures (Tpiv, where a 1:1 offspring sex ratio is produced) increase with average temperatures during incubation, but only over macroevolutionary time, while on contemporary timescales, they increase with incubation temperature variability. Limited evidence also indicates that the breadth of the logistic-shaped reaction norm decreases with temperature variability, contradicting expectations and suggesting this reaction norm feature may relate to intrinsic biological factors rather than to environmental conditions alone. In sum, these findings indicate that adaptive sex-ratio reaction norm variation within turtle species with TSD is driven by climate variability, while adjustments to the maternal behavior of nest site choice may primarily compensate for differences in climate averages.

5:00 PM - 5:15 PM

Serial founder effects and rapid phenotype evolution during Atlantic colonization in monarch butterflies

Drew Schield, University of Virginia
Megan Alderman, University of Virginia
Dylan Highland, University of Virginia
Rebecca Safran, University of Colorado at Boulder
Scott Villa, Davidson College
Jacobus de Roode, Emory University

5:15 PM - 5:30 PM

The Presence of Microbial Mutualists Limits the Geographic Distribution of Astragalus, the Most Species-Rich Plant Genus

Mike Grillo, Loyola University Chicago

Abstract:

Understanding the mechanisms that generate and maintain biodiversity remains a central challenge in evolutionary biology. While abiotic factors are often emphasized in shaping species' geographic distributions, biotic interactions—particularly mutualisms—may play an underappreciated role in limiting range size and promoting diversification. This is especially relevant for Astragalus, the most species-rich genus of plants, which exhibits strikingly patchy and restricted distributions across landscapes.

We tested the hypothesis that interactions with nitrogen-fixing bacteria (rhizobia) constrain the geographic distributions of Astragalus species and contribute to ecogeographic reproductive isolation. Focusing on ten Astragalus taxa in southern California, spanning both narrow and broad geographic ranges, we first developed species distribution models (SDMs) incorporating climatic and edaphic variables to estimate habitat suitability. While these models capture abiotic constraints, they do not explicitly account for the distribution of mutualistic partners.

To evaluate the role of rhizobia, we conducted a greenhouse experiment using soils collected from sites predicted to have high and low habitat suitability. Across 1,500+ plants, we quantified nodulation success as a proxy for successful plant–microbe interaction. Contrary to expectations based solely on abiotic suitability, nodulation occurred in only ~25% of soils and did not differ between high- and low-suitability habitats for any taxon. Furthermore, follow-up experiments revealed that rhizobia limitation can occur at very fine spatial scales, even among soils collected within a single field.

These results demonstrate that compatible rhizobia are not ubiquitously distributed across the landscape and can limit plant establishment independent of abiotic conditions. Such spatial heterogeneity in mutualist availability provides a mechanistic explanation for the patchy

distributions observed in Astragalus. More broadly, our findings suggest that plant–microbe interactions can contribute to ecogeographic reproductive isolation and may play an important role in the diversification of this exceptionally species-rich genus.

Phylogenetic Comparative Methods II

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Neo-sex chromosomes are not correlated with ecology or environment in eutherian mammals

Jimmy Choi, University of California
Polly Campbell, University of California Riverside
Jonathan Hughes, Arizona State University

Abstract:

The XX/XY chromosome system is highly conserved in therian mammals. Despite this evolutionary persistence, multiple variant sex chromosome systems exist in mammals. The potential contribution of genomic conflict to the evolution of neo-sex chromosomes has been studied extensively, while the influence of climate and ecology on the emergence and persistence of neo-sex chromosomes is less well understood. Building on previous literature that suggests ecoclimatic factors can influence intralocus sexual conflict and other forms of genome evolution, we tested whether neo-sex chromosomes in mammals are associated with these factors. We conducted a phylogenetic logistic regression in three representative mammal families using a dataset of variant mammalian sex chromosomes and a database of tetrapod traits and environmental associations. We also incorporated a dataset of mammal karyotypes to test for potential signatures of meiotic drive. When using a single phylogeny, none of the seven ecoclimatic variables tested nor chromosome morphology were significantly correlated with neo-sex chromosomes. However, correlations between neo-sex chromosomes and both range size and mean annual temperature were sensitive to differences in tree topology, demonstrating the importance of accounting for alternative evolutionary hypotheses in comparative methods.

4:30 PM - 4:45 PM

A hierarchical Bayesian framework for simultaneously inferring evolutionary and intraspecific covariances applied to great ape dental development

Levi Raskin, University of California
Maja Šešelj, Department of Anthropology
Bárbara Bitarello, Department of Biology
Wonseop Lim, Department of Integrative Biology

Jacky Li, Biostatistics Division
Mackie O'Hara, Department of Biology
John Huelsenbeck, Department of Integrative Biology

Abstract:

Inferring the evolutionary history of extinct and extant species is a core goal of evolutionary biology, but intraspecific variation and small sample sizes can bias inferences of evolutionary processes. Phylogenetic methods that accommodate intraspecific variation on a species-specific basis exist for univariate, uncorrelated continuous traits. However, for multivariate, correlated continuous traits, the only available methodologies assume that the covariance structure is shared across all tips. This assumption often is frequently violated, particularly when sample sizes differ across species, or when rapid evolution and restructuring occurs within a clade.

Through the normal inverse Wishart conjugacy, we infer a unique variance-covariance matrix for each species in the phylogenetic tree as well as the species mean. We then model the evolution of this true species mean on a given phylogenetic tree under multivariate Brownian motion and jointly infer the evolutionary variance-covariance matrix alongside the intraspecific parameters. We demonstrate the utility of this model by applying it to a great ape, modern human, and Neandertal developmental dataset of lower canine perikymata counts per decile.

Perikymata are growth increments visible on the surface of dental enamel that reflect approximately one week of enamel deposition. The distribution of perikymata across the tooth crown is highly variable within and across great apes, and perikymata cannot always be observed across the entire crown in a given individual. By jointly estimating inter- and intraspecific variation, we show that modern humans and Neandertals exhibit substantial overlap in perikymata distribution, as do most other great apes when compared within genera. We also show that later-forming enamel evolves substantially faster than cuspal enamel across the great ape clade, suggesting a mosaic of developmental and evolutionary constraints. Jointly modeling inter- and intraspecific variation more robustly characterizes evolutionary rates and covariances, and we expect this framework to be broadly applicable across macroevolutionary questions.

4:45 PM - 5:00 PM

Leveraging deep learning to infer the evolution of chromosome size and count

Raymond Castillo, Washington University in St. Louis
Rosana Zenil-Ferguson, University of Kentucky
Michael Landis, Washington University in St. Louis

Abstract:

Variation in chromosome number and size can be observed widely in both plants and animals, largely being a product of structural changes in genome architecture. The specific mechanisms that influence this also vary widely as observed in plants. Plants have a long history of repeated whole-genome duplication (WGD) followed by subsequent re-diploidization. This diploidization process is

guided by both cytological diploidization (e.g. fusion) and genic fractionation. Current chromosome evolution models like ChromoEvol and ChromoSSE aim to characterize chromosome number, yet few consider the morphology and size of the chromosomes themselves. One reason for this limitation is due to the constraints of state-dependent speciation extinction models have on state-space size. Here we present a novel model that explicitly models chromosome size and number, allowing us to model events outlined in ChromoEvol and ChromoSSE in addition to new event types that can govern chromosome size and count such as fusion and fission. Due to the sheer size of the state space in our model, ranging from thousands to millions of unique states, we leverage deep learning, using the Python package phyddle, to obtain parameter estimates. Simulations are conducted using either a birth-death process or over a fixed topology. We outline the accuracy of parameter estimates under different model conditions and different methods of encoding empirical data.

5:00 PM - 5:15 PM
Evaluating phylogenetic support for Paleoptera across multiple frameworks and simulation

Aaron Goodman, University of Illinois Urbana-Champaign
Dominic Evangelista, University of Illinois Urbana Champaign

Abstract:

A classic problem of insect phylogenomics is the relationships among the three major winged insect lineages (Odonata, Ephemeroptera, and Neoptera) – the Paleoptera problem. While most transcriptomic studies support a sister relationship between Odonata and Ephemeroptera (Paleoptera), substantial conflicting support persists. While confident cases are elusive, past research suggests that identifying sources of conflicting signal, and correcting for them, could hypothetically resolve these kinds of difficult phylogenetic controversies that are all-too-common. Here, we assess support for the three competing hypotheses of the Paleoptera problem (Paleoptera, Metapterygota, Chiastomyaria) using a highly curated transcriptomic dataset. By integrating complementary approaches for tree inference, data-quality filtering, and support evaluation, we develop a multifaceted pipeline to maximize phylogenetic signal, disentangle sources of error, and identify conflicting signal across loci. This holistic framework allows us to generate hypotheses about the causes of phylogenetic uncertainty and test their plausibility using simulation. Results from quartet-based analyses mostly supported Paleoptera, although alternative topologies were also recovered frequently. Gene-likelihood comparisons revealed strong model sensitivity, with approximately 42% of loci changing their preferred topology between model-aware and model-free approaches. Furthermore, anomaly-zone analyses, among-lineage rate heterogeneity (ALRH), and simulation tests suggest that incomplete lineage sorting and branch-length asymmetry contribute to conflict at this node. Our results refine support for Paleoptera while also providing a general framework for disentangling persistent phylogenomic conflict at other contentious nodes across Insecta.

5:15 PM - 5:30 PM

The evolution of ant symbiosis traits in lycaenid caterpillars

Trey Scott, Harvard University
Naomi Pierce, Harvard University

Abstract:

Symbiotic interactions where different species live together often result in partners evolving novel symbiosis traits. An interesting case of this is in caterpillars of butterflies in the family Lycaenidae. Lycaenid caterpillars use novel organs to gain protection from ants. In addition to ant manipulating organs, lycaenid caterpillars tend to evolve carnivorous diets far more often than other caterpillars. Our understanding of how these novel organs and diets evolved has been limited by the lack of a well sampled phylogeny for the Lycaenidae. To fill this gap, we have generated a genus-level phylogeny of the Lycaenidae. Using ample life history data, we found that ant association drives the emergence of novel organs and carnivorous diets in lycaenids. Lycaenids may thus represent a useful model for understanding how symbiotic interactions affect the evolution of new traits.

Sexual Selection and Conflict

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Sexual conflict and gene conversion shape the maintenance of repetitive sequences on the sex chromosomes of Drosophila melanogaster

Adolfo Delgado, Texas A&M University
Mahul Chakraborty, Texas A&M University

Abstract:

The non-recombining Y chromosome of Drosophila is a critical locus for sexually antagonistic genes, yet its highly repetitive sequence has obscured our view of male-limited repeats involved in sexual conflict. We investigate the Stellate-Suppressor of Stellate (Ste/Su(Ste)) system, an example of genomic conflict where X-linked selfish elements (Ste) are silenced by Y-linked piRNA-producing arrays (Su(Ste)). Because Drosophila males lack meiotic recombination, these sex chromosomes evolve through distinct mechanisms of concerted evolution that operate in the absence of crossing over. Using repeat-aware assembly merging of long-read sequencing data, we resolved the Y-linked Su(Ste) array across three strains of Drosophila melanogaster, providing the first complete map of genetic variation of these repetitive arrays. We find X-linked Stellate arrays exhibit localized homogenization between adjacent units, consistent with distance-limited gene conversion. In

contrast, Y-linked Su(Ste) arrays show exceptional homogeneity across their entire ~2.5 Mbp array, likely to counteract the mutational decay due to the lack of recombination in Y (Muller's ratchet). Within the Su(Ste) array, we identified distinct alternating domains of homogenization, which suggest that the absence of recombination, potentially coupled with a specialized 3D architecture, facilitates long-range concerted evolution within the chromosome. These dynamics reflect distinct selective pressures: while Stellate copy number is constrained by its toxic overexpression in males, Su(Ste) is under selection to maintain high copy numbers and sequence identity to ensure effective piRNA-mediated silencing. Our work suggests a model wherein sexual conflict and gene conversion facilitate the evolution and maintenance of a complex repeat landscape in nonrecombining chromosomes.

4:30 PM - 4:45 PM

Independent origin of genomic imprinting in placental fish

David Reznick, University of California
Ying Zhang, Department of Pathobiology
Polly Campbell, University of California Riverside
Alec Kingsley, Dept. of Biology
Yuridia Reynoso, Department of Evolution
Yuan Kang, Dept. of Anatomy
Chen-Che Jeff Huang, Dept. of Anatomy
John Werren, University of Rochester
Xu Wang, Auburn University College of Veterinary Medicine

Abstract:

Genomic imprinting results in biased expression of one parental allele. Such non-Mendelian expression occurs in angiosperms and placental mammals, which share having an active paternal genome during maternal offspring provisioning. It is hypothesized that imprinting modulates conflict between maternal control of resource allocation and paternal control of resource acquisition. If true, then imprinting should evolve in any organism that evolves a placenta. Here, we demonstrate genomic imprinting in a placental poeciliid fish, Poeciliopsis prolifica. Using transcriptomes from reciprocal crosses between two inbred strains, we identified 84 protein-coding genes with robust evidence of imprinting in P. prolifica placenta. These include a pair with opposing effects on glucose metabolism that are imprinted in a fashion that potentially resolves parental conflict. Our discovery is the first demonstration of genomic imprinting in a non-mammalian vertebrate and supports the potential role of imprinting in resolving parental conflict.

4:45 PM - 5:00 PM

Bagworm moths: a new model for studies of genome evolution across variable levels of sexual dimorphism, from mild to extreme.

Christina Watkins, The University of Florida
Andrew Mongue, University of Florida

Abstract:

Sexual dimorphism is intriguing because each sex within a species shares the same genomic information while manifesting striking, sex-specific phenotypes. Although this topic has received substantial attention, inferences are often limited as most examined systems exhibit mere modifications of a shared body plan. Therefore, systems containing varying degrees of dimorphism are needed to clarify how sex-specific phenotypes arise. One such system is the Bagworm moths (Lepidoptera: Psychidae). In this conserved ZZ/Z0 system, females exhibit a continuum of body plans: fully winged, half-winged, wingless, and vermiform (which lack most typical adult characters). Males retain fully developed wings/ appendages. Paired with peculiar reproductive ecologies, Psychidae provide a powerful model for examining how variation in sexual dimorphism shapes genome evolution.

Here, we introduce Psychidae as a comparative system, present preliminary results, and outline efforts to characterize genomic variation using a phylogenetic framework. Leveraging publicly available data and in-house generated chromosome-level assemblies, we explore how shifts in female form relate to genome architecture, including structure, divergence rates, genetic novelty, and heterozygosity. Initial analyses reveal overall highly conserved synteny, with gene movement onto and off the Z chromosome largely confined to vermiform lineages. The Z chromosome also contains proportionally more novel genes than autosomes in highly dimorphic species. Expression patterns indicate increased female-biased novelty in the winged-to-wingless transition, while vermiform evolution involves novel genes expressed in both sexes. Together, this work highlights Psychidae as an integrative system for the examination of sex chromosome dynamics, chromosome rearrangement, and sexual dimorphism within a single evolutionary framework.

5:00 PM - 5:15 PM

Evidence for a genetic correlation between parasite resistance and female mate preference

Payton Schaefer, University of Cincinnati
Michal Polak, University of Cincinnati

Abstract:

Female avoidance of parasitized mates is widely documented in animals, suggesting that parasitism plays an important role in sexual selection. If females prefer parasite-free males and parasite resistance is heritable, theoretical models predict the build-up of genetic covariance between resistance and female preference. However, empirical tests of this prediction are rare. We examined the effect of ectoparasitic mites, Gamasodes pachysetis, on female mate choice in their natural host, Drosophila albomicans. In the laboratory, currently parasitized males elicited more rejection from females than never-parasitized and previously parasitized males. These rejection responses were associated with reduced copulation success, indicating female preference for parasite-free mates. We then conducted twelve generations of artificial selection for increased parasite resistance. Resistance increased consistently across three replicate lines, indicating that

resistance is heritable. Females from selection lines were also less likely to mate with parasitized males than control females, consistent with a correlated response in female mate preference to selection for resistance, suggesting a genetic correlation between resistance and preference. These findings provide rare empirical support for the predicted genetic coupling of these traits.

5:15 PM - 5:30 PM
Modeling the Resolution of Sexual Conflict using a Network Approach

Andy Grieve, University of Virginia
Katja Kasimatis, University of Virginia
Nicholas Landry, The University of Virginia

Abstract:

Sexual conflict arises because males and females share most of their genome while experiencing opposing selection on shared traits. Numerous molecular mechanisms (alternative splicing, gene duplication, etc.) have been proposed to resolve this conflict by decoupling fitness effects between the sexes. However, existing theoretical models typically examine these mechanisms in isolation and do not address how genomes are biased towards available resolution pathways or how this choice is constrained by regulatory architecture. We developed a network-based theoretical framework that treats sexual conflict resolution as a dynamic process occurring within shared gene regulatory networks. In this model, genes, transcripts, and proteins are represented as nodes connected by regulatory and functional interactions, while different resolution mechanisms are implemented as modifications to network structure, parameters, or topology. The model is dynamic, allowing regulatory interactions and node states to evolve under mutation and sex-specific selection. Network properties such as connectivity, modularity, robustness, and node centrality were quantified to capture biologically interpretable features of sexual conflict, including the number of genes indirectly affected by antagonistic selection, the extent to which regulatory changes propagate across the genome, and the stability of sex-specific regulatory states once they emerge. Model outputs included time to conflict resolution, trajectories of transient genetic load during adaptation, and sensitivity analyses identifying regulatory architectures that favor rapid but costly versus slower but more stable resolution pathways. This framework generates testable predictions about when different resolution mechanisms are expected to dominate and what genomic or transcriptomic signatures, they should leave behind. By integrating population genetics with network theory, this work helps to advance sexual conflict research from descriptive case studies toward a predictive, mechanistic understanding of how conflict is resolved across genomes, providing a foundation for empirical tests in natural populations and experimental evolution.

Systematics

06/23/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM
Why taxonomy matters: lessons from ray-finned fishes

Thomas Near, Yale University

4:30 PM - 4:45 PM
Genetic data challenge morphological species boundaries in North American mantleslugs

Ashlyn Silliman, Mississippi State University
Megan Smith, Mississippi State University

4:45 PM - 5:00 PM
Integrative insights into the evolutionary history of Jamaican onychophorans (Onychophora, Peripatidae)

Pooja A. Anilkumar, The George Washington University
Gonzalo Giribet, Museum of Comparative Zoology
Tom Nguyen, National Museum of Natural History
Hannah Wood, Smithsonian Institution
Gustavo Hormiga, The George Washington University

Abstract:

Onychophora (velvet worms) are exclusively terrestrial panarthropods with limited dispersal abilities and highly conserved morphology. The phylum currently comprises more than 230 accepted extant species in two families, Peripatidae and Peripatopsidae. Members of Peripatidae occur across the Neotropics, West Africa, India, and Southeast Asia. Within the Neotropics, peripatids form the clade Neopatida, with most species assigned to the genera Epiperipatus, Macroperipatus, and Peripatus, which have been circumscribed largely by body length. However, relationships within Neopatida remain difficult to resolve because of nomenclatural uncertainty and outdated taxonomic descriptions. Across the Caribbean, 22 species of onychophorans have been reported from 12 islands. Of these, Jamaica harbors five endemic species, each currently placed in a distinct genus: Epiperipatus lewisi, Macroperipatus clarki, Peripatus swainsonae, Plicatoperipatus jamaicensis, and Speleoperipatus spelaeus, representing a unique case among Caribbean onychophorans. Previous studies using Sanger sequencing and ultraconserved elements (UCEs) included fewer than ten Jamaican specimens, which formed a clade and challenged the validity of these generic distinctions. In this study, we aim to assess the true species diversity and evolutionary relationships of Jamaican onychophorans within the island as well as in

relation to Caribbean and mainland taxa. To achieve this, we expanded taxon sampling from eight to 24 specimens, incorporating both freshly collected material from type localities as well as historical museum material, but were not able to include Speleoperipatus spelaeus. Our results reveal that Plicatoperipatus jamaicensis has a broader distribution across Jamaica than previously recognized, with pronounced population structure between eastern and western regions of the island, as well as within these populations. Phylogenomic analyses, combined with preliminary morphological observations from scanning electron microscopy (SEM), micro-computed tomography (micro-CT), and light microscopy, suggest that the diversity of Jamaican onychophorans may be overestimated, with our data supporting three species rather than five. Overall, this study highlights the value of integrative approaches for revealing the true diversity and evolutionary relationships within this understudied animal group.

5:00 PM - 5:15 PM

Systematics, divergence time, biogeography, and trait evolution of the dragonfly genus Erythemis Hagen, 1861 (Anisoptera: Odonata)

Katherine Montana, American Museum of Natural History
John Abbott, Alabama Museum of Natural History & UA Museums Department of Research and Collections
Kendra Abbott, Alabama Museum of Natural History & UA Museums Department of Research and Collections
Lacie Newton, Department of Biological Sciences
Rhema Uche-Dike, American Museum of Natural History
Aaron Goodman, University of Illinois Urbana-Champaign
Seth Bybee, Brigham Young University
Rob Guralnick, Florida Museum of Natural History
Jessica ware, Ware Lab

Abstract:

The dragonfly genus Erythemis Hagen 1861 comprises 10 species distributed across the Western Hemisphere with a variety of genital morphologies, abdomen shapes, and flight activity levels. Here we resolve intrageneric relationships of this group, reconstructing the most comprehensively sampled phylogeny for Erythemis based on anchored hybrid enrichment (AHE) data. Using an Erythemis fossil as calibration, we estimate the divergence time of the genus to be most likely about 25 million years ago, around the transition between the Oligocene and Miocene. A reconstruction of the ancestral range of the genus reveals a likely origin in central and South America, with subsequent dispersal into the Caribbean. We also perform a likelihood-based ancestral character state reconstruction to test morphological synapomorphies for the group: interspecific variation in male genitalia morphology is notable, with certain penis characteristics evolving multiple times. We also find variation in abdomen shape and size among species that could be linked to dispersal patterns. Thus, our phylogeny allows us to explore the evolutionary history of flight adaptations, and related thermoregulation, in a changing climate and geological landscape, also discussing the decoupling of genital evolution from phylogenetic relationships.

5:15 PM - 5:30 PM

Combing through louse evolutionary history: expanding knowledge of Anoplura

Kayce Bell, Natural History Museum of LA county
Priscilla San Juan, Natural History Museum of Los Angeles County
Lance Durden, Georgia Southern University
Edward Stanley, Florida Museum of Natural History
Jessica Light, Texas A&M University
Julie Allen, Virginia Tech

Artificial Selection

06/24/26: 9:30 AM - 10:45 AM

9:45 AM - 10:00 AM

Demographic history, selective sweeps, and gene network domestication of Asian rice revealed by 3,485 accessions

Shujun Ou, The Ohio State University

Abstract:

The origin and diversification of Asian rice (Oryza sativa) remain contentious owing to confounding effects of demographic history, introgression, and selection. Here we reanalyzed whole-genome sequences of 3,485 cultivated and wild rice accessions (17.7 million SNPs) to disentangle these processes. We identified a shared domestication bottleneck approximately 13,000–15,000 years ago that reduced effective population size to 0.1%, and show by forward simulation that this bottleneck alone can generate the polyphyletic patterns underlying the multiple-origin debate. Local ancestry analysis, after removing introgressed regions, supports a single domestication from the Or-3A ecotype in the Pearl River basin of southern China. Machine-learning sweep classification reveals that soft sweeps predominate across all cultivated subpopulations, with ecotype-specific selections in stress tolerance, nutrient uptake, and grain quality driving post-domestication diversification. Selected genes in cultivated—but not wild—rice exhibit significantly elevated co-functional network connectivity and density, demonstrating that domestication preferentially targeted functionally connected gene modules. Within the flowering-time regulatory network, histone-modification factors show the highest selection rate (68.8%), followed by transcription factors (41.7%), while downstream integrators remain conserved. These findings reframe crop domestication as a network-level evolutionary process.

10:00 AM - 10:15 AM
Line Cross Analysis of Aggression in Betta splendens

Kenzie Laird, Texas A&M University
Paige Maxa, Texas A&M University
Kiedon Bryant, Texas A&M University
Andres Barboza, Texas A&M University
Heath Blackmon, Texas A&M University

Abstract:

Aggression is a deeply conserved behavioral trait shaped by both natural and sexual selection. Understanding the sources of variation in aggression remains a central question in behavioral ecology. Betta splendens (Siamese fighting fish) provide an exceptional model for studying aggression as domestic strains have been selectively bred for male fighting ability for over 600 years, while wildtype populations retain ancestral behavioral phenotypes (Ramos and Gonçalves 2019). We compared aggressive behavior between male and female B. splendens from domestic, wildtype, first-generation hybrid, second-generation hybrid, and backcrossed strains. Aggressive displays were video recorded and quantified through the use of machine learning algorithms. Findings on wild type and domestic fish in this study corroborated the findings of previous studies in the field. The addition of hybrid cohorts under a line cross analysis framework allowed for the elucidation of the genetic architecture underlying this aggressive phenotype.

10:15 AM - 10:30 AM
Parallel selection across agricultural weed genomes

Acer VanWallendael, North Carolina State University

Abstract:

Agricultural weeds include some of the best contemporary examples of rapid eukaryotic evolution under both natural and artificial selection, showing repeated evolution of traits such as herbicide resistance and phenology. However, it remains a challenge to diagnose the genomic, environmental, and chance factors that contribute to any particular population of a species becoming resistant, partially because most studies focus on either a single species or a single generation. To better understand how parallel selection drives genetic variation across space, we sampled tissue from five nuisance weed species with different mating systems and genome structure at twenty locations in the southeast as well as one outgroup in Michigan. These species include Amaranthus palmeri (dioecious diploid), Erigeron canadensis (native selfing diploid), Cyperus esculentus (invasive asexual holocentric), Ipomoea purpurea (invasive outcrossing diploid), and Sorghum halepense (invasive perennial tetraploid). This project is designed to be replicated yearly to follow population-level allele frequency changes over time using pooled whole-genome sequencing and annotation of rapidly evolving genes. In the first year, we found clear differences in population genetic structure across outcrossing and selfing/asexual species. We tracked genetic variation in genes related to herbicide resistance and metabolism across space to

detect parallelism. These results contrast the roles of mutation and gene flow driving genetic diversity across species facing similar selection, but different life history traits. In future years, measuring directional changes in allele frequencies in these same populations will allow testing of hypotheses about the drivers of evolution rate in plants under high artificial selection pressure.

Computational Biology

06/24/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Integrative Machine learning framework for rice phenotype prediction-Generalization tests and consilience with association studies

Minju Kim, Fordham University
Sonal Gupta, New York University
Michael Purugganan, Center for Genomics and Systems Biology
Steven Franks, Fordham University
Simon Groen, University of California

9:45 AM - 10:00 AM

Preserving plant RNA or: How I learned to stop worrying and love phyloherbariotranscriptomics

Alexa Tyszka, University of Illinois at Chicago
Joseph Walker, University of Illinois Chicago
Drew Larson, Indiana University

Abstract:

Transcriptomic studies enhance our knowledge of the tree of life and are a cost-effective means of obtaining large amounts of genetic information. The most restrictive step of obtaining transcriptomes is preserving RNA using cold temperatures. Ultracold preservation is thought to be necessary due to the fragility of the molecule. However, RNA persists for decades in herbarium specimens and mammal skins preserved in museums. The influence a lack of ultracold storage has on RNA preservation in plant tissues on a short time scale is unknown. I will discuss some promising avenues of obtaining RNA using different treatments, with the aim of describing the relationship between dessication and RNA quality. What might preserved plant specimens be suitable for, and how can we address RNA degradation across long and short time scales? How can we make informed choices about the advantages and disadvantages of each treatment condition we use?

10:00 AM - 10:15 AM

PhyDA: phylogenetic data augmentation for robust genomic modeling under sparse data conditions

Heather Sestili, Carnegie Mellon University

Abstract:

Machine learning enables powerful tools for genomic analysis, driving significant advances in gene therapies and revealing new insights in comparative genomics. However, in many cases, small datasets limit the effectiveness of these approaches. Deep learning models of cell type-specific enhancer accessibility — regulatory elements that are known to control gene expression and are key to these analyses — thrive on large, diverse training datasets. When sufficient data is available, these models can accurately capture complex biological patterns. However, when data is scarce, a frequent concern with rare cell types and studies with non-model organisms, model performance can decrease substantially. Multiple-genome alignments may provide a promising way forward in settings where data is limited. In this study, we introduce Phylogenetic Data Augmentation (PhyDA), a novel data augmentation method based on orthologous sequences, regions of the genome that share an evolutionary origin across different species. For each enhancer sequence in the training set, PhyDA adds corresponding orthologs in related species, expanding the size of the positive set in a way that honors phylogenetic relationships. We show that PhyDA improves machine learning model performance in sparse-data scenarios. These results suggest improvements for gene therapies in rare cell types, and comparative genomics approaches across non-model organisms.

10:15 AM - 10:30 AM

Subgenome differentiation in a N. American tetraploid fish

Johnathan Lo, UC Berkeley

Abstract:

Whole genome duplications (WGDs) have long been a subject of fascination in evolutionary biology (e.g. Ohno). These sudden increases in genetic material are rare in vertebrates and concentrated primarily among amphibians and fish. While the subject of much evolutionary theory, sequencing technologies have only recently matured to an extent where it is possible to deeply explore the evolutionary and adaptive consequences of WGDs. Studying WGDs can reveal genomic patterns in diversification, such as biased gene loss, gene family expansions, expansions of repetitive elements, and the timing of these occurrences. Here we performed long read sequencing and genome assembly of 13 species of the tetraploid genus Catostomidae, which is one of the most speciose families of fish native to North America. These genomes present a compelling paradox to researchers - a whole genome duplication coupled with relatively stable karyotypes over deep evolutionary time, arising from the fusion of relatively similar progenitor lineages. We find not only substantial lineage specific differences in gene loss over time, but also a shared amplification of repetitive sequences post-duplication that may be involved in maintaining separation between

subgenomes with otherwise high similarity. We identify a variable number tandem repeat that distinguishes subgenomes in a clade-specific pattern, and show extensive subgenome dominance both with subgenome-specific loss of function mutations and differential accumulation of large structural variants. Finally, we identify recurrent chromosomal fusions associated with unique signatures of subgenome dominance across clades. Together, we trace the evolutionary consequences of an ancient tetraploidization event in high resolution over 60 million years providing unique insights into the origins and impact of karyotype evolution.

10:30 AM - 10:45 AM
Machine learning prediction of plant polyploidy from target capture data

Fahimeh Rahimi, University of Florida
Jessie Pelosi, University of Arizona
Gordon Burleigh, University of Florida
Juannan Zhou, University of Florida

Abstract:

Polyploidy is a pervasive feature of plant evolution and plays a central role in adaptation, speciation, and diversification. However, inferring ploidy levels across diverse plant samples remains challenging. With the increasing use of targeted capture sequencing, existing methods typically rely on read frequency–based approaches.

Here, we develop a machine learning framework to infer ploidy directly from targeted capture data. Using GoFlag datasets, we trained convolutional neural networks (CNNs) for individual probe loci to classify samples as diploid or polyploid, and evaluated whether combining information across multiple probes improves prediction accuracy. Models were trained and tested on 616 fern samples with ploidy levels determined from chromosome counts.

Our approach achieves high predictive performance, reaching up to 90% accuracy for individual loci and outperforming existing methods such as nQuire and nQuack, which use genome-wide data. We further identify characteristics of loci associated with improved prediction and show that model performance is relatively robust to variation in read depth. We also validate our approach using an independent dataset from the fern genus Lygodium, where ploidy levels have been experimentally confirmed.

Although developed using fern GoFlag data, this framework provides a scalable approach for ploidy inference and has the potential to extend to a wide range of plant systems.

Gene Flow

06/24/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Average tree height is a reliable statistic for accurate estimation of ghost introgression in phylogenomic datasets

Ethan Tolman, Virginia Tech
Asif Iqbal Rahaman, Virginia Tech
Anton Suvorov, Virginia Tech

Abstract:

A growing body of empirical research shows that interspecific gene flow is a widespread biological force that shapes evolutionary histories across the Tree of Life. Computational approaches designed to detect introgression either employ full likelihood, including Bayesian frameworks, to directly estimate phylogenetic networks or utilize summary statistics derived directly from locus sequence alignments or estimated gene trees to map gene flow events onto the species tree. Many current methods currently have major shortcomings. The computationally scalable summary statistics and pseudo-likelihood-based techniques may provide erroneous results in the presence of so-called “ghost” introgression and rate variation between lineages. On the other hand, full likelihood methods are more accurate, but are not computationally tractable for large phylogenomic datasets. Here, we develop a novel summary statistic, based on tree heights of different gene tree topologies to reliably distinguish between sampled and ghost introgression events. We implemented this approach in the publicly accessible bioinformatic pipeline “GhostParser”. We demonstrate that GhostParser can accurately distinguish between scenarios of sampled and ghost introgression, even in the presence of rate variation between lineages.
Our methodology concurs in accuracy with the full likelihood software Bayesian Phylogenetics and Phylogeography (BPP) on empirical datasets, and outperforms BPP in our simulation conditions, both in a small fraction of the computational time. We show that GhostParser is a scalable tool for the identification of different introgression patterns in phylogenomic datasets.

9:45 AM - 10:00 AM

From lab to landscapes: range-wide patterns of variation at mito-nuclear incompatibility loci in Neodiprion pine sawflies

Able Chow, University of Kentucky
Ashleigh Glover, University of Kentucky
Jakeb Watts, University of Kentucky
Serena Limberg, University of Kentucky
Kayleigh Dobson, University of Kentucky
Catherine Linnen, University of Kentucky

10:00 AM - 10:15 AM

Inferring the demographic history of Chinese and Indian rhesus macaque (Macaca mulatta) populations from PacBio HiFi sequencing data

Erangi Heenkenda, Arizona State University

Abstract:

The rhesus macaque is one of the most widely used animal models in biomedical research, both as it resembles humans in key biological aspects and as it is characterized by a broad geographic range. Most of the individuals in research populations have been sampled from either China or India, though notably the source population of these animals has significantly shifted over time, rendering a deeper understanding of underlying population structure important for biomedical interpretation. Despite this, the demographic histories of these two populations remains poorly resolved. Here, we present the analysis of whole-genome, PacBio HiFi long-read sequencing data from 10 unrelated individuals from each population, applying four related model- and non-model based demographic inference approaches, in order to reconstruct their ancestral history. We evaluated the fit of the subsequently estimated models against the empirical data, and incorporated underlying uncertainty in the mutation rates used for scaling. We inferred a well-fitting population history characterized by substantial structure between Chinese and Indian populations, with a split time ~140,000 generations ago from an ancestral population of ~65,000 individuals. We additionally inferred the subsequent history of size change within, and gene flow between, these populations, reaching the current estimated sizes of ~220,000 individuals in the Chinese populations and ~14,000 individuals in the Indian population. The robust baseline demographic model established in this study will serve as a valuable resource for future research on this species, including for improved fine-scale recombination mapping, selection inference, and association studies.

~~10:15 AM - 10:30~~ AM WITHDRAWN

~~*Introgression and reproductive isolation in Mimulus monkeyflowers*~~

~~**Megan Frayer, Yale University**~~

Host/Parasite Evolution I

06/24/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Mechanisms of association with amoeba hosts are shared by Paraburkholderia symbionts amid differential responses based on evolutionary history

Suegene Noh, Colby College
Calum Stephenson, Washington University in St. Louis
David Queller, Washington University in St. Louis
Joan Strassmann, Washington University in St. Louis
Susanne DiSalvo, Southern Illinois University Edwardsville

9:45 AM - 10:00 AM

Monsters inside (some) of us: Elevation-dependent consequences of botfly infection in deer mice

Sarah Senese, Univeristy of Denver
Jon Velotta, University of Denver
Nathan Senner, University of Massachusetts Amherst
Zachary Cheviron, University of Montana

10:00 AM - 10:15 AM

Evolution of virulence in tripartite systems: Life-history trade-offs constrain symbiont-vectored pathogens

Senay Yitbarek, University of North Carolina at Chapel Hill

Abstract:

Background/Question/Methods

Pathogen virulence evolution is typically studied in bipartite host-pathogen systems, yet most pathogens exist within complex ecological communities involving vectors, symbionts, and host-associated microbiota. Understanding how tripartite interactions shape virulence remains a key challenge in disease ecology. The entomopathogenic nematode Steinernema carpocapsae and its mutualistic bacterium Xenorhabdus nematophila offer an experimentally tractable system spanning three trophic levels: bacteria are vectored by nematode infective juveniles (IJs) through soil into insect larvae, where they cause rapid septicemia while suppressing host immunity. Empirical work has shown that bacterial fitness peaks at intermediate bacterial loads, suggesting life-history trade-offs constrain virulence. We developed an adaptive dynamics model to identify

the eco-evolutionary mechanisms underlying this pattern, decomposing fitness into within-host (parasitic) and between-host (dispersal) components. Using invasion fitness analysis, we determined conditions under which rare mutant strains with altered virulence can invade resident populations at ecological equilibrium. We constructed pairwise invasibility plots to visualize the fitness landscape and identify singular strategies where selection gradients vanish, then assessed evolutionary and convergence stability to characterize long-term evolutionary outcomes.

Results/Conclusions

Our analysis reveals that higher virulence increases within-host exploitation by killing insect hosts before immune clearance, yet reduces nematode IJ survival during dispersal due to metabolic costs of maintaining larger bacterial populations. The evolutionarily stable virulence strategy represents an optimal balance between these competing selective pressures, determined by the ratio of vector mortality to virulence-dependent dispersal costs. This intermediate optimum is both evolutionarily and convergence stable. Our results demonstrate how ecological trade-offs spanning distinct life-history stages jointly constrain virulence evolution in symbiont-vectored pathogens. This framework extends classical virulence-transmission trade-off theory to tripartite systems involving hosts, parasites, and their symbionts, and generates predictions for how changes in vector survival or host immunity may shift optimal virulence levels.

10:15 AM - 10:30 AM

Parasite adaptation to common hosts: experimental evolution in a biological control system

Abbey Ramirez, University of Virginia

Abstract:

The Red Queen Hypothesis predicts that parasites evolve to infect common host genotypes, generating reciprocal selection that can maintain genetic diversity in host–parasite systems. Despite its prominence in evolutionary theory, experimental tests of these dynamics remain limited, particularly in applied systems where parasite evolution may influence biological control. Understanding if and how parasites evolve to infect common host genotypes has important implications for the effectiveness and application of parasites as a biological control.

Here, we use Meloidogyne arenaria, a devastating agriculture pest and its natural bacterial parasite, Pasteuria penetrans, to test whether parasites evolve to better infect the host genotype in which they are passaged on. Parasites from a genetically diverse population were passaged for five generations on four replicate lines of five host genotypes and then assayed via parasite attachment across all sympatric and allopatric host–parasite combinations. Parasites exhibited significantly higher attachment rates in sympatric combinations compared to allopatric combinations (p These findings support key predictions of the Red Queen Hypothesis while highlighting that evolutionary responses should be taken into consideration when planning and implementing biological control programs.

10:30 AM - 10:45 AM
Nutrient provisioning or generalism: two processes that enable parasites to live on nutrient deficient diets

Kelly Speer, Northern Arizona University

Life History

06/24/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM
Social context shapes male life histories under female promiscuity

Antonio Rodrigues, Texas A&M University
Rebecca Kilner, University of Cambridge
Stephen Stearns, Yale University

Abstract:

Classical life-history theory struggles to explain positive correlations between reproductive traits. Using a theoretical model, we show that male-male competition under female promiscuity produces incidental cooperation, reshaping trade-offs and generating within-population diversity. Social environment, relatedness, and mode of dispersal further mediate these dynamics, offering a unifying explanation for unexpected life-history patterns across species.

9:45 AM - 10:00 AM
Gene expression in two different food levels in Daphnia pulex

Amirhossein Nezafatianfardjahromi, University of South Carolina
Jeff Dudycha, University of South Carolina

10:00 AM - 10:15 AM
Life history evolution of southwestern U.S. plants reveal divergent strategies among annual, biannual, and perennial species

Anish Basnet, Ohio University
Joshua Brokaw, Abilene Christian University
Larry Hufford, Washington State University
John Schenk, Ohio University

10:15 AM - 10:30 AM

Following from Embryo to Metamorphosis: Tadpole Development Under Different Exposure Routes of TCDD

Camryn Kritzell, University of Houston
Raquel Salla, University of Houston
Molly Albecker, Northeastern University

Abstract:

Globally, amphibian populations are declining in part due to degrading environmental quality. Chemical pollutants, such as 2,3,7,8 tetrachlordibenzo-p-dioxin (TCDD), are an important and persistent presence in wetlands that can lower the quality of the habitat. TCDD, for instance, is a toxic thyroid hormone disruptor that affects development, endocrine systems, and survival of vertebrates. TCDD is found in trace amounts in wetlands around the globe, and one of the primary exposure pathways occurs through ingestion of contaminated food. However, earlier amphibian studies only investigated exposure through water. It is unknown whether the exposure route (through water or diet) affects survival and developmental outcomes. To determine the effect of exposure route on amphibian development, we exposed Incilius nebulifer (Gulf coast toads) tadpoles to five concentrations (0.001, 0.01, 0.1, 1, 10 µg/L) of TCDD using either food- or waterborne exposure. We tracked survival, development, and size through metamorphosis, and sampled for histological effect on the liver post metamorphosis. Our results show that although embryos show insignificant effect, outcomes at later stages are more severe when TCDD exposure occurs through dietary pathways . Of those that survived to reach metamorphosis, outcomes are driven by both concentration and exposure routes

---

Macroevolutionary Methods and Models

06/24/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Leveraging trajectory trees to summarize phylogenetic character maps

Sean McHugh, Washington University in St. Louis
Michael Landis, Washington University in St. Louis

Abstract:

When reconstructing phylogenetic character histories, biologists aim to identify distinct evolutionary trajectories, or paths of character state evolution. However, biologists typically must summarize many potential character histories for a single phylogeny. For discrete characters, few approaches exist for summarizing the number of unique evolutionary trajectories beyond the

frequency of specific events (i.e., state transition types) or the time lineages spend in each state. Here, we introduce a framework for summarizing the evolutionary trajectories of discrete character histories by compressing them into trajectory trees, where branches represent unique character-evolution pathways rather than lineages. We apply several approaches to summarize phylogenetic trees into transition trees. We include visual summaries, such as "trajectory through time plots," to compare how unique evolutionary trajectories accumulate across lineages and state transitions. We also include quantitative summaries, such as the time spent in unique evolutionary trajectories and the number of transitions that follow unique character-state transitions. This framework includes a novel compressed tree representation, called a scenario tree, that retains temporal information, ensuring that each root-to-tip path represents a unique, temporally explicit evolutionary trajectory. We use our new trajectory-wise summaries to evaluate the adequacy of commonly used continuous-time Markov models of character evolution, which are memoryless and consider only the rates between pairs of states. We conducted multiple simulation-based experiments demonstrating the utility of our novel trajectory-wise approaches. We also apply our new trajectory-wise approaches to Greater Antillean Anolis lizard biogeography and ecomorph evolution, and find that Anoles evolved along considerably more unique evolutionary trajectories than expected under simulations of our best-fitting character evolution model. The number of unique evolutionary paths accumulated in an "early burst" pattern relative to simulated trajectories, with this burst being more intense than expected across all character state transition events.

9:45 AM - 10:00 AM
bifrost: an R package for scalable inference of phylogenetic shifts in multivariate evolutionary dynamics

Jake Berv, University of Michigan
Nathan Fox, University of Michigan
Matt Thorstensen, University of Toronto
Henry Lloyd-Laney, University of Oxford
Emily Troyer, University of Michigan
Rafael Rivero Vega, University of Michigan
Stephen Smith, University of Michigan
Matt Friedman, University of Michigan
David Fouhey, New York University
Brian Weeks, University of Michigan

Abstract:

Access preprint here: https://www.biorxiv.org/content/10.64898/2026.04.12.718036v1

Abstract: High-dimensional comparative datasets, including geometric morphometric landmarks, functional traits, and other large trait datasets, are increasingly common in biology. When these datasets include a large number of traits relative to the number of taxa, they pose significant challenges for phylogenetic comparative analysis. In addition, evolutionary dynamics are often heterogeneous across phylogenies, challenging researchers to develop tools that can localize and

account for such variation when investigating hypotheses of evolutionary change. We present bifrost, an R package for detecting and characterizing shifts in multivariate trait evolution across phylogenetic trees. bifrost implements a stepwise greedy search over alternative macroevolutionary regime configurations on a phylogeny. Candidate shifts are proposed and assessed at internal nodes, accelerated with parallel model fitting where possible, and aggregated sequentially when they exceed a user-defined information-criterion acceptance threshold. The underlying model is a scalar-rate multivariate Brownian motion process fit by generalized least squares using mvMORPH::mvgls. Our framework also provides support estimates for individual shifts using information-criterion weights. We illustrate the workflow using a fossil-tip-dated phylogeny and high-dimensional landmark data for early bony fish jaws (32,508 scalar coordinate values), and discuss tuning, outputs, and limitations. bifrost extends existing phylogenetic comparative frameworks for evolutionary analysis and provides a scalable pipeline for exploring the phylogenetic natural history of large multivariate datasets.

10:00 AM - 10:15 AM
Making sense of phylogenetic signal

Donald Swiderski, University of Michigan
Miriam Zelditch, University of Michigan

Abstract:

It is now common to use Phylogenetic Comparative Methods to quantify and correct for the effect of phylogenetic signal on statistical analyses of interspecific variation. Typically, these studies report the amount of phylogenetic signal and what they did to avoid statistical error; but they don't tell you much about the phylogenetic signal. This lack of further analysis of phylogenetic signal is consistent with its characterization as "noise" and a product of Brownian motion. However, the historical relationship of phylogenetic signal to concepts like phylogenetic inertia and ancestral constraint suggests it may be more informative than that. In this presentation we will argue that phylogenetic signal merits deeper analysis. We will briefly review the relationship of phylogenetic signal to older concepts, then discuss the conceptual shift embedded in modern quantitative comparative studies. Finally, we will show that that commonly used methods have the potential to produce broad, homogeneous summaries that may obscure the variety of phylogenetic signals that could be present in a diversifying clade, but which generally remain unexplored.

10:15 AM - 10:30 AM
Multilevel analysis of modularity and integration

Miriam Zelditch, University of Michigan
Donald Swiderski, University of Michigan

Abstract:

Morphological integration is widely recognized at multiple levels, including the individual (developmental and functional), the population (genetic, environmental and phenotypic) and

lineage (evolutionary). How these levels are related has been an enduring question and some clear predictions exist, such as that, if lineages evolve by Brownian motion, the genetic covariance matrix (G) will be proportional to the evolutionary covariance (R). Few studies have compared covariance matrices across multiple levels and assessed both the heterogeneity within levels as well as the differences between them. In this analysis, we use a classic model system for studies of integration, a rodent mandible, to analyze the covariance matrices of shape at three levels: (1) development: assayed by the covariance matrix of fluctuating asymmetry, which is structured by direct interactions within developmental pathways, (2) population: phenotypic covariance matrices, and (3) evolutionary: evolutionary covariance matrices of two lineages nested within the third. We find heterogeneity within each level although covariance matrices at the same level are often proportional. The differences are far larger between levels. If the evolutionary covariance matrices are estimated assuming Brownian motion, the main dimension of variation is the direction in which evolutionary and FA covariance matrices differ; phenotypic covariance matrices are orthogonal to both of those. If branch lengths are transformed, the dominant axis of variation distinguishes FA from phenotypic variation; evolutionary covariance matrices are orthogonal to both those along the second dimension. Our results show that the structure of direct developmental interactions does not predict the structure of phenotypic integration nor does phenotypic integration predict the structure of evolutionary integration. At each level, covariance structures are reshaped by processes emerging at that level.

10:30 AM - 10:45 AM

Future diversification potential of species can be predicted by macroevolutionary models, but the predictions are unreliable and context dependent

Jan Smycka, Simon Fraser University & University of British Columbia & Charles University in Prague

Abstract:

Predicting future evolutionary potential of individual species and lineages is one of the major tasks of macroevolution as a scientific field, and such predictions could be potentially useful for large scale conservation planning. Recent years have seen the rise of rate-variable diversification models and metrics that estimate the background rates of species diversification at the extant tips of phylogenetic trees. These techniques are potentially useful for making predictions about future numbers of daughter species based on past diversification dynamics, i.e. considering a hypothetical world without human influence. Importantly, the popular tip rate methods, such as BAMM, ClaDS or DR metric, use fairly different assumptions about the variability and heritability of diversification rates, and as a consequence often give different predictions about future diversification.

Here we test the capacity of commonly used rate-variable diversification methods to predict near-future diversification using temporal slices of empirical fossil and extant phylogenies of various tetrapod groups. We do this using a newly developed approach similar to generalized linear models, allowing us to quantify the relationship between predictor tip rates and subsequent diversification rates derived from a probability distribution of numbers of daughter species after a period of time.

We find that all tested tip-rate methods have a non-zero but limited capacity to predict future diversification. Importantly, the quality of the predictions depends not only on the methods used but also on the specific phylogeny, suggesting that diversification dynamics in some taxa, such as Carnivora or Ruminantia, may be poorly predictable in principle. Our results suggest that future cladogenesis can be, to a certain extent, predicted using existing tip rate methods, but the quality of these predictions is highly variable among taxonomic groups and inference methods. This variability fairly complicates the prospective usage of diversification potential estimates in practical applications, such as species prioritisation for conservation.

Parallelism and Convergence II

06/24/26: 9:30 AM - 10:45 AM

9:30 AM - 9:45 AM

Investigating the genetic underpinnings of repeated evolution in cavefish

Marcos da Silva, Lehigh University
Aubrey Manning, Lehigh University
Eesha Gudoor, Lehigh University
Suzanne McGaugh, University of Minnesota
Johanna Kowalko, Lehigh University

Abstract:

Evolution under similar environmental conditions often results in the same traits evolving repeatedly in independent lineages. While the same traits can evolve repeatedly through changes in the same genes, or through different genes, why some genes are repeatedly targeted, and the functional consequences of perturbing these genes, is poorly understood. Cave animals are striking examples of repeated trait evolution, as multiple lineages have evolved similar traits, including loss of eyes and reductions of pigmentation. Astyanax mexicanus is a powerful model for the investigation of the genetic and evolutionary basis of cave-evolved traits, as it is a single species that has extant populations of surface fish and cavefish. . Further, there are multiple populations of cavefish, some of which have evolved traits independently such as eye loss, reduced pigmentation and reductions in sleep. Here, we assess if genes previously identified as

harboring high frequency alleles that contain coding changes relative to surface alleles in multiple cavefish populations, including the genes rgrb, mtnr1c and rgs9a, underlie cave-evolved phenotypes. We performed a series of phenotypic assays in lines of the surface morph of A.mexicanus in which mutations in these genes were generated using CRISPR-Cas9, including quantification of eye size and morphology, optomotor response (OMR), larval feeding, and sleep. This approach allowed us to assess for a role of these genes in multiple cave-evolved traits, expanding our knowledge of drivers of repeated evolution.

9:45 AM - 10:00 AM
Incomplete lineage sorting, hybridization, and the repeated evolution of wing dimorphism in Gryllus field crickets

Leonardo Gonçalves, University of Nebraska-Lincoln
Colin Meiklejohn, University of Nebraska-Lincoln
Kristi Montooth, University of Nebraska-Lincoln

Abstract:

Phylogenomic discordance is widespread across radiations, yet its underlying causes and evolutionary consequences remain unresolved for many groups. North American Gryllus field crickets provide a powerful system for examining how hybridization and incomplete lineage sorting (ILS) interact to shape diversification and trait evolution. Using a genome-wide dataset, we test three hypotheses about the origins of discordance and the role of dispersal-related traits. First, we found that both ILS and hybridization contribute to the extensive gene-tree conflict observed across the Gryllus phylogeny, but several conflict patterns cannot be explained by ILS alone. Multiple lines of evidence reveal introgression at both deep and recent nodes, producing a mosaic evolutionary history with reticulation across several lineages. Second, hybridization is disproportionately concentrated among flight-capable lineages, consistent with the idea that dispersal ability increases opportunities for interspecific gene flow. Third, introgression among flight-capable lineages could help explain repeated trait reversal across the phylogeny, suggesting that gene flow may have contributed to the re-emergence of flight in descendants of flightless ancestors. These results support the idea that traditional models of character evolution may overestimate independent trait origins when reticulate processes are ignored. Together, our findings highlight how hybridization and ILS, interacting with dispersal-linked traits, have jointly shaped the phylogenetic and phenotypic evolution of Gryllus.

10:00 AM - 10:15 AM
Specialized enhancer activity associated with convergent evolution of vocal learning

Rajee Ganesan, Carnegie Mellon University
Andrew Wang, Carnegie Mellon University
BaDoi Phan, Carnegie Mellon University
Michael Leone, Carnegie Mellon University

Heather Sestili, Carnegie Mellon University
Andreas Pfenning, Carnegie Mellon University

Abstract:

Vocal production learning, or vocal learning, is the ability to imitate sounds through social exposure. The rare trait has been observed in humans, bats, cetaceans, pinnipeds, songbirds, parrots, hummingbirds, and is believed to have independently evolved three times in birds and five times in mammals, representing a prime example of convergent behavioral evolution. All studied vocal learning species have evolved a specialized forebrain sensorimotor learning circuit that is either absent or rudimentary in their closer, vocal non-learning relatives. Previous work within the lab has found that the "regulatory code" linking genome sequence to cell-type-specific function is highly conserved across mammals. In this study, we leverage this principle to identify candidate enhancers from publicly available Zoonomia datasets, and trained machine learning models predicting open and closed chromatin across all 240 mammalian motor cortex regions. We screened for differences in regulation between vocal learning and non-learning species by applying the Tissue-Aware Conservation Inference Toolkit, a machine learning approach to study how enhancer activity conservation relates to phenotype evolution. These machine learning models can learn sequence patterns of enhancers that robustly predict whether or not they have conserved activity across evolutionary distances, allowing us to test whether enhancer conservation patterns are associated with the evolution of vocal learning. Our results revealed lineage-specific gains and losses of regulatory elements, and we show that L6 corticothalamic neurons and oligodendrocytes had the strongest enrichment with the vocal learning phenotype, suggesting key roles in vocalization-related traits through motor learning and synaptic plasticity. Additional enrichment in PV, SST, and VIP interneurons highlights modulation of cortical circuits involved in vocal learning. Future studies will include single cell integration across human, mouse, rat, macaque and the zebra finch to identify orthologous cell populations and to better understand the molecular mechanisms associated with the convergent evolution of vocal learning.

10:15 AM - 10:30 AM
Is convergence a coincidence?

Chris Muir, University of Wisconsin - Madison

Abstract:

Convergent evolution of multi-component (i.e., composite) traits across independent lineages is often taken as compelling evidence for adaptation. However, retracing the origin and refinement of composite traits is challenging because their function depends on synergistic interactions among component traits. This raises a key question: how can selection improve individual components before they function together as an integrated whole? One proposed answer is that convergence may be initiated by nonadaptive coincidence, whereby high variability and plasticity increase the probability that functional combinations arise by chance. Yet it remains unclear what patterns of trait variation among extant species would distinguish such coincidence from scenarios in which

natural selection gradually builds synergistic function from heritable variation in rudimentary forms of the composite trait. To address this problem, I developed an evolutionary quantitative genetic model of composite trait origination and refinement. The model shows that several proposed signatures of coincidence are unreliable. In fact, gradual natural selection can generate a wide range of qualitatively distinct patterns of component trait variation among extant species. As a result, existing lines of evidence do not provide a compelling basis for rejecting natural selection in favor of coincidence.

Tri-Society Symposium: The Relations We Study, The Relations We Owe: Indigenous Data Sovereignty and the Future of Evolutionary Biology Practices I

06/24/26: 9:30 AM - 10:45 AM

10:15 AM - 10:45 AM

Operationalizing Indigenous Data and Digital Sovereignty: Tribal Research Governance from End-to-End

Joseph Yracheta, Native BioData Consortium

Abstract:

The NativeBio Data Consortium is the first Indigenous-led nonprofit biodata repository and research institution operating within the geographic borders and legal jurisdiction of a Tribal Nation, the Cheyenne River Sioux Reservation in South Dakota. Its mission is to operationalize tribal sovereignty and the inherent rights of Indigenous peoples to the ownership, benefit, and self-governance of their own genetic, environmental, and social data. This talk goes beyond policy and into practice: what does it actually mean for a community to govern every stage of a research project — from question framing and sample collection to storage, analysis, and benefit sharing? Drawing on NativeBio's operational experience, this talk offers a frank account of what has worked, what hasn't, and what evolutionary biologists need to understand before approaching tribal partners.

Adaptation III

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Comparative transcriptomic analyses reveal a tolerance vs plasticity tradeoff between baseline tolerance and hardening in five populations of the splashpool copepod Tigriopus californicus

Rujuta Vaidya, Louisiana State University

11:30 AM - 11:45 AM

Dominance reversal and temporal selection on chromosomal inversions in Drosophila pseudoobscura

Stephen Schaeffer, Penn State University

Abstract:

Drosophila pseudoobscura has a wealth of gene arrangements on the third chromosome generated by a series of inversion mutations. The different arrangement frequencies vary spatially, temporally, and altitudinally. Dobzhansky in 1943 as well as Strickberger and Wills in 1966 showed extreme gene arrangement frequency shifts over consecutive months that cycle, thus, providing a model system to test hypotheses about temporal selection. In this study, dominance reversal and storage populations may be factors that contribute to stable temporal cycles. Dominance reversal assumes that an arrangement will have a dominant phenotype when beneficial and recessive when unfavored. Storage effect assumes that a population is structured into a selected population and a nonselected storage population. Here, we used the Dobzhansky as well as Strickberger and Will data to estimate fitness values and a storage contribution parameter. This approach compares allele frequencies from one time interval to the next and solves for the fitness values necessary to lead to the observed changes. The model divides the population into a selected and a storage population with a contribution frequency of f to the selected population. The fitness estimates from the two datasets show stable cycling when the storage contribution is at least 7.5%. Without a contribution from the storage population, we fail to observe stable cycling. We failed to find uniform dominance reversal except for the rare arrangements. Temperature and humidity are the two environmental variables associated with cycling. Population genomic analysis of the third chromosome arrangements implicates proteins in temperature adaptation such as odorant binding, gustatory reception, and detoxification. These genes have been implicated in transcriptomic studies of high and low temperature exposure in D. melanogaster. This study extends previous theoretical and empirical studies of dominance reversal by going beyond two alleles to eight super alleles and suggesting possible functional roles for temporal adaptation.

12:00 PM - 12:15 PM

Underlying Mechanisms of Genotypic Variation in Cold Acclimation Induction in Switchgrass

Andrew Bleich, Michigan State University
David Lowry, Michigan State University

Abstract:

Seasonal environmental variation creates strong selective pressure for plants to adapt to cyclical climatic changes. In North America, this is particularly pronounced along latitudinal gradients, where northern environments impose harsh winter cold and southern environments present heat and drought stress. In Panicum virgatum, switchgrass, these contrasting selective pressures have driven ecotypic divergence between northern and southern populations. Northern upland ecotypes must successfully acclimate to cold each fall to survive freezing winter temperatures that would otherwise cause lethal tissue damage. Plants rely on declining temperatures and photoperiod as environmental cues to initiate cold acclimation, and genotypes capable of inducing this response more rapidly may gain a competitive overwintering advantage. However, the factors driving variation in cold acclimation induction timing remain poorly understood.

To address this, we investigated variation in cold acclimation induction across southern and northern Panicum genotypes under controlled conditions simulating the progressive environmental shifts of late fall. Plants were phenotyped across a ten week period of declining temperature and photoperiod, during which we measured respiration rates, rhizome water content, and Lt50 due to cold stress. We added to these physiological measurements by carrying out an RNAseq experiment to elucidate the underlying genomic mechanisms driving the physiological processes that allow for cold acclimation.

As expected, northern ecotypes initiated cold acclimation earlier and at warmer temperatures relative to southern genotypes. However, we observed variation among northern genotypes in the rate of cold acclimation induction. During this talk I will highlight how these physiological processes drive cold acclimation induction as well show genomic evidence of intraspecific variation between the selected genotypes. Finally, I will highlight the gene modules driving the genotypic variation between Northern and Southern populations and preview some of the more interesting differentially expressed genes that are contributing to physiological processes driving cold acclimation induction.

~~12:15 PM - 12:30 PM~~ WITHDRAWN

~~*Ultrastructural basis of transparency in adult freshwater fishes*~~

~~**Miranda Sinnott-Armstrong, Duke University**~~
~~Emily Brady, Duke University~~
~~Christine Cao, Duke University~~
~~Sönke Johnsen, Duke University~~

Abstract:

Although full-body transparency is ubiquitous among the larvae of pelagic fish, transparency in the adult form is rare. Transparency becomes more challenging in larger-bodied organisms compared to small larvae, and requires modifications to at least the skin, muscle, and vasculature in order to reduce light scattering and absorption. Previous work has shown that glass frogs (Centrolenidae) sequester red blood cells in the liver which reduces absorption and facilitates transparency. Transparent fish, especially in larger adult forms, primarily evolve changes to muscle anatomy to achieve transparency. We used a variety of imaging techniques to characterize the muscle architecture in adult fish of several transparent freshwater species, including Danionella cerebrum, Kryptopterus vitreolus, and Pristella maxillaris. We compare the results in transparent species with several of their opaque close relatives, in order to understand the ultrastructural basis of transparent musculature in adult fish. We find that transparent fishes have convergently evolved reductions in nuclei, reductions in collagen, and changes to the vasculature that limit scattering and increase transparency in the adult form.

Education and Outreach

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Beyond the museum: evaluating the impact of course-based undergraduate research experiences in evolution using digital natural history collections

Jeremy Hsu, Chapman University
Katie Weglarz, Westfield State University

11:30 AM - 11:45 AM

Introducing an evolution focused assessment of graph construction competence for undergraduate biology students

Eli Meir, SimBiotic Software
Jon Herron, University of Washington

Abstract:

Science skills such as experimental design and working with data are core to the biology curriculum (e.g. AAAS 2011), yet with few validated assessments for these skills, it is difficult to know when student learning improves (Harris et al, 2023). One such skill is graphing. Undergraduate biology students have trouble constructing complete, easy to read graphs and there is a need for better ways to teach graphing (Angra and Gardner, 2017).

We've developed six GraphSmarts assessments for measuring graphing competence as part of a project to improve teaching of graphing in biology classes (Meir et al, 2023). One of the assessments, called GraphSmarts: Urban Evolution, assesses graphing in the context of differences in lizard phenotypes between urban and rural areas. The other five versions of GraphSmarts each use a different biological scenario but are otherwise isomorphic and can be used in a pre / post test format. We've recently published the Urban Evolution and other versions of the assessment (Gardner et al, 2025), and take this opportunity to introduce GraphSmarts: Urban Evolution to the evolution community.

We'll show validity data from a sampling of 852 students across 20 U.S. college classes (in review), along with a larger set of 4,838 students from over 100 classes. The data include Wright maps indicating appropriate difficulty for U.S. biology undergraduates, scores mapping as expected to different populations (faculty > upper-level > first year), similar populations of students scoring similarly ($p > 0.05$ same class across semesters), and the evolution scenario being roughly equivalent to the others in its measurement of graphing competence.

We'll discuss how GraphSmarts can be used to aid in teaching in both introductory biology and upper level evolution classes. Sample copies of GraphSmarts: Urban Evolution will be available for participants to take home.

11:45 AM - 12:00 PM
Training the Next Generation of STEM Professionals: Lessons from a Postbaccalaureate Program in Evolutionary Biology

Ana Salgado, Louisiana State University

Abstract:

Universities seek to prepare undergraduates for scientific careers, but often lack formalized mechanisms for developing the hard and soft skills essential for success in STEM. Training in evolutionary biology is well-positioned to address this gap: the field is interdisciplinary and fosters the development of in-demand skills relevant to a wide range of career pathways. The Louisiana Graduate Network in Applied Evolution (LAGNiAppE) at Louisiana State University, a one-year research training program in evolutionary biology, was designed to strengthen postbaccalaureate scholars' scientific capabilities. This talk aims to summarize scholars' outcomes and lessons learned across two cohorts.

Each year, 10 scholars joined LAGNiAppE and were assigned to work closely with faculty mentors on original research, in addition to departmental and programmatic activities like scientific and career development workshops that help them gain professional and transferable skills. Pre- and post-program surveys adapted from validated instruments were applied to each cohort using a 1–5 Likert scale, and reported means reflect general trends.

The surveys of the first two cohorts (n = 19) indicated a moderate gain in scientific thinking (mean = 3.89) and research fundamentals (mean = 3.60). Scholars also reported strong gains in belonging within the scientific community (mean = 4.22). Notably, 12 of 19 scholars reported feeling much more likely to pursue careers in bioscience, and none reported a decrease in this likelihood. These findings suggest that postbaccalaureate programs with research and professional development components effectively build STEM career readiness and represent a replicable model for addressing workforce needs in STEM.

12:00 PM - 12:15 PM

Community-Guided Biodiversity Sampling Reveals Arthropod Turnover, Dispersal, and Environmental Filtering in Baja California Sur, Mexico

Eric Stiner, California Academy of Sciences
Lauren Esposito, Islands & Seas
Christothea Herodotou, Institute of Educational Technology
Judith Taylor, The Open University
Miranda Dyson, The Open University

Abstract:

The Baja California Peninsula is home to extraordinary arthropod diversity, and the remote ranching communities that live amidst this richness hold deep-rooted ecological knowledge that can offer novel insights into biodiversity and ecosystem dynamics. These communities often lack access to scientific monitoring tools or ecological data that could bolster ranch planning and help understand the impacts and extent of localized environmental changes on biodiversity. This study examines how rancher observations of environmental change can guide biodiversity sampling and help interpret patterns of arthropod community turnover. In interviews, ranchers reported declines in pollinators, shifting insect behavior, and increasing pest outbreaks in connection with prolonged droughts, intensified hurricanes, and erratic seasonal patterns. These observations informed a community-collaborative arthropod metabarcoding survey across ranches spanning desert lowlands to foothill habitats, with ranchers contributing to field logistics, trap placement, sample collection, and interpretation of local ecological patterns. Satellite-based remote sensing was then used to evaluate whether the biodiversity patterns emerging from the field collaboration corresponded with broader landscape gradients in vegetation, elevation, and climate stress. Integrating rancher perspectives, molecular ecology, and satellite-based remote sensing, this study links fine-scale arthropod community turnover with broader evolutionary questions about dispersal, environmental filtering, and landscape connectivity. This collaborative approach shows how community-guided biodiversity research in understudied landscapes can generate locally meaningful data while also informing larger-scale studies of arthropod dispersal and adaptation across the Baja California Peninsula.

Genomics: Molecular Evolution

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Testing a novel framework for connecting phenotypic plasticity, epigenetics, and natural selection using experiments in threespine stickleback

Emily Kerns, University of Wisconsin-Madison
Changyue Yu, University of Wisconsin-Madison
Jesse Weber, University of Wisconsin-Madison

Abstract:

DNA methylation (DNAm), the addition of a methyl group to cytosine (typically CpG sites), is the most studied marker in ecological epigenetics. DNAm typically reduces cis gene expression, yet attempts to recapitulate this relationship in wild populations often fail. Here, we present a novel framework with greater predictive power for analyzing DNAm in ecological and evolutionary contexts. The methylation status of a CpG site in a single cell has three distinct states (present/absent/heterozygous), but bulk sequencing makes DNAm a continuous trait due to variation between cells. Some CpG sites are consistently methylated or unmethylated (stably methylated sites, SM) while others have intermediate methylation (IM). Previous work found that loci with IM do not reliably transmit methyl marks during mitosis and have little effect on transcription in mammalian cell lines. This led us to predict that IM is unlikely to influence phenotypes, may not be heritable, and thus largely invisible to selection. In contrast, SM is maintained because it heritably impacts phenotypic expression and is therefore under selective constraint. To test this model, we surveyed DNAm and genetic diversity across six populations of threespine stickleback (Gasterosteus aculeatus) to assess whether genetic regions surrounding SM/IM display variable signatures of selection. We then compared differentially methylated sites between ancestral marine and derived freshwater populations to determine if SM/IM play different roles in freshwater adaptation. Next, we measured plastic DNAm at IM/SM and connected these sites to transcription that contributes to variation in thermal resilience between benthic and limnetic stickleback. Finally, we used publicly available datasets from diverse metazoans to determine if the relationship between SM/IM and transcription is consistent across taxa. While analysis is still underway, all current evidence supports our model, potentially providing a new framework to better predict the adaptive potential of DNAm.

11:30 AM - 11:45 AM

Evolution of the calcium-binding parvalbumin-oncomodulin gene family across vertebrates

Oli Wood, The Ohio State University

12:00 PM - 12:15 PM
Evolution of compound eye cell types across Heliconius butterflies

Wei Lu, University of Chicago
marcus kronforst, University of Chicago

Abstract:

The evolution of visual systems is tightly linked to the diversification of visually guided behaviors. Heliconius butterflies, renowned for their diverse wing color patterns and complex visual behaviors such as mate choice, provide an ideal system to study this process. Here, we investigate the evolution of compound eye cell types and their association with behavioral loci across a complete speciation continuum in Heliconius, ranging from polymorphic populations to reproductively isolated species. Using single-nucleus RNA-seq of adult compound eyes from six Heliconius species, we examined the evolutionary lability of the peripheral sensory system. By modeling gene expression changes with the Brownian motion-based model CAGEE, we found that neuronal populations generally evolve faster than glial cells. Furthermore, photoreceptors, particularly the color-sensing R7 cells, exhibit significantly accelerated rates of gene expression evolution compared to downstream neurons and retinal support cells. Given the role of mate choice in driving visual system evolution, we focused on two species pairs with divergent visual mate preferences. We identified differentially expressed mate preference genes in photoreceptors across both species pairs. Since accelerated evolution might also yield novel cell types, we further subclustered photoreceptors and identified two novel R7 photoreceptor subtypes, expanding beyond the canonical pale and yellow R7 classifications. Finally, we identified candidate transcription factors specifying these novel subtypes. Together, our comparative single-nucleus analysis provides a comprehensive characterization of visual system cell type evolution across multiple evolutionary timescales.

12:15 PM - 12:30 PM
Evolutionary and genomic burdens of pericentric heterochromatin could be tolerated in fig and fig-wasp mutualism

Zexuan Zhao, University of Maryland
Carlos Machado, University of Maryland

Abstract:

The obligate mutualism between figs and their pollinating fig wasps is one of the most specialized interactions in nature. However, the genomic processes that contribute to the long-term entrenchment of this asymmetrical eukaryotic mutualism remain poorly understood. Our research investigates how genome architecture evolves in fig pollinators and how this architecture may reflect the evolutionary consequences of obligate dependence on Ficus hosts. In particular, we focus on pericentric heterochromatin (PCH), a form of genomic “dark matter” that has long been overlooked because it is difficult to assemble, repeat-rich, and generally assumed to be gene-poor.

Rather than being evolutionarily unimportant, these regions may preserve key evidence of how fig pollinators have become increasingly genomically constrained by their specialized mutualism with figs.

Using chromatin-conformation data, we confirmed that substantial transposon-rich PCH forms an integral B compartment of chalcid chromosomes. However, unlike in non-pollinating relatives, PCH in fig pollinators is relatively gene-rich and appears to have remained positionally stable since the origin of the fig–fig wasp mutualism. Over the long history of this association, transposable elements have spread across both intergenic and intronic regions within PCH, even though this heterochromatic environment is associated with impaired gene expression and reduced splicing accuracy.

The evolutionary consequences of retaining genes within PCH are also severe. Using multi-species population genomic data, we found that PCH rarely recombines and forms haplotypes spanning tens of megabases on metacentric chromosomes. This extreme linkage creates Hill–Robertson effects, in which linked selection leads to depleted nucleotide diversity and reduced efficacy of purifying selection against deleterious mutations. As a result, genes embedded within PCH experience a distinct evolutionary regime characterized by greater mutational load and reduced adaptive potential. Odorant receptor (OR) genes, which are essential for host recognition and mutualistic adaptation, support this model: despite the large physical size of PCH, these regions appear unable to support rapid adaptive evolution of OR genes.

Together, these findings suggest that mutualism entrenchment in the fig–fig wasp system is not only ecological, behavioral, and morphological, but also genomic. The closed developmental environment of figs, recurrent inbreeding, and greatly reduced activity outside figs may have relaxed selection against the formation of repressive heterochromatic environments around genes. More broadly, our work provides new insight into PCH evolution by leveraging the unusual configuration of relatively gene-rich heterochromatin in fig pollinators.

Host/Parasite Evolution II

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Testing for genetic trade-offs among host plants in a polyphagous butterfly

Katharina Schneider, Swedish University of Agricultural Sciences

Abstract:

The majority of phytophagous insects are specialized on one or a few host species. Physiological trade-offs with a genetic basis have been proposed as strong candidates to explain this trend

towards narrower host repertoires. However, empirical evidence for their involvement remains limited, and relative generalists are not uncommon. Using larvae of the polyphagous butterfly species Polygonia c-album (comma butterfly), we combined performance assays and differential gene expression analyses to test how short-term experimental selection for high performance on a given host affects both the transcriptional patterns and performance on alternative host plants. We found that selection on different hosts led to distinct transcriptional responses when larvae were exposed to the same host plant, with differentially expressed genes involved in metabolism and detoxification. However, there was no consistent evidence for genetically based performance trade-offs: individuals with different selection histories did not differ in their performance when reared on the same host at the end of the experiment. These findings imply that high transcriptional and physiological plasticity are maintained despite selection and play a role in the utilization and preservation of broad and diverse host repertoires. This may also provide a potential explanation for the persistence of generalist herbivores despite the common trend towards ecological specialization. We suggest that the prevalence of specialization may be better explained by host preferences of ovipositing females, rather than by antagonistic pleiotropy leading to performance trade-offs.

11:30 AM - 11:45 AM

The population genetic structure of Northern Cardinals (Cardinalis cardinalis) and their ectoparasites across ecoregions in Arkansas.

Nora Hines, Arkansas State University
Alexander Worm, Arkansas State University
Kevin Krajcir, Arkansas Natural Heritage Commission
Maureen McClung, Hendrix College
Andrew Sweet, Arkansas State University

Abstract:

Variations in climate, landscape fragmentation, and urbanization can influence the dispersal and population structure of organisms, but it is less clear how these factors can impact the dynamics of host-parasite interactions. Here, we seek to better understand how the presence of different ecoregions in Arkansas, and their geographic boundaries, affect populations of birds and their ectoparasites. Northern Cardinals (Cardinalis cardinalis) and their ectoparasitic feather lice are an excellent system to address this aim because the birds are common throughout a variety of habitats, carry multiple ectoparasitic species, and individual birds maintain stable territories. We hypothesize that the distinct ecoregions in Arkansas serve as barriers to gene flow among Cardinals and their ectoparasites, and distinct populations exist for both organisms along ecoregion boundaries. We checked 111 Cardinals for lice across 6 different ecoregions and urban, natural, and agricultural habitat in Arkansas. With these data, we calculated prevalence and abundance of the lice. We then obtained genome-wide single nucleotide polymorphisms (SNPs) from 66 Cardinals and 30 lice to assess fine-scale patterns of dispersal among different ecoregions. Our results suggest there is gene flow among Cardinals in different ecoregions, transcending

geographic boundaries. However, our results show differences in the abundance, diversity, and genetic structure of lice among ecoregions, which could indicate a barrier to dispersal among and between host individuals on a finer scale. Our results help us better understand the mechanisms behind parasite dispersal and host sharing, and the influence of landscapes on host-parasite interactions at different geographic scales.

11:45 AM - 12:00 PM

Jack of all trades or master of one: comparing microbiomes of specialist and generalist vector ectoparasites in bat hosts

Anna Kang, Northern Arizona University
Joely Corrales, Northern Arizona University
Ashley Itogawa, Northern Arizona University- Pathogen and Microbiome Institute
Kelly Speer, Northern Arizona University

Abstract:

Bats host ectoparasites, such as ticks and bat flies, that act as vectors of various pathogens, including bacteria, viruses, and eukaryotes. Complex factors can shape vector competence - the ability to acquire and transmit pathogens - including parasite intensity, assemblage of specialist and generalist ectoparasites, and ectoparasite microbiome. However, there are significant gaps in the literature regarding how the microbiome is acquired and how it influences pathogen spread, particularly when comparing generalist versus specialist vectors.

This study compares the microbiomes of both generalist (ticks) and specialist (bat flies) ectoparasites collected from the same individual bat hosts. We aimed to uncover differences in pathogen presence and bacterial interrelationships within shared hosts. We hypothesized that generalists would exhibit more diverse microbiome variability than specialists due to their exploitation of multiple hosts. We also hypothesized there would be significant pathogen presence overlap and bacterial interrelationships present between ectoparasites found on the same bat.

Ectoparasites were sampled from vampire bats (Desmodus rotundus) and Cozumelan golden bats (Mimon cozumelae) in Belize, and their microbiomes were characterized using 16S rRNA sequencing. In addition to standard microbiome standardizing techniques, we used bacterial interaction networks and random forest classification to identify bacterial interactions in the microbiomes of specialists and generalists through a shared host. We find that specialist have a more conserved core microbiome than generalists. Both ectoparasites are found to share some bacterial genera together, but they seem to operate as different microbial communities.

As tick- and bat fly- borne pathogens impact wildlife health, interdisciplinary research is necessary to address the challenges of vector-borne diseases.

12:00 PM - 12:15 PM

Host-specific PCR blockers improve detection of low abundance DNA templates in metabarcoding

Christian Weinrich, University of Iowa
Robin Bagley, The Ohio State University at Lima
Andrew Forbes, University of Iowa

Abstract:

Metabarcoding is a powerful and efficient option for surveying diverse communities. However, one limitation of metabarcoding is that abundant DNA templates have the potential to competitively exclude lower abundance templates from amplification during PCR. For example, this issue is especially pronounced when attempting to metabarcode the community of eukaryotic associates living on a eukaryotic host. One solution to this problem is the use of PCR 'blockers'. Blockers are host-specific DNA oligos with chemical modifications that prevent extension by Taq polymerase. When used with universal primers, blockers selectively interfere with amplification of host DNA while allowing amplification of non-host DNA to proceed unaffected. Here I will discuss work to create a general-purpose blocker design tool and use blockers to survey the complete 'eukaryomes' of a taxonomically diverse array of insects.

12:15 PM - 12:30 PM

Cryptic population structure of avian vampire flies on Santa Cruz Island, Galapagos

Madi Waller, University of Utah
Sarah Bush, School of Biological Sciences
Andrew Sweet, Arkansas State University
Dale Clayton, School of Biological Sciences

Abstract:

Parasites can contribute to the decline of their hosts. Endangered species of hosts face increases costs of parasitism due to the interaction between the costs of parasitism and other drivers of population decline. Patterns of parasite dispersal leave genetic signatures that can used to understand the scale of mitigation strategies required for reducing the threat of parasites on endangered hosts. Avian vampire flies (Philornis downsi) is an invasive nest parasite that threatens Galapagos landbirds including Darwin's finches. We use 186 whole genomes of avian vampire flies to quantify the dispersal of flies within Santa Cruz Island. Our results suggest that there are multiple ancestral lineages of avian vampire flies within each site. This is consistent with multiple introductions of avian vampire flies to the Galapagos that then dispersed across the island. We also find evidence of recent and ongoing dispersal between sites separated by 18km. Our observed patterns of population structure and genetic relatedness between sites were not correlated with wind direction or distance between sites. However, human mediated dispersal of flies on garbage trucks could explain the relatively high relatedness of flies between sites. Our

results suggests that populations of flies within an island are well connected through dispersal and thus any effort to reduce the population of avian vampire flies should be managed at a large scale to effectively reduce the risk of re-colonization from other parts of the island.

Paleobiology

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

A new high-throughput pipeline for processing CT scans of biological specimens

Michael Hogan, University of Michigan
Alison Davis Rabosky, University of Michigan
Haley Martens, University of Michigan
Ramon Nagesan, University of Michigan

Abstract:

The prospects of utilizing CT scans for evolutionary research can be offset by steep learning curves and lofty prices for software licenses. To improve the broad accessibility of CT scans for evolutionary research, we present a new python coded framework, called SMARTSEG, which efficiently manages and processes CT scan data for the most common types of biological museum specimens. Briefly, the pipeline isolates the primary specimen in the scan, finds two matching symmetrical structures (such as the eyes) to define the right and left sides of the specimen, and finally rotates and crops the scan to a consistent and repeatable specimen facing and orientation using the spatial position of the right and left structures. To demonstrate the broad applicability and overall robustness of SMARTSEG towards biological data, we tested over 100 unique real-world CT scan datasets spanning a broad range of specimen targets. My presentation will highlight exciting examples from these tests, including visualizations of vertebrate fossils, dried plant specimens, vertebrate skeletons, vertebrate soft tissues (dice-stained), and invertebrate soft tissues (dice-stained). The taxa represented by these scans includes centipedes, spiders, scorpions, wasps, fish, mammals, amphibians, birds, turtles, crocodilians, tuataras, lizards, and snakes. We also confirmed the repeatability of SMARTSEG using a range of input data types (e.g., Ti?, Nifti, Dicom, Nrrd) generated across six commonly used CT scanner platforms: Nikon, General Electric, Bruker SkyScan, Versa Zeiss, Varian Actis, and Animage Fidex. The most compelling utility of SMARTSEG is the systematic reduction in CT scan file sizes by removing non-specimen associated data, such as empty spaces. Other utilities of SMARTSEG include mapping and combining segmentations of anatomical structures, measuring aligned body regions at voxel-size accuracy, generating clear pdf summaries and videos for rapid quality assessment, and generating surface meshes for

downstream analyses, visualizations, and 3D printing. We plan to make SMARTSEG entirely open source and available to researchers by next summer, pending publication.

11:30 AM - 11:45 AM
Increased sexual dimorphism does not evolve in a fossilized Threespine Stickleback population following ecological release from fish piscivores

Matthew Stuart, Loyola University Chicago
Gregory Matthews, Loyola University Chicago
Michael Bell, University of California Museum of Paleontology
Yoel Stuart, Loyola University Chicago

Abstract:

Theory suggests that populations should expand their habitat- and resource-use niches when they are freed from interactions with competitors and predators—so-called "ecological release". One way that ecological release can manifest is through increased niche differences between the sexes. If this happens, then divergent niche use should drive corresponding divergent adaptation in the niche-use traits, resulting in an increase in sexual dimorphism for those traits. This outcome is sometimes called character displacement between the sexes. Using a dataset of 16 traits collected from 18 temporal samples spread across ~16,500 years of evolution of the fossil Threespine Stickleback fish, Gasterosteus doryssus, we tested the prediction that release from predation would result in character displacement between the sexes. We classified individual sex in the fossils using an imputation model built with data from populations of extant Threespine Stickleback (Gasterosteus aculeatus) of known sex. Then, we quantified the extent of sexual dimorphism at each temporal sample and tracked how dimorphism changed through time. Contrary to prediction, we found evidence for character displacement between the sexes in only one of 16 traits. Two more traits even reduced their sexual dimorphism, and the rest showed little change. This is not the only empirical absence of increased sexual dimorphism in response to ecological release, suggesting that the assumptions of the theory need to be revisited.

11:45 AM - 12:00 PM
Selection by differential survival among marine animals in the Phanerozoic

Erik Tamre, Dartmouth College
Chris Parsons, Auburn University

Abstract:

The Gaia hypothesis posits that the Earth and its biosphere function as a single self-stabilizing system, but a key challenge is explaining how this could have arisen through Darwinian evolution. One theory is that of "selection by differential survival," in which a clade's extinction probability decreases with age as it accumulates adaptations resisting environmental disturbances. While this is hard to assess during early Earth history, we can assess whether this process operated among marine animal genera throughout the Phanerozoic.

To that end, we analyzed time ranges of 36,117 extinct animal genera using fossil occurrence data from the Paleobiology Database in order to calculate marine metazoan extinction age selectivity, extinction rates, and speciation rates over the Phanerozoic. We identify four signatures of selection by differential survival: lower extinction rates among older lineages, heritability and taxonomically nested propagation of extinction resistance, reduced age selectivity during rare environmental perturbations, and differential extinction rather than speciation as the primary driver of the phenomenon. Evidence for this process at lower taxonomic levels also implies its possibility for life as a whole – indeed, the possibility of Gaia.

12:00 PM - 12:15 PM

The evolution of ants communities during the Neogene in Dominican Republic

Valentine Bouju, Museum Comp. Zool.

12:15 PM - 12:30 PM

Major radiation in jaw morphology of early ray-finned fishes following the Late Devonian extinction

Emily Troyer, University of Michigan
Zach Lyons-Weiler, University of Michigan
Rodrigo Figueroa, Harvard University
Benjamin Igielman, University of Birmingham
Richard Dearden, University of Birmingham
Abigail Caron, University of Chicago
Michael Coates, University of Chicago
Stephanie Pierce, Harvard University
Sam Giles, University of Birmingham
Matt Friedman, University of Michigan

Phenotypic Plasticity I

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:30 AM

Intergenerational consequences of maternal social isolation and predation exposure in threespined sticklebacks

Jennifer Hellmann, The Ohio State University

Abstract:

Parents routinely encounter stress in the ecological environment that can affect offspring development (transgenerational plasticity: TGP); however, parents' interactions with conspecifics may alter how parents respond to ecological stressors. During social buffering, the presence of conspecifics can reduce the response to or increase the speed of recovery from a stressor. This may have cascading effects on offspring if conspecifics can mitigate parental responses to ecological stress in ways that blunt the transmission of stress-induced transgenerational effects. Here, we simultaneously manipulated both maternal social isolation and experience with predation risk prior to fertilization in threespined stickleback (Gasterosteus aculeatus). We then assessed offspring for a variety of traits, including growth, telomeres as a proxy for oxidative stress, brain serotonin, and anti-predator behavior. If social buffering mitigates TGP induced by maternal exposure to predation risk, then we expect the transgenerational effects of predation exposure to be weaker when a conspecific is present compared to when the mother is isolated. We found detrimental effects of maternal social isolation: daughters of isolated mothers had shorter relative telomere length and hid less compared to daughters of socialized males, regardless of maternal predation exposure. We also found some evidence for interactions between maternal social isolation and predation exposure: daughters of socially-isolated mothers were longer, but only when mothers were not also exposed to predation. Despite both independent and interactive effects of maternal social isolation, we found little evidence that maternal social environments buffers offspring from the effects of predation risk. Further, effects of maternal treatment seemed to largely affect only daughters, suggesting that, similar to paternal effects in this system, maternal effects have sex-specific consequences for future generations.

11:30 AM - 11:45 AM

Intergenerational effects of wildfire pollution on physiology and behavior in three-spine stickleback fish, Gasterosteus aculeatus.

Caitlin Weid, The Ohio State University

Abstract:

Wildfires are becoming increasingly prevalent, causing the introduction of ash into terrestrial and aquatic landscapes. On short time scales, ash pollution alters physiological processes (respiration,

metabolism, reproduction) and behaviors in many aquatic organisms. However, forays into the long term effects of ash exposure on survivors and subsequent offspring are understudied; little is known about whether or not the change to physiological processes is entirely detrimental or if it can make survivors, and their offspring, more resilient in the face of re-exposure in their lifetime. This offspring priming may be dose dependent. Low doses of a stressor may create an environment where the parent primes their offspring to better handle their environment while an excessive stressor may lead to reduction in offspring quality due to resource allocation within the parental biological processes (elevated metabolic rate versus gamete production). Here, we exposed three-spine sticklebacks, Gasterosteus aculeatus, to different levels of ash pollution for an extended period of time, mimicking flow of the pollution through aquatic systems via rain runoff and river outflow. We collected survival, morphometric, and physiological data on the exposed parent generation and used sperm from the ash-exposed males to create the F1 offspring. Offspring were reared in clean water, assayed for anxiety-like behavior, and at four months post hatch, acutely re-exposed to high levels of ash pollution. We hypothesized that offspring of ash-exposed fathers would have altered boldness behaviors compared to control lineages, and that during the exposure to ash, offspring of ash-exposed fathers would have decreased stress in reaction to the exposure than those of the control lineages. We further hypothesized that the low-level pollution exposure lineages would produce offspring that had decreased stress in reaction to the ash exposure compared to the high-level exposure lineages who would have increased stress responses.

11:45 AM - 12:00 PM

Disentangling the contributions of evolution and plasticity to phenotypic change in Spirodela polyrhiza populations under light stress

Trapper Hobble, University of Pittsburgh
Martin Turcotte, University of Pittsburgh

Abstract:

As global environmental change accelerates, organisms increasingly rely on phenotypic change to cope with intensifying stressors. Such change arises through phenotypic plasticity, which allows rapid within-generation responses, and evolution, which alters genetic composition across generations. Although these mechanisms operate simultaneously and can influence one another, their relative contributions to phenotypic change under environmental stress remain poorly resolved. Theory predicts that plasticity should dominate under predictable or moderately changing environments, whereas evolution may become increasingly important when stressors exceed historical ranges. Here, I test these predictions using populations of the rapidly reproducing clonal plant Spirodela polyrhiza exposed to prolonged light intensity stress. Four mixed populations composed of genetically distinct lineages varying in plastic ability were subjected to light regimes that ranged from ecologically historic to novel intensities rarely encountered in nature. We found that differences in light intensity produced significantly different average population phenotypes, with novel light intensity leading to increased phenotypic variation between population compositions. By quantifying trait responses pre and post stress exposure, the relative

contributions of evolution and plasticity to overall phenotypic change were found to vary by light treatment. However, the magnitude of this variation differs between population composition, suggesting differences in genotypic composition produce unique responses to environmental stress.

12:00 PM - 12:15 PM
Environmental stress shapes polygenic landscapes of survival and gene expression in Drosophila

Emmanuel D'Agostino, Princeton University
Julien Ayroles, University of California at Berkeley

Abstract:

Survival is a complex life history trait. Genomic studies of viability selection have revealed thousands of alleles of variable effect sizes that contribute to longevity, and are therefore enriched in groups of older individuals. However, we know little about the robustness of this complex trait to environmental stressors: do the alleles that confer survival tend to do so uniformly across environments, or is survival in the presence of stress largely due to alleles with environment-specific effects? Further, we are also only beginning to understand how the alleles associated with survival in stressful and non-stressful environments might actually function mechanistically, and how these may differ. To address these two questions, we conducted a high-throughput viability assay in Drosophila melanogaster, subjecting outbred populations to viability selection under either the presence or absence of hexavalent chromium, a common pollutant and environmental stressor. We use a depth-aware model to leverage the uncertainty in our low-coverage sequencing data of 3000 individuals, and identify alleles that are associated with viability in context-dependent and context-independent manners. We analyze these alleles' genomic locations, and we characterize the genes that they are in according to their functions and concordance with previous studies. In parallel, we generated a TM3' RNA-seq dataset of 800 individuals to understand how chromium shifts gene expression. We identify genes differentially expressed in the presence of chromium, describe these genes, and examine to what extent they overlap the genes associated with survival in the longevity assay. Taken together, these assays characterize the degree to which the genomic basis of survival is context-dependent, and describe genomic functions of survival-conferring alleles within and across contexts.

12:15 PM - 12:30 PM
Temperature x nutrition effects on gene expression in a horn polyphenic dung beetle

Sarah Britton, University of California San Diego
Patrick Rohner, University of California San Diego

Abstract:

Phenotypic plasticity allows organisms to interact with heterogenous environments and respond to environmental change. While the mechanics of plasticity are well-studied in many systems, we are just starting to understand plasticity in response to multiple environmental factors (ExE effects). Because organisms live in multidimensional environments, it is critical to understand how these factors interact to determine developmental outcomes. The bull-headed dung beetle, Onthophagus taurus, is a classic example of nutritional plasticity with a threshold response. The allometric relationship between body and horn size in males has a threshold that separates small, hornless minors from large, horned majors. The size where this occurs is temperature-dependent in many populations (nutrition x temperature interaction). However, at the transcriptomic level we do not know how these two environmental variables interact. We raised beetles across two levels of nutrition and two temperatures and collected tissue during the pupal stage. We analyzed how patterns of differentially expressed genes change based on temperature and ask whether the gene networks that respond to nutrition are concordant across temperatures. Furthermore, we investigated how these genes are expressed in sex- and tissue-specific manors by comparing males and females and tissues with polyphenic plasticity versus linear plasticity. We find evidence for genes with significant temperature x nutrition interactions in male horns, but not in other tissues. Many of these genes are found in pathways known to regulate horn growth in this species. We also find that rearing temperature affects the structure of the gene regulatory networks in the male horns. This implies that at the transcriptomic level, certain genes or pathways may be more important in determining phenotypes in specific environments. This study emphasizes the importance of considering how additional environmental factors can alter plastic responses in complex, multidimensional environments.

Tri-Society Symposium: The Relations We Study, The Relations We Owe: Indigenous Data Sovereignty and the Future of Evolutionary Biology Practices II

06/24/26: 11:15 AM - 12:30 PM

11:15 AM - 11:45 AM

Our DNA in Your Drawers: Indigenous Data Sovereignty in Natural History Collections and Desert Plant Genomics

Krystal Tsosie,

Abstract:

Specimens are not placeless — every sequence begins somewhere, and most likely on Indigenous stewarded lands. Natural history collections and herbaria hold centuries of specimens from Indigenous lands, often without consent and rarely with benefit to source communities. As long-read genomics transforms these collections into durable, reusable global research infrastructure, governance obligations grow exponentially: from transactional consent at collection,

through ongoing stewardship, to intergenerational responsibility. Drawing on work with Arizona Tribal Nations and over 4,000 culturally significant desert plant specimens in ASU's biocollections, I present a framework for anticipatory governance — designing consent, stewardship, and community agreements before sequences enter the world, not after. Indigenous data sovereignty does not restrict science. It produces better, more durable science.

11:45 AM - 12:15 PM

Arthropods Are Kin: Putting Indigenous Data Sovereignty into Practice in Biodiversity Genomics and Field Science

Leke Hutchins,

Abstract:

The rise of metagenomics and high-throughput sequencing in biodiversity studies has rapidly expanded the scale of data collection from Indigenous lands, making a sovereignty-grounded approach to the full data life cycle — from question framing to data storage — imperative. This talk demonstrates what IDSov looks like when you actually do fieldwork: negotiating data agreements with farming communities, attributing arthropod genomic data to the land it came from, and designing research questions that serve the community first. It is a worked example for any evolutionary biologist ready to try.

Adaptation: Inference of Selection

06/24/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Shared range, independent solutions: the genetic basis of adaptation of two sympatric tubeworm species in the face of high gene flow

Monique Van Dorssen, Monash University

Abstract:

Whether closely-related species adapt through shared or independent genomic pathways, and what role structural variants play, remains poorly understood, limiting our ability to predict species' responses to environmental change. We use whole-genome resequencing of two sympatric sister tubeworm species, Galeolaria caespitosa and G. gemineoa, sampled across ~2000 km of coastline to characterise and compare the genomic basis of local adaptation between species. Despite similar dispersal potential and exposure to similar environmental pressures, species differed in how adaptive differentiation was distributed across the genome. In G. caespitosa, differentiation was concentrated in two haploblock regions against a background of genome-wide panmixia,

consistent with structural variants maintaining local adaptation under high gene flow. In G. gemineoa, differentiation was more broadly distributed, though elevated divergence outside discrete haploblocks likely reflects lineage divergence and population structure rather than local adaptation — a distinction supported by haploblock frequencies co-segregating with two ancestral lineages. Despite these contrasting architectures, both species showed genomic associations with similar environmental variables (principally salinity, temperature, and oxygen), yet the underlying genes involved were largely independent between species. Together, these findings demonstrate that closely-related sympatric species can follow largely independent genomic routes to adaptation under shared selective pressures, though disentangling adaptive from demographic contributions to genomic differentiation remains a challenge in species with complex lineage histories.

2:45 PM - 3:00 PM
Testing for genomic signatures of adaptation in a widespread urban butterfly across three cities

Katie McManus, Temple University
Rachel Spigler, Temple University

Abstract:

Urbanization creates novel environments that impose strong selection pressures on organisms. Species can persist in cities through existing phenotypic plasticity, adaptive genetic change, or a combination of both. The cabbage white butterfly (Pieris rapae) reaches high abundances in urban areas despite substantial environmental challenges, making it an ideal system for investigating the mechanisms underlying urban adaptation. Although this species exhibits plastic responses to urban environmental pressures such as temperature, whether rapid, adaptive allele frequency shifts have evolved alongside this plasticity remains unknown. In this study, we use a landscape genomics approach to identify putatively adaptive loci associated with urbanization and test for parallel genomic evolution across cities. We sequenced 173 male P. rapae collected from urban and non-urban sites across three metropolitan regions (Cleveland, Pittsburgh, and Philadelphia) in the Eastern United States and performed genotype-environment association (GEA) analyses to identify allele frequencies that covary with urban environmental gradients. By comparing patterns of allele frequency shifts across cities, we assess whether the same genomic regions consistently respond to urbanization. This work provides insight into the predictability of genomic evolution in urban environments and establishes a set of candidate loci for future functional studies of urban adaptation in this widespread insect species.

3:00 PM - 3:15 PM
Putatively adaptive variation across a climate gradient in island fence lizard populations

Max Sprute, California State University

3:15 PM - 3:30 PM
The Genomics of Urbanization in House Mice

Megan Phifer-Rixey, Drexel University

Abstract:

Urbanization introduces a suite of major abiotic and biotic changes, e.g., shifts in temperature, pollution, the built environment, and diet. These changes can, in turn, impact the evolutionary trajectory of wildlife. Here, we compare populations of wild house mice (Mus musculus domesticus) from urban and rural areas in three major metro regions in the northeastern United States (New York City, NY, Philadelphia, PA, and Richmond, VA) to investigate evolutionary responses to urbanization. We found clear and consistent morphological and genomic differences between our sampled populations, including (1) differences in body size, (2) lower genetic diversity and higher relatedness in rural populations, and (3) shared genomic signatures of urban adaptation across cities. We also compared patterns of gene expression and microbiome diversity to better understand the impacts of habitat. Finally, combining this data with publicly available data from European populations, we investigated the ancestry and demographic history of these populations expected to represent early expansion of house mice in the United States. Patterns suggest a complex history of contributions from different European regions. Together, these data shed light on the evolutionary history of house mice in the northeastern US and the impacts of urbanization on that trajectory.

Coevolution I

06/24/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM
Population genomics of local adaptation to climate in an obligate pollination mutualism

Jeremy Yoder, California State University Northridge

2:45 PM - 3:00 PM
Comparative genomic and functional proteomic interrogation of mammalian resistance to rattlesnake venoms

Matthew Holding, University of Michigan
Meilyn Ward, University of Michigan
Suneel Apte, Cleveland Clinic
Laura Haynes, University of Michigan

Mark Margres, University of South Florida
Daniel Martin, Cleveland Clinic
Marjorie Matocq, University of Nevada
Drew Schield, University of Virginia
Rebecca (Becca) Tarvin, University of California Berkeley
David Ginsburg, University of Michigan

Abstract:

Coevolution is generally considered a driving force of organismal complexity and the maintenance of genetic diversity. Yet, tractable natural systems for the study of multi-trait coevolution are rare. Snake venoms have emerged as models for the molecular evolution of a complex predatory phenotype, while the molecular basis of the coevolved resistance to venom in prey is poorly characterized. We have combined comparative genomics and high-throughput functional proteomics to better understand the potential for a complex "interactome" between coevolving rattlesnakes and their rodent prey. Using comparative genomics, we interrogate the potential of gene duplication to fuel venom resistance: an expanding frontier in venom biology. We find hallmarks of rapid birth-death dynamics and positive selection in a tandem gene array of serine protease inhibitors (serpins) in rodents. We next explore the functional significance of serpin copy number evolution by recombinantly expressing the full set of 12 paralogous gene duplicates found in the genome of the Big-eared woodrat (Neotoma macrotis), a species known for resistance to protease-rich rattlesnake venoms. Two of the most highly expressed serpin paralogs inhibited diverse rattlesnake venom serine proteases, suggesting they serve as mammalian serum resistance factors. In a complementary approach, we used functional proteomics to profile each protein in the blood serum of venom-resistant California ground squirrels that is cut by the proteases found in snake venom, identifying several novel interactions as well as some that validate our approach. We classify the identified proteins as likely venom targets or resistance factors and analyze them in a population genomic framework. Our results provide evidence that the serpin genes are highly evolvable among rodents, generating functionally diverse venom inhibitors, and that the molecular basis of snake venom susceptibility and resistance in mammalian prey is as complex as the venoms themselves.

3:00 PM - 3:15 PM

Saved by the symbiont: environmental stress intensity and endosymbiont-mediated stress response determine evolved host complexity

Kiara Johnson, Michigan State University
Camila Mendoza, Carleton College
Daya Tucker, Carleton College
Alexander Lalejini, Grand Valley State University
Anya Vostinar, Carleton College
Emily Dolson, Michigan State University

Abstract:

3:15 PM - 3:30 PM

Identification of a putative tetrodotoxin-binding protein in the coevolutionary arms race between the Sierra garter snake (Thamnophis couchii) and newts (genus Taricha)

Kerry Gendreau, Virginia Tech
Jessica Reimche, University of Nevada
Kait Malewicz, Virginia Tech
Robert del Carlo, University of Nevada
Haley Moniz, University of Nevada
Butch Brodie, Jr.
Normand Leblanc, University of Nevada
Karen Schlauch, University of Nevada
Joel McGlothlin, Virginia Tech
Chris Feldman, University of Nevada

Genomics: Adaptation

06/24/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

The relative contribution of structural and single nucleotide variation to selective sweeps

James Hemker, Stanford University
Bernard Kim, Princeton University
Dmitri Petrov, Stanford University

Abstract:

Recent positive selection can leave signatures of sweeps in the genome. Using the H12 statistic which leverages haplotype frequencies, we identify regions under putative positive selection in a population of Pennsylvanian Drosophila melanogaster. We show that these regions are likely true partial sweeps, as they are enriched for genes and show charactersitics signs of genetic draft. Our top hits find classic examples of recent adaptation for pesticide resistance at the Cyp6g1, CHKov1, and Ace loci. The two former sweeps are driven by transposable-element mediated structural variation, and the latter is driven by a series of nonsynonymous SNPs. The extent to which structural variants versus SNPs underlie the full spectrum of sweeps is not well understood. By leveraging high quality short-read and long-read sequencing, we observe the full spectrum of mutations from single nucleotides to large structural variants across all of our sweep regions, and we ask if certain classes of mutations are likely to be driving the sweeps. We find that only 20-30% of sweeps can possibly be driven by structural variation, and the rest are likely driven by SNPs.

2:45 PM - 3:00 PM

Repeated Evolution of Glyphosate Resistance in Lolium multiflorum Lam. Across the Continental United States

Adrian Veron Zarate, The Pennsylvania State University
Julia Kreiner, University of Chicago
Caio Brunharo, Pennsylvania State University

Abstract:

The evolution of glyphosate resistance in Lolium multiflorum Lam. is a striking example of repeated adaptation to strong selection in agricultural landscapes. L. multiflorum occupies an unusual dual role as both cultivated cover crop and agricultural weed, raising the question of whether resistance alleles spread via gene flow among managed and weed populations or arose independently — a question prior regional studies have begun to address, but that remains unresolved at the continental scale. To do so, we used whole-genome resequencing of 336 individuals from glyphosate-resistant and susceptible populations, representing 12 states across the US. We first characterized the frequency of known resistance mutations, including copy-number variation (CNV) and non-synonymous mutations in EPSPS, the gene encoding the glyphosate target site. We then conducted a genome-wide association study (GWAS), controlling for population structure and CNV status, to identify additional loci associated with resistance. GWAS identified glyphosate resistance-associated loci on chromosomes three, four, and five. Accounting for CNV resolved this to a single non-target site locus. Strong haplotype structure in the region confirms this locus has been under positive selection in glyphosate-resistant populations, while high haplotype diversity suggests this mechanism evolved multiple times independently, consistent with convergent evolution rather than spread through gene flow across the US. We identified candidate genes that have not been previously associated with glyphosate resistance, providing new targets for rapid detection and further herbicide resistance management.

3:00 PM - 3:15 PM

The Hawaiian Drosophila Genomes Project: Investigating the genomic mechanisms of an adaptive radiation

Jocelyn Wang, Princeton University
Augusto Santos Rampasso, Princeton University
Bernard Kim, Princeton University
Samuel Church, New York University

Abstract:

Adaptive radiations are iconic evolutionary examples of the rapid generation of biodiversity, which makes them particularly useful in understanding the genomic mechanisms of diversification more generally. One of the best examples is the adaptive radiation of Hawaiian drosophilids (vinegar flies), which gave rise to vast ecological and morphological diversity unseen in other lineages of the family, with ~700 described species, many of which are ecologically specialized on a single native

plant family. While historical work documented the ecology of these species, the genomic mechanisms that led to this diversity remain largely unknown. To answer these mechanistic questions, we recently initiated the Hawaiian Drosophila Genomes Project, which combines field work and natural history with advances in genome sequencing technology (e.g., Oxford Nanopore, Hi-C, Illumina) to generate high quality genome assemblies from single flies. Even with the smallest flies yielding down to 25ng of gDNA, we are able to get near-chromosome level assemblies (>25Mbp contig N50). To date, we have collected 1800+ flies across two field trips and have currently sequenced 187 genomes representing 146 species spanning all major species groups and most sublineages. In addition to generating genomic data, we created a relational database (using SQL) and are maintaining all collection information, vouchers, specimen images, ecological data, and sequencing data to streamline analyses. With these data, we aim to resolve phylogenetic relationships of Hawaiian drosophilids and their non-Hawaiian relatives and characterize the roles of different genomic processes in their evolutionary history and diversification. As Hawaiian ecosystems are increasingly threatened by climate change, invasive species, and habitat loss, we aim to answer fundamental questions of a classic adaptive radiation while also providing open-access genomic data and tools for use by other researchers, conservationists, and stakeholders.

3:15 PM - 3:30 PM

Polygenic adaptation via genome-wide allele-frequency shifts in an extended phenotype

Clarissa de Carvalho, George Washington University

Abstract:

Understanding the genomic consequences of natural selection is central to explaining adaptive evolution and how genetic diversity is shaped and maintained. Although numerous studies have connected genetic change to natural selection, most have focused on major-effect loci. By contrast, polygenic adaptation is difficult to detect because evolutionary responses are distributed across many small-effect loci, leaving its genomic consequences poorly understood. Here, we integrate genomic mapping with experimental selection to examine the genomic signature of polygenic adaptation on gall size in the tephritid fly Eurosta solidaginis, an extended phenotype induced on goldenrod plants (Solidago altissima). Genome-wide association analyses in E. solidaginis showed that gall size is heritable (~41% of phenotypic variance explained) and highly polygenic, with no detectable major-effect loci. Field experiments across replicate populations reveal that parasitoid attacks select for larger galls, whereas bird predation favors smaller galls. Whole-genome pooled resequencing detects correlated genome-wide allele-frequency shifts across replicates following both selection events, consistent with widespread linked selection. Critically, loci most strongly associated with gall size are also among those showing parallel allele-frequency changes after parasitoid-mediated selection. Our findings provide rare empirical evidence linking the polygenic architecture of a trait to genome-wide evolutionary change in natural populations.

Hybridization I

06/24/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Genomic signatures of isolation and limited introgression across an elevational contact zone in whiptail lizards

Felipe Eduardo Alves Coelho, Rutgers The State University of New Jersey
Adrian Garda, Universide Federal do Rio Grande do Norte
Frank Burbrink, American Museum of Naural History
Marcelo Gehara, American Museum of Natural History

Abstract:

Understanding how reproductive isolation is maintained despite geographic contact remains a central challenge in evolutionary biology. Contact zones where recently diverged species meet reveal the balance between gene flow and the forces that maintain species boundaries, including selection, local adaptation, and landscape-mediated dispersal barriers. Elevational gradients are particularly informative natural laboratories because environmental conditions shift rapidly over short distances, potentially generating barriers to gene flow. These dynamics remain poorly explored in South America despite the region's exceptional biodiversity. Here, we investigate a contact zone along an elevational gradient in Chapada Diamantina, eastern Brazil, where the lowland lizard Ameivula ocellifera and the highland Ameivula nigrigula meet. Using low-coverage whole-genome sequencing from two elevation transects, we applied complementary population genomic approaches, including spatially explicit ancestry estimation, migration surface modeling, and hybrid index analysis, to characterize the nature and extent of divergence and gene flow between species. Our results reveal genomic differentiation with a sharp elevational turnover in ancestry and a well-defined migration barrier at the contact zone. Hybrid index distributions and heterozygosity patterns are consistent with a tension zone maintained by selection against hybrids: genuine intermediates are rare, observed heterozygosity falls below Hardy-Weinberg expectations, and no individual shows fully parental genomic composition, suggesting a historical signature of limited introgression. Gene flow appears constrained by selection barriers, though environmental factors such as elevation and slope may further restrict dispersal across the gradient. Together, our results suggest that elevational gradients can maintain genomic boundaries, contributing to diversification in heterogeneous tropical environments.

2:45 PM - 3:00 PM

What roles have polyploidy and hybridization played in the evolution of eastern Boechera stricta?

Magie Williams, Michigan State University
Emily Josephs, Michigan State University
Adrian E. Platts,

Terezie Mandakova, Masaryk University
Hassan Tarabai, Central European Institute of Technology

3:00 PM - 3:15 PM
Integrating Gene Tree Signals with Machine Learning to Infer Introgression Events

Sarthak Mishra, Indiana University Bloomington
Matthew Hahn, Indiana University

Abstract:

Introgression is a major source of gene tree discordance. Several methods have been developed to unravel the history of gene trees that include introgression. Most notably, these include F-statistic–based tests, network-based methods such as PhyloNet and SNaQ, and signal-contrast methods such as DAFT + djiNNI. DAFT uses gene tree attachment patterns to detect introgression and djiNNI uses nearest-neighbor interchange (NNI) transformations to infer the direction of introgression. However, as powerful as DAFT + djiNNI are, it is still challenging to infer the the optimal set of biological events underlying gene tree discordance. Here, we present a machine learning approach that takes the output of DAFT and djiNNI and provides a parsimonious explanation of the evolutionary history. We show that our approach can merge different introgression pairs detected by DAFT into a single introgression event and can accurately reconstruct the history of a set of gene trees.

3:15 PM - 3:30 PM
Intermediate or transgressive? Hybrid morphology and song in Gryllus crickets

Isaac Hudson Foy, University of Denver
Hannah Eckert, University of Denver
Robin Tinghitella, University of Denver
Thomas Firneno, Juniata College
Ella Mathews, University of Denver
Erica Larson, University of Denver

Abstract:

Behavioral isolation contributes to species boundaries when mating signals diverge and are no longer recognized across species. In the field crickets Gryllus firmus and Gryllus pennsylvanicus, barriers to reproduction are incomplete, allowing hybridization despite differences in morphology, habitat preference, and more cryptically: calling song. To initially attract mates, crickets rub specialized structures on their wings together to produce loud calling songs, directly linking morphology to mating behavior. Here, we analyze how wing morphology and song characteristics vary across the two species and their hybrids. Using geometric morphometrics of sound-producing wing structures, file tooth counts, and bioacoustic analyses of chirps and pulses, we assess differences between species and whether hybrids show intermediate or transgressive

traits. Together, these results clarify how morphological variation works in tandem with mating signaling to contribute to behavioral isolation in a hybridizing system.

3:30 PM - 3:45 PM
Genome-wide patterns of divergence and introgression between two hybridizing Andean Warblers with marked plumage differences

Laura Cespedes, University of Chicago

Abstract:

Hybrid zones resulting from secondary contact provide powerful natural systems for understanding how species form and are maintained in the face of gene flow. We used population genomic data to investigate divergence, hybridization, and phenotypic differentiation in the Myioborus ornatus–melanocephalus Redstart species complex, a rapidly diversifying group of Andean cloud-forest warblers that includes an extensive hybrid zone between two forms (chrysops and bairdi) with striking differences in plumage coloration.

Using ddRAD-seq data (n = 219), we showed that genetic variation across the Myioborus complex is structured primarily by regional Andean topography, with several genetic breaks aligning with major barriers, as well as evidence of isolation by distance. In contrast, chrysops and bairdi, with striking plumage differences, exhibit low genome-wide differentiation and form 230km wide hybrid zone characterized by advanced-generation hybrids, with potential evidence for asymmetric introgression of plumage traits.

Genome scans of low-coverage whole-genome resequencing (n = 18) revealed CCDC19 as a candidate gene potentially underlying differentiation in melanin-based head coloration between chrysops and bairdi, consistent with its previously hypothesized role in plumage patterning in another avian hybrid zone.

Building on these results, we have generated whole-genome resequencing dataset (n = 149; mean coverage = 16×) from the hybrid zone. The sequencing reads were aligned to a newly available Myioborus reference, alowing us to characterize genome-wide patterns of introgression and local ancestry for a more detailed understanding of the genetic architecture of plumage differentiation. We will further study how selection and recombination maintain phenotypic boundaries despite ongoing gene flow.

Phenotypic Plasticity II

06/24/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Genetic modification of stress response pathways underpins the genetic assimilation of cellular differentiation

Dinah Davison, Augusta University

Abstract:

The evolution of cellular differentiation has occurred repeatedly across the tree of life, giving rise to diversity of complex life we see today. We examine whether this repeated transition may have been facilitated by plastic responses to the environment that were later stabilized by developmental-genetic changes. We use the volvocine green algae as a model system as this clade contains undifferentiated multicellular species, species with environmentally induced somatic differentiation, species with undifferentiated cells and developmentally regulated somatic cells, and species with germ-soma division of labor. We examine a multicellular volvocine algae species, Eudorina, which has been historically characterized as undifferentiated but can develop a small proportion of plastic somatic cells following exposure to cold shock. We exposed Eudorina cultures to repeated cold shock and characterized the differentiation status of our lines more than 30 generations after the cessation of the cold treatment. Somatic differentiation evolved rapidly, with most lines showing changes in the regulation of somatic cell development and several lines evolving obligate somatic cells. The increase in the proportion of colonies that were differentiated was correlated with an increase in the number of somatic cells per differentiated colony. The repeated evolution of differentiation was shaped by the selection imposed by cold shock, as differentiated colonies were more likely to survive cold shock. Moreover, genome sequencing revealed that the regulation of multiple genes associated with the response to cold stress were altered. Taken together, our results highlight a novel pathway by which somatic cells can evolve and demonstrate that selection can rapidly drive the repeated transition to differentiated multicellularity via the modification of plastic responses to the environment.

2:45 PM - 3:00 PM

Thermal plasticity and reproductive mode interact to shape movement and morphology in Paramecium caudatum

Miyauna Incarnato, University of Nebraska-Lincoln
Alexandra Kosmicki, University of Nebraska-Lincoln
DeAnthony Rothwell, University of Nebraska-Lincoln
Kyle Coblentz, Colby College
John DeLong, University of Nebraska-Lincoln
Kristi Montooth, University of Nebraska-Lincoln

Abstract:

A predictive understanding of trait evolution in the context of thermal ecology requires an understanding of how trait thermal plasticity shapes traits and trait heritability. The unique genetics of ciliated protozoa, with a germline micronucleus and a highly reorganized macronucleus where gene expression occurs, provide potential for enhanced trait plasticity that is linked to meiosis and sex. In many Paramecium species, cell division can occur by asexual mitosis, or cells can undergo meiosis and genetic exchange with another cell during conjugation, which is required for a new macronucleus to be made. We used a quantitative genetic framework that tests whether the development of a new macronucleus by Paramecium caudatum, which is coupled to sex, imparts greater potential for trait plasticity in response to the two thermal environments. We found that temperature and reproductive mode interact to affect mean cell area and gross speed, but that this varies among genetic families. While overall we observed the expected response of smaller cells at warmer temperatures, many families' cells that developed their macronucleus at warmer temperatures reversed this trait plasticity. These gene-by-environment-by-reproductive mode interactions have the important evolutionary consequence that narrow-sense heritability, estimated by parent-offspring regression, differs across reproductive modes and temperatures. Accounting for this variation in trait plasticity will be important in predictive models of trait evolution, particularly when protists cycle between clonal reproduction and sexual conjugation in the wild.

3:00 PM - 3:15 PM
How social interactions shape the evolutionary dynamics of quantitative traits

Andrea Chen, Cornell University

Abstract:

Genetic diversity is shaped not only by mutation, drift, and selection, but also by ecological interactions that determine how genetic variation is expressed and exposed to selection. Social interactions provide one such context: individuals in groups can influence one another's expressed traits, potentially linking short-term ecological responses with longer-term evolutionary change. Here, we extend models of indirect genetic effects by incorporating explicit genetic architecture in an individual-based simulation of quantitative trait evolution. We compare three mechanisms by which social groups affect individuals: copying the group average, the fittest group member, or the most extreme group member.

Under stabilizing selection, these mechanisms produced distinct genotype–phenotype relationships and differed in how much genetic variation was maintained. Stronger social influence generally increased genetic variation, suggesting that social effects can buffer genetic differences from selection. After an environmental shift, only copying the fittest group member produced an immediate adaptive phenotypic response, but this short-term benefit was often accompanied by slower long-term genetic adaptation. In fluctuating environments, the fitness consequences of sociality depended on the interaction rule, shift magnitude, and fluctuation frequency.

These results show that social group structure can shape genetic diversity and adaptation across ecological and evolutionary timescales. Whether sociality helps or hinders adaptation depends on what individuals copy, how strongly they copy, and how the environment changes.

3:15 PM - 3:30 PM
Seasonal transition reveals cryptic genetic basis of monarch migration bet-hedging

Samuel Stratton, University of Michigan - Ecology and Evolutionary Biology
Delbert Green, University of Michigan

Abstract:

Bet hedging is predicted to evolve in unpredictably varying environments and, as such, expected to be a major force in species persistence through rapid climate change. Despite a robust theoretical framework, mechanistic descriptions of bet hedging in natural animal populations are rare, hindering our understanding of how such responses operate in nature. Here, by characterizing the functional genetic basis of the iconic migration of North American monarch butterflies (Danaus plexippus), we detail a diversifying bet-hedging migration strategy adopted by monarchs at the transition between summer non-migratory to fall migratory conditions. Physiological and behavioral components of migration are distinctly induced throughout the season, and each is regulated by tissue-specific transcriptional modules. A distinct directional flight state emerges at the seasonal transition that generates “mid-summer migrants”. Specifically at the seasonal transition, behavioral variation is genetically controlled by a substantial amount of cryptic genetic variation—thousands of loci throughout the genome linked to expression of hundreds of flight behavior-relevant genes in the brain. Mid-summer variants are enriched in exons and 3’UTRs that are predicted to lead to increased functional genetic variation. Monarch butterflies appear to have adapted to the highly variable environmental conditions across their breeding range by evolving diversifying bet hedging at the seasonal transition, potentially enabling their surprising resilience to climate fluctuations. These results suggest that diversifying bet-hedging strategies can arise from cryptic genetic variation in quantitative traits, which may be a common mechanism for species to generate phenotypic diversity.

3:30 PM - 3:45 PM
Sex differences in phenotypic plasticity across an environmental stressor gradient

Anthony Fiumera, SUNY Binghamton
Sarah Bases, SUNY Binghamton
Emily Yarbrough, Binghamton University

Phylogenetic Theory and Methods

06/24/26: 2:30 PM - 3:45 PM

2:30 PM - 2:45 PM

Into the treeverse: Exploring the effects of topological uncertainty on comparative methods

Remington Motte, University of Arkansas
Brian O'Meara, University of Tennessee - Knoxville
Jeremy Beaulieu, University of Arkansas

2:45 PM - 3:00 PM

Biology's Einstein moment: Specifying Lineal Frames of Reference

Matt Haber, University of Utah

Abstract:

We are currently in the midst of what I call Biology's Einstein moment. This is the rejection of absolute biological history, namely that there is an invariant, privileged biological history against which other histories are measured or deviate from. Instead, biologists must specify theoretically and empirically motivated frames of lineal reference. This is already informing and advancing biological practice, theory, methods, and more, and is a significant and important feature of contemporary biology. Here I argue that is worth identifying and naming this shift, and encouraging a deeper and broader embrace of it.

3:00 PM - 3:15 PM

A Statistical Optimization Technique to Inform Statistical Resampling Assessments of Phylogenetic Reconstruction Reliability

Byungho Lee, Michigan State University

Abstract:

Phylogenies represent the evolutionary history of a set of taxa and are typically reconstructed using computational analysis of genomic or other genetic sequence data. A common question is to ask whether a phylogenetic estimate is trustworthy. Felsenstein introduced the influential application of nonparametric statistical resampling to place confidence intervals on a reconstructed phylogenetic tree. Since then, this task – referred to as phylogenetic support estimation – has become a de facto requirement in systematics and wherever reconstructed phylogenies are reported. And algorithmic development efforts have continued to build upon Felsenstein's original method.

In this study, we propose a novel statistical optimization technique to improve statistical resampling assessments of phylogenetic tree support. The technique uses a statistical criterion as a means to assess re-estimation difficulty of different resampled replicate datasets and more intelligently allocate computational effort, given the computationally difficult optimization problems that are addressed during re-estimation in this context. We couple the new statistical optimization technique with a recently introduced sequence-aware resampling method named RAWR, and we evaluate the performance of these methods using simulated and empirical benchmarking datasets. The new method is also used to conduct a case study of Darwin's finches. We find that the resulting phylogenetic support estimates offer comparable or often improved type I and II error compared to the original RAWR method, at the cost of additional computational runtime. Our study outcomes point the way to future algorithmic enhancements and better informed statistical resampling approaches.

3:15 PM - 3:30 PM
Net Bootstrap Support: Robust and Efficient Confidence Limits for Phylogenomic Inference of Organismal Relationships

Sudip Sharma, Temple Universirty
Sudhir Kumar, iGEM @ Temple

Abstract:

Phylogenomics becomes an indispensable part in building a robust and well-resolved Tree of Life. Phylogenomic analysis of a superalignment concatenates hundreds or thousands of genomic segments, providing a straightforward, computationally efficient, and statistically robust framework for inferring species relationships. However, the standard bootstrap method can produce overly confident support for incorrect inferences based on superalignments because it fails to account for the heterogeneity of phylogenetic signals within the superalignment, which stems from incomplete lineage sorting (ILS), data errors, and other biological processes. To detect such erroneous inferences, researchers need to produce and deliberate on the concordance of inferences derived from many complex and computationally demanding analyses that require knowledge of data partitions. This study demonstrates that analyzing phylogenomic subsamples with bootstrap upsampling overcomes the overconfidence drawback of the standard bootstrap analysis of the superalignment approach. We found that bootstrapping multiple small, randomly selected site subsets can detect the presence of phylogeny variation signals across the dataset, similar to that detected using data partitions. We present the Net Bootstrap Support (NBS), which accounts for this phylogenetic variation in bootstrap confidence estimates. NBS values showed performance comparable to multispecies coalescent analyses in the presence of ILS and outperformed them for datasets simulated with gene tree estimation errors, while requiring no prior knowledge of data partitions. NBS analyses of phylogenomic data from rodents, fungi, and carnivorous plants corroborated the performance observed in simulated datasets and even mitigated overconfidence

resulting from some data errors. NBS calculations are computationally efficient, with a low memory footprint and significant time savings, making the NBS approach well-suited for big-data molecular phylogenetics on both desktops and high-performance computing systems.

3:30 PM - 3:45 PM
Phylogenetic inference using composite likelihood

Laura Kubatko, The Ohio State University
Shelby Moshier, The Ohio State University

Coevolution II

06/24/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM
Mito-nuclear coevolution during stickleback rapid radiation

Changyue Yu, University of Wisconsin-Madison
Jesse Weber, University of Wisconsin-Madison

Abstract:

Mitonuclear interactions are predicted to influence adaptive evolution, yet their role during recent ecological diversification remains unclear. Threespine stickleback (Gasterosteus aculeatus) provides a powerful within-species system to address this question because repeated postglacial colonization of freshwater habitats has generated independent radiations that sample from substantial standing mitochondrial genetic variation in the marine ancestor. Here, we investigated how mitochondrial lineage identity and environmental transitions jointly shape evolutionary change in nuclear-encoded mitochondrial genes across populations. Mitochondrial phylogenetic analyses revealed strong population structure and deeply divergent mitochondrial haplotypes, indicating potential for lineage-specific mitonuclear interactions. Comparative analyses of molecular evolution across oxidative phosphorylation (OXPHOS) modules showed heterogeneous divergence, with elevated dN/dS in nuclear assembly factors and mitochondrial ribosomal proteins relative to core structural subunits. Population genomic analyses further identified strong parallel allele-frequency shifts in nuclear-encoded OXPHOS genes during independent freshwater colonization events. Across broad geographic regions, 73.6% of shared SNPs exhibited concordant directional changes, demonstrating highly repeatable nuclear responses to freshwater environments. Genome-wide association analyses indicated that mitochondrial lineage identity significantly structured nuclear allele-frequency divergence, although the strength of this effect differed between regions. Variance partitioning suggests that geographic region explains a larger proportion of genome-wide nuclear divergence, whereas mitochondrial lineage contributed comparable effects at many loci and exhibited significant interactions with locality. Together, these results

reveal a hierarchical pattern of mitonuclear evolution during stickleback adaptive radiation. Parallel allele-frequency shifts reflect strong environmental selection associated with freshwater colonization, whereas mitochondrial lineage identity modulates the evolutionary trajectories of particular nuclear genes. Concentration of adaptive signals in a limited subset of regulatory OXPHOS genes suggests that mitonuclear co-adaptation targets key functional nodes controlling respiratory-chain efficiency during rapid ecological diversification.

4:30 PM - 4:45 PM
Within-host competition and genome evolution in animal-associated Xenorhabdus bacteria

Farrah Bashey-Visser, Indiana University
Ryan Awori, Elakistos Biosciences

Abstract:

Signatures of selection in microbial genomes are often linked to biotic interactions, notably resistance to host immunity or bacteriophage attack. Here, we highlight the importance of competitive interactions, specifically between conspecific bacteria, in shaping microbial genomes, using animal-associated Xenorhabdus bacteria. Different strains of Xenorhabdus bacteria can co-infect an insect host, which simultaneously promotes strong selection for competitive dominance as well as opportunities for horizontal gene flow. We found that Xenorhabdus genomes contain among the highest proportion of phage-related genes across Bacteria, and that variation among strains in their total number of protein-coding genes is largely predicted by variation in the number of phage genes per genome. A universal, yet highly variable, Xenorhabdus phage-related locus encoded xenorhabdicin tailocins, a key weapon in bacterial competition. The xenorhabdicin tailocin locus varied markedly in length both across and within species. Deletion of the tail fiber gene of two X. nematophila strains resulted in the loss of their intraspecific killing ability, while complementation experiments restored or shifted killing profiles, demonstrating that the tailocin locus is responsible for intraspecific killing and the tail fiber gene its specificity. Further, we linked genes in the tailocin locus to broad differences in intraspecific killing profiles of 37 regionally sympatric Xenorhabdus bovienii strains. The diversity of these genes and their rearrangements within the locus challenges our understanding of tailocin mechanics. Specifically, we hypothesize that tailocin specificity may be altered upon induction, such that a single clonal lineage could produce multiple tailocin types . Additionally, we propose that some tailocin loci carry genes conferring self-resistance. Thus, we suggest that competition within insect hosts may be fostering diversification of these microbial weapons in natural populations.

4:45 PM - 5:00 PM
Why sex? Host-parasite coevolution and mutation maintain outcrossing

Michelle McCauley, Florida International University
Levi Morran, Emory University
Janna Fierst, Florida International University

Abstract:

The ubiquity of sex despite its costs is a major evolutionary question. Many hypotheses have been proposed to explain the prevalence of biparental outcrossing, but none can individually resolve the question. The Red Queen hypothesis predicts that outcrossing is only maintained when parasites impose significant costs on their hosts. Alternatively, mutation-based hypotheses are only predicted to maintain outcrossing when mutation rates are substantially high. However, neither highly virulent parasites nor high mutation rates are as common in nature as outcrossing itself. The idea that multiple factors may act together to favor outcrossing, or the "pluralistic approach," has been popular for decades as a solution to broaden the applicability of individual hypotheses. Here, I briefly present results of an evolution experiment which tested the pluralistic approach using antagonistic coevolution between Caenorhabditis elegans worms and the bacterial parasite Serratia marcescens, along with altered C. elegans mutation rates using chemical mutagenesis. I identified combinations of parasite and mutation rate that maintain outcrossing where one factor alone does not. Next, I review potential evolutionary mechanisms that could underpin the maintenance of outcrossing under these conditions, and I present preliminary phenotypic and genomic data and their relevance to these mechanisms.

5:00 PM - 5:15 PM

Emergent properties in network structure offer clues to the macroevolutionary persistence of specialized mutualisms

Lianjie Zhang, South China Botanical Garden
David Hembry, James Madison University
Kai Hao, South China Botanical Garden
Youheng Wu, South China Botanical Garden
Gang Yao, South China Agricultural University
Qilin Sun, South China Botanical Garden
Tingting Liu, South China Botanical Garden
Shixiao Luo, South China Botanical Garden

Diversification

06/24/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Investigating the impact of biased taxon sampling on diversification rate estimates

Sigournie Brock, Iowa State University
Bruno do Rosario Petrucci, Iowa State University
Tracy Heath, Iowa State University

4:30 PM - 4:45 PM
Ecological drivers of biodiversity dynamic shifts of terrestrial amniotes during the Permian-Triassic climatic crises

Shelley Wang, Princeton University

Abstract:

Understanding the impact of environmental shifts on biodiversity across broad taxonomic, geographic, and temporal scales can provide fundamental insights into the drivers for the rise and fall of clades throughout Earth's history. Crucially, they represent a unique historical perspective on how climate change-induced mass extinctions can re-shape global biodiversity dynamics—a timely issue in the face of modern anthropogenic climate change. However, the fate of terrestrial organisms, such as land amniotes, have been challenging to assess relative to marine systems because of their patchier fossil record. Here, we combine an expanded fossil occurrence dataset and recent advances in machine learning to infer diversification dynamics through time for amniotes (reptiles and synapsids) during the largest set of biotic crises of the Phanerozoic: the Permian-Triassic (P-T) mass extinction events. Further, we use ecological niche modeling based on high resolution paleoclimatic data to predict their optimal niche ranges across these events. Our results across all models provide unambiguous support for high extinction rates and a massive drop in net diversification for synapsids during the P-T. However, contrary to long-standing ideas, reptiles and temnospondyls did not undergo a global mass extinction at the end of the Permian. Instead, reptiles underwent massive taxonomic radiation, with highest net diversification rates early in the Triassic, at both regional and global levels. Ecological niche modeling corroborates these findings, indicating suitable niches for reptiles contracted later, and recovered sooner, relative to synapsids. Rate of temperature shift and seasonality were the most important factors influencing niche suitability and extinction rates for all tetrapod clades, despite their incredibly disparate body plans and physiologies, indicating these were the key environmental drivers determining clade survival and success across the successive climate crises of the P-T transition.

4:45 PM - 5:00 PM
Island evolution in geckos: An global perspective

Yuanxing Liao, University of Kentucky
Phillip Skipwith, University of Kentucky

Abstract:

Islands have long been viewed as evolutionary laboratories by ecologists and evolutionary biologists. Species that colonized islands therefore tend to be welcomed by an environment which lacks interspecific competitors and predators they encountered on mainland, but over time, faced with increasing intraspecific competitions. With these processes acting on the islands, together

with the prolonged isolation, species that inhabit them tend to show marked differences with their mainland relatives. On a longer evolutionary time scale, these differences could show up as elevated rate of diversification and morphological traits for island taxa. Here, we will use one of the most complete, in terms of number of species included, gecko phylogeny to date to test whether colonizing islands will confer species with a higher rate of diversification and morphological traits. Among its 2450 or so species, almost 40% of gecko species have its range confined exclusively to, or have its range extended to islands, making it an ideal system to study island evolution. We will perform GeoHiSSE model in RevBayes to compare diversification rate between island and mainland clades. We will also estimate tip rates using MiSSE model and identify rate shifts using R package RRphylo, and check if these rate shifts correspond to island colonization. Finally, we will test the rate of morphological evolution on islands using morphometric data, using R package OUwie and others. Preliminary results show that the diversification rate does not differ between island and mainland taxa.

5:00 PM - 5:15 PM
Global patterns of niche evolution and partitioning in Cyperaceae

Adeyinka Aduragbemi, Texas A&M University
Daniel Spalink, Texas A&M University

Abstract:

The ecological niche is central to understanding broad-scale patterns of biodiversity and species coexistence. The sedge family (Cyperaceae) is the third largest monocot family, with over 5,700 species across 95 genera, exhibiting remarkable ecological diversity worldwide. However, comprehensive global analyses examining niche partitioning across the family remain limited. We quantified climate and soil niche occupancy across Cyperaceae and test hypotheses about relationships between niche size, phylogeny, species richness, geographic range, and divergence time. We obtained 2.86 million occurrence records for 4,694 species from GBIF and iDigBio, extracted climate variables from WorldClim and ENVIREM, and extracted soil variables from the Harmonized World Soil Database. Species niche sizes were estimated as convex hull areas in PCA space, and phylogenetic comparative methods were used to test for evolutionary signal and niche-richness relationships. Climate and soil niche sizes were strongly correlated at both the species (R^2 = 0.320, $p < 2 \times 10^{-16}$) and genus levels (R^2 = 0.902, $p = 2.85 \times 10^{-47}$). Phylogenetic signal was weak for climate niche size ($\lambda \approx 0$) but moderate for mean soil niche size (λ = 1.0, p = 0.002). Total niche size strongly predicted genus richness (climate: R^2 = 0.72; soil: R^2 = 0.72). Species with larger niches occupied broader geographic ranges (climate: R^2 = 0.49; soil: R^2 = 0.31). No significant relationship was found between divergence time and niche overlap among sister species (ρ = −0.038, p = 0.34). These results indicate that edaphic niche evolution is phylogenetically conservative, while climate niche evolution is dynamic and labile. The positive relationship between niche size and richness supports ecological opportunity driving diversification. The

absence of time-dependent divergence suggests niche evolution reflects lineage-specific diversification rather than conservatism.

5:15 PM - 5:30 PM
Evolution's wonderland: rules of body shape diversification in the deep sea

Elizabeth Santos, Ohio State University
Sarah Friedman, University of California
Chris Martinez, University of California

Hybridization II

06/24/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM
The mating game: mating behaviors and success in haploid hybrid males (genus Neodiprion)

Jakeb Watts, University of Kentucky
Sofia Novoa, University of Kentucky
Alyssa Chiarello, University of Kentucky
Ava Milliner, University of Kentucky
Shirin Soni, University of Kentucky
Alexis Roof, University of Kentucky
Gabrielle Kronenberg, University of Kentucky
Serena Limberg, University of Kentucky
Kayleigh Dobson, University of Kentucky
Catherine Linnen, University of Kentucky

4:30 PM - 4:45 PM
Patterns of gene expression in hybridizing field crickets, isolated by a fertilization barrier

Scott Melander, University of Denver
Alyson Emery, University of Denver
Emily Moore, University of Nebraska-Lincoln
Erica Larson, University of Denver

Abstract:

Postmating prezygotic barriers play a critical role in maintaining species boundaries, yet the mechanisms underlying these barriers remain incompletely understood. In a field cricket hybrid zone between Gryllus firmus and Gryllus pennsylvanicus, seminal fluid proteins (SFPs) are strong candidates contributing to reproductive isolation. Traditionally, sperm production has been

attributed to the testes, while accessory glands are thought to produce ejaculate fluid and SFPs. However, recent evidence from Drosophila indicates that both tissues express genes encoding SFPs, suggesting both tissues are involved in ejaculate composition. This raises the question of which tissue is primarily driving divergence and contributing to reproductive barriers.

To address this, RNA sequencing was used to investigate regulatory divergence in gene expression across tissues. By focusing on differential gene expression rather than sequence variation, this study examines whether shared genes are expressed at different levels between species. Data were collected from five cricket species (G.firmus, G.pennsylvanicus, G.veletis, G.rubens, and G.lineaticeps) across five tissues: testes, accessory glands, head, thorax, and leg, generating a total of 125 RNA-seq libraries.

Results show that while both testes and accessory glands express SFPs, the testes exhibit substantially greater divergence in overall gene expression and SFP related genes, with particularly strong divergence observed in G. firmus. Additionally, accessory gland associated genes tend to be X-linked, whereas testes associated genes are more frequently autosomal. These findings suggest that testes may play a dominant role in driving regulatory divergence and contributing to reproductive isolation in this hybrid zone.

4:45 PM - 5:00 PM

Differential gene expression and regulation of the neo-sex chromosomes in hybrid mountain pine beetle

German Lagunas-Robles, Indiana University
Gabrielle Coffing, Indiana University
Matt Hansen,
Jim Vandygriff,
Medhavi Verma, Indiana University
Barbara Bentz, USDA Forest Service
Ryan Bracewell, Indiana University

Abstract:

Sex chromosomes are known to play a disproportionately large role in speciation and the evolution of reproductive incompatibilities. Most studies have traditionally focused on understanding the X chromosome since the Y is often highly degenerated, challenging to study, and is not easily implicated in incompatibilities. Young sex chromosomes, so called neo-sex chromosomes, provide an opportunity to study the evolution of reproductive incompatibilities as neo-Y degeneration is an ongoing process. To explore the dynamics of gene regulation and reproductive isolation in a neo-sex chromosome system, we explored the young neo-sex chromosomes of the mountain pine beetle (MPB) Dendroctonus ponderosae. MPB is comprised of three Y-haplogroups that vary in the degree of postzygotic reproductive incompatibilities in genetic crosses. In this study, we first generated PacBio long-read Iso-Seq to refine previous neo-Y annotations. We then performed reciprocal crosses between populations that 1) have different neo-Ys and 2) show some level of reproductive isolation in the form of hybrid sterility. We generated RNA-seq data (heads and testes) from hybrid

males and the pure populations. We then 1) characterized gene dosage, 2) explored aberrant expression in hybrids, and 3) evaluated misregulation of dosage compensated genes in hybrids.

5:00 PM - 5:15 PM

Spatial simulations of island hybrid zones reveal importance of multiple isolating mechanisms in speciation

Ethan Gyllenhaal, Texas Tech University / Cornell University
Lluis Mercade Goma, Texas Tech
Elsie Shogren, Wake Forest University
J. Albert Uy, Biology
Benjamin Haller, Cornell University
Joseph Manthey, Texas Tech University
Philipp Messer, Cornell University

Abstract:

How species attain secondary sympatry is a fundamental goal of speciation research. Oceanic islands act as natural laboratories for understanding the origin of species but oftentimes rely on inferences based on distribution patterns. One classic observation in birds relates to the “taxon cycle” hypothesis, where widespread, dispersive taxa that favor coastal habitats and endemic taxa that favor interior, forested habitats co-occur. Several genomics studies suggest that such cases in closely related species are often accompanied by past gene flow, suggesting a stage of hybridization as an intermediate step in sympatry in such cases, but one that is unlikely to be observed. The two avian hybrid zones in the South Pacific exemplify opposing outcomes of secondary contact spectrum, with the Myzomela honeyeaters of the Solomon Islands showing evidence of coexistence and Pachycephala whistlers of Fiji experiencing high gene flow. The two pairs are starkly different in key factors relating to coexistence, with evidence for assortative mating, genetic incompatibilities, and ecological divergence in the honeyeaters, and only plumage divergence in the whistlers. To understand which of these factors shape the outcome of secondary contact, we performed geographically explicit population genetic simulations based on these island hybrid zones. We evaluated the role of assortative mating, local genetic incompatibilities, ecological divergence, and dispersal syndrome divergence. We found that elevated dispersal in one taxon was most important for establishing secondary sympatry while ecological divergence allowed stable co-existence of two gene pools. The pre- and post-mating barriers we modeled hindered initial secondary contact but were ultimately key for the co-existence of genetic clusters Our simulations highlight the role of multiple axes of divergence in shaping the outcomes of speciation and suggest a mechanism linking the taxon cycle hypothesis to distributional patterns in closely related Pacific birds.

Mutualism

06/24/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Gene family expansions underpin context-dependency of arbuscular mycorrhizal symbiosis.

Damian Hernandez, University of Toronto
Gwendolyn Pohlmann, University of California - Santa Barbara
Michelle Afkhami, University of Miami

Abstract:

As environments change at unprecedented rates during the Anthropocene, understanding context-dependency – how species regulate interactions to match changing environments – is crucial. However, generalizable molecular mechanisms underpinning context-dependency remain elusive. Combining comparative genomics across 42 angiosperms with transcriptomics, genome-wide association mapping, and gene duplication origin analyses, we show for the first time that gene family expansions undergird context-dependent regulation of species interactions. Gene families expanded in mycorrhizal fungi-associating plants display up to 200% more context-dependent gene expression under low phosphorus, low potassium, and high salinity stress during mycorrhizal symbiosis compared to 10,000 random subsamples of all plant gene families. Additionally, we find that gene families expanded in mycorrhizae-associating plants contain double the genetic variation associated with mycorrhizal benefits to plant fitness (i.e., mycorrhizal effects on the amount of seed pods). Moreover, we discover these gene family expansions arise primarily from tandem duplications with >2-times more tandem duplications genome-wide, indicating gene family expansions continuously supply genetic variation allowing fine-tuning of context-dependency in species interactions throughout plant evolution. In short, gene family expansions arising from tandem duplications underpin genetic regulation and fitness effects of context-dependency likely providing the genetic complexity plants need to mediate symbiotic interactions in complex and variable environments.

4:30 PM - 4:45 PM

Microbial symbioses drive species range shifts in the face of global change.

Kevin Ricks, University of Toronto

Abstract:

Global change is introducing novel stressors that are rapidly altering species distributions. However, the intrinsic drivers that determine a species' resilience to these changes, whether through rapid adaptation or range shifts, remain poorly understood. We hypothesized that mutualistic interactions significantly shape a population's capacity to respond to climate stress.

While mutualisms provide clear benefits, interdependencies between partners may generate coevolutionary constraints; stress on one partner can cascade to the other, limiting their adaptive capacity.

We evaluated this hypothesis by comparing range dynamics across the legume family. Legumes provide a powerful natural experiment to test this: while most associate with symbiotic rhizobia, soil bacteria which provision nitrogen in exchange for plant carbon, approximately 15% are non-symbiotic. Comparing range shifts between these groups allows us to evaluate the impact of mutualisms on species' resilience to novel stressors. Using a century of time-stamped GBIF occurrence data derived from herbaria and citizen science, we constructed spatio-temporal occupancy models for ~6,000 legume species with varied symbiotic status to characterize their range dynamics in the face of global change.

We found species' range shifts in response to climate change depended on their interactions with mutualistic rhizobia. Non-symbiotic legumes rapidly shifted their ranges to higher latitudes and altitudes, successfully tracking environmental shifts and maintaining their populations. In contrast, symbiotic legumes largely failed to shift their ranges dynamically. Consequently, their probability of occurrence has rapidly decreased, with increased rates of habitat loss associated with increasing climatic stress.

These results suggest that mutualisms can become a significant ecological and evolutionary burden under rapid climate change. These mutualisms may generate "two-body problems" for range shifts. Indeed species may be anchored by their mutualistic partners that possess differing environmental tolerances. Ultimately, interspecific dependencies may limit species resilience under global change.

4:45 PM - 5:00 PM
Dead End or Detour? Symbiont Loss and Alternative Strategies in an Obligate Nematode–Bacteria Mutualism

Morgan Familo, Indiana University - Bloomington
Farrah Bashey-Visser, Indiana University

Abstract:

Obligate mutualisms are tightly integrated partnerships essential for host survival and reproduction. However, these associations are susceptible to destabilization and the potential for symbiont loss. We examined the consequences of symbiont loss in the obligate mutualism between the entomopathogenic nematode Steinernema affine and its bacterial symbiont Xenorhabdus bovienii. Prior work showed that S. affine can emerge from insect hosts without carrying bacteria, despite the symbiont's key role in successful infection. We evaluated fitness consequences of symbiont status by measuring nematode survival during the free-living stage and reproductive success on insect hosts. Three hypotheses were tested: (1) the Dead-End Hypothesis, where bacteria-free nematodes fail to infect hosts; (2) the Rescue Hypothesis, where nematodes

re-acquire symbionts from conspecific infected hosts; and (3) the Free-Loading Hypothesis, where nematodes transiently persist by exploiting hosts infected with heterospecific symbionts. Survival assays compared longevity among nematodes carrying native bacteria, non-native bacteria, or no bacteria. Infection experiments measured host mortality and nematode emergence under coinfection treatments. As expected, nematodes carrying their native bacteria exhibited the highest reproductive success. Nematodes lacking bacteria show reduced infectivity and fail to reproduce without symbionts, supporting the Dead-End Hypothesis; although, rescue occurs when they coinfect a host with symbionts. Nematodes carrying non-native bacteria display intermediate fitness, suggesting a cost to mismatched symbiosis. Additionally, given the opportunity nematodes were able to re-acquire their native bacterial symbiont when given the opportunity, suggesting that freeloading on heterospecific infections may provide a temporary bridge until native symbionts are obtained. These findings highlight the importance of symbiont specificity while revealing unexpected flexibility within an obligate mutualism.

5:00 PM - 5:15 PM

Horizontal gene transfer enables an apicomplexan lineage to transition from intracellular parasite to extracellular commensal.

Peace Uche, University of Rhode Island
Laura Eme, University of Rhode Island
Chris Lane, Univ. Rhode Island

Abstract:

The phylum Apicomplexa consists of >5000 unicellular eukaryotes that were thought to be exclusively intracellular parasites. However, the discovery of the extracellular commensal lineage, Nephromyces, challenges the traditional view of this group and provides an opportunity to study evolutionary transitions in symbiotic lifestyles. Nephromyces is a symbiont inhabiting the renal sac of molgulid tunicates and also maintains a complex symbiosis with multiple bacterial endosymbionts. This unusual system provides a unique opportunity to investigate how symbiosis shapes metabolic and lifestyle evolution in eukaryotes. Here, we used transcriptomic data from Nephromyces isolated from the renal sac of Molgula manhattensis to determine whether horizontal gene transfer (HGT) has shaped its metabolic repertoire. Candidate HGT genes were identified via sequence similarity searches and taxonomic filtering, followed by phylogenetic reconstruction against diverse bacterial and eukaryotic homologs. Ongoing analyses have identified 305 Nephromyces genes that cluster with bacterial lineages rather than with other apicomplexans, consistent with horizontal gene transfer. Donor-group distributions show that these genes are predominantly derived from Proteobacteria (44.3%) and Bacteroidota (13.1%), consistent with the bacterial endosymbionts known to reside within Nephromyces. Many of these genes are associated with metabolic pathways, including carbohydrate, amino acid, and purine metabolism, suggesting they play a role in nutrient cycling within the symbiotic consortium. Overall, our results suggest that HGT allowed Nephromyces to regain metabolic capacity and transition back to an extracellular life.

5:15 PM - 5:30 PM

Genetic variation in symbiosis traits within species rivals variation among species in the legume genus Medicago

Corlett Wood, University of Pennsylvania
Chang-Yu Chang, University of Pennsylvania
Jazmine Rud, University of Pennsyvania

Phylogenomics and Phylogeography

06/24/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Phylogenetic Relationships and Biogeographic History of Five-toed Jerboas

Lexi Baca, University of New Mexico
Danielle Parsons, University of New Mexico
Jason Malaney, New Mexico Mususem of Natural History
Batsaikhan Nyamsuren, National University of Mongolia
Kimberley Cooper, UC San Diego
Joseph Cook, University of New Mexico

Abstract:

Arid landscapes of Central Asia have experienced repeated climatic oscillations, structuring biodiversity by driving lineage divergence, range shifts, and secondary contact across populations and species. These evolutionary and biogeographic processes provide a powerful framework to understand how independently evolving populations arise and persist across desert environments. The five-toed jerboas (Orientallactaga), comprising three sympatric and syntopic species (O. sibirica, O. balikunica, O. bullata), provide an ideal system for integrating mitochondrial and nuclear genomic data to investigate the evolutionary and biogeographic history of arid-adapted species. We generated an additional 77 cytochrome b sequences to expand upon existing GenBank records, totaling 422 samples spanning Central Asia. Phylogenetic and species delimitation analyses reveal deeply divergent mitochondrial lineages structured across Central Asia, particularly within the widespread O. sibirica. We also generated genome-wide single-nucleotide polymorphisms (SNPs) using double-digest restriction site-associated DNA sequencing (ddRADseq; n=108) to investigate divergence, geographic structure, and gene flow among these co-occurring taxa. Demographic, phylogenomic, and introgression analyses consistently recover the three species as monophyletic with little evidence of admixture despite sympatry. The integration of mitochondrial and nuclear genomic data presented here provides evidence that past climate oscillations resulted in historical divergence through range shifts followed by secondary sympatry, structuring the modern diversity of arid-adapted species across shared landscapes in Central Asia.

4:30 PM - 4:45 PM

Diversification of cactus on Neotropical rocky outcrops in relation to landscape and paleoclimate

Maria Alves-de-Lima, Universidade Estadual de Campinas (UNICAMP)
Lucas Mello, Universidade Estadual de Campinas
Fernando Franco, Universidade Federal de São Carlos
Juliana Palmeira Garcia, Federal University of São Carlos
Vera Solferini, Inst. Biology

Abstract:

Background: Limestone outcrops in the Brazilian Dry Diagonal function as island-like habitats, harboring a specialized flora with high levels of endemism. Despite their ecological importance, the evolutionary processes driving the diversification of their associated biota remain poorly understood. Cereus calcirupicola is a polymorphic columnar cactus endemic to these outcrops.

Aims: We aimed to investigate the phylogeographic history of C. calcirupicola and evaluate the efficacy of the Cactaceae591 genomic probe set applicability for population-level inference.

Methods: We sampled 62 individuals from 21 localities (limestone outcrops) across the Cerrado and its ecotones. We retained 9,507 filtered SNPs from targeted sequencing of Cactaceae591 regions. Our multidisciplinary approach integrated population genomics (F statistcs, DAPC, sNMF, TESS, and AMOVA), maximum-likelihood phylogenetics, climatic niche modeling (CNM), historical demography reconstruction (Stairway Plot), and Approximate Bayesian Computation to test diversification scenarios (DIYABC).

Results: We found high differentiation among outcrops (pairwise FST up to 0.470), indicating that local populations act as unique genetic reservoirs. We also identified a hierarchical genetic structure of clusters, explained in part by weak barriers. ABC for these clusters revealed a history of successive vicariance and a recent secondary contact event. CNM suggested significant habitat expansion during the Last Glacial Maximum and range retraction during the Last Interglacial, identifying the South cluster's range as a stable climatic refugium. The dates of demographic events indicate that historical declines are signatures of lineage diversification, and the projection of dates from generations to 'years ago' matches warmer periods of the late Pleistocene.

Conclusion: C. calcirupicola maintains moderate to high genetic diversity and high polymorphism among localities. The genetic patterns are consonant with sustained ancestral polymorphisms and gene flow among major clusters, with hierarchical isolation on the landscape and congruence to climatic oscillations. Ongoing habitat destruction by mining causes local extinction, which represents a loss of unique diversity for the species. Also, pipelines for population-level use of Cactaceae591 were developed.

4:45 PM - 5:00 PM

Rapid diversification of the Tropical Andean flora and its association with gene tree discordance

Diego Paredes-Burneo, University of Arkansas
Fabian Michelangeli, The New York Botanical Garden
Jeremy Beaulieu, University of Arkansas
Laura Lagomarsino, Louisiana State University

Abstract:

The flora of the Tropical Andes is exceptionally species-rich and has offered opportunities to study the drivers of high biodiversity. These mountains have hosted multiple recent, rapid diversifications following uplift. Climatic oscillations have dynamically shifted the elevational distribution of populations, with repeated cycles of isolation and secondary contact. Although climatic oscillations during mountain uplift are often invoked to explain the exceptional plant diversity of the Tropical Andes, the processes driving elevated diversification rates remain unresolved. Hybridization and incomplete lineage sorting are widespread across taxa, and richness is uneven across the region, pointing to complex, heterogeneous diversification dynamics. Given that higher elevation ecosystems are geologically younger in the Tropical Andes, I aim to test whether evolutionary processes, such as hybridization and ILS, increase along an elevational gradient. I generated a phylogenomic dataset for an Andean endemic clade and combined it with multiple, publicly available datasets for Andean taxa across the angiosperm tree of life. I used gene tree discordance as a proxy of underlying evolutionary processes operating during diversification. Gene tree discordance is high across the Tropical Andean flora, but contrary to expectations, it decreases with elevation. This pattern suggests reduced opportunities for hybridization at higher elevations, where populations have experienced greater isolation, whereas lower elevations may have facilitated population connectivity and increased hybridization. Incomplete lineage sorting, another common source of discordance, is also expected to be more prevalent in larger populations due to higher levels of polymorphisms. Additional analyses along a latitudinal gradient reveal heterogeneity in climatic niche evolution within a high Andean clade, where species-rich regions are associated with lower rates of evolution in temperature seasonality, suggesting more constrained niches and potentially consistent with greater population isolation. Together, these results indicate that the evolutionary processes underlying recent, rapid diversification are uneven across the Tropical Andes.

Sex and Recombination

06/24/26: 4:15 PM - 5:30 PM

4:15 PM - 4:30 PM

Structurally polymorphic sex chromosomes do not inhibit gene flow in the common frog

Melissa Toups, University of Louisiana at Lafayette

4:30 PM - 4:45 PM

Multiple independent origins of neo-sex chromosomes in Dendroctonus bark beetles

Gabrielle Coffing, Indiana University
Medhavi Verma, Indiana University
Harshita Sharma, Indiana University
Scott Geib, USDA ARS
Ryan Bracewell, Indiana University

Abstract:

Sex chromosomes have repeatedly evolved across the tree of life. Although the general processes that lead to highly heteromorphic X-Y (or Z-W) chromosomes are well established, less is known about the tempo of Y chromosome degeneration following recombination suppression. The early stages of Y degeneration can be studied in species with neo-sex chromosomes, as neo-Ys are initially gene rich due to fusions with one or more autosomes. Dendroctonus bark beetles are an emerging system for studying Y chromosome evolution and degeneration as they are known to have neo-XY chromosomes in multiple lineages. However, the history of sex chromosome to autosome fusions and the degree of Y degeneration in these species has been limited to karyotypic data. Here, we have assembled and annotated chromosome-level genome assemblies for eight Dendroctonus species, comprising sixteen total genomes (male and female from each species) using a combination of PacBio long-reads, Hi-C, and RNA-seq. With the addition of two publicly available genomes, we analyzed three species with putative ancestral chromosomal configurations (14AA + XY) and five species with neo-sex chromosomes (5AA + neo XY, 6AA + neo XY, & 11AA + neo XY). Using comparative analyses, we found there have been three independently formed neo-sex chromosomes in Dendroctonus. By estimating divergence times using gametologs, we show that autosomal fusions to the ancestral X occurred at three distinct evolutionary timepoints, resulting in neo-sex chromosomes of three different ages: young, intermediate, and old. The three species that share the ‘old’ neo-sex chromosomes have neo-Ys that have experienced extensive gene loss and proliferation of LTR elements. In contrast, a single species with the most recently formed neo-sex chromosome exhibits recombination suppression over only half of the neo-XY pair, with the non-recombining portion of the neo-Y showing TE proliferation. Overall, we find that the Dendroctonus

genus is a promising system to explore neo-Y chromosome degeneration at different evolutionary timescales.

4:45 PM - 5:00 PM
Sex chromosome fusions drive karyotype evolution in Aeshna dragonflies amidst conserved Odonate background

Zhaobo Hu, University of Louisiana at Lafayette
Melissa Toups, University of Louisiana at Lafayette

5:00 PM - 5:15 PM
The very earliest stages of sex chromosome evolution

Richard Meisel, University of Houston

5:15 PM - 5:30 PM
Structural and Functional Divergence of Sex Chromosomes in Poecilia picta

Joelle Lafond, University of Toronto
Yuying Lin, University of British Columbia
Lydia Fong, University of British Columbia
Judith Mank, University of British Columbia

Abstract:

Poecilia species provide a unique system for studying sex chromosome evolution, exhibiting diverse sex determination systems (XY and ZW), varying levels of sex chromosome differentiation, and rare instances of dosage compensation in fish. Poecilia picta stands out due to its highly degenerated Y chromosome and the presence of dosage compensation, with this species being the first fish known to exhibit it. However, the specific extent of Y degradation, and its current content, remained unclear due to an absence of a high-quality Y assembly. Here, we detail that the Y chromosome has undergone substantial shrinkage, has lost most of its gene content, and have been accumulating transposable elements to a very high rate. Additionally, we observe an unexpectedly high rate of gene movement from the X chromosome to autosomes, likely driven by selection to maintain gene dosage in males, as the Y chromosome no longer provides a second copy. These findings highlight the profound genomic consequences of Y chromosome decay and dosage compensation, shedding light on the evolutionary pressures shaping sex chromosome dynamics in fish.

Poster Session 1

06/21/26: 6:00 PM - 8:30 PM

A-01

Enhanced reproductive investment in invasive populations: a comparison of floral stalk length of Reynoutria japonica

Cady Spelman, Westfield State University
Jordan Stallworth, Westfield State University
Katie Weglarz, Westfield State University

Abstract:

Japanese knotweed, Reynoutria japonica, is a perennial plant native to Asia that has spread throughout Europe and North America. This species damages ecosystems by outcompeting native plants and reproducing rapidly from rhizome fragments. Reynoutria japonica is not restricted to asexual reproduction. Genetic variation is introduced through sexual reproduction via long, thin floral stalks covered with numerous small, white flowers. Invasive species are often hypothesized to thrive in their invaded ranges without the burden of coevolved predators and pathogens, enabling greater allocation of energy to growth and reproduction. We aimed to determine whether Japanese knotweed in its invaded range allocates more energy to sexual reproduction, enhancing the species' expansion. To address this question, we examined flower stalk length as a metric of reproductive capacity. We assume that longer flower stalks will hold more flowers, thus increasing reproductive potential. We hypothesized that the invasive populations of this plant would have more resources to devote to the development of floral structures, increasing reproductive potential in the invaded range. Using herbarium specimens of Japanese knotweed, we measured floral stalks lengths from the native and invaded range. We measured both the average longest stalk length (native n=42, invasive n=50, temporal range: 1887-2017), representing maximum reproductive potential, and the average overall stalk length (native n=62, invasive n=52, temporal range: 1863-2023), representing mean reproductive potential. We predicted that non-native Japanese knotweed would have longer flower stalks, on average, in comparison to specimens from native regions. Our investigation yielded conflicting results, showing support for longest stalk length but not for mean stalk length. These results suggest that in invaded regions, there is a difference in maximum floral stalk output, but the overall distribution of floral stalk size remains similar.

A-02

Comparison of leaf areas of japanese knotweed in its invasive and native ranges

Zachariah Frailey, Westfield State University
Alana Parrott, Westfield State University
Katie Weglarz, Westfield State University

Abstract:

Japanese knotweed is native to Asia and was brought over as a landscaping plant in the late 1800s. Its rhizomatic reproduction contributes to its rapid spread and management. We hypothesized that the leaf area of Reynoutria japonica, commonly known as Japanese knotweed, would be larger in places where it is invading in North America compared to its native range in Asia. Our study contributes to the understanding of morphological differences across native and invasive ranges. By understanding the morphology of the plant across multiple ranges, and also determining whether patterns in leaf area are consistent with expectations from the enemy release hypothesis. In this study, using GBIF herbarium images and ImageJ, we measured leaf area from 50 native and 79 invasive specimens (1863-2023) to compare morphological differences across ranges. The standard deviations and means were calculated, and a t-test was performed to understand the significance of the data. The mean for the invasive range was 57.94, the standard deviation was 33.38, and the mean of the native range was 35.90. The standard deviation was 29.13. We noticed that the invasive range leaf areas are more sporadic in value, but have a higher range on average. The p-value collected was < 0.05, showing that our data is statistically significant. In the invaded range, Japanese knotweed exhibits significantly larger leaf areas, potentially due to reduced biotic constraints in the invaded range. Understanding that Japanese knotweed has a larger average leaf area in the invaded range may help inform management by clarifying morphological shifts during invasion. These results contribute to understanding morphological shifts associated with invasion and may inform future control efforts.

A-03
Temporal shifts in lined seahorse distribution along the U.S. east coast

Cadence Eder, University of Delaware
Hannah King, University of Delaware
Rachel Loughran, University of Delaware
Elizabeth Sargent, University of Delaware

Abstract:

Hippocampus erectus, the lined seahorse, is a coastal fish species listed as vulnerable due to habitat loss associated with development, including erosion, pollution, sedimentation, and loss of submerged aquatic vegetation (SAV) and estuaries. Following World War II, the U.S. experienced a sharp increase in coastal development, particularly during the 1960s. Here, we investigate whether lined seahorse populations have shifted in distribution along the U.S. East Coast following this coastal development boom. We hypothesized that lined seahorse populations would demonstrate a northern-shifted distribution after 1960. Such a shift would allow for greater avoidance of regions with the most prominent coastal development and consequential SAV loss, while largely maintaining the species' geographic range. In order to explore this, we compiled sighting and specimen records from digitized natural history databases, including iNaturalist and the Global Biodiversity Information Facility (GBIF), and split the data into two sets: one before 1960 (n=334) and the other from 1960 onward (n=1966). We quantitatively compared the latitudes of each data

set using a two-sample t-test, not assuming equal variance (Welch's t-test), and found that the latitudinal distribution differed significantly between time periods ($p < 0.05$). Through further analysis, it appears that lined seahorse populations are moving south over time, rather than moving north as we hypothesized. This may be due to an actual shift in the population's distribution, or biases resulting from the number of people recording sightings in Florida and other southern states. This pattern may reflect temperature tolerance in lined seahorses, but could also be influenced by sampling bias and regional differences in observation effort. By understanding what is causing this pattern, we can better recognize how to conserve this vulnerable population.

A-04

Putting sea serpents on the modern map: updating spatiotemporal distributions of oarfish (R. glesne, R. russelii) with digitized natural history data

Alex Montana, University of Delaware
Rachel Loughran, University of Delaware
Elizabeth Sargent, University of Delaware

Abstract:

The two oarfish species in the genus Regalecus, despite being the longest bony fishes, are poorly known and hard to differentiate. The two species were classified as allopatric, with R. glesne being antitropical and R. russelii being tropical, before many of the digitized natural history records for the genus became available. Since updated digitized occurrence records may include previously inaccessible data, we hypothesized that they would provide expanded distributions for both Regalecus species. Here, we analyzed updated Regalecus occurrence records, comparing data from before and after 2010. Digitized natural history records suggest that both species occur outside of their expected antitropical/tropical zones. For R. glesne ($n = 460$), we observed two clusters, one ($n = 153$) between 45°S to 30°S, and one ($n = 217$) between 15°N and 45°N. Of those records, 27% occurred within the northern tropics. For R. russelii ($n = 100$), we observed only one cluster ($n = 86$) between 20°N and 35°N, with only 8% occurring within the tropics. When mapped, data suggested that R. glesne are seen most often in the Atlantic and Indopacific, while R. russelii are mostly confined to the Pacific. A review of the literature suggests that both species have similar prey species, predators, and larval stages. However, preliminary data suggests that R. russelii may occupy a deeper range, placing it farther from surface currents that influence dispersal. Additional efforts to catalog the distribution of larval and adult distributions of Regalecus are needed, as digitized natural history records challenge the accepted understanding of species ranges.

A-05

Land cover patterns of the American red squirrel (Tamiasciurus hudsonicus)

Tirzah Simmons, Widener University
Mariah Lynch, Widener University
Janice Krumm, Widener University

Abstract:

Tamiasciurus hudsonicus, the American red squirrel, is a member of the Sciuridae family, recognized for its adaptability across diverse environments. These squirrels play a key role in forest ecosystems, particularly through seed dispersal and forest regeneration. Our central research question asks how occurrence records of American red squirrels vary across land cover types, with the goal of informing habitat protection strategies. We hypothesized that the squirrel observations would be highest in urban areas, recognizing that the data included opportunistic observations, which means the dataset may reflect sampling bias. In fall of 2025, we used the Global Biodiversity Information Facility (GBIF) database to compile a dataset of 27,373 georeferenced occurrence records. We mapped the occurrences in QGIS to visualize patterns across land cover types and extracted land cover classifications for analysis. Our analysis shows that red squirrels are widely distributed across North America, occupying a range of environments. The three most common land cover types associated with sightings were urban areas (n=7,225), temperate or subpolar needleleaf forests (n=5,850), and mixed forests (n=4,321). Urban areas had the highest number of recorded occurrences, which may reflect the adaptability of the red squirrel and the higher observation effort in human-dominated landscapes. Our results highlight the ecological flexibility of red squirrels and provide a foundation for understanding how land cover influences distribution. Future research should examine how specific habitat features and geographic patterns influence red squirrel behavior and distribution.

A-06

Ash and avifauna: abundance of Ardea herodias in east Tennessee before and after the 2008 Kingston coal ash spill

Lily Norton, Carson-Newman University
Jessica Evans, Carson-Newman University

Abstract:

The Great Blue Heron (Ardea herodias) is an effective bioindicator of aquatic ecosystem health due to its longevity and high tropic position, which make it susceptible to the biomagnification of environmental contaminants. As such, declines in population abundance of Ardea herodias may indicate that an environment is contaminated with pollutants. In December 2008, the Kingston Fossil Plant coal ash spill released over one billion gallons of ash containing bioaccumulative heavy metals, including selenium, into the Emory, Clinch, and Tennessee Rivers. Selenium is known to impair avian growth and reproduction, and previous studies in Kingston, Tennessee documented its bioaccumulation in A. herodias. However, the impact on long-term population-levels of A. herodias within the affected waterways remain unstudied.

We hypothesized that Great Blue Heron population levels will decline in the years following the spill, as a result of bioaccumulative contaminants impacting survival or reproduction. Fourteen years of observation data (2002-2015) were retrieved from eBird via GBIF, focusing on the impacted reaches of the Emory, Clinch, and Tennessee Rivers, as well as Watts-Barr reservoir. Data were partitioned into pre-spill (2002-2008) and post-spill (2009-2015) periods. A one-tailed, two-sample t-test was used to compare annual observation frequency between these time intervals.

While recordings showed a slight initial decline post-spill, statistical analysis yielded a p-value of 0.325, indicating no significant change in overall abundance of Ardea herodias in the pre-spill period compared to the post-spill period. These results suggest that while local populations accumulated selenium, levels may not have reached the threshold necessary to trigger long-term population declines. This study highlights the importance of monitoring the abundance of high trophic-level species following an environmental disaster to assess species and ecosystem-level resilience. Recovery of higher trophic level species may reflect the reestablishment of lower trophic levels and overall ecosystem resilience following disturbance.

A-07
Comparing ruby-throated hummingbird population declines: Tennessee vs. national trends

Bo McGhee, Carson-Newman University
Jessica Evans, Carson-Newman University

Abstract:

The Ruby-Throated Hummingbird (Archilochus colubris) is the only species of hummingbird that regularly breeds in the eastern United States. Populations of these hummingbirds steadily increased until 2004, however, A. colubris began to experience a nationwide population decline of 17% between 2004 to 2019. Deforestation, an increase in the use of pesticides, climate change, and collisions with buildings directly contributed to their decline.

While research indicates a nationwide decline in A. colubris, few studies have focused on population trends at a smaller geographic scale. We used this study to determine if population levels of A. colubris declined in the state of Tennessee at the same rate as national levels. Tennessee has experienced environmental degradation similar to what has been observed at a national level; We hypothesized that Tennessee populations of A. colubris would see a decline of 17%, equal to that of national levels. Observation data was gathered from eBird using GBIF. Search criteria were limited to the state of Tennessee, and observation records that occurred between 2004 and 2019. Meaningful data including individual count, date of observation, and location of observation was retained, while information not relevant to this study was removed. Approximately 145,000 data records were retained for this study. Data was visualized using QGIS and a linear regression analysis was calculated to observe population trends.

Our analysis indicated that during 2004-2019, Tennessee populations of A. colubris experienced a 22% annual increase in the number of recorded sightings. Our findings indicate that, although Tennessee populations have been subjected to the same pressures driving national declines, they have not exhibited comparable population losses. Understanding population changes is highly complex, highlighting the importance of continued monitoring of A. colubris.

A-08
Use of moon jellyfish as a bioindicator of poor coastline health associated with human impact

Nikolas Monte, Colorado State University
Peyton Michaelsen, Colorado State University
Addison Nord, Colorado State University
Tanya Dewey, Colorado State University

Abstract:

Anthropogenic actions, including acidification and eutrophication, affect Earth's aquatic ecosystems by increasing phosphate and nitrate concentrations while decreasing dissolved oxygen and pH, making water chemically inhospitable for supporting life. Moon jellyfish (Aurelia aurita) are a common food source for a variety of animals, from sea turtles to fish. With Aurelia aurita thriving within unfavorable marine conditions, large population blooms in areas impacted by humans suggest they may be indicators of adverse conditions. We hypothesized that the A. aurita population size would increase in response to factors associated with poor coastline health (increased nitrate, decreased dissolved oxygen, decreased pH, and increased phosphorus). We focused on human observations and material sample occurrence data from the Global Biodiversity Informatics Facility (GBIF) in the North Sea. We obtained 3,458 occurrences from two decades of occurrences (2000 - 2010 & 2010 - 2020) and each decade's surface-level pH, dissolved oxygen, nitrate, and phosphorus from the Bio-ORACLE marine database. We ran t-tests for each of the chosen variables, comparing them with occurrence data from each decade subset to test for significant differences. Of all these factors, only nitrate had a statistically significant impact on the presence of A. aurita in the last 20 years. Nitrate readings compared to occurrences over the two decades increased by 21%. Aurelia aurita population growth seems to follow increases in nitrate, which may suggest that A. aurita serves as a bioindicator of coastline water quality. Future research should incorporate field measurements of abiotic conditions at sites of frequent large moon jellyfish blooms to identify more direct relationships.

A-09
Immigration and adaptation: differing leaf shape across ranges in purple loosestrife (Lythrum salicaria)

Aviel Spurgeon, Northeastern State University
Elizabeth Waring, Northeastern State University

Abstract:

Lythrum salicaria, commonly known as purple loosestrife, is a flowering wetland plant native to Eurasia. It was introduced to North America in the 19th century and has proliferated ever since, being classified in many states as a noxious weed. While current research indicates that the species' environmental impact may not be as severe as once believed, it nevertheless serves as a well-documented example of successful naturalization in a human-introduced species. There are significant morphological differences in L. salicaria across its native and introduced ranges, however no recent studies have examined whether the migration to regions of higher annual light availability impacted the overall shape of the species' leaves. This project examined shape (as quantified by the ratio of leaf width to length) by measuring the leaves of digitized herbarium specimens (via iDigBio) from both North America (n=53) and Europe/Asia (n=44). We hypothesized that leaves from North American plants would exhibit different width-to-length ratios than those from native Eurasian populations, indicating acclimation and potential adaptation to novel environmental conditions. A single leaf from each specimen was chosen for measurement using ImageJ, and the ratio was calculated by taking the maximum width of the leaf over its total length. It was found that the leaves of North American plants had a significantly ($p < 0.001$) smaller average ratio (mean=0.22) than the Eurasian plants (mean=0.29), indicating that leaves of plants in the introduced range are typically narrower relative to their length than those from native populations. While further research is necessary to ensure that this outcome is not a consequence of simple phenotypic variation, our results suggest that L. salicaria may be an ideal candidate for future work examining the adaptive potential of invasive plant species.

A-10

Investigation of the relationship between wing melanization and interspot frequencies of Pieris rapae European and North American populations

Lydia Wang, Anoka-Ramsey Community College
Pheobe Swenson, Anoka-Ramsey Community College
Jenna Bechtold, Anoka-Ramsey Community College
Kristen Genet, Anoka-Ramsey Community College

Abstract:

Pieris rapae, commonly the Cabbage White Butterfly, is a globally known agricultural pest and model organism. The small butterfly originated in Europe and West Asia and has since diversified into 6 other genetically distinct populations: West North America, East North America, Siberia, New Zealand, and Australia. This study focused on two phenotypic differences between European and North American populations: average proportional wing melanization and interspot presence. It was hypothesized that there would be significant differences in melanization trends between the two populations, but interspot presence analysis would not show a significant difference. Proportional melanization was calculated from measurements of wing length and width, and the areas of melanization of apex and spot regions. Interspot melanization recorded as present or absent. A chi-square test of independence revealed significance between interspot presence only

during the summer for both sexes. The number of butterflies with/without interspots was highlighted in stacked bar graphs. During analysis for proportional melanization, sex was controlled as females have an additional spot (Cu3) that males lack. Season was also controlled as wing melanization in P. rapae is plastic with climate (cool or warm) depending on when they emerged from chrysalis and with resource availability. Represented by box and whisker plots, The range of melanization was greatest for both populations and sexes during the summer . This follows known trends of P. rapae melanization: there is greater spot melanization during summer months than in spring months. A two-sample t-test concluded that the differences in melanization between the continents was significant for males during the spring and females during the summer. T-test results for males during summer and females during spring were insignificant. It is uncertain why males and females differ in significance for melanization by season, but it is worth considering for future research of P. rapae. Additionally, a two sample t-test highlighted a significant difference between wing melanization when interspot presence is taken into account. This suggests that these traits could influence one another, and is an interesting connection to interspots in P. rapae that should be further studied.

A-11
The effects of latitude on wing melanization of Pieris rapae

Judith Hadley, Anoka-Ramsey Community College
Kristen Genet, Anoka-Ramsey Community College

Abstract:

Wing melanization of Pieris rapae is important for thermoregulatory behavior. With different amounts of light, melanization might vary over different latitudes and seasons. We examined the effect latitude has on the melanization of Pieris rapae. A data set off 899 butterflies from the continents North America and Europe, containing both female and male specimens, was used to test melanization by standard ImageJ threshold methods. The data was put to a linear regression model analyzing season and sex. Male butterflies in spring were found to have a statistically significant relationship between altitude and melanization. There was so significant relationship with females in either season or males in the summer. The results suggest that males in the spring are affected by latitude, due to possible season thermoregulatory behavior. More samples and more locations may help clarify how latitude effects Pieris rapae melanization.

A-12
Wing size responses to climate change in Pieris rapae, using museum specimens from 1865 to 2020

Spencer Saba, Anoka-Ramsey Community College
Audrey Mann, Anoka-Ramsey Community College
Samuel Saba, Anoka-Ramsey Community College
Maryam Majeed, Anoka-Ramsey Community College
Kristen Genet, Anoka-Ramsey Community College

Abstract:

The cabbage white butterfly (Pieris rapae) is a great model species when studying the effects of climate change, P. rapae is a globally distributed species, present on all continents except for South America and Antarctica. P. rapae use their wings for thermoregulation, which is why global climate change over time may contribute to their changing wing size. The objective of this study is to investigate how climate change has affected cabbage white butterflies wing size over the last 200 years. Our hypothesis is that climate change will cause P. rapae wing size to increase over time. We predicted older specimens would generally have smaller wing sizes increasing steadily over time. Using image analysis P. rapae wing length and width were measured. We examined the data from 406 museum specimens from the years 1865 to 2020. We used linear regression to evaluate the relationship between wing size and time. We found that the butterfly's wing length had a statistically significant increase over time while wing width did not. The linear regression test yielded a small r2 value, indicating that time explains only a portion of the variation in wing length. Overall, our hypothesis was supported because the increase of temperature over time did affect wing size. However, this trend was only present in the case of wing length. These results provide statistical evidence that wing size in P. rapae has responded to climate change, highlighting the value of historical specimens for studying phenotypic responses over time.

A-13

The effects of benthic-pelagic ecology on evolutionary rates of body shape of Leuciscidae

Ren Horn, University of Illinois Urbana Champaign
Milton Tan, Illinois Natural History Survey

Abstract:

The evolution of body shape can be influenced by habitat characteristics, such as association with the benthos in fishes. Ecological shifts between benthic and pelagic habitats in fishes have been previously shown to affect rates of morphological evolution due to inhabiting a new niche. One fish family that shifted between benthic and pelagic habitats is minnows (Leuciscidae). Previous research demonstrated that pelagic species evolve more slowly in trophic traits than benthic species, despite a higher rate of speciation. However, how habitat preference drives other aspects of fish morphological evolution was not studied. We developed a novel unbending method for mitigating non-biological shape variation due to preservation artifacts affecting posture. This was tested against the unbending method in the R package LOST that uses a similar method to TPSutil. Our approach was similar to LOST in accuracy, with much greater computing speed, and greater flexibility in the types of curves that can be fit. We then quantified shape for 2,684 specimens across 274 species of North American Leuciscidae. With mouth angle as a proxy for benthic association, we tested how mouth angle correlated with evolutionary rates of body shape by dividing species into quartiles by mouth angle. We found no significant difference in rates of body shape evolution among mouth angle quartiles using compare.evol.rates (geomorph). Ongoing

MuSSCRat analysis in RevBayes to account for background evolution are being performed. These findings will provide further insight into the role of ecological shifts in driving functional trait evolution in diverse clades.

A-14
Mapping the evolution of novel resonators in the bat nose

Sophia Garrote, University of Washington

A-15
Encephalic Cavity in Anteaters (Xenarthra, Vermilingua): Anatomy and Evolutionary Implications

Francisco Costanzo, Universidad de Buenos Aires

Abstract:

Anteaters (Vermilingua) are a group of placental mammals exhibiting adaptations for myrmecophagy. While the cranial anatomy of the three extant genera (Cyclopes, Tamandua, and Myrmecophaga) and three extinct genera (Palaeomyrmidon, Protamandua, and Neotamandua) is well-documented, their endocranial morphology remains largely unexplored. Recent advances in computed tomography have enabled non-destructive access to endocranial structures, providing novel anatomical insights.

We performed clinical CT and micro-CT scans on adult crania from all known Vermilingua genera and juvenile Myrmecophaga specimens. Using these scans, we reconstructed 3D digital models of the encephalic cavity to analyze and compare the diverse brain morphologies qualitatively.

In general, the encephalic cavity of Vermilingua is anteroposteriorly elongated, except in Cyclopes, whose brain appears notably globular in lateral view. Among extant genera, the olfactory bulbs in Cyclopes are fused medially and less prominent, whereas in Myrmecophaga, they are more expanded and anteriorly separated. Tamandua exhibits an intermediate condition. Fossil genera Protamandua and Palaeomyrmidon show fused olfactory bulbs resembling Cyclopes but with an expansion similar to Tamandua and Myrmecophaga. In lateral view, the dorsal surface of the cerebral hemispheres is flat in all genera except Cyclopes and juvenile Myrmecophaga, which present a convex profile. The cerebellar morphology is consistent across the group, except for the petrosal lobes (paraflocculi), which are highly prominent in all genera but nearly absent in both juvenile and adult Myrmecophaga.

These findings suggest that heterochronic processes (pedomorphosis) previously proposed for Cyclopes' cranial structure may also shape its encephalic morphology. Furthermore, the presence of pronounced paraflocculi across extinct anteater genera might indicate arboreal or semi-arboreal habits.

This study contributes to understanding the evolutionary adaptations in Vermilingua and highlights the interplay between cranial and encephalic morphologies in their ecological and evolutionary contexts.

Los osos hormigueros (Vermilingua) son un grupo de mamíferos placentarios que exhiben adaptaciones hacia una alimentación mirmecófaga. Se conoce la anatomía craneana de tres géneros de Vermilingua vivientes (Cyclopes, Tamandua y Myrmecophaga) y tres extintos (Palaeomyrmidon, Protamandua y Neotamandua), pero su morfología endocraneal es prácticamente desconocida. Recientemente, la tomografía computada ha permitido un acceso no destructivo a las estructuras endocraneales, otorgando herramientas para obtener información anatómica novedosa. De esta manera, se sometieron a tomografías clínicas y microtomografías cráneos de adultos de todos los géneros de Vermilingua conocidos y cráneos juveniles de Myrmecophaga. Posteriormente, para cada uno de ellos se ha reconstruido el modelo digital 3D de la cavidad encefálica con el objetivo de analizar cualitativamente y comparar entre ellas las distintas morfologías cerebrales. En general, la cavidad encefálica en Vermilingua presenta una morfología anteroposteriormente elongada excepto en Cyclopes, cuyo cerebro es notablemente globular en vista lateral. Entre los géneros vivientes, los bulbos olfatorios de Cyclopes son poco prominentes y fusionados medialmente, siendo más expandidos y separados entre sí anteriormente en Myrmecophaga, y observándose condiciones intermedias entre estas morfologías en Tamandua. En Protamandua y Palaeomyrmidon, los bulbos olfatorios se encuentran fusionados como en Cyclopes, pero con una expansión similar a la de Tamandua y Myrmecophaga. En vista lateral, la superficie dorsal de los hemisferios cerebrales es plana en todos los géneros, con excepción de Cyclopes y juveniles de Myrmecophaga que muestran un perfil convexo. Las circonvoluciones cerebrales presentan un patrón parecido en la mayoría de los osos hormigueros, con giros laterales y lobulos piriformes marcados. Contrariamente, Cyclopes tiene una superficie notablemente lisencefálica. La morfología cerebelar es similar en todo el grupo, a excepción de los lóbulos petrosos (paraflóculos), muy prominentes en todos los géneros estudiados pero casi ausentes en Myrmecophaga juveniles y adultos. Estos resultados indican que los procesos heterocrónicos (pedomorfosis) previamente

A-16
Analysis of the transition from oviparity to viviparity in the C. drosophilae supergroup

Lynsey Blevins, University of Virginia
Wystan Byers, University of Virginia
Katja Kasimatis, University of Virginia

Abstract:

Many birthing strategies exist across eukaryotes, including oviparous egg-layers and viviparous live-birthing. Mechanisms of each of these have been characterized across species, however transitions between oviparity and viviparity within a genus are poorly understood. Within the largely oviparous Caenorhabditis nematode genus, independent transitions to viviparity have been

observed in several species, such as C. drosophilae. This transition is ideal, as unlike its oviparous close relative C. sp30, C. drosophilae appears to live-birth larvae. Using a trio of related species, we investigated the mechanisms of C. drosophilae's viviparity, and whether it represents a fitness cost compared to oviparous relatives. We quantified the variation in egg laying behavior across five different temperatures to assess under what conditions each species would lay eggs versus larvae. We found that C. drosophilae almost exclusively live-birth L1 larvae except under extreme temperature conditions. Additionally, we showed that sister species, C. sp2, has an intermediate live-birth strategy while the trio outgroup, C. sp30, is almost exclusively oviparous. These data suggest a continuum of egg laying variation rather than a distinct transition to viviparity. We supported these findings by exposing mated females to serotonin, a chemical stimulant of egg-laying muscles. The serotonin analyses supported that physiological mechanisms to lay eggs are still present in C. drosophilae. We then compared the lifespan and fecundity of mated females to examine if a trade-off exists between these fitness axes and if it differs across species. Our analyses suggest lifespan varies by genetic background, but that mating has little negative impact on median lifespan. Moreover, we found no significant difference in total fecundity between C. drosophilae and C. sp30. Together, these findings present the transition from oviparity to viviparity in the C. drosophilae supergroup as non-discrete and potentially adaptive, showing a continuum between birthing strategies, rather than two discrete options.

A-17
Is Leg Length Correlated with Net Diversification Rates in Daddy-Long-Legs?

Pranil Panda, University of Wisconsin-Madison

A-18
Linking personality and physiology: boldness and resting metabolic rate in Hyla chrysoscelis

Ali Bruton, Oklahoma State University
Rachel Jacks, Oklahoma State University
Alyssa Stockebrand, Oklahoma State University
Matías Muñoz, Oklahoma State University
Michael Reichert, Oklahoma State University

Abstract:

Within a species, individuals display consistent variation in behavior (i.e., animal personality), but the cause and adaptive benefits of such variation are not well characterized. Individuals also vary substantially in resting metabolic rate, reflecting variation in energetic state and physiological demand. Because metabolic rate affects how individuals acquire and expend energy, it may play a role in generating among-individual differences in behavior. Behaviors associated with risk-taking, exploration, and activity are especially likely to be shaped by energetic requirements, suggesting that physiological variation could underlie consistent behavioral strategies. We hypothesize that

variation in boldness will correlate to variation in resting metabolic rate. We specifically predict that boldness of male H. chrysoscelis will positively covary with metabolic rate. Boldness, in this case defined as readiness to explore a novel, potentially dangerous environment, is one measurable and repeatable personality trait. In amphibians, boldness may shape how individuals navigate their environment, locate breeding habitats, and their mate attraction strategy. Boldness has been shown to positively correlate with resting metabolic rate in several taxa, suggesting a general physiological–behavioral linkage. Male Cope's gray tree frogs (Hyla chrysoscelis), show repeatable variation in resting metabolic rate, which may therefore contribute to among-individual differences in behavior. This may indicate how individuals explore their environment, which could affect risk taking and breeding behavior. To assess boldness, we recorded male exploration of a novel environment and the latency to exit a shelter. We measured the resting metabolic rate of each individual by measuring oxygen consumption during their inactive period. Personality trials and metabolic rate data were correlated to test for relationships between boldness and resting metabolic rate. These results indicate the extent to which physiology determines the expression of a behavior that likely has important consequences for fitness.

A-19
Eco-evolutionary dynamics in a Batesian mimicry complex over spatial and temporal scales

Ashley Hoguet, Tulane University
Samridhi Chaturvedi, Tulane University
Jake Grossman, St. Olaf College

Abstract:

Batesian mimicry is a classic example of adaptive evolution and provides compelling evidence for natural selection in the wild. Under frequency-dependent selection, palatable mimics that resemble unpalatable models gain a fitness advantage because predators avoid them based on the model's visual phenotype. Although previous studies have shown that selection for Batesian mimicry can maintain the geographic distribution of mimics, the effects of climate change on phenology and future distributions of both models and mimics remain poorly understood, largely due to lack of long-term, large-scale abundance data for all species involved.

Here, we leverage a well-studied Batesian mimicry system centered on the pipevine swallowtail, Battus philenor, as the unpalatable model and four palatable mimics (Limenitis arthemis, Papilio glaucus, Papilio polyxenes, and Papilio troilus). Using 46 years of continental-scale observational data from the North American Butterfly Association, we address three questions: (1) Does model abundance influence the maintenance of the mimicry complex across space? (2) Does model phenology predict mimic phenology, and have these phenologies shifted over time? (3) Does change in the model's range affect future mimic distributions?

We find that both the model and its mimics have experienced significant phenological shifts over time. Despite this, the mimicry complex is maintained even in regions where the model is rare, with

distinct geographic transition zones. Finally, projected changes in the model's distribution strongly predict future distributions of the mimics, indicating tight ecological and evolutionary coupling among species within this mimicry complex. Together, our results suggest that interacting species engaged in Batesian mimicry are likely to respond in concert to climate change. More broadly, our study highlights the power of large-scale, long-term citizen science monitoring programs combined with integrative modeling approaches to address evolutionary questions and predict species responses to global change.

A-20
Encoder-like protein hub reconciles robustness and evolvability in the avian craniofacial network

Carmen Sánchez Moreno, University of Arizona
Alex Badyaev, University of Arizona

Abstract:

How can a conserved regulatory network produce precise, locally specific outcomes across the multitude of developmental and ecological contexts over evolution? Flexible subcellular compartmentalization of multivalent proteins is a powerful but understudied source of dynamic modularity, in which context-sensing proteins reposition within the cell to connect or disconnect parts of a network and so open access to alternative regulatory states. Here we build a comprehensive atlas of avian beak morphogenesis to test whether subcellular compartmentalization affects the regulatory repertoire of a deeply conserved craniofacial protein network across hundreds of developmental contexts. We find that, in both the upper and lower jaw, the network resolves into a small hub of context-sensing proteins – calmodulin (CaM), transforming growth factor beta II (TGFβ2), and fibroblast growth factor 8 (FGF8) – whose links to a context-invariant protein core depend on where in the cell the proteins co-localize. We show that this hub of context-sensing proteins more than doubles the repertoire of regulatory states the network expresses at any given observed stage and, across development, allows nearly complete exploration of the network regulatory configurations without adding or removing its elements. Thus, these proteins behave as encoder-like hubs – multivalent proteins whose localization-dependent interactions compress diverse mechanical and biochemical inputs into specific regulatory outputs, such that specialization and changeability increase together rather than trade off as is commonly assumed. This organization lets a compact, conserved network sustain continuous development while undergoing remarkable developmental expansion, ultimately providing a mechanistic framework that could reconcile ecological precision with the evolutionary lability evident in avian beaks.

A-21

Toe-pads as a functional trait associated with parental care and habitat use in neotropical poison frogs

Juan Ramírez-Morales, Grupo de investigación en Evolución
Maribel Rojas-Montoya, Universidad del Quindío
Mileydi Betancourth-Cundar, Facultad de Educación
Juan D. Carvajal-Castro, St. John's University
Bibiana Rojas, Department of Interdisciplinary Life Sciences

Abstract:

The superfamily Dendrobatoidea are a diverse lineage with high phenotypic, behavioral, and ecological variation. A key trait of their biology is parental care, which includes clutch attendance and the transport of tadpoles to water bodies where they complete their metamorphosis. In some species, tadpoles are deposited by males in arboreal phytotelmata located up to 20 m above the ground; in these species, males exhibit wider toe-pads than females. However, it remains unknown how this trait changes across species with different reproductive microhabitats and between sexes when the female is in charge of parental care. In this study, we evaluate (1) whether toe-pads size differs between species that transport tadpoles to arboreal phytotelmata and those that do not, and (2) whether there are intraspecific differences between males and females depending on which sex is responsible for tadpole transport. To assess how toe-pads size is associated with the sex performing parental care and the type of phytotelmata used for tadpole deposition, we used standardized photographs obtained both in the field and from natural history museum collections. We measured body size and toe-pads width in males and females across Dendrobatoidea species. Subsequently, we will perform a phylogenetic comparative analysis to control for the effect of phylogenetic relationships among species. Our results show differences in toe-pads size associated with the reproductive microhabitat and but not in the sex responsible for transport. This suggests an evolutionary relationship among reproductive ecology, sexual selection, and functional morphology, offering new perspectives on the role of functional traits in the evolution of parental care in amphibians.

A-22

The role of host plant shifts on speciation in North American butterflies

Jaden Johnson, Hope College
Cody Porter, Hope College

A-23
Characterizing Genetic Basis of Flower Color in Leptosiphon parviflorus

Alysha Schjelderup, University of California

Abstract:

A central question in evolutionary biology asks whether adaptation is primarily driven by few large- or many small-effect size mutations. Despite the extensive theoretical foundation surrounding this argument, empirical examples for either position remain underrepresented. If one of these mechanisms is predominantly responsible for adaptation in natural populations, a general framework for understanding when and how adaptation is likely to occur in natural populations can be developed. The annual wildflower Leptosiphon parviflorus can offer insight towards this knowledge gap, as its color polymorphic flowers are associated with variation in soil and climate conditions throughout its range. At one location in California, pink-flowered plants are locally adapted to harsh serpentine soils while nearby white-flowered plants generally struggle to survive in such conditions. The genetic mechanism responsible for differential adaptation to harsh serpentine soils in the pink morph remains unknown but can provide empirical insight for adaptation through polygenic or oligogenic traits. The pigment responsible for producing pink flowers is a product of the anthocyanin biosynthetic pathway, which is associated with environmental stress tolerance traits across many angiosperm taxa. We hypothesize that floral pigments pleiotropically influence environmental stress tolerance of serpentine soils in this species. By identifying the locus associated with a putatively adaptive flower color trait, we eventually hope to address whether flower color pleiotropically controls environmental stress tolerance. Here we present the methodological process of a pooled genome-wide association study (GWAS) alongside a scaffold-based reference genome to identify candidate loci that correspond to pink flower color in L. parviflorus. We identify a prominent region of the genome where allele frequencies differ between pink- and white-flowered plants, suggesting that flower color either pleiotropically controls environmental stress tolerance in this species or that there are multiple loci in tight linkage. This result is consistent with an empirical example of few large-effect loci contributing to adaptive evolution, supplementing our understanding of how adaptation is most likely to occur in natural populations.

A-24
Evolutionary Game Theory Model of Balancing Selection

Kir Morozov, Bryn Mawr College
Bárbara Bitarello, Department of Biology
Olivia Chu, Bryn Mawr College

Abstract:

Balancing selection (BLS) is an evolutionary force that adaptively maintains genetic diversity in populations through a variety of mechanisms, including heterozygote advantage. BLS modeling and

detection techniques are not currently on the same advanced level as for other selective modes. Recent studies suggest that balancing selection may be more prominent than previously thought. We build a model of heterozygote advantage, one of the mechanisms of balancing selection. Model is based in Evolutionary Game Theory (EGT), which uses classic Game Theory principles to investigate evolutionary outcomes of players in a population. It is classically assumed each player's goal is to maximize individual success. EGT, however, focuses on maximization of the entire population's success, making it highly applicable to cases of balancing selection.

The textbook example of sickle cell allele interactions with malaria is used for demonstration of the model. Data-informed stochastic simulations were run to investigate the changes in sickle cell allele frequency over time under several conditions. Simulations produce replicable results that closely match reality, where such checks are possible, and follow selective logic. Our model could thus be expanded to cover more than heterozygote advantage and used as a basis for future studies of a wide range of selective cases.

A-25
Environmental Stress Influences Phenotypic Diversification and Biofilm Formation in Pseudomonas fluorescens

Sameera Haque, University of Houston

A-26
Facultative Sex Improves the Efficiency of Natural Selection on Lowering Mutation Rates

Camila Chavez Pinero, University of Houston

Abstract:

Mutation plays a key role in evolution, and yet most mutations are deleterious and can negatively impact the survival and reproductive success of organisms. Therefore it is essential to understand how mutation rates evolve, particularly in relation to different reproductive strategies. We investigate how the evolution of mutation rate is influenced by different modes of reproduction under the assumption that all mutations are deleterious. Using simulations, we compare obligately sexual, obligately asexual, and facultatively sexual populations. While one might expect facultative sexuals to show intermediate behavior between pure strategies, we find that they reduce their mutation rate more efficiently than either obligate sexual or asexual populations. This advantage comes from the ability of facultative sexuals to combine the benefits of both recombination and asexual reproduction while avoiding their costs. Our results demonstrate that reproductive strategy can affect the efficiency of natural selection in lowering mutation given all mutations are deleterious. As a next step, we aim to expand the model to include beneficial mutations. This addition will provide insight into the interplay of beneficial and deleterious mutations and how it impacts mutation rate evolution under different reproductive strategies

A-27
The birth, life and death of sex chromosomes in the African clawed frog Xenopus muelleri

Samantha Potts, McMaster University
Ben Evans, McMaster University

Abstract:

The evolutionary history of sex chromosomes often follows a “life cycle” characterized by birth, death and aging. New sex chromosomes arise when a sex-determining mutation occurs on an autosome, and recombination around the sex-determining locus is arrested. Some sex chromosomes, such as those of mammals, persist throughout evolutionary time and reach an advanced stage of divergence and degeneration. In some taxa, ancient, degenerated sex chromosomes are eventually lost. Other sex chromosomes, such as those of African clawed frogs (genus Xenopus), are relatively young and homomorphic due to frequent sex chromosome turnover events that occur within this group. Rapid sex chromosome evolution among Xenopus has led to the eight non-homologous sex chromosomes that have been observed so far in this genus. One Xenopus species, the tetraploid X. muelleri, is an example of recent sex chromosome turnover that has resulted in young, homomorphic sex chromosomes. We leveraged RNA-Seq data mapped to a new reference genome from the closely-related species X. borealis to explore sex-linked genome architecture and expression in X. muelleri. We found that female-biased transcripts and female-specific SNPs are enriched in a 24Mb region on chromosome 4L, providing new insights into the functional evolution of sex-linked regions and the early stages of sex chromosome evolution.

A-28
Insights into the evolution of coloniality and life history traits in jellyfish

Sam Abrams, University of California
Cory Berger, University of California
Todd Oakley, University of California

Abstract:

The polyp life stage of medusozoans (jellyfish and hydroids) can form colonies with diverse architectures, ranging from mat-like encrusting colonies to complex upright or pelagic forms. The timing and distribution of transitions in coloniality are unknown, as are the relationship between colony form and other key life history traits and its impact on patterns of speciation and extinction. Medusozoa’s uncertain phylogeny has posed a challenge for reconstructing trait evolution, but we used a new, well-resolved species tree to reconstruct colony evolution. Ancestral state reconstructions showed five independent gains of coloniality and seven secondary losses, as well as over 40 transitions from simple encrusting colonies to complex upright colonies. Most colonial species belong to a single clade newly established by our phylogeny. Our results suggest that simple encrusting colonies are an evolutionary intermediate between solitary polyps and complex

colonies. Complex colony architecture was highly correlated with the presence of polyp polymorphism and losses of the medusa stage, showing that key life history characters often evolve together. Stochastic character mapping indicated that simple colonies first evolved in the Precambrian, and the frequency of transitions to upright colonies has steadily increased over time.

Additionally, colonial lineages outnumbered solitary lineages only 200 million years after the first gain of coloniality, and there have been more lineages with upright colonies than any other polyp form for the last 140 million years. Surprisingly, however, we found no evidence that coloniality or medusa loss influence diversification rates, suggesting that other factors are the primary drivers of clade-level diversity. Altogether, this study illustrates how life-history traits have evolved and diversified within this ancient clade of animals.

B-01
The molecular regulation of floral ultraviolet (UV) patterns

Justin Chan, The University of British Columbia

B-02
Yeast Mutation Rates Are Highly Correlated With Reactive Oxygen Species and Nutrient Limitation

Mark Lee, University of Wisconsin-Madison

B-03
Repeated Colonization rather than Local Diversification explains Murine Rodent Diversity in the Indian Subcontinent

Chethana Nair, UT Austin

B-04
Divergence of drought resistance strategies in ecogeographically isolated Monkeyflowers

Rachel Pitt, Binghamton University
Jay Sobel, Binghamton University

Abstract:

Early stage divergence is often driven and maintained by multiple factors, including pollinator preferences and local adaptation. Ecogeographic reproductive isolation can limit gene flow and promote divergence in traits such as drought resistance. Drought resistance strategies are typically categorized as avoidance, tolerance, or escape. Sticky monkeyflowers (Diplacus aurantiacus),

native to southwestern Oregon and California, occupy semi-arid environments and exhibit much variation. The ecotypes longiflorus and calycinus are in the earliest stages of parapatric divergence with distinct floral morphologies associated with different pollinator syndromes. Longiflorus occurs in southwestern California while calycinus occupies more inland regions, including the Sierra Nevada mountains. In addition to floral divergence, these ecotypes differ in several physiological and morphological traits, including stomata density, resin production, anthocyanin concentration, and trichome density. Longiflorus exhibits traits consistent with drought tolerance and avoidance, with higher anthocyanin and resin concentrations, and greater stomatal density. In contrast, calycinus flowers earlier, suggesting a favor for drought escape in more inland, harsh environments. This study addresses how divergence in drought resistance strategies manifest across natural populations along an ecogeographic cline. Specifically, whether these trait differences are directly linked to drought resistance or reflect other selective pressures.

B-05
Genome-wide association analysis of life-history and dispersal traits in wild populations undergoing natural range expansion

Gabriel Rizo, Colorado Mesa University

B-06
Genetic Divergence and Signatures of Selection Between Locally Adapted Ecotypes of Arabidopsis thaliana

Stephanie Tirado Rojas, Purdue University

B-07
Genome-wide signatures of recent positive selection overlap genes involved in neuronal development in black-capped chickadees

Sara Padula, University of Colorado Boulder
Georgy Semenov, University of Colorado Boulder
Theresa Burg, University of Lethbridge
Scott Taylor, University of Colorado Boulder

Abstract:

Food-caching chickadees provide a powerful system for studying the evolution of spatial memory in the wild. Black-capped chickadees (Poecile atricapillus) are non-migratory songbirds that cache tens of thousands of seeds during periods of abundance and rely on spatial memory to recover those caches during winter. Populations experiencing harsher climates exhibit enhanced spatial memory performance and larger hippocampi with increased neuron numbers and neurogenesis, and differences in hippocampal gene expression associated with these traits have been

documented across populations. However, the evolutionary processes shaping this cognitive variation remain poorly understood.

Here, we investigate how selection at both range-wide and local scales may contribute to genomic variation associated with spatial memory in black-capped chickadees. We hypothesize that spatial memory is an important target of selection in this species, such that some genomic regions will show signatures of recent positive selection across the range, and that environmental heterogeneity, particularly variation in winter temperature and snow conditions, will drive genotype–environment associations at loci related to spatial memory.

To test these hypotheses, we analyzed whole-genome resequencing data from 28 individuals sampled across North America. We first characterized population structure using principal component analysis and ADMIXTURE, and evaluated isolation by distance to assess the contribution of geographic structure. We then tested for genotype–environment associations using LFMM and Sambada, and identified candidate regions under selection using SweepFinder2 and Tajima's D. Finally, we assessed overlap among candidate loci identified by these approaches and evaluated whether these regions intersect with genes previously implicated in spatial cognition through genome-wide association studies and differential gene expression in the hippocampus.

By integrating population structure, environmental association, and selection-based analyses, this study aims to identify candidate genomic regions involved in spatial memory and to disentangle the roles of shared and spatially variable selection in shaping cognitive traits across the range of a wild bird species.

B-08

Determining genetic mechanisms behind the repeated evolution of cave traits in the Mexican tetra (Astyanax mexicanus)

Maya Enriquez, University of Minnesota Twin Cities
Stefan Choy, Lehigh University
Johanna Kowalko, Lehigh University
Suzanne McGaugh, University of Minnesota

Abstract:

The Mexican tetra fish, Astyanax mexicanus, is a unique model for evolution being that there exist two phenotypes: the surface phenotype which lives in surface rivers, and the cave phenotype which lives in completely dark underground freshwater caves. Cave fish exhibit troglomorphic traits such as eye loss, increased sensitivity in sensory modalities besides vision, and behaviors such as significantly reduced sleep compared to surface fish. Genetic reconstruction suggests cavefish developed from ancestral surface fish that colonized cave environments, but the genetic architecture underlying these drastic changes in phenotypes are unknown. Additionally, these reconstructions indicate that several independent colonizations of cave environments occurred. It is not known whether cave traits appeared through similar or divergent mechanisms across these cave populations.The purpose of this study is to characterize the parallel evolutionary trajectory of

complex cave traits across three different cave populations. We are using quantitative trait locus (QTL) mapping to determine the genetic architecture of three complex traits in cave A.mexicanus: sleep reduction, increased neuromast density, and the interaction between starvation and sleep length. For one surface and three cave populations (Pachón, Molino and Tinaja) we used behavior tracking software to estimate sleep over 24 hours at two different time points and under different feeding regimes to examine the plasticity of sleep response in response to nutrient availability. After recording sleep, we additionally quantified the number of neuromasts within a facial anatomical region (suborbital 3) associated with increased sensitivity and response to vibration across all four fish. At the conclusion of the experiment, fin clips were taken from each fish that went through the pipeline and sequenced in order to conduct QTL analysis. Preliminary results suggest that neuromast quantity may be correlated with sleep in some populations and not others, suggesting a different genetic basis and evidence for parallel evolution.

B-09
Specialized enhancer activity associated with convergent evolution of vocal learning

Rajee Ganesan, Carnegie Mellon University
Andrew Wang, Carnegie Mellon University
BaDoi Phan, Carnegie Mellon University
Michael Leone, Carnegie Mellon University
Heather Sestili, Carnegie Mellon University
Andreas Pfenning, Carnegie Mellon University

Abstract:

Vocal production learning, or vocal learning, is the ability to imitate sounds through social exposure. The rare trait has been observed in humans, bats, cetaceans, pinnipeds, songbirds, parrots, hummingbirds, and is believed to have independently evolved three times in birds and five times in mammals, representing a prime example of convergent behavioral evolution. All studied vocal learning species have evolved a specialized forebrain sensorimotor learning circuit that is either absent or rudimentary in their closer, vocal non-learning relatives. Previous work within the lab has found that the “regulatory code” linking genome sequence to cell-type-specific function is highly conserved across mammals. In this study, we leverage this principle to identify candidate enhancers from publicly available Zoonomia datasets, and trained machine learning models predicting open and closed chromatin across all 240 mammalian motor cortex regions. We screened for differences in regulation between vocal learning and non-learning species by applying the Tissue-Aware Conservation Inference Toolkit, a machine learning approach to study how enhancer activity conservation relates to phenotype evolution. These machine learning models can learn sequence patterns of enhancers that robustly predict whether or not they have conserved activity across evolutionary distances, allowing us to test whether enhancer conservation patterns are associated with the evolution of vocal learning. Our results revealed lineage-specific gains and losses of regulatory elements, and we show that L6 corticothalamic neurons and oligodendrocytes had the strongest enrichment with the vocal learning phenotype, suggesting key roles in

vocalization-related traits through motor learning and synaptic plasticity. Additional enrichment in PV, SST, and VIP interneurons highlights modulation of cortical circuits involved in vocal learning. Future studies will include single cell integration across human, mouse, rat, macaque and the zebra finch to identify orthologous cell populations and to better understand the molecular mechanisms associated with the convergent evolution of vocal learning.

B-10

Interspecific interactions drive evolutionary divergence in thermal physiological traits among species but no evidence from within species comparison: multi-scale tests in Japanese Plestiodon

Shouta Iyoda, Kyoto University
Ryotaroh Yanagihara, Kyoto University
Teppei Jono, Kyoto University

Abstract:

The thermal niche partitioning hypothesis is widely assumed to be an evolutionary mechanism driving divergence in thermal physiology among competing species. However, empirical tests based on sympatric-allopatric comparisons remain limited, leaving the scale at which these processes operate unclear.

Here, we tested whether interspecific interactions drive divergence in thermal physiological traits using a comparative framework across Japanese Plestiodon lizards. Specifically, we combined 1) an interspecific comparisons of preferred body temperature (Tpref) across seven species along a latitudinal thermal gradient, 2) a detailed comparison of microhabitat use and thermal physiological traits between two sympatric species (P. toyamai and P. marginatus), and 3) an intraspecific comparisons of P. marginatus populations between sympatric and allopatric islands.

At the interspecific level, environmental temperature did not explain variations in Tpref. However, consistent with the hypothesis, P. marginatus showed significantly higher Tpref than its sympatric congener, P. toyamai. Microhabitat and physiological comparisons further supported this, showing that P. marginatus occupied more open, warmer environment and exhibited higher thermal traits relative to P. toyamai. In contrast, inter-population comparisons of P. marginatus revealed no clear evidence of difference between sympatric and allopatric populations, indicating a scale-dependent pattern. While divergence was evident at the specific level, it was absent within the species. This discrepancy may be attributed to strong behavioral buffering, where precise thermoregulatory behavior reduces selective pressures on thermal physiological traits following ecological release after isolation from conspecific at the last glacial maximum. Considering the no effects of environmental temperature on the evolution of thermal physiology of Plestiodon species, these results highlight strong behavioral buffering in Plestiodon. However alternative mechanisms such as species filtering cannot be ruled out. Further research is necessary to distinguish the relative influence of interspecific interactions and other evolutionary driver in shaping the higher thermal physiology of P. margintus.

B-11
Historical Demography of the Livebearer Phalloceros leptokeras along a Coastal Brazilian Watershed

Ana Carolina Almeida Fernandes, Federal University of Rio de Janeiro
Ana Cristina Petry, Universidade Federal do Rio de Janeiro
Marcio Silva Araujo, São Paulo State University (UNESP)
Pablo Rodrigues Gonçalves, Federal University of Rio de Janeiro (UFRJ)

Abstract:

Geological and climatic changes are drivers of demography in freshwater organisms, particularly where hydrological connectivity fluctuates through time. We investigate how Quaternary marine transgressions and landscape heterogeneity have shaped the demographic history of the livebearing fish Phalloceros leptokeras across the Macaé river basin, southeastern Brazil. We sampled ten populations along the three geomorphological compartments of the watershed (mountain escarpment, foothills, and coastal lowlands), and analyzed genetic variation between and within compartments using mitochondrial (COI) and nuclear (RAG1) markers. Using Approximate Bayesian Computation, we evaluated alternative demographic scenarios associated with marine transgressions and regressions. Our results revealed significant spatial structure between compartments and differing demographics within each one of them. The coastal lowland population maintained relatively stable effective sizes, the foothill population exhibited bottleneck signatures followed by expansion, and the mountain population showed signals of long-term demographic expansion. The genetic stability of the lowland population is unexpected given the recurrent marine transgressions that affected this compartment since the last glacial maximum. However, the existence of freshwater refugia associated with lagoons and wetlands likely facilitated stepping-stone dispersal from the main population source represented by the neighboring Paraíba do Sul river along the coastal plain and maintenance of a larger effective size. In contrast, demographic contraction in the foothill population is consistent with the isolation imposed by rising sea levels, which may have restricted dispersal and reduced effective population sizes. Expansion in mountain populations likely reflects greater environmental suitability by increases in wetted area since the last glacial maximum, allowing population growth through time. Together, these patterns suggest that eustasy produces uneven demographic responses mediated by landscape features within a single river basin. By integrating demographic responses with long-term environmental dynamics, this study reveals an unusual population structure shaped by historical processes, divergence and connectivity in coastal watersheds.

B-12
Chromosomal rearrangements and segmental deletions contribute to gene loss in squamates

Buddhabhushan Salve, IISER BHOPAL

Abstract:

Background

Genomic rearrangements, including segmental deletions, duplications, translocations, and inversions of DNA segments, can contribute to gene losses, thereby reshaping genome architecture and potentially resulting in functional consequences. In squamates, karyotypic evolution mainly involves chromosome number reduction through fusions and microchromosome to macrochromosome translocations, although fissions have also contributed to diversification in several lineages. Despite these dynamics, the evolutionary processes and underlying genetic mechanisms driving chromosomal rearrangements and associated gene losses in squamates remain poorly understood.

Results

In this study, we analysed chromosome/scaffold-level assemblies of 261 squamates, corroborated by short-read, long-read, and transcriptomic data. We found multiple lines of evidence for the putative loss of 53 genes in the squamate lineage. Synteny and phylogenetic analysis revealed that, among the 53 unretrieved orthologs, 14 are lost in squamates with no retained paralog, 15 show ortholog loss with retained paralogs, and 24 remain as unretrieved orthologs. Furthermore, we find that many of the genes lost from squamates are organised in syntenic clusters and are involved in essential immune functions—raising important questions about the role of paralogs in compensating for the function of lost genes, strengthening the 'less-is-more' hypothesis in the squamate lineage.

Conclusions

Together, our comparative genomic analyses highlight that the loss of crucial genes in squamate lineages has occurred primarily through inter- and intrachromosomal rearrangements, including segmental deletions. These findings offer insights into the evolutionary loss of genes involved in macrophage differentiation and inform the development of novel pharmaceutical approaches for modulating immune responses.

B-13
Who wins and why? uncovering the genomic basis of resistance polymorphism in a snail–parasite system

Oluwaseun Adu, Oregon State University
Michael Blouin, Oregon State University
Stephanie Bollmann, Oregon State University
Javier Calvelo, Oregon State University

Abstract:

Schistosomiasis, a neglected tropical disease transmitted by freshwater snails, causes significant morbidity and mortality in endemic communities, particularly in sub-Saharan Africa. With the WHO targeting elimination by 2030, identifying snail genes controlling resistance to schistosome infection could offer novel strategies to break transmission cycles. Using a pooled-seq GWAS

approach, we mapped genetic variation in the BgBAR population of Biomphalaria glabrata snail associated with resistance to the SmVEN population of Schistosoma mansoni parasite. Scanning for allele frequency differentiation between infected and uninfected snail populations via 10 kb sliding-window Fst analysis and Fisher's exact test, we identified a genomic region with a high Fst peak exceeding the null-hypothesis-generated mean. We validated this region using PCR markers on independently genotyped BgBAR populations. The identification of a previously unknown region on chromosome 16 in this study highlights the importance of examining specific host-parasite population combinations to uncover resistance-associated regions and advance our understanding of coevolutionary dynamics in host-parasite systems.

B-14
Differing genomic selection on reciprocal hybrids in contrasting habitats

Matthew Billings-Chiu, Grinnell College
Jill Love, Tulane University
Kathleen Ferris, Tulane University
Caroline Dong, Grinnell College

Abstract:

Adaptation to environmental conditions can drive phenotypic divergence, reproductive isolation, ultimately culminating in speciation. Under secondary gene flow, the differing selection on reciprocal hybrids in divergent parental habitats may influence the rate and direction of gene flow, and ultimately the evolutionary outcome of hybridization. The forces acting on reciprocal hybrids are not yet well understood and further, identifying the specific genomic regions and mechanisms remains an area of great interest. We performed an evolve-and-resequence field study using Monkeyflowers in Yosemite National Park. Mimulus guttatus and Mimulus laciniatus are closely related North American wildflowers that are adapted to contrasting microhabitats but incompletely reproductively isolated. We created F2 reciprocal hybrids between M. guttatus and M. laciniatus, then transplanted hybrids and parents into native meadow and granite outcrop sites. We used whole genome pooled sequencing to sequence pools of individuals before and after natural selection in sites. Preliminary results suggest that there are regions of the genome experiencing different strengths of selection between habitats in one reciprocal cross, with further gene annotation currently underway. This work will provide a deeper understanding of the role of natural selection in the dynamics of speciation and hybridization.

B-15
Integrative Approaches to Floral Resource Allocation: Macroecological and Trait-Based Predictors of Reproducitve Output in Mentzelia (Loasaceae)

Campbell Hauschild

B-16
Temporal dynamics of parallel evolution under elemental limitation

T Goldberg, University Loyola Chicago
Caroline Turner, Loyola University Chicago

Abstract:

Evolutionary repeatability may vary not only across environments but over time. As organisms evolve, genetic changes and epistatic interactions influence the fitness impact of subsequent mutations. We sought to test how repeatability of evolution changes over time in populations adapting to different environmental constraints.

Previously, we ran a 12-week evolution experiment with populations of Escherichia coli in carbon-limited, nitrogen-limited, and alternating carbon/nitrogen-limited environments. Populations exposed to nitrogen-limitation showed higher repeatability than populations evolved solely in carbon-limitation, with all but two populations evolving mutations in one of two nitrogen-starvation response genes. Evidence suggested that initial selection under nitrogen-limitation was governed by strong positive selection for a small number of key mutations, in contrast to the large number of initial mutations under positive selection in carbon limitation.

To test how selection and repeatability changed over time, we evolved the same populations from the first experiment under the same conditions for an additional 12 weeks. We hypothesized that the initial parallelism we observed under nitrogen-limitation was due not to a lack of potential beneficial mutations, but rather the availability of a few large-benefit mutations that outcompeted smaller-benefit mutations via clonal interference. We therefore expected to observe decreased repeatability in nitrogen-limitation after an additional 12-weeks as more numerous small-benefit mutations appeared following fixation of high-benefit mutations.

B-17
Using phylotranscriptomics to disentangle the fastest radiation of plants

Tomi Jacobs, University of Illinois Chicago
Joseph Walker, University of Illinois Chicago

Abstract:

Aizoaceae (ice plants) are one of the most rapidly radiating plant families on Earth, yet the phylogenetic relationships underlying this diversification remain unresolved. In this study, phylotranscriptomic analysis of 39 Aizoaceae taxa was done by both coalescent and concatenation species tree estimation with information-theoretiy gene tree quality assessment, concordance analysis, and functional annotation of duplicated gene families. Transcriptomes were assembled using Semblans, a bioinformatics pipeline, and quality was evaluated using BUSCO & Transrate. Gene trees were inferred from 4,845 ortholog clusters extracted from 15,818 homolog gene families. To evaluate the influence of gene tree quality on species tree inference, four (4) datasets

were created through filtration: ALL = 4845, PYTH (Pythia phylogenetic difficulty score) = 2,092, BIPART (Relative Tree Certainty Assessment scores) = 450, BOTH (Intersection between PYTH & BIPART) = 432. Species tree topology was the same with ALL & PYTH and BIPART & BOTH. Gene tree concordance analysis revealed strong support at the node subtending Rushioideae (Node 11) but high conflict within the clade itself. Duplication analysis and panther annotations for gene functions at node 11 identified gene families involved in stress response, building up of lignified cells (associated with wide band tracheids) and proteins essential for xylan deposition in the secondary cell wall of xylem vessels.

B-18

Defense conferred by trichomes differs in effectiveness against different types of herbivory in Medicago lupulina

Samantha Hickman, University of Pittsburgh
Corlett Wood, University of Pennsylvania

Abstract:

Many plant defense traits are general and protect against herbivory from a range of antagonists. Trichomes, defensive hairs occurring on the plant surface, are one such trait. However, not all herbivores are interchangeable; insect herbivores fall into several distinct feeding categories, including leaf-chewing and piercing-sucking. We tested whether trichomes are equally effective against these two types of herbivory in Medicago lupulina, a wide-spread wild legume. We used lab-based choice assays to test the preference of two different types of insects, aphids and earwigs, which we selected to represent piercing-sucking and leaf-chewing herbivory, respectively. We also observed and analyzed patterns of herbivory in a large field experiment by tracking the presence of aphids and holes left by leaf-chewers. We found that trichomes did not deter aphids nor earwigs in the lab-based choice assay. However, the field experiment, trichomes affected aphids and leaf-chewers differently; we found that leaf-chewers were more deterred by trichomes than aphids. Overall, this tells us that trichomes are a more effective deterrent against leaf-chewers than against piercing-sucking insects. Earwigs, though, eat other insects as well as plants, which indicates that omnivorous leaf-chewers are undeterred by trichomes. Understanding the exact types of herbivores that trichomes are effective against allows us to infer how the composition of insects in a given environment could exert selective pressure on plants to influence the evolution of trichomes. In addition, this understanding sheds light on how naturally occurring plant defenses, like trichomes, might be utilized for agricultural pest control.

B-19

PopGenHelpR: An R package to streamline and facilitate informed population genomic analyses and visualization of genetic ancestry, diversity, and differentiation

Keaka Farleigh, University of Virginia

Mason Murphy, Bowling Green State University
Christopher Blair, City University of New York
Tereza Jezkova, Miami University

Abstract:

Analyzing large population genomic datasets requires an interdisciplinary skillset. Beyond a knowledge base in genetics and population biology, population genomic analyses involve computer science and statistics, representing a barrier for researchers without experience in those fields. PopGenHelpR seeks to lower this barrier by enabling researchers to perform population genomic analyses and generate near-publication quality figures in a streamlined and informed fashion. PopGenHelpR allows users to estimate genetic diversity within populations as well as differentiation among populations and individuals from single nucleotide polymorphism data. PopGenHelpR includes commonly used measures such as observed heterozygosity and FST. PopGenHelpR also provides five previously unavailable measures of heterozygosity, including the proportion of heterozygous loci and homozygosity by locus. Additionally, PopGenHelpR integrates widely used visualization tools in population genomics that normally require additional software packages, such as ancestry bar charts, piechart maps, and genetic differentiation heatmaps. Moreover, PopGenHelpR is minimally dependent on other R packages, reducing its chance of being removed from public networks. The PopGenHelpR website also provides tutorials and educational resources. Altogether, PopGenHelpR provides resources for informed analyses and effective visualization, making PopGenHelpR a valuable tool for many researchers. PopGenHelpR is available on the Comprehensive R Archive Network and GitHub (https://github.com/kfarleigh/PopGenHelpR).

B-20
From Sequence to Survival in the Houston Toad : Genomic Diversity, Fitness, and DNA-based Age Estimation

Xiyuan Guan, Purdue University

Abstract:

Amphibians face an unprecedented global extinction crisis, with habitat loss, disease, and climate change driving population declines worldwide. Conservation interventions such as captive breeding and reintroduction now essential management tools, yet their long-term success depends on maintaining sufficient genomic diversity to sustain adaptive potential in wild populations. The Houston toad (Anaxyrus houstonensis), a critically endangered amphibian endemic to Texas, exemplifies both the promise and challenges of reintroduction-based conservation: while intensive management has achieved notable success at some sites, fundamental questions remain about whether released populations retain adequate genomic diversity to cope with future environmental challenges, how individual genetic characteristics influence post-release fitness, and how age structure can be assessed and incorporated into demographic models of population viability. This poster describes four integrated research aims: (1) constructing a chromosome-level reference

genome for Houston toad; (2) tracking genomic erosion in captive versus wild-reintroduced cohorts to evaluate whether diversity is maintained at levels sufficient for long-term population viability; (3) quantifying how parental genetic divergence and individual heterozygosity influence offspring survival and reproductive success; and (4) developing and validating a DNA methylation-based epigenetic clock using known-age captive individuals for non-invasive age estimation in wild populations. This work will directly inform adaptive management decisions for Houston toad recovery and establish a translatable genomic monitoring framework for other non-model taxa facing extinction.

B-21
Examining Intraspecific and Interspecific Gene Expression Variation in Cold-acclimated Chickadees

Lucas Florsheim, University of Colorado Boulder

Abstract:

Patterns of gene expression provide insight into how populations and species adapt to local environments. Whether within species variation across environmental gradients mirrors between species variation across similar gradients is an outstanding question that is relevant for understanding both local adaptation and, potentially, the maintenance of species boundaries. We conducted two 6-week cold acclimation common garden experiments using wild-caught black-capped (Poecile atricapillus) and Carolina (P. carolinensis) chickadees and their hybrids. Black-capped chickadees came from both Colorado and Pennsylvania, while Carolina chickadees and hybrids came from Pennsylvania. Following the experiment, we used RNA-seq data from pectoralis muscle to compare the gene expression profiles of closely related, hybridizing, black-capped and Carolina chickadees, as well as gene expression between geographically distant black-capped chickadee populations. This design allows for direct comparison of expression divergence between species and between geographically distant populations within a species. Gene expression divergence was substantially greater between geographically separated populations of the same species than between different species occupying the same environment. These results suggest that local environmental factors may drive strong regulatory divergence within species, in some cases exceeding expression differences between closely related species that reside in similar environments.

B-22
Comparative metagenomic analysis of bat flies and their primary endosymbionts.

Joely Corrales, Northern Arizona University
Kelly Speer, Northern Arizona University

Abstract:

Microbial endosymbionts are essential for biological processes in their hosts and are reliant on host internal environments. Host-microbe interactions have facilitated the diversification of insects with specialized diets (e.g., obligate sanguivores), and enable their respective hosts to obtain vital nutrients through microbial provisioning (e.g., vitamin B). Despite our understanding of their functional role, we lack knowledge surrounding how these host-endosymbiont interactions are maintained through evolutionary time. Specifically, how selection and host genetic structuring influences the accumulation of deleterious mutations in the small genomes of endosymbiont. Bat flies provided an excellent model for this analysis as diet and environment are controlled for by their respective bat host life history.

To determine if bat fly genetic structure covaries with endosymbiotic genetic structure, I will use single nucleotide polymorphisms (SNPs) from short-read WGS to compare the genetic structure of bat flies to their endosymbionts. I hypothesize that endosymbiont genetic structure will covary with that of their hosts. Therefore, if the host genetic structure is more homogenous, the microbial endosymbiont genetic structure will mirror that.

To determine how genetic structure impacts functionality and deleterious mutation accumulation, I will reconstruct gene regions to examine distribution of mutations within and outside of genes of the B vitamin synthesis pathway with de novo and reference guided genome assemblies. I hypothesize that a more homogenous genetic structure will be associated with higher genetic functionality and longevity within the entire bacterial population. Inversely, a more heterogeneous genetic structure would be associated with gene loss and fewer functional genes. Bat flies within large, admixed populations are less likely to accumulate deleterious mutations than those in small, isolated populations; therefore, if host and bacterial structure covary, we might expect to see corresponding patterns in the frequency and retention of genes involved in vitamin synthesis pathways (i.e, vitamin B).

B-23
Investigating the genetic basis of polymorphic mimicry in a freshwater mussel

Nathaniel Neal, SSE
Jingchun Li, Ecology and Evolutionary Biology
Scott Taylor, University of Colorado Boulder

Abstract:

Mimicry, wherein organisms evolve elaborate resemblance signals to deceive predators, prey, or hosts, provides some of the most striking examples of trait evolution. Many freshwater mussels of the Unionidae family present specialized tissue extensions, called mantle lures, that mimic small prey items to entice and facilitate parasitization of host fish. The genetic basis of such lures is unknown, but Lampsilis fasciola (Rafinesque 1820; “wavy-rayed lampmussel”) provides a uniquely tractable system to investigate this mimicry. Two distinct lure phenotypes are present among L. fasciola: (1) the darter fish mimic lure that has eyespots, tissue extensions which mimic fins, and

mottled black, tan, and white pigmentation; and (2) the orange, leech mimic lure which lacks eyespots and tissue extensions. Not only do the polymorphic phenotypes co-occur within populations, but we have identified both phenotypes among full siblings in a single brood. We performed whole-genome sequencing at a mean depth of 14.1X coverage for 20, full-sibling, L. fasciola mussels (10 per phenotype). We mapped reads to a Sinanodonta woodiana reference genome and used 5kb sliding-window FST plots and principal components analysis to evaluate genetic differentiation between the two respective lure phenotypes. Multiple regions on a single chromosome scaffold showed elevated divergence (mean FST = 0.00066; 99th percentile FST = 0.147) spanning 240 genes. Initial gene ontology analysis of peak regions (top 1% FST) revealed enrichment for terms related to ion transport and pH regulation. Preliminary RNA-seq analysis, based on a single replicate per phenotype, indicated differential expression in mantle lure tissue of genes associated with pigmentation and muscle contraction. While phenotypic consequences remain unclear, these patterns suggest divergence in physiological processes potentially associated with lure phenotypes. Sampling and whole genome sequencing of populations across the species range combined with RNA sequencing of common-garden-reared individuals will further clarify the genetic framework of polymorphic mimicry.

B-24
Prevalence and mediators of an amphibian fungal disease on the nearshore California Channel Islands

Jennifer Hu, California State University

Abstract:

Globally, amphibian populations are declining at alarmingly high rates, partially due to chytridiomycosis, a disease caused by Batrachochytrium dendrobatidis (Bd). Island amphibians are more vulnerable to this aquatic pathogen, as they evolved in isolation with limited disease exposure. Because Bd can survive without a host in water, mud, and damp debris, its spread across bodies of water can be mediated by non-amphibian vectors. Bd was established on the California Channel Islands in the 1970s, but no study has assessed its prevalence and intensity on live island amphibians. I will quantify spatial variation of Bd among and within the three islands where the Pacific chorus frog (Pseudacris regilla) occurs. I hypothesize that Bd prevalence is associated with human density, as footwear can contribute to pathogen mediation.

I will sample adult frogs and record location data at 12 sites each on Santa Rosa, Santa Cruz, and Santa Catalina Islands (n = 15 frogs/site, 540 total). Frogs will be swabbed for Bd using a standard protocol. Pathogen presence will be detected via qPCR, and fungal load will be estimated from internal transcribed spacer (ITS) copy numbers. I will rank sites by human density by measuring distance from locations of human traffic, such as hiking trails, campsites, and harbors, then refine binning with iNaturalist observations. I will test my hypotheses using ANOVA analyses. Though the Pacific chorus frog is a reservoir species on the continent and able to tolerate much higher fungal loads without succumbing to disease, island frogs have evolved in isolation. Thus, it is possible that

island frogs are more susceptible to this disease. These preliminary results of my study will contribute to our understanding of near-shore island disease dynamics and may inform conservation and biosecurity plans for the islands' only native frog.

B-25
Cognition Mediates Fitness Under Environmental Stress and Parasitism

Clarissa Guzman, University of Texas at Austin

Abstract:

This study investigates the relationship between cognition and reproductive success in birds within the framework of the cognitive buffer hypothesis. The cognitive buffer hypothesis predicts that enhanced cognitive abilities promote behavioral flexibility and confer evolutionary advantages, such as enhanced foraging and provision, spatial memory, communication. Using citizen science data aggregated by the NestWatch project dataset encompassing over 400 predominantly North American bird species, we analyzed reproductive outcomes for approximately 185 species with available comparative brain data. We tested how cognition, measured as residual brain size, relates to reproductive success, quantified by the number of fledglings. We further evaluated how cognition interacts with environmental conditions and brood parasitism by incorporating measures of climatic variability and parasite presence at both egg and nestling stages. We found no consistent main effect of relative brain size on reproductive success, indicating that cognitive effects are strongly context dependent. Species with larger relative brain sizes exhibited improved reproductive performance under harsher environmental conditions, consistent with the cognitive buffer hypothesis. In contrast, under brood parasitism, larger-brained species showed reduced fledging success but a lower probability of complete reproductive failure, suggesting partial mitigation of parasitism costs. Environmental harshness reduced the probability of parasitism at both the egg and nestling stages; however, this effect was moderated by brain size, with larger-brained species more likely to experience parasitism under harsh conditions at the egg stage but less likely to support successful parasite development at the nestling stage. Together, these results demonstrate that cognition does not universally enhance reproductive success but instead shapes how species respond to environmental and biotic challenges, highlighting the context-dependent nature of cognitive advantages in avian evolution.

B-26
Defining the Human-AI Boundary in Bioinformatics; A Framework for AI-Augmented Skill Acquisition in Computational Biology.

Oluwatimileyin Okeseni, University of Illinois at Chicago (UIC)

Abstract:

Background:

AI tools for generating pipelines analysis, interpreting genomic data outputs, and even automating ecological models are now freely accessible to students at every level of training. Yet a critical and largely unexamined question follows this shift: Is learning taking place when a student delegates a bioinformatics task to AI, or they are bypassing the cognitive work that learning requires?

Objectives:

This doctoral research aims to (1) operationalize a conceptual boundary between AI augmentation and AI replacement in computational biology skill acquisition; (2) develop and validate a human-centered, AI-assisted learning framework built around this boundary; and (3) evaluate whether the framework equitably builds bioinformatics competency in students from underrepresented communities, using transcriptomics and invasive species modeling as the biological learning contexts.

Proposed approach:

First, a Modified Delphi process with bioinformatics educators and learning scientists will produce a validated rubric defining where AI should and should not mediate student learning, distinguishing tasks that require human analytical ownership from tasks where AI scaffolding is appropriate. Second, the framework will be applied to two real biological problems: RNA transcriptomes analysis and invasive species modeling, allowing students to produce scientifically valid outputs. Third, a quasi-experimental pre/post intervention study will deploy the framework with underrepresented undergraduate students, measuring skill acquisition and AI dependency patterns against a controlled group trained through conventional approaches.

Significance:

This research aims to offer the first empirically grounded model for preserving human analytical agency in AI-assisted bioinformatics training, with direct implications for workforce development, research reproducibility, and equity in the life sciences. In an era where AI can do the analysis, the question this research insists on asking is: can the student?

B-27
From Decimation to Density-Dependence: Waterbuck in Gorongosa National Park

Hannah Gellert, Stanford University
Katherine Solari, Stanford
Robert Pringle, Princeton University
Dmitri Petrov, Stanford University

Abstract:

Defaunation, particularly the loss of megafuana or large-bodied mammals, is a continuing concern amid today's ongoing biodiversity crisis, with populations being especially susceptible to overexploitation, habitat loss, climate change and more. In Gorongosa National Park, the

Mozambican Civil War (1977-1992) decimated megafaunal populations. However, since 2004 the park has committed to large-scale rewilding. No species has responded as dramatically to these efforts as the waterbuck (Kobus ellipsyprymnus). The waterbuck population decreased from 3,000 to 140 due to the war but has since rebounded to an estimated 64,000 waterbuck in the most recent aerial counts. Waterbuck are a widespread African antelope whose genomic diversity remains poorly characterized in the southeastern and southern portions of their range. Here, we present the first genomic baseline for waterbuck in Mozambique with samples from Gorongosa National Park and Coutada 11 (a nearby hunting concession) and compare them to other populations throughout the waterbuck range. We also investigate evidence of microgeographic structure of the waterbuck population within Gorongosa National Park.

B-28
Analyzing the Taphonomy of a Miocene-age Threespine Stickleback Fish Series

Matthieu Weinberg, Loyola University Chicago
Emily Hallett, Loyola University Chicago
Yoel Stuart, Loyola University Chicago

Abstract:

The 10-million-year-old Truckee Formation near Hazen, Nevada, preserved a 20,000 year long sequence of fossilized threespine stickleback fish (Gasterosteus doryssus). The fish are fossilized in diatomite, the siliceous shells of ancient diatoms that were continuously deposited on the Lake Truckee floor. This depositional setting allows a high-resolution, near-continuous record of morphological evolution, stasis, and local extinction. The series captures an ecological replacement of a low-armored stickleback lineage by a high-armored stickleback lineage. Understanding the paleoecology of this replacement can help explain why it happened. Here, we present the taphonomy, or fossilization and depositional context, of this stickleback fish series in an attempt to reconstruct paleoecology through time. We photographed approximately 4,000 fish from this series and quantified trends in taphonomic disarticulation of the skull, fins, ribs, vertebral column, and general skeleton, each indicative of an ecological process. For instance, disarticulation of fin elements of an otherwise perfectly articulated fish is evidence of decay at low temperatures. We also noted trends in anoxia-induced muscle convulsions (tetany), evidence of a low-oxygen environment. We reconstruct temperature, depth, and oxygen content throughout the time series. Given the Truckee Formation's temporal resolution, abundance of specimens, and expansive evolutionary phenomena, analyzing the taphonomy that underlies these patterns can further our understanding of stickleback evolutionary history.

C-01
Mitochondrial introgression in North American red-backed voles is facilitated by co-introgression at nuclear-encoded mitochondrial genes

Ben Wiens, University of Kansas

Jocelyn Colella, University of Kansas

Abstract:

Mitochondrial genomes encode for the proteins and RNAs that serve as the basis for aerobic respiration and energy production. Yet mitochondria depend on the nuclear genome for hundreds of additional genes whose products engage in core metabolic processes (N-mt genes). Despite strong selective pressure for coevolved mitonuclear interactions, there are numerous examples of mitochondrial introgression across species barriers. Mitonuclear co-introgression, a process whereby alleles at N-mt genes move across species boundaries in concert with mitochondrial genomes, has been suggested as a mechanism whereby species could capture heterospecific mitochondria while avoiding mitonuclear incompatibilities, but evidence for this phenomenon is sparse. We test for evidence of mitonuclear co-introgression in two discordant populations (Clethrionomys gapperi nuclear genomes, C. rutilus mitochondrial genomes) of North American red-backed voles using whole genome resequencing. We find that N-mt genes in both populations are significantly enriched for C. rutilus ancestry, with evidence of co-introgression at eighteen N-mt genes. Notably, two N-mt genes directly associated with mitochondrial translation are fixed or nearly fixed for C. rutilus ancestry in both discordant populations and analyses of genetic variation at these genes suggest recent selective sweeps. We pair these findings with mitochondrial phylogenies, recent demographic histories, and recombination maps, which support a scenario of ongoing introgression in British Columbia but cessation of gene flow in Southeast Alaska. Together, our results show that mitochondrial introgression in North American red-backed voles is adaptive and that mitonuclear incompatibilities are overcome through mitonuclear co-introgression.

C-02
Uncovering the Evolutionary Adaptation of Helaeomyia petrolei (Diptera: Ephydridae)

Ying Fei Lin, Virginia Tech
Ethan Tolman, Virginia Tech
Nurislam Shaikhutdinov,
Sean Campbell,
Phoebe Fu,
Parul Johri, University of North Carolina
Giar-Ann Kung, Natural History Museum of Los Angeles County
Jessica ware, Ware Lab
Bernard Kim, Princeton University
Anton Suvorov, Virginia Tech

Abstract:

The oil fly, Helaeomyia petrolei, is a unique extremophile that spends most of its life cycle in native asphalt as well as tar pits—one of the most extreme habitats on Earth. How can the oil fly survive, while all other metazoans die in this extremely toxic environment? To date, our understanding of its

phenotypic and molecular adaptations to a hydrocarbon-rich, hypoxic environment remains very limited. In this study, we aim to uncover the morphological and genetic basis of extremophily in H. petrolei using comparative approaches. Specifically, we examined larval and adult morphology with high-resolution imaging, assembled a high-quality H. petrolei genome, and investigated the gene families that might be related to extreme environmental adaptation. This work provides a foundational resource and advances our understanding of the genetic and anatomical adaptations that enable survival in one of the most challenging niches.

C-03
Range-wide population genomics of the eastern oyster reveals divergent environmental adaptation and parasite mitigation strategies between two ancestral groups

Madeline Eppley, Northeastern University
Katie Lotterhos, Northeastern University Marine Science Center

Abstract:

Identifying adaptive loci from wild populations is a priority for designing multi-trait genomic selection programs for aquaculture, particularly as climate change necessitates breeding for resilience to novel and variable environments. One such desired trait is parasite load mitigation, an urgent priority for aquaculture scientists and shellfish growers alike as they look to source broodstock that will perform positively under projected future intensification of marine diseases. Parasite load is theoretically debated to be mitigated by two non-exclusive strategies. With targeted adaptation, specific immune-related loci mitigate load. Comparatively, general heterozygote advantage and linkage disequilibrium can work in tandem to produce immune advantage across the genome. To close this gap, we conduct the first range-wide genomic study for the eastern oyster (Crassostrea virginica) across thousands of miles (Texas, USA to Eastern Canada) using a 200K SNP array. We use population structure analyses to identify two ancestral groups with a phylogeographic break between the Gulf and Atlantic coasts (FST = 0.06). We then statistically test parasite mitigation hypotheses by examining the relationship between individual-level parasite load and underlying genotype for each ancestral group. We find divergent adaptation strategies, where (1) logistic regression reveals general genome-wide heterozygosity mitigates parasites in Gulf oysters, but not in Atlantic oysters; and (2) Gulf and Atlantic ancestral groups have divergent targeted loci in statistical association with infection, sharing no overlap at the SNP, gene, or pathway level. Lastly, we identify three genes from heat shock protein families involved in adaptation to both high temperature and parasite resistance - a biologically significant response as parasites proliferate under high temperatures. Our results ultimately identify genomic targets for aquaculture breeding programs aimed at climate resilience and contribute to a growing body of evidence that marine species with a previously thought propensity for genetic panmixia can exhibit structure and adaptive differentiation across the seascape.

C-04

Comparative genomics of evolutionary transitions from marine to freshwater among Fundulus killifish species

Tatum Bernat, University of California
Gio Madrigal, University of Illinois
Julian Catchen, University of Illinois at Urbana-Champaign
Martin Tresguerres, University of California
Fernando Galvez, Louisiana State University
Andrew Whitehead, University of California Davis

Abstract:

Evolved differences in osmoregulatory physiology have allowed fishes to colonize vastly different habitats and much remains to be learned about the genomic variation that underlies the array of osmoregulatory strategies. Euryhaline species are physiologically flexible, tolerating a wide range of salinities. In Fundulus killifish, euryhaline lineages have repeatedly and independently radiated from marine to freshwater environments, which is accompanied by a loss of euryhalinity and a gain of freshwater specialization. These evolutionary transitions provide a unique opportunity to apply comparative genomic methods to investigate the mechanisms supporting osmoregulatory plasticity across species. We hypothesized that the loss of euryhalinity would manifest as patterns of protein sequence or protein family evolution that differ between those with euryhalinity and those which have lost this flexibility (stenohalinity); if specialized protein function is important for euryhalinity but not for stenohalinity, then we predict that those protein sequences will be less conserved in derived freshwater species. Additionally, proteins important for derived freshwater specialization should show accelerated evolutionary rates due to directional selection. Gene family expansion or contraction may also underlie loss of euryhalinity or gain of freshwater specialization. We found divergence in the rates of gene family evolution and the rates of protein sequence evolution, offering insight into the mechanisms that support both osmoregulatory flexibility and freshwater specialization. Complementary to these findings, we are also interested in using euryhalinity as a model for discovering the mechanistic basis of a reversible form of phenotypic plasticity. To this end, we are performing comparative gill transcriptomics and physiological experiments to synthesize our functional understanding of the evolution of diverse osmoregulatory strategies, integrating inference from genomic variation, genome function, and physiological responses.

C-05

How are they connected? Indirect evidence for dispersal rates in two tortoise beetle species

Stef Linden, Boston University
Lynette Strickland, Boston University

Abstract:

Charidotella sexpunctata and Deloyala guttata are two tortoise beetles that can be found throughout North and South America. Their life cycles are closely associated with plants in the Convolvulaceae family, especially Convolvulus arvensis in Massachusetts. While C. arvensis is widespread, patches can often be isolated from each other by distance and geographic barriers. This project investigates the genetic relationship between individuals in different populations to determine the spatial structure of the community and infer how much interbreeding is occurring. To do this, individuals were collected from seven populations across Massachusetts and their DNA was extracted and sent for ddRAD sequencing. The STACKS pipeline was used to align reads and estimate FST, then STRUCTURE was used to uncover evidence of admixture. These results suggested that distance is not a barrier to reproduction for either species in Massachusetts, implying that the beetles are able to travel over 200 kilometers. Understanding the population structure of tortoise beetles will inform the direction of future research into how individuals travel between populations and will contribute to a clearer picture of how dispersal evolves in insects.

C-06
Do Large-Brained Birds Favor Cognition-Based Sexual Selection?

Marissa Sidell, University of Texas at Austin
Eliza Hoffman, The University of Texas at Austin
Junco Cerezo Arrillaga, The University of Texas at Austin
Carlos Botero, University of Texas at Austin

Abstract:

Many animals produce sexual signals across multiple modalities, but it remains unclear why some become more prominent than others. One possibility is that different modalities reflect different aspects of sexual selection, including mate attraction, competition, condition, or cognitive investment. In passerine birds, functional vocal repertoire size may reflect neural investment in vocal production and storage, whereas body size dimorphism and plumage dichromatism may more strongly reflect competitive ability, condition, or diet. We tested whether phylogenetically corrected relative brain size predicts the probability that vocal repertoire is the dominant signal among three measured sexual traits: vocal repertoire size, tarsus sexual dimorphism index (SDI), and plumage dichromatism. Each trait was converted to a within-dataset empirical quantile across 172 passerine species, and the trait with the highest quantile was classified as the dominant modality. Phylogenetic logistic regression showed that larger relative brain size was associated with a higher probability of repertoire dominance ($\beta = 3.97$, SE = 1.98, $p = 0.045$, $n = 172$). We then compared mean signal quantiles in the top and bottom quartiles of relative brain size. In small-brained species (bottom quartile, $n = 43$), mean quantiles were similar across repertoire, tarsus SDI, and plumage dichromatism (0.46, 0.45, 0.44). In large-brained species (top quartile, $n = 43$), repertoire had the highest mean quantile, followed by tarsus SDI and plumage dichromatism (0.68, 0.60, 0.41). Bayesian phylogenetic models supported this pattern: in large-brained species, repertoire exceeded plumage dichromatism (posterior estimate = 0.27, 95% HPD: 0.16 to 0.38) and tarsus SDI (0.19, 0.08 to 0.31), while no pairwise differences were detected in small-brained

species. These results suggest that relative brain size shapes the prominence of vocal repertoire as a sexual signal in passerine birds.

C-07
Conceptualizing the speciation continuum from a big-picture perspective.

Rosie Zhong, University of Michigan EEB department

Abstract:

The speciation continuum concept reflects the view that speciation is a continuous process, and this term has become well-established in the speciation literature over the last decade. However, there have been substantial difficulties in seeking a definition for the concept, and it remains nebulous in the literature. Here, I aim to elucidate the speciation continuum concept by describing characteristics broadly applicable across the tree of life, rather than forcing a single definition. This includes discussion of the dimensionality of the speciation continuum, as well as examining how diverging populations might progress along the continuum. Concepts outlined are not inherently new to evolutionary biology, but they provide a useful conceptual and analytical framework that informs evolutionary theory, and even act as a foundation for comparative and experimental studies of speciation.

C-08
ihgti: an ensemble machine learning tool for identifying horizontally transferred genes from bacteria and fungi in insect genomes

Johnathan Spaulding, Florida International University
Janna Fierst, Florida International University

Abstract:

Horizontal gene transfer (HGT) also known as lateral gene transfer is the transfer of genetic information from one organism to a different organism non-sexually. During this phenomenon DNA sequence such as gene/genes or a chromosome is transferred from the host organism to the recipient organism. This natural phenomenon is well known to occur in bacteria; however, it has also occurred in viruses, fungi, plants and insects. With multiple sources documenting HGT occurring in an array of insects from different families. This opens the door to using machine learning (ML) methods to leverage the available insect HGT data, to create an ML model that can identify bacterial and fungal candidate transferred genes in insects.

C-09
Phylogenomics and gene-flow among the Gray-throated white-eye (Zosterops rendovae) complex with whole-genome sequence data

Chase Perkins, University of Kansas Biodiversity Institute

Abstract:

The avian genus Zosterops (Family: Zosteropidae), is diverse and widespread, consisting of over 100 currently recognized species occurring from Africa to Australasia and Oceania. Due to the rapid and recent diversification of this group and cyclic patterns of connectivity, phylogenetic signals are obscured by gene-flow and incomplete-lineage sorting. Here, we focus on the three allopatric montane populations of the Gray-throated White-eye (Z. rendovae sensu lato) complex, variably treated as one polytypic species or three distinct species. This group is distributed on three islands in the Solomon Islands, primarily in montane forest: Makira Island (Z. rendovae), Guadalcanal Island (Z. oblitus), and Bougainville Island (Z. hamlini). The Makira and Guadalcanal populations have been shown to be sister to one-another, but only limited genetic information has been available for the Bougainville population. Here we use the first whole genome sequence data for the Bougainville population, in concert with whole genome data for the Makira and Guadalcanal populations, to determine the patterns of gene-flow and how these inform our phylogenetic inferences of the group.

C-10
Do geographic barriers drive genetic differentiation in ground-dwelling Platymantis frogs from geologically complex Philippine islands?

Faben Tesfazion, Department of Ecology and Evolutionary Biology & Biodiversity Institute
Kier Mitchel Pitogo, Department of Ecology and Evolutionary Biology & Biodiversity Institute
Lucas DeCicco, University of Kansas
Rafe Brown, Biodiversity Institute and Department of Ecology and Evolutionary Biology
Ana Motta, KU Biodiversity Institute and Natural History Museum

Abstract:

Speciation is inherently unpredictable, shaped by processes both internal and external to diverging populations. Nevertheless, broad patterns of population divergence are well documented to allow tests of expected speciation trajectory. One of the most widely recognized patterns is isolation-by-distance, which predicts that genomic differentiation increases with geographical distance. However, it remains unclear whether this pattern holds in topographically and geologically complex island systems, where multiple barriers (e.g.: lowland, mountains, seas, etc.) may influence population divergence. Here, we test whether genomic differentiation increases with geographic distance and whether marine barriers contribute more strongly to differentiation than terrestrial barriers. Using populations of ground-dwelling Platymantis frogs that diversified within the Mindanao Pleistocene island complex in the southern Philippines, we modeled pairwise genomic differentiation (FST) as a function of least-cost geographic distance, accounting for Pleistocene sea-level oscillations, and barrier type (terrestrial vs. terrestrial + marine). Performing model selection tests showed that including both distance and barrier variables slightly improved model fit (AIC = -123.1) compared to distance alone (AIC = -121.8). Results reveal a positive but non-linear relationship between genomic differentiation and geographic distance. Unexpectedly, populations separated by just terrestrial barriers (within island pairs) showed greater genomic differentiation

than populations separated by both terrestrial and marine barriers (between-island pairs). Modeling FST as a function of distance and barriers explains 35.4% of observed genomic divergence (33.9% when modeling as a function of distance alone).These findings highlight the importance of complex terrestrial landscapes in shaping divergence within island systems and suggest that small but topographically heterogenous islands may promote substantial lineage diversification, potentially explaining why some island systems, such as the Philippines, are exceptionally diverse.

C-11
Diversity and Prevalence of Environmental Nontuberculous Mycobacteria in Texas

Maritza Estrada, University of Texas at Tyler

Abstract:

Non-Tuberculosis Mycobacteria (NTM) belong to the Mycobacterium genus, which also includes tuberculosis (M. Tuberculosis) and leprosy (M.Leprae), and require a host to survive and transmit from host to host. Whereas NTM are opportunistic pathogens commonly found in the environment, such as water, dust, and soil. Although most NTM exposures do not cause infections, people with lung abnormalities or immunocompromised systems are at higher risk. NTM infections can cause chronic lung disease, lymphadenitis, skin infections, or widespread disseminated disease. Their distribution is influenced by specific climate and environmental factors, like pH and temperature. Rising global temperatures, extreme weather, and altered hydrology have led to increased NTM exposure, with infection rates rising by approximately 4.0% and 4.1% per 100,000 persons per year. Because NTM distribution is influenced by climate and environmental factors, like pH and temperature, higher temperatures are likely to promote their growth and increase exposures. Our study aims to understand the current presence of NTM in the environment and future distribution across certain Texas regions.

C-12
Agent-based modeling trait-mediated survival and management influence of cutthroat trout evolutionary outcomes

Trinity Kassuhn, Auburn University
Janna Willoughby, Auburn University

Abstract:

Rainbow trout (Oncorhynchus mykiss), though non-native, have been established in western U.S stream systems since the 1800's. Their hybridization with native cutthroat trout (Oncorhynchus clarkii) has produced hybrid 'cutbow' trout, introducing life-history traits and environmental tolerances not present in native populations. These interactions complicate predictions of how cutthroat trout will respond to rapid environmental change under ongoing management and genetic introgression. To address this challenge, we developed an agent-based model (ABM) to examine

how trait-dependent survival and harvest of non-native and hybrid individuals influence population dynamics and adaptive trajectories under temperature change in a theoretical river reach. The model simulates non-native, native, and hybrid individuals over 300 years within a theoretical river reach. Each individual is assigned a quantitative trait locus (QTL) representing thermal tolerance, inherited through parental averaging. Survival depends on age and environmental penalties on QTL modeled as a sigmoidal curve. We evaluated management scenarios with varying harvest rates targeting hybrid and non-native individuals. Under no harvest, simulations resulted in loss of native populations and the formation of a hybrid swarm. Harvesting scenarios targeting 50% caught hybrids and either 10% or 25% caught non-native trout achieved a similar increase in native thermal tolerance (QTL ~0.15 to ~0.42), but produced distinct demographic outcomes. Lower non-native harvest maintained a mixed population with few hybrids, whereas higher non-native harvest resulted in reduced non-native abundance and increased hybrid prevalence. This model provides a theoretical framework for understanding eco-evolutionary responses to management under environmental change and will be expanded to incorporate spatial heterogeneity and more mechanistic genetic architectures.

C-13
GhostParser: A Scalable Introgression Detection Framework

Asif Iqbal Rahaman, Virginia Tech
Ethan Tolman, Virginia Tech
Anton Suvorov, Virginia Tech

Abstract:

Introgression is a form of gene flow in which genetic material is transferred among species via migration, hybridization, and backcrossing, producing reticulate evolutionary histories rather than strictly bifurcating trees. It can introduce alleles that facilitate local adaptation, niche expansion, or rapid responses to environmental change, but can also import deleterious variants that increase genetic load and distort phylogenetic and population-genetic inferences. Phylogenomic studies have revealed widespread introgression across the tree of life, yet detecting and characterizing gene flow remains challenging because incomplete lineage sorting (ILS), introgression among sampled lineages, and ghost introgression from unsampled or extinct lineages can generate similar patterns of gene tree discordance. Ghost lineages in particular can cause site-pattern and branch-length methods to misidentify donors and recipients or distort divergence time estimates. A large body of methods exists, from scalable summary-statistic approaches based on site patterns or gene tree summaries to full-likelihood multispecies-coalescent methods such as BPP, which can be accurate but are often infeasible for practical datasets. This has motivated us to build GhostParser, a scalable summary-statistics framework that uses triplet-level gene tree frequencies and tree-height distributions to classify each species triplet as showing no introgression, sampled, or ghost introgression.

Given a hypothesized species tree, a collection of gene trees, and outgroup taxa, GhostParser analyzes all ingroup triplets with a three-stage statistical pipeline that uses discordant tree counts,

a two-sample Kolmogorov–Smirnov test on tree-height distributions, and a median tree-height comparison to distinguish ILS from sampled and ghost introgression scenarios. Across simulated and empirical datasets, GhostParser matches or exceeds the accuracy of full-likelihood software like BPP while remaining computationally scalable to large phylogenomic datasets. Users can install GhostParser from pre-built wheels or source distributions and integrate it into existing phylogenetic workflows, and our pure-Python, multiprocessing-based implementation is manifold faster than any other tool with similar accuracy.

C-14
Limited hybridization between introduced Celastrus orbiculatus and C. scandens

Cody McManus, Williams College
Luana Maroja, Williams College
Connor Connolly, Williams College

Abstract:

Hybridisation is a fascinating phenomenon that can lead to adaptive or maladaptive increases in genetic variation. While speciation often involves full reproductive isolation, there are cases in which individuals of two species are capable of producing viable offspring. Oftentimes, this hybridisation comes with negative consequences for one or both of the species, and results in hybrids with developmental issues and sterility. Two species which are known to hybridise are the rare native climbing vine Celastrus scandens L. (American bittersweet) and the introduced common invasive species C. orbiculatus Thunb. (Asian bittersweet) (Zaya, 2014), which are the study organisms for this thesis. We collected leaf samples from 18 locations in three US states, one Canadian province, and one sample from the People's Republic of China in order to assess the hybridisation between these two species. Specifically, we uploaded 528 leaf photos into the LAMINA computer programme to analyse fluctuating asymmetry, a common phenotypic result of developmental instability in hybrids. We also performed RFLP analysis on chloroplast segments for all 186 samples, to identify the maternal species. We used 23 samples through Illumina ddRADSeq to evaluate the extent of hybridisation in various populations. Our results showed the presence of only one hybrid of C. orbiculatus ancestry and no C. scandens hybrids within our sampled area, despite initial appearance. We discuss the implications for conservation of C. scandens, which is a protected species in many localities.

C-15
A Conservation Data Disconnect: Why Conservationists Need Evolutionary Biology Data

Clayton Hale, University of Georgia
Anna Wyngaarden,
Annabel Lewis,
Magie Williams, Michigan State University
Jennifer Cruse-Sanders, State Botanical Garden of Georgia

Jill Anderson, Department of Genetics
Seema Sheth, North Carolina State University
Susana Wadgymar, Davidson College
Emily Josephs, Michigan State University
Megan DeMarche, University of Georgia

C-16

Leveraging a system of Poecilia hybrids to study trait genetic architecture and speciation

Sophia Haase Cox, Stanford University
Tristram Dodge, Stanford University
Kelsie Hunnicutt, Stanford University
Rhea Sood, Stanford University
Theresa Gunn, Stanford University
JJ Baczenas, Stanford University
Stepfanie Aguillon, University of California
Manfred Schartl, University of Würzburg
David Reznick, University of California
Cameron Ghalambor, Norwegian University of Science and Technology (NTNU)
Molly Schumer, Stanford University

Abstract:

Poecilia reticulata, the common guppy, is well known for its extreme intraspecific variation in male coloration and life history traits. Extensive research on P. reticulata populations in Northern Trinidad has shown that male pigmentation and a suite of life history phenotypes rapidly and repeatably evolve in response to predation regime. While most ecological research has been centered in Trinidad, P. reticulata has a broad natural range across northern South America. In northern Venezuela, P. reticulata co-occurs with sister species P. wingei. Poecilia reticulata and P. wingei can produce viable offspring in lab crosses and are thought to hybridize in the wild, but the strength of reproductive isolation between species and potential negative consequences in hybrids are unknown. We plan to leverage the hybridization of these species to investigate evidence of hybrid incompatibilities and perform QTL mapping of pigmentation and life history traits that differ between the two species. By producing crosses between various strains of P. wingei and P. reticulata, we aim to characterize the extent and genetic basis of reproductive isolation, and identify if pigmentation or life history traits of known ecological importance contribute to incompatibilities. As a first step, we used Oxford Nanopore Technology (ONT) long read sequencing to generate a high-quality reference genome assembly of Poecilia wingei. This research will provide insight into whether rapidly evolving traits under high selection within a species can also serve as important contributors to the formation of reproductive isolation between diverging lineages.

C-17
Against the Current: Does "Fast-Stream" Life Shape Tadpole Skin Evolution?

Quang Pham, Cornell University
Molly Womack, Cornell University

Abstract:

Anurans (frogs and toads) are the most diverse and widespread amphibian order, with most described species maturing through a larval (tadpole) stage that exhibits extraordinary morphological diversity across taxa. The extensive morphological diversity present during early anuran life history is fascinating yet underexplored, which limits our understanding of large-scale patterns in anuran evolution and diversification. Many species show specialized morphological adaptations to distinct freshwater habitats, including lentic (still) and lotic (fast-flowing) water environments. Tadpole skin, as the body's outermost barrier and a key physiological interface, may facilitate adaptation to diverse niches; thicker and more durable skin structure could protect species from excessive mechanical stress exerted by fast flowing currents, whereas thinner structure could facilitate efficient skin respiration in hypoxic standing water bodies. Here, we use histology and phylogenetic comparative methods to investigate tadpole skin morphological diversity and evolution, relative to habitats as well as body size within a phylogenetic framework. Our results address major knowledge gaps in tadpole biology and provide important baseline information about the evolution and diversification of the largest organ in anuran larvae.

C-18
Exploring host-associated and sex-based morphological variation in the Perilampus neodiprioni parasitoid

Salahuddin Mohammed, The Ohio State University
Robin Bagley, The Ohio State University at Lima
Sarah White, The Ohio State University

Abstract:

Ecological speciation generates biodiversity when divergent natural selection across environments promotes reproductive isolation. In multitrophic systems, divergence at one trophic level can cascade to associated organisms in a process known as sequential divergence. Sequential divergence is poorly understood, but it may be further explored through plant-insect-parasitoid (lethal parasite) systems, where ecological speciation of insects on plants may allow a divergence cascade in parasitoids. For example, we consider the parasitoid wasp, Perilampus neoprioni, which attacks pine-eating Neodiprion sawflies. Although broad geographic analyses in the Pinus–Neodiprion–Perilampus neodiprioni system suggest host-associated morphological variation in parasitoids, it remains unclear whether these patterns persist when geographic variation is minimized. To address this, we analyzed 60 sympatric by-catch specimens of P. neodiprioni reared from three Neodiprion host species (N. lecontei, N. pinetum, and N. virginianus) collected along a

latitudinal transect from Lexington, Kentucky to Southern Ohio. We measured total body segment lengths (head, thorax, and abdomen) as well as facial traits, including eye height, eye distance, and malar distance. Parasitoid sex, parasitoid color, and Neodiprion host sex were recorded for each specimen. We evaluated the associations of host species, parasitoid sex, and their interaction with each morphological trait. All measured traits varied significantly with parasitoid sex, with females exhibiting larger measurements than males. Host-associated differences were also detected, particularly between parasitoids reared from N. virginianus and those from N. lecontei and N. pinetum. Notably, this divergence pattern parallels host evolutionary relationships, as N. virginianus is more distantly related to N. lecontei and N. pinetum, which are sister species. Therefore, parasitoids from more distantly related host species demonstrated greater morphological differentiation. These findings demonstrate that host-associated morphological divergence in P. neodiprioni persists at a fine geographic scale, supporting the potential for sequential divergence in externally feeding insect–parasitoid systems.

C-19
Immune response as a measure of hybrid fitness in a Gryllus system

Hannah Eckert, University of Denver
Isaac Hudson Foy, University of Denver
Erica Larson, University of Denver

Abstract:

An organism's immune function can provide insight into physiological differences across species and the potential fitness consequences of hybridization. Two closely-related field cricket species, Gryllus firmus and Gryllus pennsylvanicus, hybridize in the eastern United States, producing F1 hybrids as well as later-generation (F2) hybrids and backcrossed individuals. Previous studies suggest that hybrids may experience evolutionary disadvantages that impact overall fitness.

To investigate immune variation in this system, we quantified hemocyte counts and measured the melanization response to foreign bodies across parental species, F1 hybrids, F2 hybrids, and backcrossed crickets. These metrics serve as indicators of innate immune function.

We found significant differences in melanization response among groups. F1 hybrids exhibited melanization levels more similar to G. firmus, whereas F2 hybrids more closely resembled G. pennsylvanicus. In contrast, hemocyte counts showed less pronounced differentiation across groups. These results suggest that components of immune function may shift across hybrid generations.

C-20

Can genomics resolve uncertainty in conservation unit status for Western Canada's only native turtle?

Tate Linden, University of British Columbia
Evelyn L Jensen, Newcastle University
Michael Russello, University of British Columbia Okanagan

Abstract:

Conserving pre-existing genetic variation is paramount to species' ability to adapt and persist. To conserve genetic variation, wildlife can be managed in conservation units, such as evolutionarily significant units (ESUs) or designatable units (DUs) in Canada. DUs must meet two criteria: discreteness (i.e., evidence of lack of gene flow) and evolutionary significance (i.e., evidence of unique adaptations or evolutionary history). Genetic data are routinely employed to satisfy the discreteness criterion, yet few studies have used empirical genomic approaches to address the significance criterion. Western painted turtles (WPTs; Chrysmeys picta bellii), the only native turtle in Western Canada, provide an excellent case study for integrating genomics within the Canadian DU framework. A previous WPT study found evidence for up to six discrete units based on microsatellite loci. However, this work did not address the significance criterion and the most recent status assessment retained the historical number of three DUs. Here, we employed whole genome sequencing of 92 individuals from 18 populations spanning the native WPT distribution in British Columbia to: 1) evaluate discreteness using neutral genomic variation; 2) explicitly test significance through environmentally-associated variation at putatively adaptive loci; and 3) recommend the number and distribution of DUs. Thus far, we have completed sequencing and generated genotype likelihoods using the ANGSD pipeline. Putatively adaptive SNPs will be identified via genotype-environment association analyses. Subsequent network, clustering, and principal component analyses will use neutral SNPs for evaluating discreteness and putatively adaptive SNPs to test the significance criterion. Our future work will expand to range-wide sampling to predict climate maladaptation and develop a genotyping tool for applied conservation. This work will test a framework for using genomic data to explicitly inform conservation unit delineation in Canada, the U.S.A., and beyond.

C-21
Under pressure: Evolving heat and drought tolerance in Ipomoea purpurea

Emma Foster, University of Michigan
Regina Baucom, University of Michigan

Abstract:

Global changes have accelerated significantly over the last century, leading to more frequent occurrences of drought and higher average temperatures. Rather than facing certain extinction, some species have the ability to persist via migration, acclimation, and/or adaptation. Adaptation through rapid evolution of tolerance may play a key role in plant species persistence as environments shift. Tolerance is described as an organism's ability to minimize the negative effects a stressor may have on fitness. In this study, we used a resurrection approach to determine how Ipomoea purpurea populations' tolerance to heat and drought stress has changed over time. We exposed three populations with maternal lines from 2003, 2012, and 2016 to heat-only, drought-only, heat & drought, and control conditions, and used relative biomass as a proxy for fitness to determine tolerance. Preliminary results suggest that the evolution of tolerance to heat and drought stress is population-specific, reflecting environmentally dependent evolution. Future work using a greater time scale and quantitative genomic techniques would inform how environmental pressures may be impacting evolutionary trajectories among populations in the long term.

C-22
High-throughput assessment of plant selection on free living and symbiotic rhizobia

Bianca Campagnari, UC Riverside

Abstract:

Rhizobia are bacterial symbionts that provide essential nitrogen fixing services to agriculturally and ecologically important legumes. Free living rhizobia compete to form nodules on legume roots, where the enter into symbiosis with the host and release billions of descendents back to the soil upon the end of plant growth. Despite the noted impact of selection in the free living stage on symbiotic quality, free living rhizobia are rarely studied due to the difficulty of isolating rhizobia from other free living microbes. Here, I use high throughput automation to isolate and sequence Bradyrhizobium communities across free living and plant associated compartments from the wild California legumes Acmispon strigosus and Acmispon americanus. I will infer gene sets selected for in each compartment, and assess how divergent selection pressures across compartments drive gains and losses of symbiotic competence on ecological time.

C-23

The accidental virulence hypothesis: The correlation between resistance to predation and virulence in Saccharomyces cerevisiae

Ana Kothandram, The College of William and Mary
Armaan Salchak, The College of William and Mary
William Rice, The College of William and Mary
Sam Boyle, The College of William and Mary
Helen Murphy, The College of William and Mary

Abstract:

Opportunistic pathogens are microbes that can thrive in two ecological niches: the open environment and an animal host. Survival in an animal host is not a necessary component of the life cycle, so the selective pressures that lead to adaptations for host exploitation remain an open question. The accidental virulence hypothesis provides one explanation for the evolution of opportunistic pathogens, positing that selective pressures in the environment can favor traits which coincidentally increase pathogenicity. One such pressure is amoeba predation, which would favor traits that allow microbes to avoid engulfment by amoeba. These traits would coincidentally allow escape from immune cells, whose mechanisms of phagocytosis use the same cellular processes as amoeba. Using a collection of 1,011 isolates of the yeast Saccharomyces cerevisiae from across the world and various ecological niches, this project examined the relationship between resistance to amoeba predation and virulence in yeast isolates. Each of the 1,011 strains was co-cultured with the social amoeba, Dictyostelium discoidieum, and predation levels were estimated. We found a wide-range of predation resistance levels, which appeared to be associated with both evolutionary history (clade) and ecological origin of the isolate; wild isolates (trees, soil, etc.) were particularly resistant. A genome-wide association study implicated genes in the TOR pathway as possible targets that influence predation resistance. A subset of yeast isolates exhibiting high and low levels of predation were injected into larvae of the wax moth Galleria mellonella to observe their virulence. In contrast to our hypothesis, strains with lower levels of predation resistance were more virulent. Instead, yeast growth rate appeared to play a stronger role in virulence, as fast-growing isolates overstimulated the immune system causing damage to the host. Our findings provide an in-depth understanding of the evolution of virulence in these opportunistic pathogens.

C-24

Invasion, hybridization, and speciation: The breakdown of reproductive isolating barriers in the San Francisco Bay

Timothy Legare, University of Illinois Urbana-Champaign
Rebecca Fuller, University of Illinois

Abstract:

Hybridization between previously isolated lineages, once thought uncommon, is now recognized as a regular consequence of anthropogenic disturbance. Chief among the drivers is species introduction, which can rapidly erode reproductive isolating barriers (RIBs) that took millions of years to evolve. Understanding which features of novel environments and invaders themselves facilitate RIB breakdown is both a pressing conservation concern and a window into how RIBs evolve, are maintained, and can be disrupted. Here, we used Restriction-site Associated DNA sequencing (RADseq) to investigate whether RIBs have broken down between Lucania goodei and L. parva following their co-introduction into the San Francisco Bay (SFB). These two species co-occur in Florida, where there are high levels of behavioral, ecological, and post-zygotic isolation. We present clear evidence that these two species are hybridizing frequently in the SFB. Using population genomic analyses, we trace the origin of the introduced L. parva population to an allopatric source in the Pecos River, NM, likely arriving as a hitchhiker during sportfish stocking. L. goodei appears to have originated from Florida, though the specific source drainage remains unresolved. Additionally, we have begun preliminary analyses to determine whether the introduction is ongoing and to estimate the founding population size for each species. This project is an important first step that will guide our efforts to determine why and how stable RIBs broke down in the novel environment of the San Francisco Bay.

C-25
Transposable Element Dynamics Across Diverging and Hybridizing Lineages of Blue Butterflies

Garima Setia, Tulane University
Diana Tataru, Utah State University
Zachariah Gompert, Utah State University
Samridhi Chaturvedi, Tulane University

Abstract:

Transposable Elements (TEs) are mobile genomic sequences that comprise the majority of genome content in eukaryotes. TEs generate insertional mutations that disrupt gene regulation, thereby creating genomic incompatibilities between diverging lineages, which can lead to speciation. However, which TE families are responsible for generating these incompatibilities remains poorly understood, particularly in natural and non-model hybrid systems. Here, we investigated the temporal aspect of TE dynamics in two ways: (1) we conducted a deep-time analysis of TEs across eight chromosome-level Polyommatini assemblies and (2) characterized TE dynamics across the Lycaeides butterfly complex, comprising two parental species (L. idas and L. melissa) and hybrid lineages at both ancient (Jackson Hole, ~15,000 years) and recent (Dubois) stages of divergence. We first established which TE families are actively expanding across the broader clade by annotating TE landscapes in the eight Polyommatini assemblies. Population-scale data from 1,504 individuals of the focal Lycaeides parental species was used to validate genome assembly annotation and characterize TE insertion polymorphisms. Ancestry-informative TE insertions were estimated from Oxford Nanopore long-read data from 39 individuals spanning parental and hybrid

lineages. TE content ranged from 52% to 80% across assemblies with no phylogenetic signal, demonstrating lineage-specific expansion patterns. Young TE content positively correlated with genome size (Pearson r = 0.775, p = 0.024), whereas old TE content did not, suggesting that recently acquired insertions are the primary driver of genome size variation. Across all three analyses, two TE classes consistently emerged as major contributors to lineage differentiation: LTR retrotransposons (Gypsy and unclassified families) and DNA/Helitron elements. The consistent identification of these families across deep-time, population, and hybrid scales suggests they are central to the genomic divergence observed in blue butterflies, in accordance with the documented roles of these elements in lineage differentiation across eukaryotes.

C-26
Distinguishing state-dependent trait evolution from ecological filtering in comparative data

Shih-Na Liu, Virginia Tech
Josef Uyeda, Virginia Tech

Abstract:

Differences in trait distributions across habitats, diet groups, or other discrete ecological states can arise through multiple non-mutually exclusive mechanisms, including differences in how traits evolve within each state (state-dependent trait evolution) and whether transition probabilities between states are trait-dependent (ecological filtering). While these mechanisms can produce similar observed trait distributions in comparative data, they correspond to very different biological processes. Here, we develop a generalized Markov model that jointly models trait evolution within each state and transitions among discrete ecological states, where between-state transition rates are explicitly allowed to depend on trait values. We use simulation to test the statistical power to distinguish the extreme case where similar trait distributions arise strictly from state-dependent trait evolution versus strictly from ecological filtering, and characterize the conditions under which these processes are identifiable.

C-27
Creating and characterizing the transgenic tools to explore the function of genes in non-model animal species

Madeline Ranly, University of Dayton
Ava Kelly, University of Dayton
Thomas Williams, University of Dayton

Abstract:

Loss Of Function (LOF) and Gain Of Function (GOF) experiments are the most successful approaches for uncovering the role of genes in animal development, physiology, behavior, and evolution. The former approach removes a gene's function to reveal its necessity, while the latter adds a gene's function to reveal its sufficiency. These experiments have been utilized for thousands

of genes in limited model organism species, such as the fruit fly Drosophila melanogaster. However, model organisms do not have a monopoly on the traits and phenotypes that are compelling to study. Thus, the full potential of genetic inquiry requires the ability to perform LOF and GOF experiments in what can be considered non-model species. Here, we will present our progress in creating and characterizing genetic tools for LOF and GOF experiments in non-model fruit fly species Drosophila malerkotliana. Success here will unleash the ability to investigate how evolutionarily conserved genes have shaped the gain, loss, and modification of traits among fruit flies. These tools will also be of use to scientists studying gene function in other animal genres, classes, and perhaps even phyla.

C-28

Investigating the presence of immune priming in the cnidarian model organism Exaiptasia diaphana

Carly Travers, Texas State University
Lauren Fuess, Texas State University

D-01

Connecting the trans-regulators of an evo-devo trait to their direct target genes through genetic, genomic, and biochemical approaches

Devon Seibert, University of Dayton
Ashley Williams, University of Dayton
Eliana Williams, University of Dayton
Thomas Williams, University of Dayton

Abstract:

Gene Regulatory Networks (GRNs) control the orchestrated spatial and temporal patterns of gene expression that are responsible for trait development. The gain, modification, and deconstruction of GRNs logically must be major causes of trait evolution. In spite of this perceived importance, the evolution of few, if any, traits is thoroughly understood at the scale of a GRN. This shortcoming has several causes. One is the difficulty of finding the breadth of GRN transcription factors and mapping these to their binding sites in cis-regulatory sequences of their downstream realizator genes. Another is the need for GRN studies to occur in experimentally tractable species for which closely-related species exist that possess ancestral, modified, and secondarily lost phenotypes. One suitable model trait is the gain, modification, and loss of sexually dimorphic abdomen pigmentation in the lineage of Drosophila melanogaster and its close relatives. We will share updates from our genetic, genomic, and biochemical studies that are mapping the regulatory connections between the key transcription factors of a pigmentation GRN and their realizator genes that comprise a pigment metabolic pathway.

D-02

How Do Population Size Differences Shape Genome Evolution over 7,500 Generations from SNPs to Karyotypes? Microscopic vs. Macroscopic Multicellularity in Yeast

Luis Felipe Cedeño Pérez, Georgia Institute of Technology
William Ratcliff, Georgia Institute of Technology
G. Ozan Bozdag, Georgia Institute of Technology

Abstract:

The transition from unicellular to macroscopic multicellular life represents a major evolutionary transition with profound consequences for population genetics. Multicellular organisms necessarily exist at lower population densities than their microscopic counterparts, fundamentally altering effective population size (Ne) and the balance between selection and drift. Reduced Ne is predicted to weaken purifying selection, increase fixation of neutral and slightly deleterious mutations, and reduce clonal interference. However, testing this framework has been challenging, as comparisons across extant species confound population size with phylogeny, ecology, and mutation rate.

The Multicellularity Long-Term Evolution Experiment (MuLTEE) provides a unique experimental setting to test the effects of population size. From a single microscopic snowflake yeast ancestor (~30 µm radius), fifteen replicate populations evolved for >7,500 generations (1,500 days) under selection for large size and fast growth. Ten populations evolving under oxygen limitation remained microscopic (~50 µm radius), while five populations without this constraint evolved macroscopic size (~5 mm). This size divergence corresponds to a divergence in Ne three orders of magnitude smaller in macroscopic populations, allowing us to disentangle the effects of Ne from confounding variables.

To test how Ne differences shape the selection/drift balance and generate distinct signatures of genome evolution, we sequenced isolates and populations from both lineages at 3,000, 5,000, and 7,500 generations using short- and long-read sequencing. Macroscopic populations show 5 times more fixed or near-fixed mutations, while the SNP spectrum in microscopic populations is shaped by clonal interference. Building on our published 1,000-day work (Tong et al., 2025), populations continue diverging at the ploidy and karyotype level through 1,500 days, with macroscopic populations sustaining aneuploidies accumulated during the size transition. We also explored structural variation in autosomes and mitochondrial genomes. Together, this work demonstrates divergent signatures of genome evolution driven by effective population size differences in a long-term evolution experiment.

D-03
Divergent Oxygen Strategies of Aquatic Vertebrate Regenerators

Madison Adams, Louisiana State University
Igor Schneider, Louisiana State University

Abstract:

Myoglobin is a critical protein for oxygen transport and storage in vertebrate muscle tissue, but examples of myoglobin serving roles in the brain, heart, and epithelial tissues contrast this traditional definition. Our preliminary findings indicate that both fin regeneration-capable species Senegal bichir (Polypterus senegalus) and West African Lungfish (Protopterus annectens) express myoglobin not only in the muscle but also in the wound epidermis, with expression induced by injury. This widespread non-muscle expression suggests unexplored functions of myoglobin, particularly in vertebrate regeneration. While most vertebrates possess a single myoglobin gene, Polypterus and lungfish harbor multiple gene copies, with duplicates expressed in distinct cell types during fin regeneration. The functional roles of these duplicates remain unknown. We hypothesize that conserved myoglobin gene duplications provide specialized metabolic advantages during regeneration, such as facilitating oxygen availability in avascular regenerating tissue. To test this, we selected two highly expressed myoglobin gene duplicates from each species for functional evaluation. Hybridization Chain Reaction Fluorescence In Situ Hybridization (HCR-FISH) is used to resolve spatial and quantitative patterns of myoglobin expression at the cellular level. Additionally, a CRISPR-generated zebrafish myoglobin knockout line will be used to assess fin regeneration in the absence of myoglobin. Together, this work reveals unique oxygen management strategies supporting fin regeneration and challenges the traditional definition of myoglobin as a muscle-restricted protein.

D-04
Testing cascade reinforcement with experimental evolution

Veronica Baquero, University of South Carolina
Graham McLaughlin, University of South Carolina
Brian Hollis, University of South Carolina

Abstract:

Populations that evolve some reproductive isolation during isolation are often expected to lose it after secondary contact, but complete reproductive isolation can instead evolve through reinforcement. Reinforcement occurs when natural selection strengthens reproductive barriers because hybridization is often costly. We experimentally modeled reinforcement by introducing LHm-GFP migrant males into replicate IV populations and maintaining these populations for over 140 generations under four regimes that differed in selection against hybrids (Control, No Selection, Intermediate, Strong).In this study, to test cascade reinforcement, we used migrant males from a never-before-encountered population (Dahomey and Valaís) to examine whether reinforcement-associated mating traits in the evolved populations also appear in crosses with this new population. We hypothesize that reinforcing selection has led to the evolution of female mating traits (willingness to mate and mating latency) that reduced hybridization.

D-05
Hybridization and Host Immunity: MHC Variation and Parasite Susceptibility in Rattus

Cheyenne Graham, University of Michigan
Kayce Bell, Natural History Museum of LA county
Jillian Myers, University of Michigan
Keelan VanderHart, University of Michigan
Aishani Moradia, University of Michigan
Isabella Valdebenito, University of Michigan
Grace Havern, University of Michigan
Evelyn Tanaka, University of Michigan
Cody Thompson, University of Michigan
Kelly Speer, Northern Arizona University

Abstract:

Rodents in the genus Rattus are among the most globally successful invasive mammals and are reservoirs for numerous pathogens affecting wildlife, agriculture, and human health. Two widespread species, R. rattus (black rat) and R. tanezumi (Asian house rat), now occur sympatrically in regions in Asia, South Africa and parts of the United States due to human-mediated dispersal, creating opportunities for hybridization. Hybridization may influence host immunity by introducing novel alleles at immune-related loci such as the Major Histocompatibility Complex (MHC), which plays a key role in pathogen recognition. This study investigates hybridization and immunogenetic diversity in R. rattus and R. tanezumi populations from Los Angeles, California. We ask whether hybridization occurs between these species, how MHC variation differs between parental species and hybrids, and whether MHC diversity is associated with endoparasite load and diversity. To assess host species identity, mitochondrial DNA (CytB) sequences from 50 museum specimens were compared with reference sequences. Preliminary phylogenetic analyses identified R. rattus and R. tanezumi individuals. Ongoing work includes determining hybrid ancestry through phylogenetic analysis of nuclear genes (ATP5A1, DHFR), characterizing MHC class II exon 2 diversity, and identifying helminth parasites through morphological and molecular approaches. Together, these analyses will test whether hybridization influences immunogenetic diversity and parasite susceptibility in invasive Rattus populations. Due to their invasive nature and ability to act as pathogen reservoirs, understanding how hybridization influences the immunogenetic diversity and parasite susceptibility among Rattus species, may help clarify how invasion impacts disease dynamics and pathogen spillover risks.

D-06
SPARCnet RaMP: Impacts from the First Year of a Postbaccalaureate and Mentor-Training Program in Ecology

Caitlin Fisher-Reid, Bridgewater State University

D-07
The impact of coinfection on population stability and chaos

Fernando Melara Barahona, Vanderbilt School of Medicine

Abstract:

Parasites play an outsized role in mediating the persistence and stability of host populations. Flour beetles (Tribolium spp.) have long served as classic examples of population dynamics under both disease-free and infected conditions, with elegant combinations of theory and experiments demonstrating, for example, that cannibalism rates can push populations from stability to chaos. As with most organisms in nature, however, flour beetles rarely face just one parasite species, and co-infecting parasites can antagonize or facilitate each other through resources and immunity. To test the prediction that non-neutral interactions would qualitatively alter population stability, we first raised flour beetles (Tribolium castaneum) in infection-free, single-infection, or coinfection microcosms and quantified relative prevalence and parasite intensity. Next, we reworked a classic stage-structured discrete-time model to include single and multiple infections and performed sensitivity and bifurcation analyses to identify the most important (co)infection-associated parameters for population stability. The model predicts that stability is highly sensitive to parasite transmission mode regardless of infection multiplicity, but facilitation among parasites rapidly drives populations into oscillations and chaos under realistic conditions. This study identifies an important mechanism for explaining population variability and highlights the importance of within-host mechanisms for driving dynamics at higher levels of biological organization.

D-08
How sex-specific regulation of the pleiotropic gene foraging shapes behavioral traits in Drosophila melanogaster

Elizabeth Makovec, University of Toronto
Allan Edelsparre, University of Toronto
Marla Sokolowski, University of Toronto
Ina Anreiter, University of Toronto Scarborough

Abstract:

Sex differences are common sources of variation in populations. Males and females can differ in morphology, gene expression, and behavior, and certain genes can affect the sexes differently. Just as a gene can affect the sexes independently, a gene can affect multiple independent traits. This can be between the sexes, where a gene influences one trait in one sex and a different trait in the other, or within a sex, where a gene influences multiple independent traits. This phenomenon is known as pleiotropy. Pleiotropy involves the regulation of multiple independent traits, and some of these traits could be sexually dimorphic. This raises the question of how a pleiotropic gene regulates sex differences. A bottom-up approach, looking at a candidate pleiotropic gene, can help us investigate how pleiotropic genes regulate sex differences. One example of a pleiotropic gene

that has sexually dimorphic traits is the highly complex gene for. This gene has four independently regulated promoters that contribute to its pleiotropy. This gene is associated with multiple phenotypic traits, and many of these traits exhibit differences between the two naturally occurring allelic morphs of the gene: rover and sitter. However, not much is known about sex differences within these traits. One phenotype that has been found to have both rover-sitter differences and sex differences is dispersal, making dispersal a useful phenotype to study the interaction of pleiotropy and sexual dimorphism. We are using genetically modified lines that have a sitter genetic background and express the rover version of one of the four promoters of this gene, to investigate the sex-specific regulation of this gene and how it shapes the sexually dimorphic traits dispersal and activity.

D-09
Does Mode of Larval Development Influence Dispersal Capacity and Genetic Connectivity in the Ocean?

Sofia Orellana, Loyola University Chicago
Nicholas Alde, Loyola University Chicago
Tauana Cunha, Loyola University Chicago

Abstract:

The duration of larval stages in marine invertebrates is expected to influence dispersal capacity and affect population connectivity and gene flow. While some studies find positive correlations between pelagic larval duration and dispersal, contradictory findings exist. Previous studies often targeted only one or two species, in different geographical contexts and using few genetic markers, limiting comparisons and generality. Here we apply a comparative genomic approach using 10 species of intertidal gastropod mollusks distributed throughout the Pacific coast of Panama to test how larval developmental mode affects dispersal and connectivity. Using Illumina sequencing data, we first estimated genome sizes and assembled draft genomes for each species, which vary from 250 Mb to 1430 Mb in size. 3RAD data for an average of 75 individuals per species was mapped to the reference genomes to characterize population structure through PCA, admixture analysis, and FST, revealing several cryptic lineages. To test the hypothesis, we will compare isolation-by-distance patterns between species with short-lived and long-lived larvae using phylogenetic ANOVA. Our design increases power to detect differences, accounts for species relatedness, and minimizes confounding environmental factors, providing a powerful test of developmental mode as a predictor of marine connectivity.

D-10
Micro-morphological variation in Pocillopora grandis is associated to temporal changes of corallite development

Jason Tuang-tuang, Centro de Investigaciones Biológicas del Noroeste
Michael Hellberg, Louisiana State University
David Paz-García, Centro de Investigaciones Biologicas del Noreste

Abstract:

Species identification of many reef-building corals rests on features of the corallite that change in plastic response to environmental conditions and through the course of normal colony growth. This study investigates seasonal variation and developmental progression of the micro-structures of Pocillopora grandis from two reef sites with contrasting flow conditions. Analyses of electron micrographs revealed seasonal variations in the columella and septa that are linked to corallite development. We propose five distinct developmental stages, which show similar frequencies between the two sites. Stages 2a and 2b, however, are more frequent at the low-flow site during warmer months. Corallite diameter of stage 1 was smaller than the other stages ($p < 0.001$) and corallite diameter and depth were positively correlated ($r2 = 0.98$) at all stages. These findings suggest that some putatively diagnostic traits used for identification of P. grandis show seasonal variation that in turn correlates with changes in water temperature, corallite development, and reproduction. These developmental stages offer a framework for interpreting skeletal characteristics in P. grandis, which in turn affects growth, taxonomy and physiology under changing environmental conditions. A recognition of seasonal changes in corallite development facilitates better understanding of how micro-structures can vary in response to both biological and environmental factors without necessarily reflecting plasticity.

D-11

Snakes on islands: Evolutionary processes underlying the insularization of land bridge island populations of Bothrops sp. off the Southern coast of Brazil

Harold Gibbs, Ohio State University
Peri Bolton, Ohio State University
Michael Sovic, Freedom Genomics
Andrew Mason, The Ohio State University
Inacio de Azevedo, CeTICS/Laboratório Especial de Toxinologia
Felipe Grazziotin, Instituto Butantan

Abstract:

Evolutionary differentiation (“insularization”) of island populations off the Southern coast of Brazil has long been argued as potentially contributing to the diversity of the Atlantic Forest biodiversity hotspot. However, the evolutionary mechanisms that underlie this process for specific taxa remain unclear. Here, we analyze whole genome sequence data from individuals from three island and two reference mainland populations of Bothrops sp. pitviper snakes to explore the mechanisms responsible for the diversification of island populations. Populations of snakes on nearby Quemada, Alcatraz, and Franceses islands are all genetically distinct and show reduced diversity relative to reference mainland populations likely due to smaller effective sizes. Phylogenetic analyses show that the Franceses population forms monophyletic clade with the North mainland population and the two southern island populations (Quemada and Alcatraz) are sister taxa to each other in a clade that also contains the South mainland population. Historical demographic

modeling dates the origin of the Quemada and Alcatraz populations to roughly 22,000 ybp and the origin of the unsampled lineage that is the ancestor of the island populations to ~ 500,000 ybp. Finally, genome scans show evidence for selection in island populations at multiple regions of the genome, some containing genes that can plausibly be linked to island phenotypes. Our results support the idea that insularization results in the adaptively distinct lineages on these islands that could contribute to high levels of mainland diversity. They also suggest the new hypothesis that island populations may arise from a long-standing unsampled "shelf lineage" that undergoes repeated colonization-extinction dynamics linked to specific islands that is driven by fluctuations in ocean levels during the recent Pleistocene.

D-12
Population genetics of Tadarida brasiliensis and their mites across North American landscapes

Aleana Savage, University of Michigan
Kelly Speer, Northern Arizona University
Daniel Becker, University of Oklahoma
Michael Cove, North Carolina Museum of Natural Sciences

Abstract:

Tadarida brasiliensis is a migratory, cosmopolitan species that frequently roost in anthropogenically altered landscapes. Nine subspecies of T. brasiliensis have been described, but phylogenetic mtDNA studies show limited, or no, structure throughout their North American range. However, high gene flow in the region could be masking population differentiation at markers previously studied. There is evidence of geographically restricted gene flow across relatively short distances compared to their dispersal capabilities, and it remains unclear how often adjacent mainland populations overlap. Anthropogenic change can drive isolation by resistance in other mammals, but less is understood about the regional movements of migratory bats using urban and non-urban habitats. Next Generation Sequencing (NGS) can detect subtle population structure that mitochondrial sequencing does not detect but assessing population connectivity among local populations requires high-resolution markers. Ectoparasites could provide key insight into regional movements and connectivity of bat colonies. Mites are commonly found on T. brasiliensis throughout their range, and geographic distinction in mite species supports their utility for examining host population connectivity.

Therefore, we will use NGS of T. brasiliensis specimens and their associated mites to investigate fine-scale dispersal patterns across anthropogenic landscapes. We will test three primary hypotheses: (1) mites will show fine scale dispersal patterns among bat populations (2) mites from T. brasiliensis in the eastern United States will show more population structure in bat populations than those from the central part of their U.S. range, as T. brasiliensis in the eastern U.S. are putatively resident and less migratory than central colonies, and (3) population connectivity will be reduced in areas with high urbanization. This work will examine the utility of parasites in assessing

how urbanization and migratory behavior may influence gene flow in a widespread, ecologically significant species.

D-13
Shell and Sequence: A Genomic Investigation of the Native North American Freshwater Mussel, Fusconaia flava (Unionidae)

Kussum Ghimire, Loyola University Chicago
Tauana Cunha, Loyola University Chicago
Sean Keogh, National Museum of Natural History

Abstract:

High-quality genomic data are now considered foundational for biodiversity studies, enlightening the genetic basis of biological traits, ecological interactions, and population dynamics. Yet freshwater mussels (Order Unionida) remain severely underrepresented in genomic resources despite their immense diversity and threatened status. Fusconaia flava, the Wabash pigtoe, represents an ideal species for addressing fundamental questions about freshwater mussel groups. It is widely distributed across North America and demonstrates resilience across diverse habitats where other related Unionidae species have declined, suggesting a genomic background that may hint at adaptive advantages. In this project, we are generating a reference genome for F.flava. High molecular weight DNA was extracted with multiple methods to compare yield, purity and integrity, resulting in several micrograms of DNA with peaks exceeding 50 Kpb. Long-read sequencing is ongoing with Oxford Nanopore Technologies for initial assembly. Genomic data from Illumina sequencing will be used to estimate the genome size with a K-mer approach (predicted to fall between 2-3 gigabases based on other freshwater bivalves). Additional Hi-C data will be used for scaffolding with the ultimate goal of generating a chromosome-level assembly. This will be annotated with RNAseq data and used to characterize gene content and function, repetitive elements, and chromosomal architecture. This new resource will enable a follow-up transcriptomic investigation on the genomic basis of ecomorphological variation across populations distributed in contrasting river environment systems.

Keywords: Bivalvia, Mollusca, Mussel, HMW DNA, Genomics

D-14
The evolution and origins of alpine daisies in North America

Joseph Kleinkopf, Cornell University
Hannah Marx, Cornell University

Abstract:

The origins of alpine plants have been debated in science for centuries. Some have posited that alpine plant species are derived from those of the arctic, which migrated southwards during glacial periods and upwards during the interglacials of the Last Glacial Maximum (Arctic hypothesis).

Others have posited that alpine plants are derived from non-arctic lowland species (Lowland hypothesis). Recent large-scale studies have found evidence to suggest that alpine plant assemblages are the result of migration from arctic or other alpine regions, upward biome shifts, and in-situ speciation, though the importance of each varies continentally. Here, we test hypotheses on the origins of alpine species in North America in Erigeron L., a widespread and charismatic group of daisies that is species-rich and found across nearly all habitat types. We utilize target-capture sequencing and a species-tree approach to reconstruct phylogenetic relationships in this group, and state-dependent speciation models to test our hypotheses.

D-15

Creating reference genomes for two novel species of deep-sea snails from different oceans (Zeidora, Fissurellidae)

Afrah Khan, Loyola University Chicago
Tauana Cunha, Loyola University Chicago

Abstract:

Genome-level DNA data remain scarce for gastropods, despite being one of the most diverse animal groups in the oceans. Deep-sea gastropods are especially underrepresented in genomic databases due to challenges with sampling, preservation and high-quality DNA extraction. The project addresses this gap by generating the first reference genomes for two new species of slit-limpets of the genus Zeidora, one from the Pacific and the other from the Atlantic Ocean, both collected during independent deep-sea expeditions in 2021. High-molecular-weight DNA was extracted from both specimens and is being sequenced using Oxford Nanopore Technologies (ONT) for long read data. Illumina short-read data was generated to estimate genome size and heterozygosity using a K-mer frequency approach, and will be used to improve assembly accuracy. The Pacific specimen has an estimated genome size of 1.59 Gb and a heterozygosity of 1.41%, while the Atlantic specimen has an estimated genome size of 1.62 Gb and heterozygosity of 1.53%. De novo genome assembly will be performed using flye, with additional HiC data for scaffolding into chromosomal-level assemblies. By producing reference genomes for two geographically distinct Zeidora species, this study will contribute novel genomic information to an underexplored lineage of marine invertebrates and provide a foundation for future comparative and population-level studies.

D-16

Using machine learning to study the evolutionary dynamics of the interplay between liver transcription factor binding and enhancer activity across mammals

Alexander Okamoto, Carnegie Mellon University
Kuanyang Fang, Carnegie Mellon University
Junjie Ma, Carnegie Mellon University
Madeleine Kellogg, Carnegie Mellon University

Andrew Bellesis, Carnegie Mellon University
Irene Kaplow, Carnegie Mellon University

Abstract:

Genome sequencing is quickly outpacing the generation of experimental datasets necessary to understand the genetic mechanisms underlying the phenotypic diversity observed across species. While collecting experimental datasets from primary tissues across hundreds of species is infeasible, one promising solution is machine learning. Machine learning models can be trained on experimental data from model species and then used to make predictions based on genomic sequences for hundreds of other animals. We are using machine learning to study the evolution of the binding of transcription factors (TFs), proteins that help activate genes, in the mammalian liver. We are training machine learning models to predict the binding of three TFs (CEBPA, HNF4A, and CTCF) with available binding data from primary liver tissue of multiple species and then predict TF binding in over 400 mammals using their genomic sequence. Using this dataset, we will explore TF binding dynamics and the relationship between TF binding and enhancer activity across Mammalia. TF binding dynamics have the potential to uncover the mechanisms underlying the phenotypic differences between mammals resulting from differences in gene expression.

D-17
A CURE to teach undergraduates about the evolution of multicellular complexity

Dinah Davison, Augusta University

D-18
The regulation of the Drosophila melanogaster pale gene and its evolution during the origin of a dimorphic pigmentation trait

Ashley Williams, University of Dayton
Devon Seibert, University of Dayton
Thomas Williams, University of Dayton

Abstract:

The coordinated expressions of trait building, so-called “realizator”, genes in the appropriate cell types and developmental stages are two impressive outcomes of the genetic and molecular mechanisms of morphological evolution. For each realizator gene, its pattern of expression is anticipated to result from the interaction of a combination of transcription factors to binding sites within one or more cis-regulatory element (CRE). A question that remains murky is to what extent these similar patterns of realizator expression require their CREs to be bound by similar combinations of transcription factors. One model trait that may shed light on this question is the sexually dimorphic pattern of abdomen pigmentation that evolved in the lineage of Drosophila (D.) melanogaster fruit flies. This male-specific pattern of melanic pigmentation on

the posterior abdomen results from the spatial-, temporal-, and sex-specific deployment of a pathway of metabolic genes. While the CREs for several of these pathway genes have been well-studied, the biochemically first acting gene, known as pale, has received little attention. Here, we will share insights from studies on the regulation of the D. melanogaster pale gene and how this regulation and pale expression evolved during the origin and diversification of this pigmentation trait.

D-19
Genetic basis of tolerance to combined heat and chemical stressors in a beneficial insect

Sarah Britton, University of California San Diego
Patrick Rohner, University of California San Diego

Abstract:

Organisms face numerous anthropogenic stressors, both biotic and abiotic, that are often combined in complex, multi-stressor environments. Rapid adaptation to newly introduced environmental stressors depends heavily on existing genetic variation in a population. Since natural selection acts on multiple covarying traits simultaneously, evolution in complex environments depends not only on variation in individual traits, but also on their covariance. We investigate how a beneficial agricultural insect, the black scavenger fly Sepsis neocynipsea, responds to stress from heat and ivermectin, a veterinary antiparasitic drug that is lethal to a broad range of arthropods. We took a quantitative genetics approach to analyze the effects of these stressors and their genetic basis. We ask whether these stressors have additive or interactive effects on survival and whether there is genetic variation in resistance to these stressors alone or in combination. We conducted a fully factorial experiment with heat stress and ivermectin stress across 40 isofemale lines. We find that heat and ivermectin combined are more lethal than the additive effects of either stressor alone, with sex- and size-dependent effects. Furthermore, we show that genetic lines differ in their response to these stressors alone but also in combination, providing evidence for GxExE effects. Finally, we show that tolerance to heat and ivermectin have a positive genetic correlation, which may facilitate future adaptation. This study elucidates how organisms in complex, multi-stressor environments are affected by these anthropogenic changes in the short term and the potential for longer term adaptation.

D-20
Understanding the DNA sequence encodings and molecular mechanisms of gene expression regulation through the study of the fruit fly bric-à-brac genes

Eliana Williams, University of Dayton
Thomas Williams, University of Dayton

Abstract:

Well-developed and healthy animals depend on the faithful and robust expression of their genes in the correct cells and life-stages. Mutations that alter gene expression are suspected to be major contributors to evolution, disease risk, and even the cause of genetic disorders. Thus, it is of high importance to understand the DNA sequences and molecular mechanisms of gene expression control and how mutations can result in altered expression. The Drosophila melanogaster fruit fly bric-à-brac (bab) genes provide an opportune model to study gene expression regulation, as bab expression is complex and differs in closely-related species. We are teasing out which DNA sequences control the activity of the anterior element, a regulatory sequence that activates bab expression in the anterior dorsal abdomen segments during the pupal metamorphic stage. Insights will set the stage for future studies into how this anterior element function evolved from a more-broad ancestral capability.

D-21
Whole-genome sequencing of historical museum specimens reveals evolutionary history of island populations of a North American songbird

Henry Rosato, University of Minnesota
Keith Barker, University of Minnesota

D-22
Aggregation and Collation of Texas Crayfish Museum Specimens to Determine Their Current Conservation Statuses

Adrian Alvarez, University of Texas at Tyler
Jared Dickson, Texas Parks and Wildlife
Archis Grubh, Texas Parks and Wildlife Department
Ryan Shartau, Washington State University
Joshua Banta, University of Texas at Tyler

Abstract:

Crayfish account for over half of the macroinvertebrate biomass in many ecosystems and serve as crucial bioindicators because of their behavioral and physiological adaptability to environmental changes. Despite being home to approximately 52 native crayfish species, Texas currently lacks protective regulations. This gap is primarily because of insufficient information regarding their distribution and occurrences within the state, including their statuses as Species of Greatest Conservation Need (SGCN). This study focuses on compiling and comparing crayfish museum records with current iNaturalist field survey data across Texas to address these knowledge gaps and recommend updates to SGCN statuses. Five species not currently protected exhibited significant range contraction by over half of their historic range, recommending their addition to SGCN. Further sampling in historic regions and beyond is recommended for all species for a better understanding of their range in Texas.

D-23
High-powered mapping reveals stable G2P map, but unpredictable architecture of adaptation

Jess Smiley-Rhodes, Stanford University

Abstract:

The extent to which adaptation can be predicted, particularly for traits with complex genetic bases, is unknown. We leveraged a model complex trait, model species, and high-powered longitudinal sampling design to test the efficacy of genomic prediction of complex trait variation and evolution in ecologically relevant settings. We monitored genome-wide allele frequencies and pigmentation variation in genetically diverse populations of Drosophila melanogaster across seven generations of evolution in both field mesocosms exposed to natural environmental fluctuations, as well as mesocosms housed in a controlled, lab-based setting. At two time points throughout trait evolution, we conducted a high-powered, tail-based mapping of pigmentation, producing a well-resolved genotype-phenotype map that reaffirms canonical pigmentation genes and unveils novel loci. While we were able to use this map to correctly infer the direction of pigmentation evolution in both the field and lab mesocosms, the particular loci responding to selection, and thus architecture of adaptation itself, were largely unpredictable. We suggest this unpredictability to be a result of pleiotropic constraint, which was more pronounced in the field, relative to the lab-based environment. Finally, we quantified a striking stability of the genotype-phenotype map across genetically diverged populations, demonstrating that shifting epistatic landscapes associated with the evolutionary process itself do not alter trait architecture and preclude phenotypic prediction, provided the mapping is sufficiently powered. In concert our results highlight both the promise and limitations of genomic prediction, and exemplify the challenges of applying lab-based studies of complex traits to their evolutionary dynamics in the wild.

D-24
Patterns of biodiversity across depth gradients: natural experiments in marine lakes

Hashel Orquiz, University of California
Michael Dawson, University of California

Abstract:

Abiotic conditions shape patterns of biodiversity through environmental filtering, which influences community composition, species distributions, and local adaptation. Environmental gradients and their effects on population-level genetic structure have been extensively studied across latitude and elevation, but less so across depth. Marine lakes are ‘natural laboratories’ that provide a suite of depth-related environmental gradients, providing an ideal environment to study how vertical gradients may drive genetic variation and fine-scale local adaptation. Mixed marine lakes exhibit relatively constant environmental profiles, whereas stratified lakes have distinct layers and steep

environmental gradients. Given the more uniform water column in mixed lakes, we expect little to no change in diversity with increasing depth. In contrast, the steep environmental gradients and more extreme conditions in stratified lakes are expected to result in selective forces that drive distinct patterns of biodiversity and genetic structure. Using environmental data and species richness measured across depth, we analyzed the relationships between temperature, pH, dissolved oxygen, and salinity against species richness in 15 marine lakes in Palau, Micronesia. Contrary to our hypothesis, preliminary results show decreasing diversity with increasing depth in both mixed and stratified lakes. Further analyses will determine which environmental factors are the primary drivers of these patterns and how species' vertical ranges compare across lakes with distinct stratification. We expect to find genetic signals of selection to occur exclusively in organisms inhabiting stratified marine lakes, where differential environmental pressures across depth may lead to fine-scale local adaptation. As climate-driven shifts in abiotic conditions intensify, it is critical to determine the primary drivers of biodiversity patterns to anticipate how future change will impact sensitive ecosystems such as marine lakes.

D-25
Lack of evidence for coevolution in a sexually transmitted nematode and its dung beetle hosts

Patrick Rohner, University of California San Diego
Avi Khanna, UC San Diego

Abstract:

Symbioses with high transmission fidelity, such as those spread sexually or inherited vertically, are thought to facilitate coevolution between pairs of symbionts. However, coevolutionary dynamics may be impacted by symbiont life history or host choice. The nematode Diplogastrellus monhysteroides has been found on the genitalia of several dung beetles, with the symbiosis initially described in Onthophagus taurus but later noted in other sympatric species of Onthophagus. Nematodes are passed between adult beetles through copulation and maternally passed onto offspring. Previous research shows that this association is consistent with a facultative, sexually-transmitted mutualism, as dung beetles benefit from increased larval growth when nematodes are present and nematodes benefit from transportation between suitable habitats when associating with hosts. However, it is unknown how common this symbiosis is within host species, whether hosts differ in infection frequency, whether it is observed across a broader range of dung beetle taxa, and whether nematodes and dung beetles co-speciate. To address these questions, we sampled various dung beetles throughout the West Coast of the United States. Surprisingly, we find that D. monhysteroides are found on a much broader range of partners than just Onthophagus beetles, with newly identified hosts being separated by at least 45 million years of evolutionary divergence. However, despite this divergence time, we find little evidence for co-divergence in nematodes based on 18S rRNA sequences, providing evidence against co-speciation driven by sexual and maternal transmission. In addition, we found that rates of symbiotic association vary strongly between host species, potentially indicating context-dependence to the relationship's

benefits. This suggests that other mechanisms, such as frequent host switching or free-living dispersal, may impact this symbiosis. Taken together, our observations highlight the complexity of coevolutionary dynamics and help clarify when symbioses may fail to drive speciation.

D-26

Pacific-wide population genomics in Acropora hyacinthus: speciation, gene flow, and local adaptation

Benjamin Moran, UC Davis
Rachael Bay, University of California

Abstract:

Growing evidence suggests that many morphologically defined coral species contain multiple genetically distinct groups, or cryptic taxa. These complex patterns of genetic diversity present a challenge to traditional conservation, but also an exciting opportunity to reveal the fundamental processes by which species diverge genomically and ecologically. The table coral, Acropora hyacinthus, is one such cryptic complex, with recent population genetic and phylogenetic work describing numerous cryptic sympatric groups, some of which may represent independent species. However, previous studies have been limited in geographic extent, sample size per location, or in the number of genetic markers surveyed. As such, the relative strength of within-location population structure vs. isolation by distance at the oceanic scale, the extent of historical and contemporary gene flow between taxa, and the degree to which cryptic taxa may share adaptive genetic variation, remains unclear. I will present the work of a collaborative network combining 1300 new and existing A. hyacinthus samples from over 40 sites throughout the species' Pacific range. We are subjecting these sequences to a standardized whole-genome sequencing and genotyping pipeline, and using this unique dataset to create a clearer and broader view of diversity within the A. hyacinthus complex. We will distinguish cryptic population structure from the effects of allopatric divergence, and estimate effective migration rates across the range of each cryptic clade. We will also identify admixed individuals and infer the history of gene flow across the complex, revealing the degree of long-term reproductive isolation between taxa. Finally, we will perform genotype-environment association within each taxa to infer loci involved in local adaptation, and quantify the extent to which adaptive alleles are shared across taxa. Together, our work will reveal the evolution of this ubiquitous coral at the Pacific scale, and create a rich resource for future A. hyacinthus research and conservation.

D-27

Structural Blue Coloration and Collagen-Related Gene Expression and Population-Level Divergence in Gymnopithys Antbirds

Trayvond Russ, LSU

Abstract:

Antbirds (Thamnophiladae) are a highly specialized family of neotropical birds that remain understudied. A subset known as “ant-following birds” forage on arthropods and small vertebrates flushed by swarms of army ant species such as Eciton burchellii. Ant-following birds vary in levels of specialization. While obligate ant-followers rely heavily on ant swarms, occasional followers forage more independently. Some obligate ant-followers such as the genus Gymnopithys, possess unique periocular skin coloration (bare skin surrounding the eye), which could be used as an honest signaling trait in interspecific competition. Periocular coloration in birds is poorly studied, despite structural skin coloration occurring in over 250 known bird species. The blue coloration has been shown to be achieved from coherent scattering of light via quasi-organized collagen fiber arrays. However, the genetic mechanisms underlying collagen organization remain unexplored. Previous work in our lab identified significant gene ontology terms associated with collagen fibers, using a differential gene expression analysis between sister species of Gymnopithys with and without blue periocular tissue. Here, I expanded this dataset by incorporating additional specimens possessing greater phenotypic variation. Phenotypic variation was mapped using photographic data from the Macaulay Library, generating a gradient of blue periocular color intensity across Central and South American populations. This phenotypic variation was evaluated alongside population-level genetic differentiation to explore potential associations between coloration and genomic differentiation. Our results describe the molecular basis of blue periocular coloration, and highlight its potential ecological relevance and taxonomic value.

D-28
The Role of Mating System Variation in Shaping the Evolution of Sex-Biased Genes

Morjina Solaiman, University of Idaho
Sarah Flanagan, University of Canterbury
Adam G Jones, University of Idaho

Abstract:

In many species, sexual selection drives the evolution of sex-biased gene expression, with a disproportionate number of genes often showing male-biased expression, particularly in reproductive tissues such as the testes. However, little is known about gene expression patterns in species where sexual selection acts strongly on females, especially in sex-role–reversed systems. Within the family Syngnathidae, both reproductive role reversal and mating system variation are present: in monogamous systems, sexual selection acts weakly on females, whereas in polygamous systems, sexual selection acts strongly on females. This study aims to address this gap by examining transcriptomic differences across polygamous and monogamous syngnathid species. We performed a comparative tissue transcriptomic analysis of two syngnathid species with contrasting mating systems: one polygamous species (Syngnathus scovelli) and one monogamous species (Hippocampus erectus). We quantified the abundance and range of expression levels of sex-biased genes and estimated the nonsynonymous-to-synonymous substitution ratio (dN/dS) to detect signatures of positive selection. Genes with $\log_2$ fold changes >

2 and p-values < 0.05 were identified as significantly differentially expressed sex-biased genes. Overall, we observed a higher number of sex-biased genes in the polygamous species compared to the monogamous species, and reproductive tissues exhibited the greatest expression differences relative to somatic tissues. Our findings suggest that species experiencing stronger sexual selection pressures harbor more sex-biased genes and exhibit higher evolutionary rates. These results contribute to ongoing debates about whether sexual selection and sexual conflict drive the evolution of sex-biased gene expression across species and mating systems.

E-01
CFTR Modulators Alter Host-Pathogen Dynamics in CF Staphylococcus aureus Infections

Guy Snow, University of Iowa
Jose Zapata, University of Iowa
Thomas Zaputil, University of Iowa
Anthony Fischer, University of Iowa
Benjamin Chapin, University of Iowa
Natalie Blake, University of Iowa
William Gerhardt, University of Iowa
Netachi Nwizu, University of Iowa
Kayanna Gomez, University of Iowa
Maurine Neiman, University of Iowa
Justin Krogh, University of Iowa
Valerie Reeb, University of Iowa
Alexis Zaputil, University of Iowa

Abstract:

Background. Antimicrobial resistance (AMR) is a major public health problem that arises through evolution imposed by antibiotic-mediated selection. In cystic fibrosis (CF), chronic bacterial infection and frequent antibiotics select for AMR. The 2019 introduction of Elexacaftor/Tezacaftor/Ivacaftor (ETI) for CF treatment improves clinical outcomes and reduces the need for antibiotics. We leverage the natural experiment posed by the reduction in antibiotic use after 2020 to determine the fate of AMR in people with CF (pwCF).

Methods. We collected Staphylococcus aureus from 128 pwCF before and after ETI between 2018 and 2024. We scored for methicillin-resistant S. aureus (MRSA) and performed whole-genome sequencing (WGS) on S. aureus isolates to track the evolutionary fate of MRSA. We considered four possible causes for decreased AMR: (1) loss of S. aureus, (2) loss of genes conferring AMR, (3) point mutations restoring antibiotic susceptibility, and (4) outcompetition of resistant strains by emerging antibiotic-susceptible strains.

Results. We examined 531 S. aureus isolates (47% MRSA) before and 670 isolates (36% MRSA) after ETI, a significant reduction in MRSA. Among 63 pwCF with baseline MRSA, 74.6% retained MRSA after ETI. Among those who lost MRSA, 50% did not culture S. aureus and 45% had a new strain of S. aureus that was methicillin susceptible (analysis still pending for 5%). In one subject who

retained MRSA, we found point mutations in mecA indicating newly evolved methicillin-susceptible S. aureus (MSSA).

Discussion. MRSA frequency decreased with removal of antibiotic pressure although most subjects with MRSA continue to have MRSA. Loss of MRSA occurred both by loss of S. aureus and by strain displacement with new MSSA. On rare occasions, we capture evolution of MSSA from MRSA. This work suggests while AMR is costly to S. aureus, re-evolution of antibiotic susceptibility can be a lengthy process.

E-02
Linkage and the loss of short stamens in Arabidopsis thaliana

Natalie Dresdner, Michigan State University

Abstract:

How do genetic correlations between traits contribute to evolutionary processes? This study investigates the role of genetic linkage in an unexplained geographic cline of floral trait loss in Arabidopsis thaliana. A diagnostic characteristic of the Brassicaceae family is the arrangement of four long stamens and two short stamens in each flower. These short stamens are adaptive in outcrossing and have lost this function in highly selfing A. thaliana. Short stamens demonstrate incomplete loss across A. thaliana's native range, with fewer stamens produced at lower altitudes and latitudes. We hypothesized that short stamen number is genetically correlated with one or more traits involved in altitudinal adaptation, thus shaping the altitudinal cline in population mean short stamen number. We grew recombinant inbred lines from a cross between high and low altitude parents and measured a suite of phenotypic traits for each plant. We found a correlation between mean short stamen number and days to flowering, supporting a hypothesis of pleiotropy or linkage disequilibrium between the two traits. Ongoing study will seek to further explain the geographic variability in loss of this ancestral trait and explore how alternative mechanisms to direct selection shape evolution.

E-03
Genomic Characterization of Two Intertidal Tardigrades Occupying the Same Microhabitat in Biscayne National Park

Kevin Murillo, FIU
Alexis Mas, Florida International University
Pushpalata Kayastha, Florida International University
Jason Pienaar, Florida International University

Abstract:

Intertidal tardigrades from the Miami, Florida region were investigated using genomic sequencing and comparative analysis. Two taxa were examined: Archechiniscus biscaynei and Echiniscoides sp. nov. Archechiniscus biscaynei, is a type locality originally described in 2012 from Biscayne

National Park. The original description is based only on morphology without any genomic data. Found In the same area, a new species of the genus Echiniscoides is being described based on morphology, morphometrics, and DNA barcodes. Whole-genome sequencing was performed on both Intertidal genera using single specimen and Multiple Displacement Amplification (MDA) to investigate conserved genomic regions shared between them. A eukaryotic BUSCO analysis was done to verify the accuracy of each assembly. The BUSCO score for Archechiniscus biscaynei was 80.0%. The BUSCO score for Echiniscoides sp. nov. was 63.9%. This preliminary data expands the currently limited genomic information for intertidal tardigrades. and furthers the possibility for future research on the evolution of conserved genes in tardigrades.

E-04

How did highly modified webs evolve in cribellate orb-weaving spiders? Using UCE based phylogenetics to reconstruct web evolution in Uloboridae.

Steven Casey, University of Massachusetts Lowell
Shoyo Sato, Harvard University
Gustavo Hormiga, The George Washington University
Gonzalo Giribet, Harvard University
Jessica Garb, University of Massachusetts Lowell

Abstract:

Spiders in the family Uloboridae build a wide range of web types, from horizontal orb webs to highly modified capture webs. Examples of this include the single line webs of Miagrammopes and the spring-loaded triangle web of Hyptiotes. Research into the silk of this family has uncovered that the silk Hyptiotes uses to launch itself forward to catch prey has a unique protein composition; it is highly enriched with proline, possibly to facilitate its unique functional requirements. Despite this diversity in web architecture and silk composition, phylogenetic relationships within Uloboridae remain poorly resolved, and there is no comprehensive molecular phylogeny of the family. Without a well-resolved family phylogeny, whether these web reductions occurred sequentially or independently remained an open question. We sequenced museum samples targeting ultraconserved elements (UCEs) using a spider specific probe set, combining these data with UCE loci extracted from any available uloborid genome or transcriptome. From this, we constructed a comprehensive phylogeny of Uloboridae, covering 16 of the 20 accepted genera. Ancestral state reconstructions mapping web modifications show that web reductions occurred multiple times in the family. The relationships elucidated in this study will inform future research into the evolution of the varied webs of the family as well as that of the underlying silk proteins.

E-05

Mapping network properties of C. elegans transcriptional factors to the regulation of differential expressions

Kuankuan Hu, University of Virginia
Katja Kasimatis, University of Virginia

Abstract:

Gene regulatory networks (GRNs) describe the regulatory relationships among all or a subset of genes in a genome. A directed network model in which nodes represent genes and edges represent regulatory effects can capture the structures and dynamics of a GRN. This network-based framework enables realistic and holistic modeling to reveal emergent properties - such as robustness and modularity formation – and provides more interpretable explanations of regulatory sequence evolution. Caenorhabditis nematodes are ideal systems for bridging in silico and in vivo approaches, as they exhibit diverse mating systems, are amenable to CRISPR-based genome engineering, and possess well- characterized cell lineages. Using C. elegans transcription factor (TF) data, we identified a strongly connected component (SCC) comprising 453 TFs. Within this SCC, six TFs exhibit significantly higher betweeness centrality than null expectations – that is, the shortest paths between all gene pairs most frequently pass through this set of TFs. This pattern suggests that these TFs are structurally important and likely participate in multiple regulatory pathways. We examined the null mutant of the gene nhr-86, which perturbs one of the six focal TFs. The level of differential expression varied considerably among recorded direct cis-regulatory targets, with over 100 genes showing significant differential expression between the wildtype and nhr-86 null strain. Further investigation will assess the correlation between variation in robustness and redundany and the properties of GRN modules. Additionally, we correlate phenotype severity with changes in expression to evaluate functional consequences. Together, this modeling framework provides an effective new paradigm for generating more precise hypotheses regarding the consequences of and constraints on regulatory sequence evolution through the lens of genome-wide interactions.

E-06
Phylogenomics of Solomon Island Flycatchers Reveal Complex Evolutionary Relationships Within Genus.

Lukas Westermann Salas, Biodiversity Institute
Ryan Andrews,
Robert Moyle, University of Kansas

Abstract:

Speciation is one of the fundamental evolutionary processes that generate the immense biodiversity we observe on our planet. Island systems have historically been used to investigate biogeography and speciation due to their isolation and potential for rapid species diversification. For instance, monarch flycatchers (Aves: Monarchidae) have been used to study the origin of avifauna across Pacific islands. Despite this, previous phylogenetic work on this family is limited, based on restricted sampling and few loci. One such genus is Monarcha, comprised of several species native to the Solomon Islands. Here, we use genomic data and comprehensive sampling of the Northern Melanesian Monarcha to disentangle the phylogenetic relationships within the

genus and clarify its evolutionary history. We identified single nucleotide polymorphisms (SNPs) and used those as a basis for a variety of phylogenetic and population genetic analyses. Our analyses reveal a well-supported species-level topology that renders Monarcha castaneiventris paraphyletic. Additionally, we uncover evidence of gene flow between M. castaneiventris and both M. richardsii and the more widespread M. cinerascens. Our data also reveals possible species-level divergence of M. castaneiventris megarhynchus, which is found on the deeply isolated southernmost island of Makira and surrounding small islands. These findings highlight the need for taxonomic revision within this clade. More broadly, these results clarify where members of the Monarcha genus fall within the speciation continuum, adding to the growing body of literature showcasing the complex evolutionary relationships of taxa diversifying within island systems.

E-07
Gene duplications facilitate dietary specialization in a mammalian herbivore

Nathaniel Carlson, University of Utah
M. Denise Dearing, University of Utah

Abstract:

Extreme dietary specialization on a single plant species (monophagy) has evolved only a handful of times in mammalian herbivores. Mammals are thought to be constrained to a generalist dietary strategy by an inability to tolerate high doses of individual plant toxins; and by feeding on multiple species, herbivores effectively "dilute" their exposure to any single compound. To date, well-documented cases of monophagy in mammals occur at the species level, making it difficult to pinpoint the evolutionary basis of monophagy due to the degree of divergence between reproductively isolated species.

To overcome this limitation, we compare a monophagous specialist population of a mammalian herbivore—the desert woodrat (Neotoma lepida)—with nonspecialist populations to understand how monophagy evolves in mammals. Specifically, we investigate a population of desert woodrats from Death Valley, California, that feeds exclusively on the foliage of honey mesquite (Prosopis glandulosa), exposing them to high concentrations of toxic alkaloids.

Using population genetic analyses of more than 200 desert woodrat genomes, we found that genes encoding hepatic detoxification enzymes are enriched for signatures of selection in mesquite-specialist woodrats. In particular, CYP2D, a cytochrome P450 enzyme that metabolizes alkaloids across mammalian species, shows a strong signature of selection in mesquite specialists. This selection is associated with a massive gene duplication, with approximately five copies in nonspecialists compared to more than 30 copies in mesquite specialists.

Together, these results suggest that elevated detoxification capacity is required for monophagous specialization in mammalian herbivores. They also add to a growing body of evidence that

duplication of detoxification genes is a key genetic mechanism underlying toxin tolerance in mammalian herbivores.

E-08
Multi-track drifting: ecological, allopatric, and hybrid divergence in the gall wasp Antistrophus silphii

Brendan O'Loughlin, The Ohio State University
Bryan Carstens, The Ohio State University

Abstract:

Speciation is a central concept in evolutionary biology, yet the genetics underpinning different modes of speciation are not well understood. The gall wasp Antistrophus silphii presents an ideal model system for comparing different modes of speciation and their effects on the genome. This species induces globular stem galls on at least 10 different species of the sunflower-like genus Silphium across eastern North America, occupying a much larger host range than any of its close relatives. Preliminary genetic data suggests that this species may be a cryptic complex, with at least four distinct lineages that each diverged via different mechanisms. The most basal lineage inhabits the Piedmont region of the Southeast U.S. and is separated from Midwest lineages via allopatry. Within the Midwest lineages, two lineages appear to be sympatric and segregated by host plant choice, while the third may be a hybrid of Midwest and Southeast ancestry. Therefore, divergence within the Antistrophus silphii complex may be simultaneously driven by allopatric, ecological, and hybrid speciation. Future work will include species delimitation and validation from whole-genome data, comparison of different genomic patterns across lineages undergoing different modes of divergence, and the evolution of ecologically relevant genes across different lineages.

E-09
Let's Stick Together: Investigating the Distribution of Micro-Multicellular Phenotypes Across 1,000 Isolates of S. cerevisiae

Macie McGraw, College of William & Mary

Abstract:

Multicellularity and adhesion are important microbial adaptations to stress. Brewer's yeast, Saccharomyces cerevisiae, is a facultatively multicellular microbe, meaning that it can exist as a single-celled microbe or form multicellular structures. These structures may be beneficial in environments with ethanol toxicity and nutrient limitation. Yeast has been observed to form a variety of multicellular phenotypes, including biofilms, flors (floating mats) and pseudohyphae. Aside from these complex multicellular structures that can be seen by the naked eye, S. cerevisiae can form microscopic multicellular aggregates, which are the focus of this study. Cell aggregation is not a uniform trait across S. cerevisiae strains, and can vary depending on

aggregation mechanism and growth medium. One form, known as “flocculation,” is reversible cell-cell adhesion and is often selected for in beer-brewing environments to facilitate yeast precipitation from the liquid beer pitch. In this study, using a panel of 1,000 strains of yeast isolated from ecological niches and geographic locations around the world, the distribution of micro-multicellular phenotypes across the global population of S. cerevisiae was investigated. Potential factors that may contribute to the distribution of micro-multicellularity were tested, including environment of isolation, genetic background (phylogenetic clade), and flocculins, members of the FLO gene family which encode adhesive cell-surface proteins. Our results indicate that specific environments of isolation, such as biofuel environments, are correlated with aggregating phenotypes; however, environment of isolation explained very little variation in the distribution. Clade, or evolutionary history, on the other hand, explained a significant amount of variance in aggregation. In addition, when yeast isolates were grown in different media, we found bi-directional phenotypic plasticity, where some isolates exhibited aggregates only in nutrient-poor conditions, while others exhibited aggregates only in nutrient-rich conditions. Most observed aggregates did not disperse in deflocculation buffer, suggesting adhesion is mediated by the kin-recognition flocculin Flo11. Overall, these results indicate that long-term evolutionary history plays an important role in shaping multicellular phenotype, and that the trait of yeast aggregation is diverse not only in aggregate size and pattern, but also in degree and direction of plasticity in nutrient limited conditions.

E-10
You Are What You Eat: An analysis of the gut microbiome of larval Dryophytes cinereus

Jesus Villalobos, University of Houston

Abstract:

Rising salinity levels from environmental and anthropogenic causes negatively affect freshwater organisms, especially amphibians, which have particularly sensitive early life stages. Understanding the host-microbe interactions of these organisms may give us insight into how to adapt to inevitable environmental changes. In this study, we looked at coastal and inland populations of Dryophytes cinereus tadpoles, a species of frog that has been shown to have a predisposition to higher salinity tolerance, to gain a deeper understanding of host-microbe interactions in their vulnerable stages of life. After exposing tadpoles in permeable containers over 9-days in both coastal and inland wetlands, the organisms' gut coils were removed and sequenced. We looked at any differences between populations reared in coastal or inland environments, and whether any microbes influenced tadpole growth. We saw that the gut microbiome from tadpoles placed in inland wetlands had significantly greater richness than that of tadpoles placed in coastal wetlands. Furthermore, coastal tadpoles in inland wetlands exhibited significantly hicher shannon diversity than inland tadpoles. We also found that coastal wetlands had a positive effect on tadpole growth. Lastly, we found the microbial composition is not only linked to environmental and host-origin efects bt also to host growth, and the top families associated with growth are aquatic algae

and protists. This may mean that microbiome-growth associations in tadpoles may reflect environmental food-web structure and feeding ecology rather than strictly endogenous gut symbiosis

F-01
Investigating the pleiotropic effects of spdt in Drosophila melanogaster

Jalen Major, University of Houston
Farnam Ghaemmaghami, University of Houston
Richard Meisel, University of Houston

Abstract:

Mating behaviors often evolve under sexual selection and are governed by complex gene regulatory networks. Genes within these networks can have widespread pleiotropic effects that can weaken the response sexual selection thereby constraining adaptation. However, we lack a mechanistic understanding of how genes within these networks interact to limit the adaptive response to selection. To address this gap, we are studying the Drosophila melanogaster gene speed date (spdt), which encodes a transcription factor that may downregulate the expression of an odorant binding protein, Obp56h, which in turn reduces male copulation latency. Decreased copulation latency is male beneficial, yet this phenotype is not observed naturally in Drosophila. We artificially elevated spdt expression in the neurons and used RNA-seq to measure gene expression in the head of male and female flies. We hypothesize that the pleiotropic effects of spdt are sexually antagonistic against females.

F-02
What is the Influence of Elevation and Ridgeline Orientation on Gene Flow?

Nick Nighswander, University of Mississippi
Ryan Garrick, U. Mississippi

Abstract:

Mountain landscapes compress environmental variation across short distances, promoting local adaptation, genetic divergence, and speciation. Ridgeline orientation is a particularly underexplored driver of these processes: in the northern hemisphere, east-west ridgelines generate persistent contrasts between permanently shaded north-facing and sun-exposed south-facing slopes, producing divergent temperature and moisture regimes that may limit dispersal and gene flow across ridge crests. North-south ridgelines, by contrast, expose both flanks to direct sunlight at different times of day, resulting in greater diurnal swings but less persistent thermal divergence between slopes. Whether ridgeline orientation translates into measurable genetic divergence remains largely unknown. We leverage a natural experiment in the U.S. Interior Highlands, a recognized biodiversity center encompassing two adjacent ranges with strikingly different topographies. The Ouachita Mountains feature strictly east-west ridgelines, while the neighboring Ozark Mountains exhibit irregular, non-directional ridgelines typical of an eroded plateau.

Separated only by the Arkansas River Valley, these systems share similar climatic and biotic contexts, allowing ridgeline orientation to be isolated as a variable. We focus on three co-distributed subterranean termite species (Reticulitermes flavipes, R. virginicus, and R. hageni) that share the same microhabitat, have limited dispersal capacity, and serve as replicate taxa for testing landscape-level hypotheses. Pairwise genetic dissimilarity will be quantified from mitochondrial COI and COII sequences across localities spanning both mountain systems. Least-cost path distance matrices parameterized with cost surfaces varying in weights for elevation change and ridgeline orientation will be compared against straight-line distance using linear regression and AIC-based model selection. We predict that east-west ridgelines more strongly limit gene flow than irregular ridgelines, consistent with isolation-by-environment predictions. If supported across all three species, results will implicate slope-aspect gradients as a broadly important driver of evolutionary divergence in topographically complex landscapes.

F-03
Convergently-evolved honeypot ants show mixed signs of niche conservatism

Bianca Nogueira, Rutgers University
Omar Léon-Alvarado, Rutgers University
Lily Khadempour, Rutgers University-Newark

Abstract:

Honeypot ants represent an example of convergent evolution, where workers known as repletes, specialized in storing liquid food in their distended crops, have independently evolved multiple times across different ant genera. While seasonal resource scarcity and arid conditions are thought to drive the evolution of repletism, the role of environmental variables in this process remains unknown. With this in mind, we constructed species distribution ensemble models for 49 species to assess habitat suitability and abiotic predictors importance. Predictor importance was compared across genera and groups occupying similar geographical areas. Niche overlap and similarity were also evaluated to determine whether honeypots occupy similar environmental spaces. Overall pairwise overlap was low, with only 253 of 1176 comparisons yielding significant similarity. Similarity was primarily detected within the most speciose genera, Leptomyrmex and Myrmecocystus. Overall, Leptomyrmex distribution was mainly influenced by atmospheric bioclimatic variables like precipitation and temperature, while Myrmecocystus had soil bioclimatic variables as the most important predictors for their current distribution. This suggests that divergent niche dimensions are driving their distributions. Camponotus inflatus and Melophorus bagoti, while occupying similar geographical space, showed particularly distinctive niches, with little overlap with any other honeypot ant. Overall, species occupying the same geographical region did not show niche similarity. Our results indicate that, as a group, honeypot ant species currently do not occupy the same environmental space and are thus not subject to shared contemporary stressors. However, certain abiotic variables showed convergence signals within genera, indicating that the environmental niche is not entirely divergent. Our results suggest that contemporary environmental factors cannot fully explain the convergence of honeypot ants. In our future work, we

will examine past climatic conditions alongside ant genomic data to better understand the causes of this convergence.

F-04
Evolutionary and Transcriptomic Insights into the Parrotfish Beak

Samyah Smalley, Rice University

Abstract:

Parrotfish exhibit one of the most unique dentitions possessed by a bony fish: a highly organized beak formed of up to 1000 teeth in constantly regenerating rows. This mechanically robust adaptation allows them to scrape algae off of coral for consumption. Despite the complexity of this trait, very little research has been done on the genes and regulatory networks employed by their genome to accomplish such a feat. Further examination of the molecular evolution behind this trait gives insight on how they have come to have said trait.

F-05
Host specialization without cophylogeny in palm flower weevils

Abigail Magland, University of Chicago
Diego Souza, Field Museum of Natural History
Aline Lira, Federal Rural University of Pernambuco / Field Museum
Bruno de Medeiros, Field Museum

Abstract:

Palm Flower Weevils (Coleoptera: Curculionidae) represent a group of weevil genera, primarily in the subfamily Baridinae and tribe Derelomini (Curculioninae), that rely on palm flowers for their lifecycle. As adults, they feed on pollen and mate and oviposit in the flowers, and emerging larvae consume plant tissue. Here, we take a systematic approach to uncovering diversity and assessing host specificity among these weevils. We use weevils collected from Syagrus palms, a close relative of the coconut and the most abundant palm genus in the Neotropics, as a study system. Using species delimitation analyses and cophylogenetic models, we find weevils to be incredibly host specific but also host switchers through time.

F-06
Tracing the origin of parallel-evolving freshwater-adaptive genes in threespine sticklebacks

Kung-Ping Lin, Department of Zoology
Dolph Schluter, University of British Columbia

Abstract:

Threespine sticklebacks (Gasterosteus aculeatus) are renowned for their rapid and repeated adaptation from marine to freshwater environments following the retreat of Pleistocene glaciers. This remarkable parallel evolution is thought to be facilitated by freshwater-adaptive alleles maintained as standing genetic variation in marine populations along the west coast of North America, the species' ancestral range. A key prediction of this hypothesis is that freshwater-adaptive alleles should predate the recent colonization of freshwater habitats. Supporting evidence comes from loci such as Ectodysplasin (Eda) gene, where divergence between marine and freshwater haplotypes substantially predates the postglacial origin of contemporary freshwater populations. If freshwater-adaptive alleles originated in southern glacial refugia and subsequently spread northward, phylogenetic trees should exhibit a ladder-like topology, with southern haplotypes occupying basal positions and northern haplotypes appearing progressively derived. To test this prediction, we constructed phylogenetic trees for three chromosomal inversion regions known to contribute to freshwater adaptation, as well as the Eda locus, using samples spanning the Pacific coast from California to Alaska. Preliminary analyses reveal ladder-like phylogenetic patterns across all four regions, consistent with a northward expansion of freshwater-adaptive haplotypes following glacial retreat. These results suggest that the ancestral freshwater-adaptive alleles likely originated in populations located in present-day Washington or Oregon, providing new insights into the evolutionary history and geographic origins of standing genetic variation that fuels rapid adaptation in sticklebacks.

F-07
Salinity exposure reveals the embryonic stage as a critical bottleneck for coastal amphibian development and survival

Kayla Hancey, Utah State University
Kayla D McBride (Hancey), Department of Watershed Sciences, Utah State University, Logan, UT
Molly A Albecker, Department of Biology and Biochemistry, University of Houston, Houston, TX
Molly C Womack, Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, New York

Abstract:

Anuran (frog and toad) populations are in global decline, largely due to habitat loss and environmental changes. Moderate climate change predictions expect sea level to rise 50-100 cm in the next 70 years, with the United States Atlantic and Gulf coasts expected to face intensified impacts of rising sea levels. Predicted sea level rise poses a clear threat to amphibian populations that often occupy wetlands very near coastal areas. Despite having a wide global distribution, amphibians never occupy marine environments and were considered intolerant of salt due to their permeable skin and breeding requirements. Yet, accumulating observations and experimental evidence indicate more tolerance to salinity than previously understood, leaving uncertainty in predictions regarding coastal community resilience. This research focuses on anuran populations within five miles of coastlines near Houston, Texas and Sapelo Island, Georgia which are dual sea level rise locations with low-elevation coastlines and freshwater wetlands expected to be

inundated by 2050 under moderate sea level rise predictions. We experimentally tested salinity tolerance across life stages and species using acute (96 hr) salinity exposures and monitored survival and development for 21 days post-exposure. We found variation in species survival and notable evidence across species that the egg stage is less tolerant of salinity than the larval stage. When exposed to moderate salinity levels for relatively short periods of time, anuran eggs are unable to hatch or develop. This indicates a crucial salinity bottleneck during the embryonic stage. We plan to continue to collect data to provide evidence-based vulnerability predictions to wetland managers aiming to prevent biodiversity loss and promote resilience through anticipated environmental changes.

F-08
Innovation arising during experimental evolution: a machine learning investigation

Madeline Eggink, University of Minnesota

F-09
Molecular cloning of putative Na+-K+-2Cl- cotransporter (NKCC) cDNAs in the copepod Eurytemora carolleeae

Yeaeun Park, The Ohio State University

Abstract:

Recent shifts in global climate patterns including accelerated glacier melt and altered rainfall are cuasing rapid declines in salinity within estuaries and coastal waters, posing a severe threat to the survival of diverse aquatic taxa. The saline copepod, Eurytemora carolleeae, serves as an ideal model for studying adaptation to salinity shifts, as it has shown remarkable osmoregulatory flexibility across multiple freshwater habitats. Previous genomic studies discovered that a key feature of E. carolleeae surviving in low salinity is rapid evolution of genes encoding ion transporters. Na+-K+-2Cl- cotransporters (NKCCs) is one of the ion transporters that are most differentially expressed between the saline and freshwater populations and hypothesized to be the targets of recent natural selection. Despite their importance, specific functions and localization within the osmoregulatory organs remain poorly understood.

In this study, we successfully cloned cDNAs of the NKCC paralog 2 (NKCC-2), which is significantly upregulated during freshwater adaptation. Using Rapid Amplification of cDNA Ends (RACE) on cDNA from a saline population of E. carolleeae, we identified several candidate splice variants of NKCC-2. Most of these variants had altered NH2 regions that truncate the upstream coding sequence, predicted to result in the partial loss of several transmembrane domains. However, several splice variants include transmembrane domain segments 11 and 12, which are known to be involved in dimerization of monomers and stabilization of proteins at the cellular membrane.

Whether these alternative splicing events modulate the ion transport capacity or dimerization of NKCC-2 remains to be determined.

F-10
A chromosome-scale genome assembly of the rice stink bug (Hemiptera: Oebalus pugnax) illuminates genome structure and gene family evolution in Pentatomidae

Rokeya Akter, University of Arkansas
Mahamad Miya, Department of Entomology and Plant Pathology
Allen Szalanski, University of Arkansas
Duane McKenna, University of Memphis
RICH A, University of Arkansas

Abstract:

The rice stink bug (Oebalus pugnax; RSB) is a major agricultural pest that poses significant threats to rice production throughout the United States. Despite its importance, genomic diversity and evolutionary processes underlying plant feeding, resistance to chemical control, and adaptation in this species remain unknown. Here, we sequenced, assembled, and annotated the first high-quality reference genome for RSB and conducted comparative analyses with related hemipteran genomes to better understand its structure, function, and evolution. The assembly spans 826.62 Mb across 211 contigs, with a N50 of 17.25 Mb and the largest contig of 67.15 Mb. Hi-C-based chromosome-scale scaffolding supported six putative autosomes that together cover 94.20% of the genome. Genome-wide GC content was 30.83%, and repeats comprised 47.55% of the genome, consisting largely of interspersed elements, including DNA transposons, LINEs, and LTRs, with evidence of recent expansions. Our annotation pipeline identified 13,175 putative genes, with predicted functions for 97.87% of protein-coding genes. BUSCO analysis indicated 99.30% completeness, supporting the high quality of the assembly and annotation. Comparative analyses revealed rapid expansion and contraction of gene families associated with feeding, host specialization, and pesticide resistance. Together, these resources provide a new framework for future investigations into genome structure, function, and evolution in this economically and ecologically important insect clade.

G-01
Viral Diversity and Evolution in Wild Populations of Hesperis matronalis

Susan Lusardi, University of Michigan
Regina Baucom, University of Michigan

Abstract:

Plant viruses evolve rapidly due to high mutation rates, short generation times, and strong selective pressures that favor strains capable of evading host defenses or increasing transmission efficiency. Although substantial effort has been devoted to mitigating viral impacts in agricultural systems

through genetic modification, insecticide application, and other management strategies, the ecological and evolutionary dynamics of plant viruses in wild host populations remain poorly understood. Here, I present results from a comprehensive survey of viral diversity across populations of Hesperis matronalis. I use RNAseq and transcriptome assembly to characterize the existing viral community, compare viral taxa abundance across host phenotypes, evaluate the influence of spatial factors on viral diversity, and investigate evidence for viral strain divergence and potential speciation. These findings provide insight into the evolutionary processes shaping plant viral communities in natural systems and highlight the importance of wild plant reservoirs in understanding the emergence and persistence of agriculturally relevant viruses.

G-02

Are moths keeping pace with a changing planet? Integrating automated camera traps, environmental DNA, and traditional methods to survey nocturnal Lepidoptera communities

Alissa Doucet, University of Chicago
Sophie Picq, Field Museum of Natural History
Bruno de Medeiros, Field Museum

Abstract:

Nocturnal Lepidoptera are ecologically important as pollinators, herbivores, and prey, yet remain understudied relative to their diurnal counterparts. Traditional light-trapping methods miss species flying outside of observation windows, exclude floral interaction data, and are often too resource-intensive for community-scale, long-term monitoring. Addressing these gaps requires validated, complementary survey approaches that can capture non-overlapping subsets of moth communities while remaining scalable for eco-evolutionary hypothesis testing.

Here, I present pilot data from a multi-method nocturnal Lepidoptera monitoring framework deployed at Warren Woods Ecological Field Station (Three Oaks, Michigan) in September 2025. I compare three methods: traditional bucket light traps (Mothbucket); automated camera traps with UV and full-spectrum lighting and computer-vision identification (Mothbox); and environmental DNA (eDNA) metabarcoding from one validated substrate (flower heads) and one novel substrate (Mothbox landing stages). Both eDNA methods will target the COI barcode regions by Illumina MSeq sequencing. Three pilot Mothbox deployments spanning six data-collection nights yielded over 35,000 insect detection events, with the UV + full-spectrum lighting scheme being the most successful. Flower eDNA and Mothbox stage eDNA extractions yielded sufficient DNA concentrations for library preparation. Primer testing of moth tissue and eDNA samples is ongoing.

I predict that no single method captures the full species pool, that methods will detect non-overlapping taxonomic subsets, and that biological traits such as phototaxis, body size, and foraging behavior will predict method-specific detectability. Results will directly inform which survey approaches should be prioritized for different focal taxa in biodiversity surveys for conservation and restoration efforts, and lay the methodological groundwork for testing whether

evolutionary history structures seasonal, within-night diel activity time, and floral resource partitioning in temperate moth communities.

G-03
Comparing patterns of speciation in depth-separated species pairs of rockfishes

Jordan Pilcher, CSU Monterey Bay

Abstract:

Speciation is the evolutionary process responsible for generating biodiversity, which is critical for ecosystem structure and function. Investigating the genomic, ecological, and geological factors involved in speciation helps to better understand historic and present-day patterns of biodiversity. Rockfishes (genus Sebastes) are a remarkably diverse clade with wide-ranging phenotypes and ecology that provide a unique opportunity to investigate and compare multiple replicates of genomic speciation. Using Sebastes as a model clade, this project identifies genomic patterns of speciation across environmental and temporal gradients in depth-separated sister species pairs. We performed low coverage (~2X) whole genome sequencing for ~15 individuals of 10 species comprising 5 sister species pairs, as well as ~4 individuals of species representing candidate sister taxa to each pair. We evaluated genetic population structure for each species, identified regions of genomic divergence between species pairs, and reconstructed the demographic history, including divergence times, of the species pairs. We also assessed the function of regions of genomic divergence and evaluated these patterns based on historic palaeoceanographic conditions, providing insight into the selective forces acting on the species pairs during the process of speciation. Our findings provide insight into the genomic mechanisms of sympatric speciation and the selective environmental pressures that influence speciation.

G-04
A large-effect locus may underlie leaf lobing in Ipomea trifida: describing the variation and inheritance of leaf shape

P. Durant, University of Michigan
Regina Baucom, University of Michigan

Abstract:

Leaves in nature take on a variety of shapes and forms, from slender blades of grasses to the deeply dissected heart-shaped leaves of monsteras. Leaves are the primary photosynthetic organs of plants, and thus are a plant's main interface for gas exchange, light capture, and temperature regulation. However, despite the importance of leaves to a plant's ecological function and evolutionary success, understanding of the underlying ecophysiological mechanisms underlying leaf shape evolution remain incomplete.

Ipomoea trifida, the wild sweetpotato, provides a unique model for studying the ecology and evolution of leaf shape. I. trifida maintains a leaf shape polymorphism, in which some individuals can grow lobed leaves while others only grow simple leaves. The overarching goal of this work is to describe the variation in leaf shape in I. trifida and determine if the presence of lobed leaves is heritable.

First, I describe the leaf shape variation in present USDA ARS-GRIN I. trifida germplasm qualitatively and quantitatively using image analysis to see if traditional leaf shape metrics, like solidity and circularity are sufficient descriptors of leaf shape. I next investigate the genetic basis of leaf shape using crosses and transcriptomics. A pilot dataset suggests that leaf shape is primarily determined by at least one Mendelian locus. I then use differential expression analyses to look for differences in gene regulation between leaf shapes. Finally, I propose that common garden experiments coupled with stress treatments, such as heat, be used to investigate the fitness and ecophysiological effects of leaf shape.

G-05
Dewlap color variation and visual grasp responses across populations in a neotropical lizard

Janelle Talavera, Binghamton University - SUNY
Thomas Powell, Binghamton University (SUNY)
Lindsey Swierk, Binghamton University

Abstract:

The processes and mechanisms that drive and maintain population and species divergence are not uniform and/or consistent across taxa. There is still more to be understood about how ecological factors can shape signals among populations, and furthermore, how those signals affect communication and genetic divergence. Male Anolis lizards have brightly colored dewlaps that are used for communication (i.e. mate choice and intrasexual interactions). Anolis aquaticus is a southern Costa Rican species that exhibits intraspecific variation, as populations' dewlaps vary in color from red to yellow. We hypothesize this variation in sexual signals relates to responsiveness to colorful signals among populations. We used visual modeling to simulate anole vision and model dewlap conspicuousness to the eyes of A. aquaticus and conducted visual grasp response trials as a proxy for interest in a signal. Additionally, we predict that yellow-site and red-site lizards are genetically diverged and that genetic structure can be explained by variation in dewlap color. We employed ddRADseq genotyping for each population. We found that (1) the yellow color component (y-mean) of a dewlap varies among populations, (2) red-site lizards had an overall preference for the yellow stimulus more than the control, and (3) yellow-site lizards did not have an overall preference for any stimulus. These results show that populations vary in their responsiveness to dewlap coloration.

G-06
Genetic architecture of woodiness traits in Mimulus

Rachel Kruger, Binghamton University
Jay Sobel, Binghamton University

Abstract:

Understanding what factors allow taxa to inhabit or become dominant in novel environments is important in studying speciation. According to Dollo's Law, once a complex trait is lost through evolution, it is unlikely to be resurrected in the same form. Angiosperms are generally accepted to be ancestrally woody, yet woodiness is a complex trait that repeatedly appears in otherwise herbaceous groups of taxa –especially insular populations of species. Within the genus Mimulus (Phrymaceae), a diverse group of mostly herbaceous plants native to the western United States and Mexico, herbaceous Mimulus species are conspicuously absent from chaparral landscapes. However, in one section of the genus, Diplacus (Bush Monkeyflowers), one herbaceous species (M. clevelandii) exists sister to a woody group of taxa (M. aurantiacus). The M. aurantiacus species complex is a dominant plant group in dry, chaparral communities. This with it showing a clear phenotypic difference in woodiness compared to everything else in the genus, might suggest that the evolution of secondary woodiness in Diplacus may have allowed them to occupy a novel niche in areas with more drought. This begs the questions: Is secondary woodiness in Diplacus adaptive? Does the evolution of secondary woodiness confer ecogeographic isolation between the taxa? To begin answering these questions, we are investigating the genetic basis of the shift from herbaceousness to woodiness by performing a quantitative trait locus (QTL) analysis on M. clevelandii and M. aurantiacus, looking for associated loci in traits such as stem diameter and break strength. By understanding the genetic architecture of this phenotype—whether it is controlled by few large-effect loci or several small-effect loci, and where in the genome thesy are—we can work to understand how the divergence between herbaceous and woody proceeded in the face of gene flow, and whether it may currently contribute to reproductive isolation.

G-07
Molecular evolution of the solute carrier 4 gene family in the Arthropoda

Joshua DeRuyter, University of Wisconsin-Madison

Abstract:

The SLC4 bicarbonate transporter gene family is found throughout the animal kingdom and plays a vital role in ion transport and pH regulation. This gene family includes the Na+/HCO3- cotransporters (NBC), the Na+-driven Cl-/ HCO3- exchangers (NDAE), and the Cl-/HCO3- anion exchangers (AE). SLC4 genes are known to play a role in human kidney function, but they are poorly understood in arthropods and other invertebrates. Despite their ubiquity, little is known about the evolutionary history of SLC4 genes within Arthropoda. Thus, this study seeks to (1) reconstruct the evolutionary history of the SLC4 gene family using a phylogenetic approach and to (2) analyze

patterns of molecular evolution across the phylum Arthropoda. To achieve these goals, DNA and amino acid sequences from ~100 arthropod species will be mined from genome databases and aligned. To determine the evolutionary history of the SLC4 gene family, a phylogenetic tree will be constructed using the mined sequences. Nucleotide sites and phylogenetic branches showing signatures of natural selection will be investigated using the HyPhy software package.

G-08
Lack of evidence for co-speciation in a sexually transmitted nematode and its dung beetle host species

Patrick Rohner, University of California San Diego

G-09
Predicting the Unpredictable: Ensemble Species Distribution Modeling Reveals Critical Refugia for selected Philippines' Charismatic Megafauna Under Climate Change

NIKKI HEHERSON DAGAMAC, UT Tyler

G-10
Quantifying Color Variation in a Polymorphic Tortoise Beetle Using Patternize

Kaizia Johnson, Boston University

Abstract:

Color polymorphisms provide a valuable framework for understanding how genetic variation produces phenotypic diversity and how diversity is maintained. The tortoise beetle, Chelymorpha alternans, exhibits five genetically determined color phenotypes: metallic, rufipennis, veraguensis, militaris-a, and militaris-b making it an ideal system for studying the relationship between genotype and phenotype. While previous studies have investigated the evolutionary mechanisms maintaining these phenotypes, including differential predation and mating patterns, a quantitative assessment of within-phenotype color variation remains limited, particularly as relates to developmental color changes. To address this gap, we used the R package patternize to analyze high quality images, combined with a carotenoid analysis to examine potential relationships between pigment abundance and observed color pattern differences for two phenotypes (metallic and rufipennis) over 4 developmental time points (24 hours, 72 hours, 2 weeks, and 3 weeks). Color pattern data was analyzed using PCA, heatmaps, and dendrogram clustering to identify major patterns of phenotypic variation. Quantitative image analyses revealed substantial color variation among individuals and developmental stages, with young beetles exhibiting greater concentrations of orange pigmentation across the elytra and mature beetles displaying increased red-brown coloration throughout the same area. A principal component analysis identified developmental

stage as a major source of phenotypic variation, with young and mature beetles forming distinct clusters. Analyses of carotenoid content revealed differences among developmental stages, with higher levels of carotenoids in beetles at two weeks. Observed relationships between carotenoid concentration and patternize visualizations suggest that pigment abundance, specifically beta-carotenne may contribute to observed color-pattern variation. This approach combines computational image analysis with pigment quantification to better understand phenotypic variation in tortoise beetles.

G-12
Genetic signatures of adaptation across chile pepper domestication

Hannah Scheppler, Ohio State University
Natalia Martínez-Ainsworth2, Centro de Investigaciones Interdisciplinarias en Ciencias y Humanidades
Jelmer Poelstra, Ohio State University
Vivian Bernau, Seed Savers Exchange
Jack McCoy, University of Illinois
Michael Kantar, University of Hawaii
Lev Jardón-Barbolla, UNAM
Kristin Mercer, Ohio State University
Leah McHale, Ohio State University

Abstract:

Within the expanding field of crop landscape genomics, the chile pepper (Capsicum annuum) stands out as a model system due to the diverse uses, cultivation practices, and domestication stages found across its native Mexico. In this study, we evaluate genetic variation in a comprehensive collection of wild, semiwild, and landrace samples representing wide geographic and environmental gradients across the country. Using 169,183 SNPs, we performed complementary environmental genome-wide associations (EGWA) and selective sweep analyses to identify putatively adaptive genomic regions associated with climate and edaphic variables. We identified 516 significant environmental associations distributed across all twelve chromosomes, with 52 SNPs associated with multiple variables. Furthermore, 12 putatively adaptive loci coincided with genomic signatures of selective sweeps. Incorporating insights from population structure and geography, chile peppers present a dynamic landscape of admixture that is likely affected by local adaptation. While some adaptive signatures progress linearly from wild to domesticated stages, others reflect stage-specific adaptations, including one potential case of convergent evolution. As climate change threatens Mexico's diverse ecologies, these findings highlight conservation concerns for native crop wild relatives and landraces, as well as semiwild peppers that house unique genetic diversity. Ultimately, the adaptive markers identified here serve as promising candidates for future functional validation and climate-resilient breeding efforts.

Poster Session 2

06/23/26: 6:00 PM - 8:30 PM

A-01

BioDivA Lab: a decentralized model for collaborative biodiversity science across borders

Luisa Maria Diele-Viegas, Michigan State University

Abstract:

The BioDivA Lab is a decentralized and collaborative research network designed to transform how biodiversity science is produced, shared, and applied. Rather than operating as a traditional centralized laboratory, BioDivA connects researchers across institutions, countries, and career stages to co-develop projects in ecology, evolution, and conservation. This structure enables the integration of diverse expertise and perspectives while promoting scientific inclusivity, training, and equitable participation in research. By leveraging distributed collaboration, BioDivA facilitates the development of projects that span ecological theory, conservation applications, and innovative methodological approaches, including ecological niche modeling and eco-physiological integration. Here, we present the conceptual framework of BioDivA, its ongoing research initiatives, and its role as a model for building more open, connected, and globally engaged biodiversity science.

A-02

The mechanism of sex ratio adjustment in fig-associated Parasitodiplogaster

Justin Van Goor, University of Missouri Columbia
Peter Thompson, Animal Parasitic Diseases Laboratory
Benjamin Rosenthal, USDA ARS
Eric Haag, University of Maryland College Park

Abstract:

Genetic sex determination (GSD) is widespread in nematodes, typically via XX/XO or XX/XY chromosomal systems. Rare cases of environmental or stochastic sex determination (ESD) occur (such as in Mermithidae and some species of Pristionchus). The fig-associated diplogastrid Parasitodiplogaster presents an intriguing challenge to this pattern: across even the smallest infrapopulations, adults display a strikingly consistent 2:1 female-to-male sex ratio. This level of precision is difficult to reconcile with simple Mendelian expectations under GSD and the small nematode mating populations that have been observed. Because analogous female-biased ratios occur in hymenopteran hosts under local mate competition, mediated by environmental influences on sex allocation, ESD deserved examination for its possible role. Here, we tested (and found wanting) ESD as an explanation. We first identified multiple contigs from a novel

Parasitodiplogaster genome assembly that are homologous to autosomal or sex chromosome regions of the close relative Allodiplogaster (Koerneria) pararmatus. We then mapped reads from pooled males and pooled females and found unambiguous evidence for an XX/XO sex chromosome system in Parasitodiplogaster. Its characteristic female bias does not therefore result from environmental sex determination. Instead, alternative mechanisms must act within a genetically determined sex framework. Potential explanations—many of which are documented in other nematodes—include non-Mendelian X-chromosome segregation, sex-biased fertilization processes, or differential survival either within the fig environment or during phoretic recruitment onto pollinating wasps. The remarkable reproducibility of the 2:1 ratio suggests the possibility of an active, developmentally regulated mechanism that disproportionately eliminates males. Consistent with this idea, we observe stomatal polyphenism in Parasitodiplogaster, paralleling facultative carnivory described in Pristionchus and Allodiplogaster. This suggests the hypothesis that eurystomatous or teratostomatous morphs maturing in, or emerging from, female wasps may actively consume excess males. To discriminate among these mechanisms, ongoing work is quantifying sex ratios at the dauer stage prior to recruitment.

A-03
Investigating a symbiotic association between a Scaphopod Mollusk and a Cnidarian

Abigail Montgomery, Loyola University Chicago
Tauana Cunha, Loyola University Chicago

Abstract:

An association between a tusk shell (scaphopod mollusk) and an anemone (cnidarian) was discovered on museum specimens collected in 1996 in the Pacific Ocean, on the west coast of Oregon. Two scaphopod species have been historically documented at this locality: Fissidentalium actiniophorum Shimek 1997, which has previously been found hosting anemones, and Fissidentalium erosum Shimek and Moreno, 1996, which has never been recorded in association with anemones. Morphological shell measurements of total shell length, arc length, arc, aperture width, and aperture height for 31 specimens were taken to determine the identity of our scaphopod species. The measurements are consistent with F. erosum, expanding the range of known scaphopods hosting a symbiotic relationship with a cnidarian. DNA extractions were performed using the Omega EZNA Mollusk DNA kit, with an additional step to alleviate the adverse effects of formalin fixation. Molecular barcoding of the COI gene, as well as a genomic library is being attempted for both the scaphopods and associated anemones to compare with published data from other localities.

Keywords: symbiosis, deep sea, Scaphopoda, Mollusca, Cnidaria, historical DNA, museum genomics

A-04
Reversion of ampicillin resistance in E. coli under elemental limitation

Gabriel Wegman, Loyola University Chicago
Caroline Turner, Loyola University Chicago

Abstract:

When antibiotic resistance is costly in the absence of antibiotic selection, resistant bacteria may evolve by reverting resistance mutations or compensating for the cost via beneficial mutations in other genes. In a clinical setting, reversion is the preferable outcome because the evolved bacteria can be treated again. We sought to test how the maintenance or loss of resistance is influenced by evolutionary environments. To do so, we made use of Escherichia coli populations that previously evolved under ampicillin selection and either carbon limitation or nitrogen limitation. In that experiment, the bacteria were less likely to survive antibiotic treatment under nitrogen limitation than under carbon limitation, suggesting that ampicillin treatment is a stronger selection pressure under nitrogen limitation. Next, we isolated ampicillin-resistant clones from four populations; two evolved under nitrogen limitation, and two evolved under carbon limitation. To test the effect of genetic background and elemental limitation on the maintenance of resistance, we propagated each of these clones for 28 days without antibiotic in both carbon- and nitrogen-limited environments. Regardless of elemental limitation during the second, non-antibiotic experiment, populations that originally evolved under carbon limitation were more likely to lose resistance than those originally evolved under nitrogen limitation. This pattern appear to have been driven by a higher availability of reversion mutations in the clones that originally evolved under carbon limitation.

A-05
Effective mentorship in evolutionary genetics training: Insights from the STEGG-INTERACT RaMP

Virginia Snodgrass Rangel, University of Houston
Zachary Baquet, University of Houston
Richard Meisel, University of Houston
Rebecca Zufall, University of Houston

A-06
Fitness landscape and spatial microbiome organization jointly shape competitive dynamics in a two-species lattice model

Ramanarayanan Kizhuttil, University of California

Abstract:

Host-microbiome interactions are increasingly recognized as key determinants of host fitness and evolutionary dynamics. While experimental tools such as metagenomics and spatial transcriptomics reveal that microbiomes are spatially structured, theoretical models explicitly coupling spatial microbiome organization to host cell competitive dynamics remain scarce. Here we develop a spatially explicit agent-based model on a two-dimensional lattice where two competing host cell types each harbor a compatible microbiome. Cell fitness is governed by a set of four values encoding the compatibility or incompatibility between each cell type and the microbe occupying its patch. Through simulations across thousands of random initial conditions and systematic parameter sweeps, we identify distinct dynamical regimes corresponding to competitive exclusion and coexistence. Coexistence manifests as a quasi-stationary distribution, sustained by microbes acting as spatially distributed favorable niches toward which cells assort over time, largely independent of initial conditions. A shuffle analysis reveals a critical timescale: when spatial microbiome organization is disrupted at a rate faster than the characteristic time for cells to assort to compatible niches, coexistence collapses. Importantly, in this model, competitive exclusion is the only outcome if microbes do not substantially influence host fitness. These results suggest that spatially structured host-microbe systems, in which microbes are significant determinants of host fitness, can promote the coexistence of competing species, and that this requires not only an appropriate fitness landscape but also that spatial microbiome organization is maintained over sufficiently long timescales.

A-07
A CURE for invasive species management along Virginia's Chesapeake Bay with community engaged science

Carrie Wu, University of Richmond

Abstract:

Learning in nature fosters belonging and community, key factors that help retain diversity in STEM. A well-structured field experience can not only inspire and prepare students for scientific careers through deep immersion in the subject matter, active learning, authentic scientific research practice, but also creates shared experiences and relationships that facilitate personal growth through the formation of peer networks and cohesive learning communities. For over 10 years, students in my introductory biology course have partnered with the Virginia Department of Conservation and Recreation (VA-DCR) to identify rare relic populations of a native wetland plant and help manage an aggressively invading cryptic sister species. In what has become a signature lab module, students spend a majority of the semester help document the spread of Phragmites, an aggressively invasive wetland plant in Eastern VA and much of North America. We collect tissue samples in the field, then conduct genetic analyses to determine whether the stands contain the relic native subspecies or the highly invasive introduced variety. During field trips, students are challenged to think about effective experimental design, and work in teams to develop sampling strategies based on readings from the scientific literature. Students extract DNA and perform PCR analyses. Results from each year's class immediately informs VA-DCR management strategies in

the Chesapeake Bay. End-of-semester evaluations consistently praise this type of Course Based Undergraduate Research Experience (CURE), with students excited that their research “actually matters” outside the classroom.

A-08
Phenotypic evidence of chemotaxis in evolved pseudomonas fluorescens populations.

Oluwabusola Asenuga, Clarkson University
Chimaroke Onyeaghala, Clarkson University
Susan Bailey, Clarkson University

Abstract:

Chemotaxis is a behavior that enables organisms to move toward favorable chemical stimuli and away from harmful conditions, thereby improving survival in structured environments. In a previous experimental evolution study, we evolved P. fluorescens in a structured heterogenous environment (experimental populations) and a homogenous environment (control populations). Whole-genome sequencing of the evolved populations revealed mutations in genes associated with chemotaxis suggesting potential for evolved changes in movement behavior.
In this study, I investigated whether those genomic changes corresponded to measurable phenotypic evidence of changes in chemotaxis. To do this, a chemotaxis assay was performed using agar plates with a central glucose patch as an attractant. I inoculated evolved Pseudomonas fluorescens samples 2 cm away from the center, and directional movement of the colony toward or away from the glucose patch was quantified after 24 hours, using ImageJ. Statistical comparisons were conducted using ANOVA models in R.
Results showed that the experimental populations exhibited stronger glucose-directed movement compared with the ancestral strain. In contrast, control populations showed a less consistent pattern, with smaller differences in directional movement. These findings suggest that adaptation in structured heterogeneous environments may promote the evolution of enhanced chemotactic behavior. Overall, this study highlights the role of structured environments in shaping microbial movement and adaptive evolution.

A-09
Trust your gut: effects of antibiotics on gut integrity and feeding behavior

Eleanor Rice, Louisiana State University
Victoria Coutts, Louisiana State University
Marquise Henry, Louisiana State University
Christine Lattin, Louisiana State University

Abstract:

Synergy between gut microbes and host immuno-endocrine signaling is essential for maintaining cellular, digestive, and metabolic homeostasis in animals. Disturbances to the gut’s microbial

community (dysbiosis) impair gastrointestinal functioning and may also alter cognition and behavior. However, it is currently poorly understood how microbial dysfunction of the gut influences feeding behavior and avoidance of novel foods (neophobia), especially in free-living wild species exposed to antibiotics in agricultural settings. We administered antibiotics to wild-caught house sparrows (Passer domesticus) held in the lab and compared their behavior and physiology to a control group that received no antibiotics. We used a novel trans-epithelial electrical resistance (TEER) gut permeability assay to investigate the effects of microbial disruption on the epithelial barrier of the duodenum. Our preliminary data show that there were no differences in gut tissue permeability between birds that received antibiotics and the control group, suggesting that house sparrows may be relatively resilient to the negative effects of antibiotics on the gastrointestinal tract. Our study contributes to the ever-expanding literature on the gut microbiome and its role in physiology and behavior.

A-10
Comparative mitogenome analysis of Procambarus crayfish species

Matthew Blow, University of Texas at Tyler
Matthew Greenwold, University of Texas at Tyler

Abstract:

Several species of Texas crayfish in the Procambarus genus are listed as Species of Greatest Conservation Need (SGCN) by the Texas Parks and Wildlife Department (TPWD). However, little is known of their genome content and genetic relationship, and a search of the National Center for Biotechnology Information (NCBI) database found only five full mitogenomes of Procambarus species. To our knowledge, a comparative analysis of these mitogenomes has not been performed. This study focuses on comparing the mitogenomes of four SGCN species, P. nigrocinctus, P. nechesae, P. texanus, and P. nueces, and six partially sympatric species (P. acutus, P. kensleyi, P. simulans, P. fayettei, P. dupratzi, P. clarkii) that we collected and assembled in Texas, in addition to the five species on NCBI. We will present on the phylogenetic relationship among these 12 Procambarus species and the outgroup species Faxonius (Orconectes) luteus including the evolutionary distance (dN-dS) for all thirteen protein coding genes. These data will help inform on SGCN crayfish in Texas, provide crucial data for the development of genetic conservation assays such as environmental DNA assays, and provide data for a state genetic database for crayfish.

A-11
When phenotypic disparity doesn't match the rate of evolution

Elizabeth Santos, Ohio State University
Ryan Felice, University College London
Kory Evans, Rice University

A-12
Use of ddRAD-sequencing to diagnose cryptic species with low interspecific mitochondrial divergence

Halle Summers, The Ohio State University
Loren Ammerman, Angelo State University

A-13
Cracking Cryptic Corals: Testing the Effectiveness of DNA Barcodes for Lineage Identification in Porites Corals

Olivia Quintin, Bridgewater State University
Caitlin Fisher-Reid, Bridgewater State University

Abstract:

Ocean warming continues to threaten coral reef ecosystems, necessitating improved tools for identifying and conserving resilient coral populations. Accurate species identification is critical for effective reef restoration. Yet many coral taxa, including the massive mounding Porites lobata, contain cryptic lineages that are visually indistinguishable but genetically distinct—complicating traditional morphology-based classification. Many whole genome sequencing methods have been developed for identification; however, these methods are expensive and time consuming. Isolating and amplifying individual genetic barcode loci has been proposed as an alternative method. By lowering financial and technical barriers, genetic screening becomes accessible to a broader range of laboratories and conservation programs. This study evaluates the effectiveness of multiple DNA barcode markers for identification of Porites lobata corals. I compared the efficacy of several commonly used mitochondrial (COI) and nuclear (ITS and H2) barcoding genes in their ability to resolve genetic variation among previously identified cryptic lineages of Porites lobata. My results demonstrate that while certain barcodes provide higher resolution of these lineages than others, no single marker consistently distinguishes between closely related lineages and species—supporting a multi-marker approach. This study highlights the persistent challenge of defining species boundaries in corals Further work to strengthen the connection between affordable molecular identification and in situ reef restoration will enhance the selection of resilient genotypes, ultimately supporting more effective conservation strategies in the face of rapid environmental change.

A-14
A holobiont approach to sustainable viticulture

Ashley Itogawa, Northern Arizona University- Pathogen and Microbiome Institute

A-15
Flower size evolution in Caryophyllaceae

Chamali Harshanie Samarathunga Appuhamillage, Ohio University
Riley Rees, Indiana University
Andrea Appleton, Harvard University
John Schenk, Ohio University

Abstract:

As the reproductive organs of angiosperms, flowers are subjected to strong selective pressures, shaping their form and function. This process results in exceptionally diverse flora forms, including size, shape, and structural components, including the evolution of novel structures, such as nectaries, spurs, and staminodes. Staminodes are stamens that have lost the ability to produce viable pollens and are classified into three types based on function and evolutionary history: vestigial, fodder, and co-opted staminodes. Vestigial staminodes no longer generate viable pollens and reside in flowers as a rudiment, but the lack of research on vestigial staminodes have left us with no understanding of why they evolved. I hypothesized that the reduction of flower size associated with resources limited environments drives the evolution of vestigial staminodes. I tested my hypothesis in Caryophyllaceae. Herbarium specimens were used to record morphological data, such as sepal, staminode, and stamen number, position, and length. Sepal length was used as a proxy for flower size. A previously reconstructed time calibrated phylogenetic tree based on molecular variation was used to account for shared evolutionary history among traits. A phylogenetic ANOVA was conducted to evaluate differences in floral size among staminode conditions (absent, vestigial, and petal-like), incorporating phylogenetic structure and to evaluate the differences in floral size among flowers based on the species tree. The three staminode conditions were significantly different in flower sizes (P-value = 0.001, F-value = 4.99). Flowers with vestigial staminodes have significantly smaller flower size than flowers with petal-like structures or flowers without any staminodes, supporting the hypothesis that flower size evolution is driving the evolution of vestigial staminodes. We conclude that selection for smaller flowers drives evolutionary novelty in floral forms through the evolution of vestigial staminodes and the reduction in the number of parts in a flower.

A-16
Age-rate scaling in evolution is largely artifactual

Brian O'Meara, University of Tennessee
Jeremy Beaulieu, University of Arkansas

A-17
Choices that matter: the impact of substitution models on machine learning-based species delimitation inference

Matheus Salles, Universidade Federal do Paraná
Fabricius Domingos, Universidade Federal do Paraná

Abstract:

The choice of nucleotide substitution models is fundamental to phylogenetic inference, shaping estimates of evolutionary parameters and, consequently, downstream demographic and species delimitation analyses. As machine learning approaches are increasingly used to address these problems, it remains unclear how the substitution model used during training affects classifier performance when applied to empirical datasets, which often exhibit substantial genomic heterogeneity. We addressed this question using a controlled simulation framework to assess the impact of substitution-model misspecification on supervised inference. Multiple classifiers were trained on data simulated under three commonly used models (JC69, HKY, and GTR) and evaluated on test datasets combining multiple substitution processes across loci, thereby mimicking realistic genomic heterogeneity. Classifiers trained under a single model generalized well to mixed-model data, consistently recovering the correct demographic scenario with high posterior probability (mean > 0.86 with as few as 100 SNPs), with performance plateauing around 600-800 SNPs. Accuracy differences among training models were minimal, indicating that the demographic signal captured by the site frequency spectrum outweighs substitution-model artifacts under the conditions tested. However, this robustness is context-dependent. More complex evolutionary scenarios, such as deep divergences, strong among-site rate variation, or protein-coding data, may reduce classifier performance. Moreover, robust model selection does not guarantee accurate parameter estimation, as branch lengths and evolutionary rates remain sensitive to model misspecification. Overall, our results show that computationally efficient training under simple substitution models can be sufficient for many species delimitation applications, provided analyses are accompanied by careful validation and model adequacy assessment. More broadly, these findings offer a practical path for integrating phylogenetic modeling with machine learning while maintaining a balance between computational efficiency and biological realism.

A-18
A Framework for Assessing Effects of Temperature on Brown Dog Ticks' (Rhipicephalus sanguineus s.l.) Fitness and Vector Competence

Anna Kang, Northern Arizona University
Amanda Carter, Biological Sciences at Northern Arizona University
Joseph D Busch, Northern Arizona University
Kelly Speer, Northern Arizona University

Abstract:

Tick-borne diseases (TBDs) cause over 450,000 human cases and $19 billion in U.S. agricultural losses annually. Climate change accelerates these threats by altering the geographic range and vector competence of ectothermic vectors. Rhipicephalus sanguineus s.l. (i.e., brown dog tick) includes "temperate" and "tropical" lineages with distinct thermal niches. Recently found living sympatrically in Arizona, these lineages offer a unique system to test competing ecological models: the Climate Variability Hypothesis (predicting higher temperate lineage resilience) and the Stress-Gradient Hypothesis (predicting microbiome-mediated stress resilience). This research investigates how temperature drives genetic, microbial, and physiological changes that shape vector fitness.

Objective 1 : Use RAD-seq and mitochondrial (12S/16S) sequencing on estimated 200 ticks sampled from animal shelters, humane societies, and animal control offices to quantify genetic differentiation, reconstruct phylogenies, and evaluate how possible hybridization impacts thermal phenotypes.

Objective 2: Assess physiological and microbial plasticity of ticks by accolimating them to three diurnally fluctuating temperatures (11°C, 22°C, and 31°C) for 3 days. Mass-specific metabolic rates will be quantified via closed-flow respirometry and analyzed using a two-way ANOVA. Concurrently, 16S rRNA sequencing will map microbiome changes. PERMANOVA and Random Forest algorithms will evaluate microbial beta diversity, while Redundancy Analysis (RDA) will link specific genomic SNPs to metabolic and microbial profiles.

This research will help bridge the gap between genetic composition, microbiome analysis, and associated physiological factors to engage in a novel, multi-disciplinary method investigating vector competence. This will not only enable us to understand temperature shift impacts in tick physiology, but also serve as a foundational step to predict how environmental change will impact TBDs and inform future management practices in identifying and controlling disease spread.

A-19
Teaching transcriptomic GOterm enrichment in the classroom

Jennifer Blake-Mahmud, Hope College

Abstract:

Teaching across levels of biological organization can be a challenge as both tiny and large scales stretch student's knowledge and challenge relatability. Here we present a lab activity designed to introduce students to the world of transcriptomics. This computer-based lab uses real transcriptomic data to help students explore sex-based or tissue-based differences in gene expression. Pilot sequence data from native striped maple Acer pensylvancium trees were sequenced from samples collected and extracted by undergraduates. Initial stages of DESeq analysis and GO enrichment were performed. In this lab, students conduct the final steps of GOterm exploration investigating a comparison of their choosing. Multiple comparisons are possible, including differences within a sex between tissue types (e.g. male and female leaves) or

within a tissue type between sexes (e.g. male to female flowers). The lab is designed for 2nd through 4th year undergraduate students, many of whom will have rudimentary understandings of genetics. The lab introduces how sequencing works and the rationale for using RNA vs DNA to answer certain types of questions. We develop an analogy for gene ontology in preparation for their own GOterm exploration, which they perform using online visualizer software, Revigo. The lab has been piloted twice in an upper level undergraduate course on the ecology and evolution of sex and reproduction. It is designed to take 2-3 hours, including the introductory lecture. The lab requires computers for student use (two students per computer is adequate) and an internet connection.

A-20
The Genetic Architecture of the Northern Swordtail Nuchal Hump

Maia Jackson, Louisiana State University
Daniel Powell, Louisiana State University

Abstract:

Northern Swordtail fish (genus: Xiphophorus) are a model system known for their wide range of sexual ornaments and unique behavioral ecology. They are also a powerful system for addressing fundamental questions in evolutionary biology like “How species remain separate amid gene flow?”. The closely related sister species Xiphophorus malinche and Xiphophorus birchmanni are a particularly good example, with the extent of gene flow between them varying greatly across several independent hybrid zones. Variation in sexual ornaments across the two species may promote or inhibit hybridization between them, making investigating the genetic makeup of these traits critical to understanding the evolution of reproductive barriers.

The falling costs of whole genome sequencing has increased the power of techniques like quantitative loci mapping to uncover the genetic basis of traits that may be important for reproductive isolation between species. Because of this, we have a robust understanding of the genetic underpinnings of some ornaments in Xiphophorus like the famous sword fin extension and the male mimicry trait, the false gravid spot. However, the nuchal humpwhich can be found on the necks of some male X. birchmanni and X. malinche x X. birchmanni hybrids, is largely understudied allowing us a unique to assess if the nuchal hump also influences reproductive isolation. We are using a classical QTL mapping to identify genomic regions in the Xiphophorus genome that underlie nuchal hump variation. We expect there to be multiple regions associated with the trait–though environment is likely to play a role as well as shown in X. multilineatus. These results will inform future studies aimed at describing the nuchal hump’s genetic makeup, morphology, and its impact on sexual selection, as well as hybridization in these species.

A-21
Bacterial microbiome analysis of parasitic Epicephala moths (Lepidoptera: Gracillariidae: Epicephala) found in Texas, Louisiana and Oklahoma

Samantha Ronalds, James Madison University

Sarai Badillo, University of Texas Permian Basin
Maria Tocora Alonso, Texas Tech University
Athenia Oldham, University of Texas Permian Basin
David Hembry, James Madison University

A-22
Body size evolution in Caenorhabditis nematodes

Gavin Woodruff, University of Oklahoma

Abstract:

Body size and shape are intimately tied to an organism's way of life. As body shapes vary dramatically across phylogeny, biology aims to understand the proximate and ultimate causes of morphological divergence. Caenorhabditis nematodes exhibit variation in body size and shape. C. elegans is a long-standing model genetic system, and C. inopinata is its sister species with a highly-elongated body. Our lab aims to harness the experimental toolkit of C. elegans to understand the evolution of body shape in C. inopinata. Here, we describe ongoing projects aimed at understanding how and why C. inopinata has a divergent body shape:

• The nematode cuticle is critical for regulating body morphology in nematodes, and collagens represent highly abundant constituents of this structure. We found C. inopinata collagen genes are highly differentially expressed across postembryonic development in comparison to C. elegans. Moreover, C. inopinata has more collagen-encoding genes than any other species in the Caenorhabditis genus. We are perturbing collagen genes to understand how the evolution of collagen gene copy number and expression influences the evolution of body shape.

• rnt-1 encodes a RUNX transcription factor whose homologs regulate developmental processes across animal phylogeny. We found that while rnt-1 regulates both length and width in C. elegans, it only regulates length in C. inopinata. This functional evolution suggests potential divergence in the gene regulatory networks underlying body dimensions, which may contribute to the evolution of divergent length:width ratios.

• We are currently mapping a phenotypic body size mutant in C. inopinata generated via mutagenesis.

• C. inopinata develops slowly. Metabolic genes reveal differential expression in C. inopinata. And, a previous report suggests striking mitochondrial sequence divergence in C. inopinata. We are exploring the relationship between metabolism, developmental timing, and body size evolution in this species.

This work is supported by an NSF award (#2238788).

A-23
Unraveling the map turtle complex (Emydidae, Graptemys) in the southeastern U.S biodiversity hotspot

Karina Moreno, University of Hawaii at Manoa

Abstract:

High rates of diversification are observed to occur within biodiversity hotspots, making these key study regions for investigating drivers of species diversity. However, the rapid radiation of species within these hotspots can pose challenges for investigating their evolutionary histories. Incomplete coalescence and hybridization can obscure species boundaries and result in phylogenetic discordance that misrepresents the true species diversity. This raises a series of foundational questions, including how species boundaries are maintained in the presence of gene flow, how gene flow may contribute to or even drive divergence, and how to achieve conservation in the face of uncertain or porous boundaries among species. The map turtles, Graptemys, are a clade of river endemics that form a central component of the global biodiversity hotspot for turtles in the southeast of North America. The clade has allopatrically radiated into at least fifteen lineages within the last 1.5 million years. Despite prior molecular and morphological studies that have examined the evolutionary relationships among Graptemys lineages, their species boundaries remain poorly understood. The objectives for this study are to resolve the species boundaries, patterns of gene flow, and investigate processes of diversification within Graptemys. Genomic data was obtained for 144 specimens encompassing the geographic ranges of all described species. I used a combination of phylogenetic, network coalescent, and population genomic tests to resolve the evolutionary relationships among lineages and investigate introgressive hybridization in this clade.

A-24
The Adaptation to Acidic Environments Potentiates Pathogenicity in Bacteria

Wei-Chin Ho, University of Texas at Tyler

Abstract:

Microbes adapt to altering environmental stress with molecular and phenotypic changes favored by natural selection. For example, acidic stress appears in various natural and anthropogenic contexts. However, the rate, trade-offs, and genetic mechanisms of adaptation under persistent acidic stress remains poorly understood. More importantly, whether the adaptive results can alter the opportunity of host infection or difficulty of host treatment remains largely unexplored. To address these questions, we experimentally evolved Escherichia coli to acidic stress as a model system. Specifically, we propagated 12 replicate populations of E. coli for ~1,900 generations in Luria-Bertani media with two pH values (acidic: 4.5; neutral: 7.0) with daily transfers and shaking at 37°C. The evolved populations in the acidic environment adapted rapidly, sustaining a significant improvement in competitive fitness by (55.8 ± 7.3 %), while no significant difference was found in the neutral environment (-0.9 ± 1.5 %). Whole-metagenomic sequencing of evolved populations revealed nonsynonymous and structural mutations enriched in the genes underlying transcription and translation machineries or the enzymatic ability of dephosphorylation. Strikingly, adaptation in

the acidic environment uniquely resulted in the emergence of population-level biofilm formation and collateral resistance to translation-targeting antibiotics. Together, our results demonstrate that environments can strongly shape the speed of microbial adaptation and reveal how pathogenicity can evolve as a byproduct of new adaptation to stressful environments.

A-25

Evolutionary and ecological contributions to the honeypot ant gut microbiome.

Faith Hill, Rutgers University
Lily Khadempour, Rutgers University-Newark

Abstract:

Insects can acquire microbial symbionts through vertical, horizontal, or environmental transmission. These symbionts have the potential to aid their hosts in nutrition, pathogen resistance, and host survival. North American Honeypot Ants, Myrmecocystus spp., are ecologically dominant and their unique life histories make them interesting study systems for understanding microbial assembly. My proposed research investigates the relative contributions of ecological interactions and evolutionary history in the establishment of the Myrmecocystus gut microbiome. To understand how evolutionary history impacts the gut microbiome, I will quantify vertical transmission between unmated queens and colony members and assess phylosymbiosis in Myrmecocystus. By overlaying microbial community composition with previously compiled phylogenies, we can assess if gut microbiomes have coevolved with their hosts. To evaluate dietary transmission of microbes, I will sequence the microbiomes of Myrmecocystus' primary food sources, namely hemipteran honeydew and floral nectar, and compare them to Myrmecocystus gut microbiota. Then, using GFP transformed strains of Fructilactobacillus, I will conduct colonization assays to visually document how microbes from floral nectar move between Myrmecocystus colony members. In accordance with current literature on the microbiomes of honeydew feeding ants, I expect environmental signals and diet to contribute more to gut microbe composition than evolutionary history. My multi-layered approach will provide insight into the eco-evolutionary dynamics that drive Myrmecocystus' microbial assemblage.

A-26

Comprehensive Bayesian methods for analyzing marginal epistasis for sites, genes, pathways, and chromosomes

Fahimeh Rahimi, University of Florida
Juannan Zhou, University of Florida

Abstract:

A major challenge in understanding sequence–function relationships in evolution is the widespread presence of epistasis, where the effect of a mutation depends on genetic background. Here, we

present a family of interpretable and scalable methods to characterize the structure of epistasis across multiple biological scales.

Our framework summarizes epistasis at three hierarchical levels: (1) the propensity of individual loci to participate in interactions; (2) background-averaged interaction strengths between alleles or variants within genes; and (3) interactions among large-scale genomic features, including genes and chromosomes. Together, these provide a unified view of epistatic structure in complex genotype–phenotype maps.

We implement these methods using Gaussian process regression, projecting the inferred genotype–phenotype landscape onto orthogonal subspaces to quantify variance components associated with different orders and scales of interaction. By leveraging kernel-based representations, our approach scales with the size of the observed data, enabling analysis of large genotype spaces. We also estimate prediction uncertainty using both bootstrap-based and analytical approximations.

We apply our framework to high-throughput datasets for the AAV2 capsid protein and the SH3 domain of GRB2, and further perform genome-wide analyses of a yeast dataset comprising ~100,000 genotypes across >40,000 sites. These analyses reveal patterns of marginal epistasis at the level of SNPs, genes, and pathways, and identify interactions between gene pathways and chromosomes.

These results provide insight into how epistasis is structured across biological scales and how genetic interactions can constrain and shape evolutionary trajectories in complex genotype–phenotype landscapes.

A-27
The convergent evolution of olfactory acuity in fossorial squamates

Connor O'Boyle, Independent
Jonathan Sargent, Field Museum of Natural History
Renzo Gravito Camacho, Universidad Nacional de Colombia
Logan Ekstein, South Dakota School of Mines and Technology
Rebecca Fish, South Dakota School of Mines and Technology
Denver Suyom, University of the Philippines
Michael Stevens, Independent
Rachel Wolther, Independent
Eric Ames, Independent
Taylor Muir, Arizona State University
Cristopher Harrison, Florida International University
Graeme Gobey, Independent
Matthew Barthelotti, Independent
Miles Thomas, Independent
Arion Chao, Friedrich-Alexander University of Erlangen-Nuremberg
Nicholas Paiva, Independent
Arkanniti Adisajjana, Independent
Mitchell Bergquist, Independent
Alden Rivadavia, University of the East Ramon Magsaysay

Leon Fu, School of Visual Arts
Krista Koeller, University of Vermont

Abstract:

The elongate, limbless body plan has convergently evolved in squamates numerous times and is associated with a number of traits that are thought to be adaptations to a fossorial lifestyle. These include reduced or absent ear openings, reduced lower jaws, and reduced eyes, which reduce the animal's capacity to see and hear. However, limbless squamates are almost universally solitary predators and must use some long-distance sensory information to find prey and mates. We hypothesized that fossorial squamates rely on olfactory signals and have greater olfactory acuity than non-fossorial squamates. For this study we used computed tomography-derived digital brain endocasts to compare the relative olfactory bulb sizes of fossorial and non-fossorial squamates. We found that non-fossorial squamates have a range of olfactory bulb sizes and fossorial squamates only have relatively large ones. We also found that fossil amphisbaenians had smaller relative olfactory bulbs than their extant relatives, suggesting an improvement in olfactory acuity throughout the evolution of the lineage. This study suggests that a sense of smell may be beneficial to some surface-dwellers but poor olfactory capabilities are incompatible with a fossorial lifestyle.

A-28
Genome structure and adaptive evolution drive venom diversification in Leptodeira

Collins Awiaga, Florida State University

Abstract:

Understanding how genome architecture and natural selection shape complex adaptive traits remains a central question in evolutionary biology. Venom systems, characterized by rapidly evolving toxin gene families, provide a powerful model for studying this interplay. Here, we investigate how chromosome-scale genome organization and selection pressures drive venom diversification in the Neotropical cat-eyed snake genus Leptodeira.

We generated a chromosome-level genome assembly using Hi-C scaffolding, resolving macro- and microchromosomes and identifying the Z sex chromosome through conserved synteny with Thamnophis elegans. Genome-wide mapping of venom-associated genes revealed a non-random organization, with toxin gene families clustered within specific chromosomal regions. Phylogenomic analyses across multiple Leptodeira species and the outgroup Imantodes cenchoa provide a framework for comparative toxin evolution.

To investigate selective pressures on venom genes, we analyzed 15 toxin-associated orthogroups. Copy number variation revealed substantial lineage-specific expansion, with orthogroup OG0000007 showing pronounced increases in Leptodeira relative to the outgroup. This orthogroup exhibits strong signatures of positive selection and is associated with snake venom metalloproteinases (SVMPs), a key functional class involved in prey immobilization and tissue

degradation. Species-level comparisons further reveal differential expansion and sequence diversification, suggesting lineage-specific adaptive evolution.

These results demonstrate that venom diversification in Leptodeira is driven by the interaction between chromosome-scale genome organization, gene family expansion, and strong positive selection, with SVMPs emerging as a key axis of functional diversification.

B-01
Temporal Trends in Wing Morphology and Fluctuating Asymmetry in Painted Lady Butterflies in Response to Climatic Variation

Kayleen Sugianto, Oklahoma State University
Fabio Machado, Oklahoma State University

Abstract:

Environmental change is rapidly affecting life on Earth. Species may avoid local extinction if they can adapt morphologically, physiologically, or behaviorally to new conditions, but whether species can adapt fast enough is uncertain. Understanding these limits is essential for conservation efforts and species resilience. The painted lady butterfly, Vanessa cardui, is an ideal model for studying climate change effects because it is globally distributed and occupies diverse environments. Preliminary data from our lab show morphological change over the past century in western U.S. populations, likely in response to rising temperatures, raising the question of how much additional change this species can endure. For the study, I use museum specimens across the U.S. and measure fluctuating asymmetry in wing size and coloration patterns that may indicate adaptation to climatic change. I then gauge how much of these conditions disrupt developmental pathways and potentially constrain further adaptation. Predictions include smaller body and wing sizes along with darker wing pigmentation for specimens acquired from warmer habitats. Future steps would include conducting of common-garden experiments and laboratory work for further understanding of changes. Examining the evolutionary responses of butterflies to environmental change can enrich broader research on other species and ecosystems, deepening understandings of how organisms navigate shifting conditions and guiding conservation strategies.

B-02
Evolutionary dynamics of chronic lymphocytic leukemia (CLL) in a patch-structured model

Sydney Ackermann, University of California San Diego
Dominik Wodarz, UC San Diego

Abstract:

Chronic lymphocytic leukemia (CLL) is the most common adult leukemia in the Western world, characterized by the accumulation of malignant B cells in the blood, lymph nodes, and bone marrow. BTK inhibitors such as ibrutinib have transformed CLL management, inducing durable

responses in many patients. However, drug-resistant mutants inevitably arise, eventually driving relapse. A critical and unanswered clinical question is: for how long can a given BTK inhibitor control the disease before resistance-driven relapse occurs? Here we develop mathematical models grounded in evolutionary biology to address these questions. Previous models of CLL evolution assumed perfectly mixed cell populations. Yet, CLL grows across multiple lymph nodes and the spleen, connected by blood, i.e. it is characterized by a patch-like population structure. A new mathematical model of CLL evolution is developed that takes into account this population structure. According to this model, tumor cells can initially expand into available space within lymph nodes of normal size. As nodes fill up, further growth requires physical remodeling of the tissue microenvironment, mediated by stromal cells such as fibroblasts. To capture this we model demes with expanding carrying capacities connected by migration. When drug-resistant mutants are incorporated using stochastic modeling, a striking finding emerges: in the model with lymph node structure, the expected number of resistant mutants at any given tumor burden is substantially larger than predicted by exponential, well-mixed models that have so far been used to model CLL evolution. In other words, the population structure particular to CLL has substantial effects on evolutionary dynamics. This has important implications for understanding the emergence of drug resistance and time to resistance-induced relapse in CLL patients.

B-03
Cloning of Na+/ H+ antiporter paralogs involved with rapid freshwater adaptation in the Eurytemora affinis species complex

Teresa Popp, The Ohio State University
Carol Lee, University of Wisconsin
Peter Piermarini, The Ohio State Univeristy

Abstract:

Global salinity change is reshaping aquatic habitats and imposing strong selection on organisms inhabiting these environments. In particular, high latitude coastal environments are experiencing rapid salinity decline due to increased precipitation and melting glaciers. Repeated saline-to-freshwater invasions in the copepod Eurytemora affinis species complex provide a powerful system for studying the molecular basis of physiological adaptation to salinity decline. Previous work has identified ion transporter genes as repeated targets of natural selection during salinity change, including two paralogs of the Na+/H+ antiporter (NHA) family, NHA-5 and NHA-7. Orthologs of these putative sodium transporters have been described only recently in animals and their functions are poorly characterized. Here, we focus on the cloning of NHA-5 and NHA-7 cDNAs from E. carolleeae (Atlantic clade of the E. affinis complex). We found evidence of alternative splicing in both paralogs, suggesting that a broad diversity of transcripts may contribute to functional differences among NHA paralogs during salinity adaptation. We also cloned NHA-5 cDNAs from both saltwater (SW) and freshwater (FW) populations. Ongoing work is aimed at characterizing the respective functional properties of the FW and SW alleles of NHA-5 and NHA-7. Together, these findings will shed light on

how both allelic divergence and alternative splicing in NHA paralogs contribute to repeated adaptation during habitat salinity decline in E. affinis complex populations.

B-04
An optimized DNA extraction method for museum microbiomics

Erin Larson, Northern Arizona University
Ashley Itogawa, Northern Arizona University- Pathogen and Microbiome Institute
Teagan Mulford, Northern Arizona University
Grey Gustafson, Northern Arizona University
Kelly Speer, Northern Arizona University

Abstract:

Natural history collections have recently come into focus as an important tool for understanding microbial associations, expanding the value of specimens housed in these collections. However, most natural history specimens were preserved in ways that damage nucleic acids, requiring the development of specialized protocols to extract DNA and RNA. We present an optimized DNA extraction protocol that enables downstream sequencing of the bacterial microbiome associated with arthropods in the Northern Arizona Arthropod Collection. We compared two extraction methods: a ZymoBIOMICS Microprep DNA kit extraction, an industry standard for gut microbiome extractions, and an in-house Phenol:Chloroform protocol, designed to retain as much fragmented DNA as possible. We found that, although the Phenol:Chloroform extraction resulted in higher DNA concentration and longer DNA fragments, Kit-extracted DNA was more consistent, typically yielding higher concentration DNA and long, pure DNA. Based on this dataset, the ZymoBIOMICS Microprep DNA kit extraction protocol provides usable DNA for downstream microbiome analysis without the safety concerns of Phenol:Chloroform extractions. Our findings are a valuable first step in enabling museum specimens to be used in microbiome research.

B-05
Evolution of the most frequently detected H1 subtype swine influenza A virus (1A.3.3.3) in the United States

Isabel Novick, US Department of Agriculture
Carl Hutter, US Department of Agriculture
David Hufnagel, Centers for Disease Control and Prevention
Celeste Snyder, US Department of Agriculture
Kelly Hewitt,
Michael Zeller, Iowa State University
Amy Baker, USDA-ARS
Tavis Anderson, USDA-ARS

Abstract:

Influenza A virus (IAV) is one of the most prevalent respiratory viruses in swine with noted zoonotic (animal-to-human transmission) potential. The H1 subtype represents approximately two thirds of

detected IAV cases in swine. Within H1, there are 16 different groups of viruses classified by genetic diversity and phylogenetic topology of the hemagglutinin (HA) surface protein gene. Of the 16 groups, the 1A.3.3.3 genetic clade has been the most frequently detected every year since 2010 (20-30% of detections) and has been associated with multiple swine-to-human transmission events. We hypothesized that genetic diversification and selection on the HA gene have resulted in phenotypic change of these swine viruses. This may increase the probability of transmission in pigs and the emergence of strains that have zoonotic potential. To address this, all available IAV HA nucleotide sequences collected within the USDA IAV swine surveillance system from the 1A.3.3.3 clade were downloaded from the Bacterial and Viral Bioinformatics Resource Center and merged with reported zoonotic cases. These data include 4,560 HA genes collected 1999-2026 from 34 US states. We inferred a maximum likelihood phylogenetic tree and identified statistically supported groups within the 1A.3.3.3 clade. Bayesian phylodynamic analyses of each group revealed unique evolutionary trajectories, including clade-specific estimated substitution rates, signals of selection pressure, and protein structures. A randomly sampled set of sequences from each 1A.3.3.3 clade demonstrated evidence for greater diversifying selection on sites in dominant immune-recognized regions, but these sites varied between groups. Future analyses will assess whether diversification and selection within swine 1A.3.3.3 clades increase adaptive evolutionary potential and reduce vaccine efficiency against circulating viruses, affecting both animal and public health.

B-06

Sarah Roderick, University of Pennsylvania

B-07

Exploring genetic diversity and population structure of hemlock woolly adelgid throughout the eastern North American invasive range

Grace Forthaus, Grand Valley State University
Nathan Havill, USDA Forest Service
Charlyn Partridge, Grand Valley State University

Abstract:

Eastern hemlocks (Tsuga canadensis) are a foundation species in eastern North American forests and are crucial for water quality and ecosystem stability. However, they are under threat from the invasive hemlock woolly adelgid (HWA, Adelges tsugae), an insect responsible for widespread tree mortality. Despite the devastating impact of invasive species, the genetic mechanisms driving their rapid range expansion and adaptation remain poorly understood. Our research uses low-coverage whole genome sequencing (lcWGS) to analyze the genetic structure and genetic diversity of HWA throughout its invasive range in eastern North America. We have found that despite the large geographic distribution of invasive HWA, ranging from Georgia to Nova Scotia and westward into Michigan, there is limited genetic differentiation among these populations. Currently, these data support the hypothesis that HWA was only introduced once to eastern North America and has since rapidly dispersed via clonal reproduction. By using advanced molecular approaches, we will

increase our understanding of the population dynamics of this invasive pest, while also expanding our knowledge of how invasive populations with low genetic diversity are able to invade new habitats.

B-08
Global patterns of avian myrmecophagy: a phylogenetic perspective on ant- and termite-eating birds

Gustavo Martins, Louisiana State University
Gregory Thom, Louisiana State University

B-09
The effects of demography on genomic heterogeneity in Neotropical antbirds (Aves: Thamnophilidae)

Kristen Wacker, Louisiana State University Museum of Natural Science
Brian Smith, American Museum of Natural History
Camila Ribas, National Institute for Amazon Research
Gustavo Bravo, Harvard University
Gregory Thom, Louisiana State University

Abstract:

Avian genomes are comprised of chromosomes of markedly different sizes that have vastly different recombination rates and gene density. This variation subsequently impacts the dynamics of linked selection on individual chromosomes, yielding a heterogeneous distribution of numerous genetic features (e.g., heterozygous sites and repetitive elements) across the genome. However, chromosomes are nested within species, which themselves have highly variable effective population sizes (Ne) that shape the overall dynamics of drift versus linked selection in their genomes. Here, we characterize the landscape of genomic heterogeneity in birds and investigate how it is shaped by demography using 18 de novo reference genome assemblies from the Neotropical antbird family Thamnophilidae. Specifically, we combine demographic modeling (PSMC) and comparative genomic analyses to evaluate how species-level Ne affects variation in heterozygosity, selection, and the distribution of transposable elements across chromosomes, while controlling for phylogenetic non-independence. This work sheds light on the relationship between demography, linked selection, and genomic architecture across oner ecently diverged clade of birds.

B-10
Repeated evolution of wing dimorphism in Gryllus Crickets: Testing for shared genetic architecture across independent origins

patrick nshizirungu, University of Nebraska Lincoln

Abstract:

Wing dimorphism in North American Gryllus crickets is a model threshold trait in which long-winged (LW) and short-winged (SW) morphs co-occur as alternative life-history strategies shaped by multigenic and environmental variation. Ancestral state reconstruction suggests wing dimorphism has independently evolved from SW monomorphic ancestors multiple times, raising a fundamental question: do these independent origins share a common genetic basis, or did each lineage recruit distinct mechanisms to produce the same dimorphic phenotype?

To address this, I am using Bulk Segregant Analysis (BSA) across four wing-dimorphic Gryllus species. Outbred families are ranked by proportion of LW offspring as a proxy for parental liability;the continuous variable determining morph outcome under the threshold model. DNA from parents at the liability extremes is pooled and sequenced at ~50× coverage; regions of high allelic differentiation (FST) between pools identify candidate loci for morph determination. Cross-species synteny analysis will then test whether differentiated regions are shared across independent origins or represent distinct evolutionary solutions.

Executing this comparative framework requires species-specific reference genomes for read mapping and synteny inference. I have completed de novo assembly and validation of G. rubens: 1.86 Gb across 1,012 gap-free contigs (N50 = 9 Mb, BUSCO = 98.7%), with annotation in progress. This joins completed assemblies for G. lineaticeps and the published G. longicercus genome, establishing the reference infrastructure for cross-species comparison.

Beyond morph-associated loci, I will test for molecular signatures of relaxed selection in SW monomorphic Gryllus lineages, examining whether flight-related and juvenile hormone pathway genes show accelerated evolution following permanent loss of the LW morph. This directly links genomic architecture to the macroevolutionary dynamics of flight loss across the radiation, advancing understanding of how multigenic threshold traits are maintained, gained, or lost during species diversification.

B-11

Variability of life history traits in hybridizing field crickets as temporal reproductive isolating mechanisms

Addison Bert, Juniata College
Ryan Branton, Juniata College
Hannah Eckert, University of Denver
Alyson Emery, University of Denver
Celeste Flores, Juniata College
Katie Hackman, Juniata College
Mae Haussman, Juniata College
Isaac Hudson Foy, University of Denver
Lauren Mahkovic, Juniata College
Samuel McCammon, Juniata College
Bella Rose, Juniata College
Ken Sorokie, Juniata College

Erica Larson, University of Denver
Thomas Firneno, Juniata College

Abstract:

The alterations of climate change across the world are unprecedented in both the amount and rate of change. These changes are impacting biotic and abiotic factors of many ecosystems, and in response many species' ranges are shifting and their normal behaviors may be altered, ultimately impacting how species may interact. Insect life history traits (e.g., development, activity, reproduction) rely heavily on seasonality, being synchronized with fluctuations in light, temperature, moisture, and resource availability. Many insects withstand extreme seasonal fluctuations via diapause – a period of low metabolic activity and developmental arrest triggered by photoperiod and/or temperature - which is an important seasonal phenology, as its timing can influence other life history processes. The field cricket species, Gryllus pennsylvanicus and G. firmus, have ranges that span a large latitudinal and climatic gradient, and readily interact/interbreed in a hybrid zone along the edge of the Appalachian Mountains in the eastern U.S. Using these species, we (1) characterized the variability of diapause and development between species, populations, and hybrids, (2) characterized the level of obligacy of diapause between species and populations, and (3) characterized emergence timing for these species and populations in natural setting using a mixture of common garden experiments and passive sound recording. These experiments have given us an understanding of how variable diapause and development may be and have allowed us to characterize these life history traits and their plasticity in response to a changing climate across the entire latitudinal range of these species.

B-12
Assessing variation in wing morphology of hybridizing field crickets

Ken Sorokie, Juniata College
Isaac Hudson Foy, University of Denver
Alyson Emery, University of Denver
Hannah Eckert, University of Denver
Erica Larson, University of Denver
Thomas Firneno, Juniata College

Abstract:

Reproductive isolation can occur through behavioral isolating mechanisms when mating signals diverge and are no longer recognized between species. The North American field crickets, Gryllus firmus and G. pennsylvanicus, while diverged morphologically, ecologically, and, more cryptically, behaviorally, they readily interact/interbreed in a hybrid zone along the edge of the Appalachian Mountains in the eastern U.S. Male field crickets rub specialized structures on their wings together to produce loud calling songs to attract mates, directly linking morphology to mating behavior. We wanted to investigate the variation in wing morphology of putative hybrids from the central/southern portion of the field cricket hybrid zone. To do this, we clipped and photographed the wings of 283 crickets spanning from Maryland to Virginia. We then used geometric

morphometrics of sound producing wing structures to assess differences between species, their hybrids, and across geographic location. Along with bioacoustic data and mating trials, this work is foundational in understanding how mating signals can contribute to behavioral isolation in a hybrid system.

B-13
Metabolic stability across the lifespan of the forked fungus beetle (Bolitotherus cornutus)

Devin Gibson, Swarthmore College
Sandy Kawano, Universirty of Virginia
Edmund Brodie,
Vincent Formica, Swarthmore College

Abstract:

Terminal investment theory suggests that organisms should reallocate energy as they age, implying that age related behavioral differences should be reflected in physiological processes and detectable by respirometry. Forked fungus beetles (Bolitiotherus cornutus) can live for over 6 years, and exhibit age-related increases in aggression, courtship, mating, and egg laying. Studies in insect systems have revealed that standard metabolic rate (SMR) often scales with body mass, but relationships between age, morphology, and sex are variable among species. We tested whether SMR varied across age and sex in forked fungus beetles using intermittent flow respirometry. Surprisingly, SMR did not differ among age classes and showed no significant differences between males and females. Therefore, metabolic rate appears to remain stable as individuals age despite known variation in behavior across ages in this species. Our future work will examine if age related tradeoffs emerge during post exercise recovery following events such as combat and courtship.

B-14
Sunflower Moth Infestation Patterns in a Sunflower Resurrection Experiment

Omeid Majd, UC Riverside
RAJESH NEUPANE, University of California Riverside
Kate Ostevik, UC Riverside

B-15
The Effect of Seed Age and Size on Germination Success Across Dune and Non-dune Ecotypes of Helianthus petiolaris

Yu Tian, UC Riverside
Theodore Reitman, UC Riverside
Kate Ostevik, UC Riverside

Abstract:

Seed germination is a critical stage in plant life cycles and determines whether seeds successfully transition to seedlings. Seed size and age may influence this process, but whether ecotypic differences influence germination remains unclear. The objective of this study was to examine how seed age and size relate to germination success in Helianthus petiolaris across dune and non-dune ecotypes, and whether ecotype explains additional variation beyond these factors. Seeds were collected from ten populations within Great Sand Dune National Park during two collection years (2015 and 2025). Seed mass was measured using an analytical balance, and area and feret diameter were quantified from standardized images. Germination was assessed in Petri dish assays, and mixed-effects models were used to evaluate predictors of germination success, with population included as a random effect. Results showed that germination was higher in seeds collected in 2025 than in 2015. Germination rate also increased with seed mass, suggesting a benefit associated with greater stored reserves. In contrast, ecotype showed weak or no effect on germination success, once seed traits and seed age were accounted for. Overall, these findings indicate that aging and seed mass play key roles in germination success in Helianthus petiolaris, whereas ecotype contributes little additional variation.

B-16
Coexistence of Two Lineages in a Temporally Fluctuating Evolution Experiment

Hailey Marconi, Loyola University Chicago
Genevieve O'Bryon, Loyola University Chicago
T Goldberg, University Loyola Chicago
Caroline Turner, Loyola University Chicago

Abstract:

Although evolution of specialists within a population is common, long-term coexistence of two specialists in a temporally fluctuating environment is rare. In our evolution experiment, we propagated E. coli under fluctuating nutrient-limited conditions, alternating between nitrogen limitation and carbon limitation every 3 weeks. In this fluctuating environment, a population of E. coli arose in which two lineages coexisted through 24 weeks of evolution. One lineage increased in frequency under carbon limitation, while the other increased in frequency under nitrogen limitation. Although each lineage reached at least 75% frequency during each 3-week interval in its favored environment, neither fully swept to 100% frequency. We hypothesized that the two lineages coexisted as specialists in each of the two environments and that each would experience trade-offs in the other environment. To test this, we competed clones from the two lineages from each 3-week interval against each other. Fitness competitions at the early time points demonstrated specialization, with each lineage outcompeting the other lineage in one environment and performing worse in the other environment. However, after 9 weeks of evolution, both lineages had similar fitness in both environments. It is unclear why the lineages continued to fluctuate in proportion after 9 weeks without a significant fitness difference in either environment. Competitions of each lineage against their ancestral strains indicated that neither lineage experienced fitness trade-

offs; both lineages were more fit than the ancestor in both environments. The lack of apparent trade-offs as well as the disappearance of specialization after 9 weeks suggests that unexplored population dynamics such as frequency-dependent selection may better explain the coexistence and fluctuation of the lineages.

B-17

Contemporary evolution and developmental plasticity shape the thermal tolerance landscape across an urbanization gradient

Logan Kolaske, Case Western Reserve University
Ryan Martin, Case Western Reserve University
Sarah Diamond, Case Western Reserve University
Adaleiz Ore, Case Western Reserve University
Jansi Patel, Case Western Reserve University

B-18

Toward reference-agnostic phylogenomics from heterogeneous sequencing data

Nan Yao, Yale University
Anri Chomentowska, Yale University
Pauline Raimondeau, Yale University
Peregrine Todd,
Alison Carranza, Yale University
erika edwards, yale university

Abstract:

The fundamental requirement for resolving species relationships may be less about predefined loci than about gathering sufficient data whose evolutionary dynamics reasonably approximate a molecular clock. If so, the genomic regions most informative for tree-building could, at least in part, emerge from the data themselves rather than being specified a priori. Motivated by this idea, we explore an alignment-free framework that extracts phylogenetic signal directly from raw sequencing reads without relying on multiple sequence alignment or reference-dependent locus definition. The framework can optionally interface with reference-based workflows to produce per-locus inputs compatible with existing tree-inference methods, but we treat this as a practical bridge rather than a requirement. Because it operates on raw reads, it readily accommodates heterogeneous data types, including genome skimming, RAD-seq, target capture, and transcriptomes, and may help revive dormant datasets archived in public repositories or stored within individual laboratories. We hope this approach can lower the barrier to broader phylogenomic synthesis by making use of scattered, previously underexploited sequencing data.

B-19
Do Freshwater Mussels Influence the Nutritional Quality of Aquatic Subsidies?

Antonio John Tirotta, Louisiana State University
Lenin Chari, Louisiana State University
Sydney Moyo, Louisiana State University (Edit)
Garrett Hopper, Louisiana State University

Abstract:

Terrestrial and riparian environments are intricately linked through the exchange of resources; however, these subsidies are most often measured in terms of biomass quantity, with comparatively less attention given to nutritional quality. This nutritional quality is expected to vary in accordance with community composition, as different organisms concentrate and synthesize different nutrients. In this study, we examined whether the presence of freshwater mussel beds influences the nutritional quality of aquatic insect subsidies, and whether such variation is reflected in the condition and physiological metrics of riparian predators. We sampled web-building riparian spiders (family Tetragnathidae) and emergent insects from sites featuring and lacking mussel beds, as well as three different creeks within Kisatchie National Forest, Louisiana. To characterize subsidy quality and predator responses, we conducted fatty acid analyses on both insects and spiders, measured spider body condition, and assessed immune function. In parallel, we quantified the emergent insect community composition, biomass, and fatty acid content to characterize nutrient availability and quality. Together, these data will be used to evaluate links between aquatic community structure, subsidy quality, and terrestrial predator health. This work aims to advance understanding of how benthic community composition may influence the nutritional pathways connecting aquatic and riparian food webs. Preliminary analyses indicate no detectable differences in spider body condition between mussel and non-mussel sites.

Key words: Ferroptosis, Oxidative stress, Comparative biology, Bats, microscopy

B-20
All that glitters is genomic: Whole-genome sequencing insights into structural and pigment-based color variation in the tortoise beetle, Deloyala guttata

Sara Parker, Boston University
Lynette Strickland, Boston University

Abstract:

Coloration in nature acts as a highly tractable trait for studying the genomic and ecological bases of phenotypic variation. Additionally, body color often shapes organismal fitness, functioning in predator aversion, crypsis, mate choice, and even thermoregulation. Tortoise beetles (Cassidinae) are a highly diverse and globally distributed subfamily of leaf beetles comprised of over 6,400 colorful species. The tortoise beetle Deloyala guttata was first described as ‘variable’ by Edward

Barrows in 1979, but since, to my knowledge, there have been no further studies examining the basis of this color variation.

I expand upon Barrows initial life history account in 1979 and formally characterize elytral color variation in D. guttata. I identify phenotypes that vary along two axes; Beetles are either brown or black and have varying degrees of structural coloration ranging from extensive mottled spotting to entirely opaque elytra with no spots.

We collected beetles from three populations spanning an urban gradient from Boston, Massachusetts to Western Massachusetts. Using whole-genome sequencing combined with quantitative trait analysis of microscope images, we investigate the genomic basis of color in D. guttata. We hypothesize that this complex trait is polygenic, with multiple small-effect loci corresponding to melanin pigmentation and structural coloration. By integrating genomic data with phenotypic quantification, we establish D. guttata as a novel system for investigating how genomic differences manifest as visible diversity.

B-21
Uncovering phylogenetic relationships and cryptic diversity in Philippine Hypsipetes

Abby Perkins, University of Kansas Biodiversity Institute
Chase Perkins, University of Kansas Biodiversity Institute
Peter Willadsen, University of Kansas
Ben Wiens, University of Kansas
Kier Mitchel Pitogo, Department of Ecology and Evolutionary Biology & Biodiversity Institute
Lucas DeCicco, University of Kansas
Robert Moyle, University of Kansas

Abstract:

Hypsipetes is a genus of bulbuls (Aves: Pycnonotidae) residing in tropical forests across the Indian Ocean, including the Philippine Islands. The Philippines is home to the widespread Hypsipetes philippinus as well as seven other recognized species with more restricted ranges (H. amaurotis, H. catamanensis, H. everetti, H. guimarasensis, H. mindorensis, H. rufigularis, and the endangered H. siquijorensis). We obtained specimen-vouchered genetic samples originating throughout the Philippines to produce the first well-sampled genomic dataset for Hypsipetes in this region. We explore genomic patterns of divergence within and among these species using reduced-representation genome-wide data (RAD-seq) supplemented with publicly available whole-genome sequences. Our analyses generally support the taxonomic validity of currently recognized species while revealing several notable findings: species-level divergence between two subspecies of H. siquijorensis, supported by both genomic differentiation and morphological differences in bill size, shape, and color; a genetically distinct population of H. philippinus endemic to Lubang; phylogenetic placement of Moluccan H. affinis nested within the Philippine clade; and genomic

confirmation of the recent H. catarmanensis/H. everetti split. We also recover H. guimarasensis as sister to H. philippinus, in contrast with prior studies based on limited genetic markers. Together, these results underscore the role of island biogeography in driving diversification and highlight the conservation priority of restricted-range lineages within this radiation.

B-22
Duplication of rodent serpin genes as molecular fuel for coevolved resistance to snake venoms

Matthew Holding, University of Michigan
Meilyn Ward, University of Michigan
Laura Haynes, University of Michigan
Mark Margres, University of South Florida
Marjorie Matocq, University of Nevada
David Ginsburg, University of Michigan

Abstract:

Gene duplication can play a critical role in the evolution of functional novelty, yet our understanding is limited concerning the role of gene duplication in coevolutionary interactions. While tandem duplication is a major force in venom evolution, the potential of gene duplication to fuel venom resistance is an expanding frontier in venom biology. Serpin subfamily “A” (henceforth serpina) genes produce globular serine protease inhibitors, and serpina1 has previously been shown to inhibit snake venom serine proteases. We have characterized patterns of duplication within the tandem array of serpina genes, finding the hallmarks of rapid birth-death evolution of serpina1-like and serpina3-like genes within and between rodent lineages, and evidence for diversifying selection acting on rodent gene duplicates. To explore the functional significance of copy number evolution, we recombinantly expressed the full set of 12 paralogous duplicates of serpina3 found in the genome of the Big-eared woodrat (Neotoma macrotis), a species known for resistance to protease-rich rattlesnake venoms. Two of the most highly expressed serpina3 paralogs also inhibited diverse rattlesnake venom serine proteases, suggesting they serve as mammalian serum resistance factors. Paralogous duplication produced functional variation, including neofunctionalization to inhibit both chymotrypsin-like and trypsin-like proteases simultaneously for one venom-inhibiting paralog. We are currently using phage display and deep mutational scanning to map the mutational landscape of snake venom inhibition by these highly evolvable serpins. Our results provide evidence that the serpina1 and serpina3 genes have high evolvability and a tendency to generate novel gene copies among rodents, including functionally diverse venom inhibitors.

B-23
Better Scientific Presentation Graphics

Jacelyn Shu, University of British Columbia

B-25
Mutations in Escherichia Coli's Global Regulator H-NS Reveal Potential Insights intoTranscriptome Dynamics

Claire Cheng, Vanderbilt University

Abstract:

DNA organization remains an important phenomenon across the tree of life, but is often overlooked in prokaryotes because of their lack of histones. Although bacterial genomes lack histones in their genomes, bacterial DNA organization is conducted by nucleoid associated proteins (NAPs). H-NS, histone-like nucleoid structuring protein, is one of the most studied NAPs in Escherichia coli that acts as a global transcriptional silencer by targeting AT-rich regions of DNA. Of the genes that H-NS regulates, they are often enriched in stress and environment responses. Despite understanding H-NS as a global regulator, there is very little known about how mutations in H-NS can alter its regulatory activity and reshape the transcriptome. Using mutation identified from the Behringer Lab's long term starvation experiment, we analyzed the transcriptome utilizing RNA-sequencing and was able to identify differentially expressed genes, enriched biological pathways and global regulators. We demonstrated an increased enrichment in FNR regulated genes in our over expressed genes and consequently a decrease in expression in clpX and clpP which encodes ClpXP, a protein complex responsible for the degradation of FNR. As such, we suspect that a major molecular phenotype of the H-NS R93H mutant shows a transition to anaerobic conditions and increase in proteome stability due to decrease in FNR degradation.

B-26
Chance and Contingency Predominate Over Necessity in the Evolution of Tyrosine Kinase Activity

Michael Gardner, Purdue University
Brian Metzger, Purdue University

Abstract:

A central question in biology is the extent of predictability in evolutionary outcomes and the relative roles of chance and contingency on this predictability. Since we cannot directly observe the past, the effects of chance and contingency are unknown. However, we could infer their effects by comparing the outcomes of repeated evolutionary events. Chance predominating would cause independent evolutionary events to produce variable outcomes, while contingency predominating would cause variable outcomes to depend on where evolution started. If the outcomes of evolution were always the same, there is evolutionary necessity (the absence of chance and contingency) and there was a single route available to evolution. Unfortunately, most traits evolved only once and this analysis has been inapplicable. However, the repeated and independent evolution of tyrosine phosphorylation activity offers an exception.

Here, we determine the genetic and molecular basis for tyrosine kinase (TK) activity for one instance of its evolution: the Wee kinase family. Using maximum likelihood analysis, we reconstructed a phylogeny of related kinases and mapped known phosphorylation capabilities onto it, determining when and how the Wee family gained TK activity. We refined our analysis using structurally validated sequence alignments. Future work will use this phylogeny to reconstruct the last common ancestor of Wee and related kinases and identify the genetic changes that conferred kinase activity. We will then compare the sequences and evolutionary mechanisms against those of TK activity in other kinase families, allowing us to determine the relative roles of chance and contingency in the evolution of acquired function for the first time.

B-27
Cross-species susceptibility to harmful algal bloom toxins microcystin-LR, anatoxin-a, and saxitoxin

Kali Mattingly, SpecPro Sustainment & Environmental
Marissa Jensen-Brickley, US Environmental Protection Agency
Aabir Banerji, US Environmental Protection Agency
Kasey Benesh, SpecPro Sustainment & Environmental
Alexander Cole, US Environmental Protection Agency

Abstract:

Cyanobacterial blooms are becoming increasingly common. Bloom-associated toxins (cyanotoxins) may cause deleterious effects in humans, but effects are unknown for many other species. This is due in part to the limited number of species used in toxicology testing. Susceptibility to toxins can also be predicted by comparing target proteins for these toxins—species having functionally different proteins might have different susceptibility to a toxin. To expand our understanding of how common cyanotoxins (microcystin-LR, anatoxin-a, saxitoxin) impact a broad range of organisms, we obtained publicly available data extracted from controlled exposure experiments in the ECOTOXicology Knowledgebase (ECOTOX) and analyzed protein sequences using Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS). ECOTOX provided ample toxicity data for microcystin-LR, whereas anatoxin-a and saxitoxin each have ~one-tenth as many studies (311 publications for microcystin-LR, 32 for anatoxin-a, 28 for saxitoxin). Most studies for microcystin-LR and saxitoxin tested effects in crustaceans and fish, while more than half of anatoxin-a studies focused on algae and plants. A subset of the species with studies in ECOTOX also had protein sequences available for SeqAPASS analysis. Susceptibility predictions from SeqAPASS tended to be corroborated by ECOTOX findings. SeqAPASS predictions were also available for hundreds of unstudied species per toxin and could help inform future work. Most species received “susceptible” predictions. Fungi were often classified as nonsusceptible to microcystin-LR, a finding that aligns with proposals to use fungi for bloom remediation. For anatoxin-a, we found evidence that invertebrates may be less susceptible than vertebrates, because invertebrates lack the protein variants that have been shown to bind strongly with anatoxin-a. Our efforts to predict which organisms might be differentially affected by toxic blooms

will ultimately inform larger-scale estimates of blooms' impacts on whole aquatic communities, in the St. Louis River estuary and beyond.

DISCLAIMER: The views expressed in this article are those of the authors and do not necessarily represent the views or policies of the US Environmental Protection Agency. Any mention of trade names, manufacturers, or products does not imply an endorsement by the US Government or the US Environmental Protection Agency.

B-28
Nitrogen limitation decreases the survival of E. coli under tobramycin selection

Veera Byrne, Loyola University Chicago
Caroline Turner, Loyola University Chicago
Anja Hofmeier, Loyola University Chicago
Heather Blasius,
Alexa Schnell, Loyola University Chicago
Gabe Wegman, Loyola University Chicago

Abstract:

Antibiotics are widely used in clinical settings to combat bacterial infections. The evolution of resistance is widespread and may be influenced by the evolutionary environment. We posed the following question: How does the evolution and survival of E. coli under tobramycin selection vary between nutrient-limited environments? We evolved bacterial populations for 24 days in the presence or absence of tobramycin under either nitrogen-limited or carbon-limited conditions. E. coli were less likely to survive tobramycin exposure under nitrogen limitation than under carbon limitation, demonstrating that nutrient limitation can influence the evolution of antibiotic resistance. Under tobramycin selection, nitrogen-limited populations had much lower population sizes than carbon-limited populations, likely reducing the rate of occurrence of beneficial mutations. However, the resistance level of surviving populations did not differ between carbon- and nitrogen-limited environments.

C-01
X chromosome genetic diversity across diverse beetle taxa

Thomas Johnson, Indiana University
Ryan Bracewell, Indiana University

C-02
Heterogeneous Genomic Signatures of Adaptive Introgression in Chimpanzee Hybrids from the Sanaga River Contact Zone in Cameroon

Fabrice Kentatchime, Texas A&M University
Paul Shrurtarshi, Texas A&M University

Matthew Mitchell, The Jackson Laboratory for Genomic Medicine
Mary Gonder, Texas A&M University

Abstract:

The Sanaga River in Cameroon forms a critical biogeographic boundary between central chimpanzees (Pan troglodytes troglodytes) and Nigeria-Cameroon chimpanzees (Pan troglodytes ellioti), creating a narrow contact zone where hybridization occurs. Although previous studies have documented admixture at this boundary, the genomic architecture and adaptive potential of introgression in wild hybrid individuals remain poorly understood. Here, we use genome-wide ABBA-BABA statistics and high-resolution sliding-window f_dM analysis to characterize introgression patterns in hybrid chimpanzees from the Sanaga contact zone.

We analyzed whole-genome sequences from two hybrid individuals (LWC46 and LWC21) alongside pure P. t. troglodytes, P. t. ellioti, and bonobo outgroup samples, using Dsuite to compute D-statistics and f4-ratios across multiple trio configurations. Significant genome-wide introgression signals were detected (mean D = 0.039-0.064, Z > 3, FDR-corrected p Critically, we discovered striking individual-specific introgression patterns: approximately 349 high-confidence regions supported by ≥4 independent trios could be partitioned into LWC46-private, LWC21-private, and shared categories. This heterogeneity suggests that hybrid individuals from the same contact zone carry distinct introgressed haplotypes, potentially reflecting temporal variation in hybridization events, local selection pressures, or stochastic demographic processes.

Our findings reveal a complex mosaic of introgression in Sanaga River chimpanzee hybrids, with implications for understanding adaptive evolution at species boundaries and for informing conservation strategies for endangered chimpanzee populations in fragmented Central African landscapes.

C-03
Repeat accumulation drives the expansion of a young Y chromosome in Zaprionus davidi

Alex Preble, Indiana University
Ryan Bracewell, Indiana University

C-04
Extended Clades and Conditional Clade Distributions (CCD)

Lars Berling, Simon Fraser University

Abstract:

The inference of phylogenetic trees is typically accompanied by uncertainty quantification, for example through sampling from a posterior distribution or by generating bootstrap replicates.

However, how best to summarize and communicate the uncertainty contained in such samples remains poorly understood and is often treated only superficially.

This uncertainty is commonly summarized using a single representative tree, which serves as a backbone onto which additional measures of uncertainty are mapped.

Methods to create these representative trees have been restricted to “plain tree topologies”: trees encoding only relationships among taxa and no additional structure or information.

Inference of more sophisticated models produce annotated tree objects.

These have additional information representing nodes’ locations in the case of phylogeography, host information when inferring transmission trees, or sampled ancestor status when incorporating fossil information.

Nevertheless, these enriched representations are often reduced to a single representative tree, typically using methods developed for plain topological trees and without accounting for the resulting methodological mismatch.

Here, we introduce the concept of an extended clade and investigate an extension of the conditional clade distribution model.

We present a extended clade representation for discrete trait phylogeography, transmission trees, and stratigraphic ranges.

C-05
Despite negative fitness effects, female forked fungus beetles do not construct social niches

Sophia Springer, Swarthmore College
Vincent Formica, Swarthmore College
Edmund Brodie,

Abstract:

Using the forked fungus beetle, Bolitotherus cornutus, as a model system, we investigated whether interactions with males influence female fitness. We then determined whether females modify their behavior to avoid costly interaction types. In other words, do female beetles engage in social niche construction? After a four week long experiment in 12 semi-natural field enclosures, we found that the number of reproductive interactions with males had no fitness effect on females. However, non-reproductive interactions with males had a negative fitness impact. Despite this, we found no evidence that females modify their behavior across short time periods to avoid non-reproductive interactions with males. Our data therefore does not support social niche construction.

C-06
Molecular Pet or Parasite? Exploring selection for plasmid vertical and horizontal transfer

Elizabeth Duan, University of Washingon
Ben Kerr, University of Washington

Abstract:

A core tenet of heredity—the “vertical” transmission of genes from parent to offspring—is violated by bacterial plasmids that also move “horizontally” between unrelated cells. In nature, plasmids exhibit diverse lifestyles, ranging from "host-centric" (favoring vertical gene transfer, VGT while sacrificing horizontal mobility) to "parasitic" (favoring horizontal gene transfer, HGT at the expense of its host). However, laboratory evolution experiments often drive plasmids toward host-centric lifestyles, revealing a gap in our understanding of how to actively select for HGT. To better understand transfer selection, we developed a mathematical model of a microbial community comprising ancestral plasmid-containing, mutant plasmid-containing, and plasmid-free cells. Using local linear stability analysis, we derived an invasion criterion demonstrating that plasmid-free cell availability is the primary driver of HGT selection. We then expanded our model to simulate a prior experiment (De Gelder et al.) where a host-centric mutant successfully invaded despite the presence of plasmid-free cells. Our analysis revealed that adding plasmid-free cells was not sufficient to select for HGT—the frequency at which addition occurs relative to standard batch culture transfer (which inherently selects for VGT) is important. We found that reducing emphasis on growth increases selection for HGT. Finally, we performed a parameter sweep to predict the invasion success of hypothetical mutants across the HGT-VGT phenotypic space. By identifying key drivers of HGT selection, our study provides insight on why standard batch culture protocols fail to exert strong selection on HGT. Furthermore, we offer a framework for predicting the pleiotropic transfer mutations favored in given environmental conditions. Our study offers insight on how mobile genetic elements of major ecological and medical importance move in microbial communities.

C-07
Convergent Phenotypic Evolution and Similar Assembly Patterns in Two Insular Gecko Radiations

Phillip Skipwith, American Museum of Natural History

Abstract:

Theory posits that speciation in adaptive radiations is largely driven by ecological opportunity with concurrent morphological expansion in response to niche availability. In this study, I use a phylogenomic estimate of Australasian diplodactyloid geckos in combination with meristic and ecological data to infer patterns of ecological diversification, quantify signatures of stabilizing selection, and the factors driving speciation processes. Specifically, I focus on two relatively young

but speciose and ecomorphologically diverse assemblages from the ancient islands of New Caledonia and New Zealand. Models accounting for stabilizing selection identify shifts in adaptive optima in morphospace that largely agree with shifts in ecology identified in stochastic mapping analyses of ancestral ecological guild. Explicit texts of morphological convergence provide compelling evidence that the New Caledonian and New Zealand forms have independently converged on similar morphologies when transitioning to arboreal and generalized scansorial guilds. Understanding the relative importance of abiotic and biotic factors in shaping lineage diversification has increasingly become a focus of evolutionary biology, particularly for putative adaptive radiations. Bayesian and multiple regression analyses suggest that abiotic factors rather than interspecific competition dictate phenotypic divergence in both insular lineages. Rather, species seem to diverge phenotypically in allopatry and environmental factors, such as climate, in combination with competitive exclusion drive phenotypic overlap in sympatry.

C-08
TraitBlender V2: Synthetic Image Datasets to Evaluate Deep Comparative Methods

Caleb Charpentier, Virginia Tech

C-09
The role of coinfection in driving interspecific competition

Edith Simpson, Vanderbilt University
Hadi Alsaidi, Vanderbilt University
Ann Tate, Vanderbilt University

Abstract:

Coinfection, the infection of a host by multiple parasites, is widespread due to the ubiquitous nature of parasites. Compared to single infections, coinfections can alter disease outcomes through parasite facilitation or competitive exclusion within the host. These interactions may ultimately influence host fitness and competitive dynamics by modifying mortality, developmental time, reproduction, and population growth. In this study, we investigated the coinfection dynamics of two parasites, the eugregarine Gregarina spp. and the neogregarine Farinocystis tribolii, in two flour beetle species, Tribolium castaneum and T. confusum. We quantified parasite prevalence and intensity under both single-infection and coinfection conditions and monitored changes in host species population abundance over time. In addition, we measured life-history traits, including survival, developmental time, body mass, and gut physiology, to determine whether infection and coinfection-induced changes in these traits help explain variation in parasite-mediated apparent competition between the two host species. We found that T. castaneum exhibited significantly lower eugregarine prevalence and intensity compared to T. confusum. In contrast, Farinocystis prevalence was higher in T. castaneum than in T. confusum. In the competition experiment, T. castaneum competitively dominated in both the control (no infection) and eugregarine-exposed

treatments. However, under Farinocystis exposure and coinfection, T. confusum outcompeted T. castaneum. Notably, population sizes of T. castaneum were higher in the coinfected treatment than in the Farinocystis-only treatment. Together, these findings highlight the importance of host species identity in shaping parasite interactions and demonstrate that competitive outcomes can differ substantially between single-infection and coinfection conditions.

C-10
Population structure and chromosomal inversion in two hybridizing warbler species.

Alican Avsar, University at Buffalo
Marcella Baiz, University at Buffalo
Alix Matthews, University at Buffalo

C-11
Evolutionary ecology of montane plants

Natalie Reynolds, The University of Arizona
Katrina Dlugosch, University of Arizona

Abstract:

Climate change is impacting all life on the planet. The planet is becoming increasingly hotter, drier, and with more extreme weather events affecting species distributions across the globe. Mountain species have been retreating to higher elevations, and this phenomenon has been recorded on the Madrean Sky Islands located in the Southwestern USA. Although sub-tropical and temperate plant ranges are shifting and contracting up Mt. Lemmon. The reason why each species' range is contracting or shifting is still uncertain. My dissertation will aim to answer why sub-tropical and temperate plant species are shifting differently and whether genetic diversity or plasticity is the main player. First, I will investigate the relationship between latitudinal gradients and elevational contraction through species distribution models of 20 Asteraceae species. Next, I will use a genotype x environment analysis to determine how genetic diversity differs along a latitudinal gradient. Furthermore, I will investigate how overall genetic variation and variation in known climate-associated loci correlate to elevational contraction by looking for single nucleotide polymorphisms in the genomes of Asteraceae on Mt. Lemmon and in known climate-associated loci. Finally, I will investigate plasticity of temperate and sub-tropical plant species through reciprocal transplants on Mt. Lemmon. My dissertation will dissect the role of genetic diversity and plasticity in climate change adaptation of temperate and sub-tropical plants on Mt. Lemmon.

C-12
Effects of acoustic rearing environment on phonotaxis in female Gryllus pennsylvanicus field crickets

Susan Gershman, The Ohio State University at Marion
Troy Bowers, The Ohio State University

Abstract:

In field crickets, juvenile exposure to conspecific song can cause individuals to develop adaptive adult traits. Gryllus pennsylvanicus fall field crickets currently experience novel sounds during development like traffic sound and the song of recently introduced heterospecific field cricket Velarifictorus micado. In this experiment, juvenile G. pennsylvanicus females were reared with conspecific song, V. micado song, traffic sound or silence. In no-choice phonotaxis trials, adult G. pennsylvanicus females were presented with conspecific song as virgins, and then again after a mating opportunity. We found that females reared with conspecific song took longer to reach a speaker playing conspecific song and spent less time at the speaker than females with juvenile exposure to traffic song, V. micado song, or silence. This effect was similar for virgin and mated females. We conclude that females reared with conspecific song are choosier than females reared in other acoustic environments. Although V. micado song is within the auditory frequency tuning of G. pennsylvanicus females, juvenile exposure to V. micado song does not cause G. pennsylvanicus females to be choosier. It is also notable that exposure to traffic sound does not affect female choosiness differently than heterospecific song or silence. Finally, although mating has been found to alter female choosiness in other studies, we found little difference between virgin and mated females in the effect of acoustic environment on their choosiness.

C-13
Divergent Reproductive Plasticity in Highland and Lowland Deer Mice

Madison Tatro, University of Denver
Kelsie Hunnicutt, Stanford University
Erica Larson, University of Denver
Jon Velotta, University of Denver

C-14
Whole genome duplication, speciation and demographic history in the Phyllomedusa frog genus

Júlio César Magalhães Chaves, CUNY Graduate Center
Célio Fernando Haddad, Universidade Estadual Paulista
Michael Hickerson, City University of New York
Connor French, City University of New York
Ana Carnaval, City Collegue of New York

Abstract:

Whole genome duplication (WGD) can shape the evolutionary history of a lineage, providing new genetic material for evolutionary forces, such as mutation, drift, and selection. There are two different modes of genome duplication that result in polyploid organisms: two parent genomes are duplicated in a hybrid, known as allopolyploidy, or a genome is duplicated within a lineage, termed autopolyploidy. These phenomena are considered to be instant speciation events, and polyploids are thought to have a broader niche compared to the parental lineages. Among tetrapods, amphibians have the largest genome size variation and the lowest total number of sequenced genomes. With polyploidy being reported in 15 families, the effects of WGD in amphibians and the events that originated polyploidy are still poorly known.

To understand the effects of WGD and the demographic consequences, we use the sister species pair Phyllomedusa tetraploidea (4n) and P. distincta (2n). These two frog species exhibit different distributions in the Brazilian Atlantic Forest. The polyploid species occurs in a more seasonal environment, and is suggested to have originated via autopolyploidy from the diploid species around 300 thousand years ago.

Our goal is to clarify the demographic history of the species pair and determine the mode of WGD that resulted in polyploidy.

To answer this question, we generated RADseq data for 12 individuals of P. tetraploidea, 60 individuals of P. distincta, and one hybrid. We used ipyrad to process sequencing data and generate output files used for the following analysis. We used a PCA and STRUCTURE to visualize population structure. Site frequency spectrum was generated by easySFS and used for demographic history inference in Stairway Plot, and simulations to infer the origin of ploidy were made.

C-15
Geographic Distribution of Y-Haplotypes in Mountain Pine Beetle

Charles Pittman, Indiana University
Dana Smits, Indiana University
Medhavi Verma, Arizona State University
Harshita Sharma, Indiana University
Joe Robbins, Indiana University
German Lagunas-Robles, Indiana University
Ryan Bracewell, Indiana University

Abstract:

Sex chromosomes are known to play a large role in speciation, but the role of young, so-called neo-sex chromosomes is less well known. The mountain pine beetle, Dendroctonus ponderosae (MPB), has a neo-sex chromosome system with three geographically distinct Y haplogroups that are linked to postzygotic reproductive isolation. Where these Y haplogroups come into contact has only been broadly geographically defined. Here, we created an assay that distinguishes the neo-Ys based on simple PCR amplification. We greatly expanded our geographic sampling of MPB to narrow in on the

contact zones and assess Y haplotype movement across cryptic species boundaries. The PCR amplifies a region with an indel variation that allows us to distinguish the three Y haplogroups easily. The Y haplogroups of 527 adult males and 533 larvae/pupae from 57 collection sites were identified. We find that the Western/Eastern contact zone appears incredibly narrow, while the other hybrid zone is broad with more variable Y chromosome movement. Our results suggest that different evolutionary processes and the extent of reproductive incompatibility might alter Y chromosome movement between cryptic species.

C-16
Assembly of a new parasitoid wasp genome (Philolema latrodecti) to investigate host-parasite co-evolution

Rilquer Mascarenhas, York College - CUNY
Jessica Garb, University of Massachusetts Lowell
Michal Segoli, Ben-Gurion University of the Negev
Yael Lubin, Ben-Gurion University of the Negev
Marie Djernaes,
Trine Bilde, Aarhus University
Jesper Bechsgaard, Aarhus University
Monica Mowery, City University of New York

Abstract:

Sequencing complete genomes has the potential to aid in documenting evolutionary history and increasing our understanding of processes shaping biological diversification. Here, we present a first draft of the genome of Philolema latrodecti, a parasitoid wasp (Eurytomidae, Hymenoptera) specialized in infecting spiders in the genus Latrodetus (Widow Spiders). One species in this genus, L. geometricus, is a highly invasive species found across most continents. This invasion has been documented to negatively affect populations of native spiders through the introduction of P. latrodecti into communities with no history of evolutionary contact with this parasitoid. However, the lack of taxonomic, biogeographic and genomic information on the parasitoid hinders a systematic investigation of how this host-parasitoid co-invasion is driving changes in native spider communities. To bridge this gap, we assembled a reference genome for P. latrodecti from high accuracy long DNA reads. Additionally, we used whole genome re-sequencing to explore the phylogenetic relationships among 20 museum specimens either identified as P. latrodecti or with ambiguous taxonomic identification. The assembled genome comprises a total of 354 megabases across 61 contigs (N50: 160Mb; L50: 8). We retrieved high genome completeness scores (95%) from comparison to the Hymenopteran gene database. A maximum likelihood phylogenetic tree reveals three distinct clades across our specimens: one clade composed of P. arnoldi and two specimens from Israel previously identified as P. latrodecti, a second clade with unidentified Philolema specimens from the Phillipines, and a third clade widely spread across the globe comprising specimens previously identified as either within genus Eurytoma or Philolema. Our results suggest that this third clade represents the core clade of P. latrodecti that has recently spread across the

globe with L. geometricus. Our results also highlight the relevance of generating reference genomes for understudied groups in order to shed light on their evolution and biogeography.

C-17
Comparative genomic insights into neo-sex chromosome formation and evolution in treehoppers

Sukanya Samaddar, University of Texas at Arlington
Diogo Cabral-de-Mello, São Paulo State University
Daniela Palmer, The University of Texas at Arlington

Abstract:

Sex chromosomes have a crucial role in sex determination and reproduction in many organisms, but their evolutionary origins are surprisingly diverse. Sex chromosomes begin as an identical pair of autosomes and often differentiate from one another, forming heteromorphic sex chromosome systems (e.g., XX/XY). These heteromorphic systems are hypothesized to act as evolutionary traps that prevent subsequent evolutionary transitions of the sex chromosome system. However, heteromorphic systems can become neo-sex chromosomes through chromosomal fusions that link autosomal regions with the ancestral sex chromosome, thereby bringing new genomic regions into sex linkage. In this study, we investigate the origins of neo-sex chromosomes in a group of hemipteran insects known as treehoppers. Our cytological data indicate that at least five species carry neo-sex chromosomes (XX/XY) formed by X-autosome fusion from an ancestral state of XX/X0. For this study, we are assembling the genomes of these five species and using a genomic coverage approach to identify autosomal vs sex-linked regions. We then test whether these neo-sex chromosomes were formed by convergently recruiting the same autosome, or if these evolved by fusions involving different autosomes. Furthermore, we investigate whether the autosomes involved in fusions share similar features, such as in gene content or repetitive DNAs. This study addresses the evolutionary forces that underlie the formation of neo-sex chromosome systems, the molecular underpinnings of X-autosome fusions, and the role of chromosomal fusions in the dynamic evolution of sex chromosomes.

C-18
Impact of Plasmodium falciparum on the taxonomic composition and stability of the Anopheles coluzzii midgut microbiome

Maame Asiamah, STEGG-INTERACT
Mark Mattine, Texas A&M University

Abstract:

Malaria is a deadly disease with over 200 million cases annually, resulting in over 600,000 deaths each year. Transmitted by Anopheles mosquitoes, the malaria parasite infects and destroys erythrocytes, leading to symptoms such as headaches, fevers, seizures, and difficulty breathing. Plasmodium falciparum is known as the most lethal malaria, attacking red blood cells of all ages

and causing cerebral malaria. The sexual reproduction stage of the Plasmodium occurs in the midgut of Anopheles, when mosquitoes ingest gametocytes during a blood meal. As blood reaches the midgut, the gut microbiome activates the Anopheles's innate immune system, leading to the release of antimicrobial peptides that target the intruding apicomplexan parasite. Previous studies in captive and lab-reared mosquitoes have explored the role of certain bacterial groups, such as Serratia marcescens and Wolbachia, in suppressing or inhibiting the developmental stages of the plasmodium in the midgut; however, research on the role of the natural microbiota of wild-caught Anopheles and their interaction with the plasmodium falciparum parasite is scarce. We hypothesized that infection with P. falciparum would restructure the natural microbiome of wild-caught Anopheles coluzzii, collected from Equatorial Guinea. Preliminary results suggest a shift in community structure between falciparum-infected and non-infected groups. Although both were enriched with Achromobacter insuavis, suggesting a core microbiome, Bukholderia dominated the infected groups. In contrast, the negative groups showed a high abundance of the skin commensal bacterium Corynebacterium acnes, which has been identified in the microbiomes of many Anopheline species. Functional Biomarkers, such as zitb5, a Zinc Transporter, were detected in the negative samples, while ldh, a lactate dehydrogenase, was present in the positive samples only. Further analysis and investigations will examine the role of these bacterial taxa in inhibiting Plasmodium in the midgut of Anopheles and how they can be integrated into vector control strategies.

C-19
Exploring nutritional obligate endosymbiosis in Hawaiian endemic Iolania planthoppers

Stefan Cranston, University of Hawaii

C-20
Ecogeographic variation in plumage and morphometrics of the Common Raven (Corvus corax)

Emma Powers, Louisiana State University
Samantha Rutledge, LSU Museum of Natural Science
Terry McGlynn, CSU Desert Studies
Allison Shultz, Natural History Museum of Los Angeles
Nicholas Mason, Louisiana State University

Abstract:

Solar radiation consists of wavelengths between 300-2100 nm; 300-700 nm encompasses UV and visible (UV-Vis) light, while the remaining 700-2100 nm is near-infrared (NIR) light and falls outside of the visible range of birds yet may have important thermoregulatory implications. The common raven (Corvus corax) lives in a variety of climates from arctic to desert conditions, where they are a resident species. As residents, ravens in distinct climates experience different thermoregulatory

extremes throughout their annual cycles. Here, we examine ecogeographic associations between common raven phenotypes and the environment. Specifically, we quantify UV-Vis-NIR variation among populations using measurements from 58 raven specimens from natural history collections. We collected full spectrum reflectance data using a spectrometer, which we combined with morphometric measurements (bill size, body size, wing size, tail size), and microstructures of feather barbules. We then used QGIS to extract climate data associated with the locality of each specimen and compared those to the phenotypic data to examine ecogeographic associations across this widespread bird.

C-21
Ectomycorrhizal monodominance in the tropics: a modeling approach

Minh Tu, Louisiana State University
Rachana Rao, Louisiana State University
Gaurav Kandlikar, Louisiana State University

Abstract:

Tropical forests are renowned for their hyperdiverse tree communities, yet in forests across the tropics, patches of low diversity often occur where one or a few closely-related tree species dominates the canopy. Several mechanisms have been suggested to explain such anomalous 'monodominant' patches through different plant trait strategies such as seed masting, low seed dispersal, and slow-to-decompose litter. Although multiple mechanisms likely interact to give rise to stable monodominant patches, one notable feature of many such patches is the dominance of trees that form mutualistic associations with ectomycorrhizal (EM) fungi. This is in contrast to most other plant species in these forests, which associate with arbuscular mycorrhizal (AM) fungi. Past studies have suggested that EM-associating trees may have an advantage over AM-associating trees in low nutrient conditions due to the unique ability EM fungi have for mining nitrogen from organic matter, and moreover, that EM-associating trees might further entrench their advantage by releasing more recalcitrant litter than AM-associating trees. Here, we present a mathematical modeling framework for evaluating the role of plant–nutrient–fungal interactions in giving rise to monodominance. Our model follows the biomass dynamics of trees that associate with EM and AM fungi, and that generate litter that differs in its ratios of labile to recalcitrant nitrogen. EM and AM fungi in turn acquire nitrogen from these pools, which they can then provide to trees in exchange for carbon. We parameterized the model with empirically-justified estimates where possible, and conducted parameter sweeps for parameters lacking empirical data. In all, our work provides a quantitative basis for understanding the conditions under which tree associations with EM fungi explain patterns of monodominance in tropical forest communities.

C-22
Evolution of Collective Behavior in Multicellularity in Snowflake yeast

Hikaru Katani, Georgia Institute of Technology

Abstract:

The transition from unicellular to multicellular life represents a major evolutionary innovation in Earth's history. Our work with the Multicellularity Long-Term Evolution Experiment (MuLTEE) provides an unprecedented opportunity to observe this transition in real time, offering unique insights into the emergence of collective behavior and multicellular agency. Recent observations from the MuLTEE have revealed a phenomenon: snowflake yeast has evolved coordinated growth patterns, enabling clusters to grow and physically entangle more efficiently. Following physical fragmentation, late-evolved macroscopic strains re-form a single cohesive cluster in steady culture more readily than early macroscopic strains. We also found a pattern that late macroscopic strains increased branching frequency. We conducted time-lapse imaging to directly reveal the growth pattern, identify growth delays and angles, and assess the cell death ratio. Computational modeling confirmed that increased branching significantly accelerates and strengthens cluster entanglement.

C-23

Does coevolution increases resilience? A study on the establishment of new mutualists in a multi-mutualist yeast community

Lior Karman, UMASS BOSTON
Mayra Vidal, University of Massachusetts Boston

Abstract:

Mutualistic communities are an integral part of any ecosystem on the planet, and as every other community, they are subject to alterations. As species ranges change, some interactions can be disrupted by new mutualists. Although this is usually a naturally occurring phenomenon, human induced climate change and accidental dispersion have been pushing organisms out of their original areas of occurrence, increasing the rate of invasions by non-resident species in various ecosystems. The ability of an invasive mutualist to colonize and persist in a new community should depend partially in its initial trait values as well as the trait values of the resident community. We believe that those trait values are proportional to the amount of time each of the species in the interaction has spent coevolving with its adjacent mutualists; an older, more evolved community should be more resilient to colonization by an invader than a less coevolved community; and the invader's ability to colonize a novel community should also increase with the coevolution period it has experienced in its original community. In order to test this, we are employing a yeast system build of specially designed Saccharomyces cerevisiae strains that are either Lysine deficient Adenine overproducers or Adenine deficient Lysine overproducers; that when cultured together can simulate a multi-species mutualistic interaction in vitro. Using previously evolved communities from this system, we have isolated and recombined differently coevolved strains to create various community-invader combinations, and studied the evolution this new communities for several generations measuring the persistence of the resident and non-resident strains. Our results should improve our understanding of which variables facilitate the establishment of non-residents in new

environments, and with that we might be able to better predict and prevent the harming effects of invasions in mutualistic communities.

C-24
New methodology for studying the morphology of frog skin glands

Katherine Porras Brenes, Virginia Tech
Roberto Márquez, Virginia Tech

C-25
Genomic differentiation and host-plant adaptation in the Enchenopa binotata species complex

Satabdi Mandal, The University of Texas at Arlington
Daniela Palmer, The University of Texas at Arlington

Abstract:

Insect adaptation to host plants can be quite challenging, since plants defend themselves to restrict herbivory. Regardless, phytophagous insects have been largely successful in exploiting plant resources and often adapt to multiple closely related hosts plants. But how do insects that are adapted to a given host plant shift to new distantly related hosts? The Enchenopa binotata species complex of treehopper insects represent a remarkable example of adaptive radiation, with lineages in the complex adapted to over 20 host plant species belonging to 11 different orders. The species complex first diverged from other Enchenopa species ~17.7mya, but the majority of the complex's diversification started ~200,000 years ago. It has been posited that E. binotata have diversified through multiple instances of host-shifting and subsequent adaptation to new host plant phenology. Behavioral studies show differences among host-adapted lineages in sexual communication and maturation timing associated with plant phenology. However, our knowledge of the genetic changes behind such a wide range of adaptations is limited. In this study, we explore genomic patterns of differentiation among host-associated lineages within the species complex using a whole genome sequencing (WGS) approach. First, we generated a de novo genome assembly for E. binotata on Eastern Redbud (Cercis canadensis), which will serve as a contiguous and comprehensive reference genome for E. binotata. WGS data from E. binotata individuals representing distinct host-associated lineages will be used for genomic analyses like and to identify regions associated with divergent adaptation. Additional analyses will investigate phylogenetic relationships, patterns of gene flow and putative barrier loci, driving diversification and reproductive isolation among lineages. Together, these analyses will establish E. binotata as a model for studying the connections between host plant adaptation, genomic divergence, and reproductive isolation during the early stages of adaptive radiation of an insect species complex.

C-26
Reproductive effects of scaly-leg mites (Knemidocoptes sp.) in mountain chickadees

Sam Kruczek, University of Colorado at Boulder
Sara Padula, University of Colorado Boulder
Scott Taylor, University of Colorado Boulder
Haley L. Kenyon, University of Colorado Boulder

Abstract:

Ectoparasitic mites (genus Knemidocoptes), commonly called scaly-leg mites, can have detrimental effects on fitness and reproductive success in birds. Here, using long-term data from a nest-box transect along the Colorado Front Range, I investigated the impact of scaly-leg mite infections on mountain chickadees (Poecile gambeli), a declining species. Specifically, I analyzed the correlation between mite infections in adults and nestling number, clutch size, nestling body condition, and adult body condition as well as differences in infection rate between male and female birds. I report negative correlations between mite infection status and egg number and nestling number, but no relationship with adult or nestling body condition. Males were infected significantly more often than females, providing additional support for the well-established hypothesis that, across many taxa, including birds, males generally experience higher parasite loads than females. My results suggest that infection may lead to decreased fertility and therefore a reduction in clutch size, but that body condition of both adults and offspring are not impacted by infection.

C-27
Deep eukaryotic origins of animal polycystin-1/PKD1

Austen Theroux, Harvard University

Abstract:

Mutations in human polycystin-1 (PKD1) cause autosomal dominant polycystic kidney disease. PKD1 has a large adhesion-related ectodomain with a sperm receptor for egg jelly (REJ) domain and a GAIN autoproteolysis domain. The extracellular region is followed by an 11-transmembrane (11TM) core comprising an N-terminal 5TM module and a C-terminal 6TM module homologous to the PKD2/TRPP cation channel. A cytoplasmic PLAT domain lies between TM1 and TM2. How this chimeric architecture arose remains unclear.

A computational survey of diverse eukaryotes (using InterPro annotation, transmembrane topology prediction, and profile-HMM-based remote-homology searches with HMMER/HH-suite) identified “proto-PKD1” proteins: REJ-domain proteins with a downstream transmembrane region homologous to PKD1 TM1–TM5. Most proto-PKD1 candidates also carry a detectable GAIN domain, though sequence divergence likely obscures it in others.

Proto-PKD1 proteins occur across most major branches of the eukaryotic tree, including early-diverging Discoba, Metamonada, and Malawimonadida, indicating that the proto-PKD1 module was likely present in the last eukaryotic common ancestor. The full 11TM architecture appears restricted to Holozoa, consistent with a model in which canonical PKD1 was assembled by combining an ancestral 5TM proto-PKD1 module with a TRP-like channel module near the origin of this clade. The PLAT domain also shows a predominantly holozoan distribution. Some lineages (dictyostelids, chytrids) encode only 1TM REJ/GAIN proteins, while others (land plants, microsporidia, most terrestrial fungi) lack detectable REJ-domain transmembrane proteins.

Transcriptomic case studies in ciliate, amoebozoan, and holozoan species associate these proteins with ciliary, mating, developmental, and cell-cell recognition programs that echo the roles of PKD1 and REJ in animals. Together, these findings suggest that animal PKD1 emerged by integration of two ancient modules into a single receptor, with related proteins occupying analogous cellular contexts across other eukaryotes. The PKD1/REJ family thus illustrates how complex animal receptors can be assembled from far older eukaryotic building blocks.

C-28
Estimating introgression from gene-tree attachment patterns

Laia Pomar Pallarès, Indiana University

Abstract:

Introgression leaves characteristic signatures in gene-tree topologies, often causing discordant trees where the recipient taxa attach not only to the donor but also to other species closely related to it. Here, we present a simple framework for estimating the magnitude of introgression in a known species network using attachment counts derived from collections of gene trees. Given a species tree and a specified introgression event, the method compares how frequently the recipient taxa attach to taxa on the donor side of the tree against how frequently the sister lineage of the recipient attaches to those same taxa. Under "no introgression", these attachment patterns are expected to be similar, whereas excess attachment of the recipient lineage to the donor side provides evidence of introgression. The relative imbalance between these counts can therefore be used to estimate the introgression proportion. This framework provides an intuitive and computationally efficient way to quantify introgression directly from topology frequencies and offers a scalable alternative for analyzing complex evolutionary histories.

D-01
Behavioral, Ecological, and Evolutionary Responses of the Green Anole (Anolis carolinensis) to Brown Anole (Anolis sagrei) Invasion on the Spoil Islands of Mosquito Lagoon, Florida

Emmanuel Ezumel, Loyola University Chicago

Yoel Stuart, Loyola University Chicago

Abstract:

Character displacement reduces niche overlap between closely related species through behavioral, morphological, and ecological divergence. The invasion of the brown anole (Anolis sagrei) into the range of the native green anole (A. carolinensis), especially across the Spoil Islands of Mosquito Lagoon, Florida, provides a natural system to examine how invasive competitors drive phenotypic change. Previous studies have shown that the presence of brown anoles leads to spatial niche shifts and associated morphological changes in green anoles. Yet, the underlying mechanism remains unclear: Is it resource competition, antagonistic interactions, or intraguild predation? We examined behavioral, morphological, physiological, and trophic responses of green anoles across uninvaded (Osprey), recently invaded (Hornet), and long-invaded (Yang) islands using data from 2010, 2019, and 2024. Green anoles perched significantly higher on invaded islands, demonstrating rapid and repeatable behavioral displacement following invasion. Lamella number increased through time on invaded islands, while toepad area showed less consistent temporal divergence. Stable isotope analyses revealed enriched $\delta^{13}C$ signatures and narrower isotopic ranges on invaded islands, suggesting shifts in trophic ecology and resource use consistent with exploitative competition. H:L ratios did not differ significantly among islands. These findings suggest that character displacement in this system is likely driven by both behavioral interference and resource competition, with behavioral shifts occurring more rapidly than morphological change.

D-02
Endosymbiotic Paraburkholderia species carry diverse bacteriophages

Emily Oxender, Washington University in St. Louis

D-03
Decoding Time in the Deep: A High-Throughput Methylation Clock for Rockfish

Kinga Kotulska, University of Victoria

D-04
PopGenHelpR: An R package to streamline and facilitate informed population genomic analyses and visualization of genetic ancestry, diversity, and differentiation

Keaka Farleigh, University of Virginia
Mason Murphy, Bowling Green State University
Christopher Blair, City University of New York
Tereza Jezkova, Miami University

Abstract:

Analyzing large population genomic datasets requires an interdisciplinary skillset. Beyond a knowledge base in genetics and population biology, population genomic analyses involve computer science and statistics, representing a barrier for researchers without experience in those fields. PopGenHelpR seeks to lower this barrier by enabling researchers to perform population genomic analyses and generate near-publication quality figures in a streamlined and informed fashion. PopGenHelpR allows users to estimate genetic diversity within populations as well as differentiation among populations and individuals from single nucleotide polymorphism data. PopGenHelpR includes commonly used measures such as observed heterozygosity and FST. PopGenHelpR also provides five previously unavailable measures of heterozygosity, including the proportion of heterozygous loci and homozygosity by locus. Additionally, PopGenHelpR integrates widely used visualization tools in population genomics that normally require additional software packages, such as ancestry bar charts, piechart maps, and genetic differentiation heatmaps. Moreover, PopGenHelpR is minimally dependent on other R packages, reducing its chance of being removed from public networks. The PopGenHelpR website also provides tutorials and educational resources. Altogether, PopGenHelpR provides resources for informed analyses and effective visualization, making PopGenHelpR a valuable tool for many researchers. PopGenHelpR is available on the Comprehensive R Archive Network and GitHub (https://github.com/kfarleigh/PopGenHelpR).

D-05
A genealogical likelihood framework for detecting selective sweeps

Christian Huber, Pennsylvania State University
Mahsa Alemrajabi, Pennsylvania State University

Abstract:

We developed a likelihood-based framework to detect signatures of positive selection using gene tree–based data by identifying distortions in local genealogies relative to a genome-wide neutral demographic model. Unlike site frequency spectrum–based approaches, our framework leverages local genealogical structure directly to detect population-specific selection. In this framework, each inferred genealogy is evaluated under a null demographic model estimated using gLike, a genealogy-based demographic inference method, and compared to an alternative model incorporating a transient population bottleneck that captures the elevated coalescent rates expected under positive selection. A likelihood ratio test (LRT) is then used to quantify statistical support for selection and to localize selective sweep signals to specific branches within a three-population topology.

To evaluate performance, we conducted simulations across a broad range of demographic and selective scenarios. Preliminary analyses show that likelihood ratios are higher under selection than under neutrality, indicating power to detect selective events. In addition, the method can recover the approximate timing of the sweep and localize selection to the population in which it

occurred. We also plan to apply the framework to human genomic data from the 1000 Genomes Project to assess its utility in empirical population genetic analyses.

D-06
Genetic changes in a microbial predator-prey system after coevolution under temperature stress

Karissa Plum, University of Houston

D-07
Demographic processes shape genome-wide gene tree discordance between allopatric and parapatric populations of rattlesnakes

Ellie Faber, University of Virginia
Megan Alderman, University of Virginia
Dylan Highland, University of Virginia
Keaka Farleigh, University of Virginia
Samuel Hirst, University of South Florida
Mark Margres, University of South Florida
Drew Schield, University of Virginia

Abstract:

Genealogical relationships between closely related taxa are often heterogenous throughout the genome due to evolutionary processes such as incomplete lineage sorting (ILS), introgression, and selection. Topology weighting methods are useful for quantifying genome-wide discordance between gene trees and species trees but fall short of identifying the underlying mechanisms driving this discordance. Here, isolated populations that share a recent common ancestor can be utilized to quantify discordance that likely arises primarily from ILS, then compared with populations exchanging genes to understand how these processes affect genealogical heterogeneity. Furthermore, the integration of demographic models into gene tree-based methods can elucidate how demographic properties such as effective population size, migration rate, and divergence time might influence the degree of discordance between species pairs. We aim to understand the mechanisms driving gene tree discordance in the Speckled Rattlesnake species complex by taking advantage of this combination of approaches. This system offers comparisons between pairs of allopatric populations and populations of non-sister taxa that exchange genes in secondary contact, which we use to test relationships between gene tree discordance and genetic and geographic distance, effective migration rate, and genome-wide recombination rate variation. We predict greater gene-tree discordance in populations subject to both ILS and gene flow than in allopatric populations, when controlling for time to coalescence (as measured by e.g., dxy). By interpreting heterogeneity in the gene genealogies in the context of explicit demographic modeling, we may better understand the degree to which gene flow influences genome-wide discordance during ongoing speciation processes.

D-08
Sex in plants: birth, death, and trying to survive in a changing climate

Elena Meyer, Virginia Commonwealth University
Andrew Eckert, Department of Biology & School of Life Sciences and Sustainability

Abstract:

Plant mating systems are key determinants of fitness. Angiosperms exhibit a wide variety of reproductive strategies, including self-fertilization (or selfing), outcrossing, and mixed mating. It has been estimated that up to 43% of plant species are capable of selfing, and selfing has been hypothesized to provide reproductive assurance where opportunities for mating may be limited, such as in marginal environments. However, questions regarding the overall distribution of selfing rates across angiosperms, the maintenance of mixed-mating in the face of inbreeding depression, and the impact of self-fertilization on diversification rates remain incompletely resolved. Here, we explore the dynamics of self-fertilization across three lines of inquiry: 1) addressing systematic bias toward the study of plant species capable of self-fertilization, 2) using state-dependent speciation-extinction models to assess the impact of mating and sexual system traits on rates of diversification through time, and 3) assessing if habitat marginality as measured by species distribution models can explain variation in selfing rate across populations. We present results demonstrating a bias favoring more "interesting" mating systems, yielding a bias against studies of outcrossing species. We also utilize state-dependent speciation-extinction models to show how reproductive system traits like mating and sexual system impact diversification rates across a broadly-distributed sample of 18 angiosperm families, and discuss how these traits can be used together to improve our understanding of angiosperm reproductive dynamics. Finally, utilizing species distribution modeling, we discuss what drives population-level variation in selfing rates, and the potential implications of this for plants under a changing climate.

D-09
Novel Paraburkholderia symbionts display variance in host infection dynamics

Kaitlyn Torack, Washington University in St. Louis

Abstract:

Dictyostelium discoideum is a soil amoeba found in the soil that preys on a wide variety of bacteria, including three species of Paraburkholderia that can survive phagocytosis and persist inside amoeba cells. These species represent two independent transitions to symbiosis with D. discoideum. P. agricolaris, with a larger genome, less dependence on D. discoideum, and more variation among genomes, represents one transition. Based on their reduced genomes, P. bonniea and P. hayleyella established a relationship with D. discoideum earlier. Until last year, only 19 strains of Paraburkholderia from all 3 species had been isolated. We used species-specific primers to expand the collection to 111 isolated strains from 17 locations across the United States. We used edibility, infection frequency, and infection density as three measures of symbiotic

interactions to characterize novel P. agricolaris strains. To assess variation within P. bonniea, we used edibility assays. We found that while P. bonniea is more edible than P. agricolaris, both species display a range of edibility. For P. agricolaris, variance in edibility seems to have no relationship with genetic similarity, and the data suggest a negative relationship with infection frequency and density.

D-10
Modeling the demography of recently bottlenecked alewives

Riley Corcoran, University of Denver
Eric Schultz, University of Connecticut
Jon Velotta, University of Denver

D-11
Characterizing genomic divergence between hybridizing cricket species across a broad geographic range

Alyson Emery, University of Denver
Jose Lopez Aleman, University of Denver
Thomas Firneno, Juniata College
Michael Grapin, Juniata College
Ella Mathews, University of Denver
Elise Gellman, University of Denver
Emily Moore, University of Nebraska-Lincoln
Erica Larson, University of Denver

D-12
Effect of Artificial Light at Night on Mate Choice in Field Crickets Gryllus pennsylvanicus

Xiran Du, University of Minnesota

Abstract:

Artificial light at night (ALAN) is a common global stressor that disrupts natural photoperiods, yet its impacts on mating behaviors remain poorly understood. Beyond masking signal transmission, ALAN may also be a movement barrier for nocturnal taxa that evolved aversion to light. I hypothesize that ALAN acts as both a spatial barrier for female crickets mate searching behavior and a disruptive barrier in mate preference expression. Using the field cricket (Gryllus pennsylvanicus), I will conduct phonotaxis playback experiments using LED light strips to simulate ALAN barriers. First, I will test whether ALAN reduces the probability or efficiency of females reaching a conspecific call in no-choice and two-choice (lit vs. dark path) trials. If the hypothesis is true, I expect a lower percentage of females in reaching the speaker, and/or increased latency in light on treatment, and less than 50% of females to choose the lit side when given the dark choice.

Second, I will assess whether ALAN disrupts mate preference by pairing an attractive male song with a lit/dark path and an unattractive song always with a dark path, recording choice proportions and movement latency. If ALAN interferes with mate preference, I expect a higher proportion of females choosing the unattractive song and exhibit a longer choice latency due to conflicting song and light preference when attractive song is paired with lit path. This study will provide improved empirical data for ALAN as a movement barrier while introducing a novel mechanistic framework that ALAN interferes with decision-making and mate preferece. Beyond laboratory, this study will also offer practical insights into sustainable urban lighting design.

D-13
Phylogenomic insights into the orgins and evolution of hyperiid amphipods

Collin Gross, Smithsonian National Museum of Natural History
Karen Osborn, Smithsonian National Museum of Natural History

Abstract:

Life in extreme environments has led animals to evolve many extraordinary morphological and physiological adaptations. Hyperiid amphipods are a group of marine crustaceans that moved into pelagic habitats in the Cretaceous and since then have developed adaptations that have helped them thrive and survive in the midwater, including transparent bodies, enormous eyes, and associations with gelatinous zooplankton. Phylogenetic relationships – both within hyperiids and their place among other amphipods – have been murky and unstable since molecular tools were first applied to the group, precluding comparative studies of adaptation in this group. Using mitochondrial genome skims and barcodes for 53 out of 76 hyperiid genera plus 123 additional amphipod genera, we have produced a new phylogeny that attempts to resolve outstanding questions in hyperiid systematics, including the placement of the enigmatic genera Paraphronima and Cystisoma, whether the suborder Hyperiidea is monophyletic, and which benthic amphipod groups are sister to hyperiids. We find that Paraphronima and Cystisoma – two genera with large eyes differing in structure from other large-eyed hyperiids, form a grade leading to the small-eyed infraorder Physosomata, suggesting that a) large eyes likely evolved at least twice independently in hyperiids, and b) that these large eyes may have been secondarily lost. The relationships between hyperiids and benthic taxa remain unclear, but our tree suggests that hyperiids may have arisen from small cryptic, benthic amphipods that were commensal inside larger sessile animals, and that hyperiids may have ascended into the water column twice – i.e. the suborder Hyperiidea is polyphyletic. However, fully resolving these questions is dependent on acquiring additional genomic data on these potential sister taxa. With additional taxa and sequence data, our tree will provide a foundation for phylogenetic comparative studies of the evolution of hyperiid eyes, appendage morphologies, swimming behavior, and associations with gelatinous zooplankton.

D-14
From Ancient Adaptation to Modern Health: Reconstructing Host–Microbiome Interactions Through Time

Dina MemarMoshrefi, Pennsylvania State University

Abstract:

Ancient DNA (aDNA) has transformed the study of human evolution by enabling the direct observation of genetic change through time. Recent advances in sequencing technologies, large-scale ancient genomic datasets, and statistical approaches for detecting selection have reshaped our understanding of how humans adapted to shifts in diet, mobility, pathogen exposure, and environment. These studies have highlighted the importance of temporal genomic data for reconstructing evolutionary processes that cannot be inferred from present-day populations alone. However, most aDNA studies remain focused on the human genome in isolation, limiting our ability to investigate how broader biological systems evolved across time.

Here, we extend these evolutionary frameworks by integrating ancient human genomic and ancient oral microbiome (aOM) data to investigate the long-term dynamics of host–microbiome interactions. Focusing on northern Mesopotamia and the Iranian Plateau, regions central to early agriculture, migration, and urbanization yet underrepresented in genomic research, we combine host genetics, oral microbiome reconstruction, archaeological context, dietary evidence, and environmental data within a temporally resolved framework. Using a hypothesis-driven approach centered on loci implicated in modern host–microbiome associations, including FUT2 and ABO, we test whether gene–microbiome relationships observed in present-day populations were already present in the past and how they changed across major cultural and environmental transitions.

By integrating evolutionary genomics with ancient microbiome research, this work moves beyond descriptive reconstructions of the past and toward a deeper understanding of how host–microbe relationships evolve across time. This framework enables the identification of stable biological associations as well as more recent disruptions linked to disease, providing new insight into the evolutionary foundations of oral and systemic health. More broadly, it highlights the potential of temporally resolved datasets to improve the interpretation of modern health variation across diverse human populations.

D-15
The hexaploid genome of horsetail milkweed (Asclepias subverticillata) reveals candidate defensive-metabolite pathways in Apocynaceae

Mahamad Miya, Department of Entomology and Plant Pathology
Terrence Sylvester, Department of Biological Sciences
Center for Biodiversity Research, University of Memphis
Rokeya Akter, University of Arkansas
Duane McKenna, University of Memphis
RICH A, University of Arkansas

Abstract:

Milkweeds (Asclepias) are important models for studying plant defense, specialized herbivory, and chemically mediated coevolution, yet genomic resources for the genus remain limited. Horsetail milkweed (Asclepias subverticillata) is a toxic North American species associated with diverse milkweed-feeding insects and distinctive defensive chemistry. Here, we generated a high-quality long-read genome assembly for A. subverticillata and used it to investigate genome structure, gene content, repeat evolution, organellar genomes, candidate specialized-metabolite pathways, and demographic history. The final nuclear assembly spanned 341.49 Mb across 210 contigs, with a contig N50 of 14.22 Mb, a largest contig of 24.96 Mb, and high gene-space completeness. K-mer analyses provided evidence consistent with hexaploidy, representing the first such signal reported for Asclepias. Repeats accounted for 65.08% of the assembly, dominated by long terminal repeat retrotransposons, including a large fraction of unclassified LTRs. We annotated 24,939 putative protein-coding genes, assigned functional predictions to 97.92% of them, and identified 7,150 non-coding RNAs. We also assembled and annotated the mitochondrial genome (586,290 bp) and chloroplast genome (162,654 bp). Comparative analyses across Apocynaceae recovered conserved orthogroups as well as expanded gene families associated with defense response, stress signaling, protein phosphorylation, and membrane-associated functions. Specialized-metabolite and CAZyme analyses identified putative biosynthetic gene clusters and candidate enzyme families relevant to plant defense, including cytochrome P450s, UDP-glycosyltransferases, hydroxysteroid dehydrogenases, and progesterone 5β-reductase. Together, these resources establish A. subverticillata as a valuable new system for comparative studies of milkweed genome evolution, polyploidy, and the genomic basis of plant–insect interactions.

D-16
Evolution of defense against native parasites of C. elegans

Mandy (Amanda) Gibson, University of Virginia
Linyao Peng, University of Virginia
Tessa Batterton, University of Virginia

Abstract:

Parasite defense is the ability of a host to minimize fitness loss to parasites, and it is typically among the most variable phenotypes in natural populations. We expect this variation in defense to facilitate rapid adaptation under parasite-mediated selection. Though there has been substantial study of defense against non-native parasites of Caenorhabditis elegans, we know little about adaptation of C. elegans population to defend against parasites they encounter in the wild. To address this, we first used controlled exposures to characterize genetic variation in defense of C. elegans against its natural microsporidian parasites in the genus Nematocida. We report extensive variation in parasite defense among wild Hawaiian strains of C. elegans: some strains lost 60% of fecundity under parasite exposure, while others were unaffected. Defense covaried with life history: host strains that reproduced quickly had higher relative fecundity under exposure,

consistent with the idea that parasites diminish future reproductive opportunities. Second, we selected a genetically diverse ancestral population in the presence or absence of different species of Nematocida. After 20 weeks, lineages selected in the presence of parasites showed substantially elevated defense relative to control and ancestral lineages. Evolved defenses were moderately specific, with host lineages more defended against the parasite species with which they were selected. Together, these findings indicate significant potential for adaptation of wild C. elegans populations to defend against their natural parasites. Moving forward, we expect these evolved lineages will allow us to characterize the mechanisms and genomics of parasite adaptation.

D-17
How low is low enough? Induction of cold acclimation in locally adapted populations of a winter annual

Emily Lancaster, Purdue University

Abstract:

Phenotypic plasticity allows organisms to use environmental cues to respond to predictable environmental variation. One example of this is cold acclimation, where low non-freezing temperatures drive a cascade of changes to prepare organisms for winter in the temperate zone. As the severity of winter can vary substantially across a species' range, intraspecific variation in acclimation could lead to local adaptation due to a trade-off between freezing tolerance and growth. This variation in freezing tolerance has been documented many times. However, these studies typically use a constant 4°C to induce the acclimation process, which is not representative of natural conditions. This research aims to address this through the following questions: 1. What temperature cues induce this process? 2. How do diurnal fluctuations impact this? 3. Is there natural variation between populations in their cues? To do this, we used Swedish and Italian ecotypes of Arabidopsis thaliana, which is a well-studied system where the role of cold acclimation in local adaptation has been investigated. Here, significant differences in freezing tolerance are due to a polymorphism in a gene that encodes the transcription factor CBF2. This regulates the expression of downstream genes that are cold-inducible and show significant differential expression after acclimation at 4°C, making them excellent markers for the induction of cold acclimation. Using two of the most differentially expressed downstream targets we measured gene expression in both ecotypes after acclimation at 3 constant temperatures and 6 diurnal temperatures, providing a closer look into the induction of this process.

D-18
Day and night dependence in the expression of evolved behaviors in giant mice from Gough Island

Elsa Luebke, University of Wisconsin - Madison
Bret Payseur, University of Wisconsin - Madison

Abstract:

Day and night impose contrasting selective pressures on behavior. How behavioral divergence depends on circadian timing remains underexplored in evolutionary biology. Giant house mice (Mus musculus) from Gough Island evolved new behaviors compared to their mainland relatives, but it is unknown whether these behaviors are dependent on the time of day. We used the experimental framework of the elevated plus maze to quantify a suite of behaviors connected to anxiety and exploration to compare Gough Island Mouse and mainland mouse behaviors during the day and night. We found that Gough Island mice travelled further distances, spent more time in the middle of the apparatus, assessed risk more, and froze less than their mainland counterparts independent of day/night setting. However, divergence in percent open arm entries, percent time spent in the open arms, and propensity to jump off of the apparatus differed between day and night. These findings highlight the importance of incorporating diel contexts into studies of behavioral evolution.

D-19

The role of hybridization in genome evolution: How loss of heterozygosity impacts interactions between the nuclear and mitochondrial genomes in hybrid yeast

Edie Nissen, North Carolina State University
Nathan Brandt, North Carolina State University
Caiti Smukowski Heil, North Carolina State University

Abstract:

Hybridization between different species often reduces fitness due to incompatibilities between the co-evolved nuclear and mitochondrial genomes. Our preliminary research evolving Saccharomyces cerevisiae x Saccharomyces uvarum hybrids that have inherited either the S. cerevisiae or S. uvarum mitochondrial genome identifies mutations that may mitigate these incompatibilities by favoring alleles compatible with the inherited mitochondrial genome. These mutations, known as loss of heterozygosity (LOH), are commonly occurring in yeast and are formed when mitotic DNA breaks are repaired by break induced replication resulting in homozygosity. Using Saccharomyces hybrids as a model system, this project aims to test whether LOH acts as a mechanism to resolve mito-nuclear incompatibilities and increase hybrid fitness. To investigate this further, we are expanding laboratory evolution of interspecific hybrids to identify LOH events involved in potential mito-nuclear interactions and testing fitness effects of LOH events and reciprocal hemizygosity of candidate genes to identify mito-nuclear incompatibilities. This research will clarify the role of LOH in genome evolution and hybrid fitness, provide insight into the genetic basis of mito-nuclear incompatibility, and establish LOH as a potentially important driver of adaptation and evolutionary change.

D-20
Different prey species affect fitness and transcriptomes of their amoebal predator Dictyostelium discoideum

Heng Liang, Washington University at St. Louis
Margaret Steele, Texas Tech University
Weilong Yang, University of Nebraska–Lincoln
Kaifeng Hu, Washington University at St. Louis
Joan Strassmann, Washington University in St. Louis
David Queller, Washington University in St. Louis

D-21
Does size really matter?: Inner ear shape and vestibular constraints in metamorphic frogs

Chloe Addiego, Cornell University
Jackson Phillips, Cornell University
Molly Womack, Cornell University

Abstract:

Miniaturized frogs of the genus Brachycephalus exhibit poor landing orientation following jumps, a deficit that may stem from morphological constraints on their vestibular system. Several explanations exist, including that their inner ears may be disproportionately small relative to body size, or the shape of the inner ear itself may deviate from what is functionally typical in most frog species. To distinguish between these possibilities, we examined whether Brachycephalus inner ear morphology diverges from the typical growth path that inner ear shape follows from metamorphic frogs, which begin at body sizes comparable to Brachycephalus, to adult frogs with normal orientation abilities. Using geometric morphometrics, we landmarked inner ear structures across a phylogenetically diverse sample of frog species spanning size and life-stage categories: Brachycephalus, metamorphs, small non-Brachycephalus adults, and typical-sized adults. Principal component analysis of landmark coordinates revealed three distinct groupings in morphospace. Typical-sized adults and miniaturized non-Brachycephalus adults overlap considerably, suggesting that inner ear shape converges on a shared form across a broad range of adult body sizes. Metamorphs occupy a separate region of morphospace, consistent with a transitional ontogenetic stage in inner ear development that has not yet reached the adult form. Brachycephalus, however, cluster apart from all other groups, including metamorphs of comparable body size, indicating that their inner ear shape is not simply an arrested or scaled-down version of the typical developmental trajectory, but a genuine morphological divergence. Taken together, these results suggest that the vestibular deficit observed in Brachycephalus may reflect this derived inner ear morphology rather than body size constraint alone. Future work will expand sampling of species at each life stage and incorporate behavioral assays of jumping

orientation in metamorphs to clarify the functional relationship between inner ear shape and orientation ability across ontogeny.

D-22
Habitat versus History: Assessing the Roles of Ecology and Phylogeny in Tadpole Brain Morphological Variation

Emma Poplyk, Cornell University
Jackson Phillips, Cornell University
Molly Womack, Cornell University

Abstract:

Across tetrapods, major brain regions are homologous, yet their relative sizes and shapes vary considerably between classes and even between species.This morphological variation is thought to be influenced by multiple factors such as phylogeny, ecology, behavior, and the degree of sensory specialization; however, the extent these factors contribute to the variation remains poorly understood. Tadpoles offer a unique system to study these factors. Because tadpoles undergo metamorphosis, a dramatic reconstruction of their bodies, brain morphology in tadpoles is expected to reflect the specific sensory and ecological demands of their environment. Thus, this exploratory study aims to characterize shape variation of key brain structures in tadpoles. To investigate this, micro-CT scans of 36 tadpole species were used. We segmented the brains using VGstudio, and applied a landmark scheme to analyze structural variations via 3D morphospace. We used a principal component analysis to analyze and visualize the variation in brain shape. However, species do not seem to be clustered according to phylogeny, but rather by their ecology. An ANOVA statistical analysis test revealed that ecology was a statistically significant driver for the variation in brain shape between tadpole species. Our findings suggest that tadpole brain shape may be adapted to ecological niches rather than constrained by phylogenetic inertia. This research lays the groundwork for future studies that focus on whether tadpole brain shape is constrained by the chondrocranium, and whether individuals of the same species have significant structural variation.

D-23
Transcending limits: suctorial tadpoles over-develop their skulls to achieve specialized morphologies

Saty Paynter-Tavares, Cornell University
Jackson Phillips, Cornell University
Molly Womack, Cornell University

Abstract:

Tadpoles, much like their adult frog counterparts, form ecological guilds and evolve specialized morphology to exploit the available resources within their microhabitats. One habitat group in particular, ‘suctorial’ tadpoles, exhibits highly differentiated skull morphology from other ecological guilds. Curiously, suctorial tadpoles’ extreme skull morphology is exclusive to their larval stage; the

adult frogs of suctorial tadpoles exhibit relatively normative skull morphologies relative to other frogs hailing from other habitat groups. How do suctorial tadpoles achieve such divergent larval skull morphology? We hypothesized suctorial tadpoles' specialized morphology is achieved by overdeveloping their skull through heterochrony, which is the shift of an organism's developmental rate or timing relative to its ancestor at the same developmental stage. The interactions between shifts in timing of tadpole skull development and tadpoles' morphological specialization has been hinted at in previous literature but remains unexplored. During anuran metamorphosis, the jaw joint migrates posteriorly, and the cartilaginous skull ossifies. Thus, if we predict tadpoles to be overdeveloped, we expect them to be metamorph-like by exhibiting earlier skull ossification onset and posteriorly positioned jaw joints relative to other habitat groups. We compared relative jaw position and onset of ossification between suctorial tadpoles and four other habitat groups (referred to as "ecotypes") and show that suctorial tadpole skulls are overdeveloped through the developmental mechanisms of pre-displacement and hypermorphism. These findings highlight how heterochrony facilitates morphological specialization to an organism's environment. We encourage further exploration into the larger question of heterochrony's underrecognized contributions to speciation and diversification across the tree of life.

D-24

corpus: automating structured data retrieval from the taxonomic literature

Samuel Church, New York University
Felipe Zapata, University of California
Maciej Mańko, University of Gdańsk
Casey Dunn, Yale University

Abstract:

At the foundation of biodiversity work sits the taxonomic literature: original species descriptions, revisions, monographs, and catalogues accumulated over centuries, all containing valuable data on morphology, biogeography, and identification. This literature is the shared reference system across fields of study, but as a collection of thousands and thousands of digital publications of all kinds, it is complex, heterogenous, and not always easily accessible, especially for comprehensive data retrieval. This can represent a significant barrier to biodiversity research that can slow or limit progress when new findings often require urgency (e.g. to confront or record diversity loss). Recent developments in artificial intelligence and large-language models hold considerable promise for facilitating a synthesis of the literature. Here we present `corpus`, a new pipeline for converting a directory of pdfs into a queryable knowledge-base of text, figures, and taxonomic references. Our pipeline generates a structured dataset from thousands of pdfs within a matter of hours, and uses these data to construct a model context protocol (MCP) server to allow for large-language model driven searches across languages, structures, and formats. This pipeline can be used to increase access to the taxonomic literature and to automate tasks of building character matrices, summarizing taxonomic histories, or generating species and clade level reports.

D-25

Differential gene expression during chill coma recovery in Charidotella sexpunctata

Diksha Gambhir, Boston University
Lynette Strickland, Boston University

Abstract:

Chill coma, a reversible neuromuscular dysfunction triggered by suboptimal temperatures, has helped insects to adapt to colder temperatures. Chill coma recovery time (CCRT), the time taken by insects to become active and recover from this cold-induced paralysis, is an important physiological mechanism influencing adaptation and geographical distribution in insects. While chill coma recovery times have been studied in different tortoise beetles, the molecular mechanisms behind the chill coma recovery remains understudied in these species. In this study, we aim to understand the cold weather adaptation of tortoise beetle, Charidotella sexpunctata, through chill coma recovery. C. sexpunctata belongs to the tribe Cassidinae within the family Chrysomelidae, for which genomic resources remain limited. Currently, no chromosome-level genome assemblies exist in tribe Cassidinae. To address this gap, we first generated a chromosome-level, haplotype-resolved genome assembly for C. sexpunctata. To examine the chill coma recovery, live adult beetles of C. sexpunctata were placed in an ice bath for two hours to induce chill coma. The beetles were then collected at 0-, 2-, 5-, 7- and 9-minute intervals after the coma and RNA was extracted from the beetles at these intervals to capture gene expression during chill coma recovery. Through our study, we will identify the genes that are differentially expressed across the different time intervals during recovery and evaluate the candidate pathways contributing to cold tolerance in this species. These findings will further help in the comparative studies involved in adaptations and species distribution of tortoise beetles.

D-26
Comparative analysis of P-matrixes reveals evolution of genetic constraints on wing patterns in Polyommatinae butterflies

Bhagya Amarasinghe, Utah State University

D-27
Does male preference contribute to reproductive isolation in the California Vole, Microtus californicus?

Miles Johnstone, University of Caliifornia Riverside
Harrison Lin, University of California - Riverside
Polly Campbell, University of California Riverside

D-28

Searching for natural selection through time in ancient Fuego-Patagonia

Jillian Taormina, University of Connecticut
Christina Balentine, University of Connecticut & Dartmouth College
Marta Alfonso-Durruty,
Flavia Morello,
Miguel Vilar,
Manuel San Román,
Deborah Bolnick, University of Connecticut

Abstract:

The Americas were one of the last places on the globe to be populated by humans, with the southernmost regions of South America, Tierra del Fuego and Patagonia (Fuego-Patagonia), being occupied for the past 12,500 years. As groups of early hunter-gatherers adapted both biologically and behaviorally to the different environments of the region, populations developed varied gene pools, cultures, and languages. Groups settling in the western archipelagos relied mostly on a marine-rich diet, while groups in the eastern plains predominantly utilized terrestrial resources. This division of subsistence strategies may have led to potentially uneven adaptations, such as to arsenic-containing drinking water, or high iodine levels stemming from a marine-rich diet. Genetic adaptation to improve arsenic metabolism has been observed further north along the Andean mountains, while changes related to consuming iodine-rich seafood have been noted in other archipelago-residing and island populations. Here, we investigate potential genetic changes related to these environmental exposures using new and previously published pseudohaploid genomic data from 61 Fuegian-Patagonians dating 6,800 to 100 years ago. We ran logistic regression analyses to assess changes in the presence/absence of candidate single-nucleotide polymorphisms (SNPs) over time in ancient Fuegian-Patagonians. While most alleles showed no change over time, the two subgroups had separate alleles that did show a decreased presence over time, highlighting the consequences of specializing on different subsistence strategies. However, no significant trends were identified in the presence/absence of candidate SNPs through time in the marine subsistence or terrestrial subsistence groups, nor in the full Fuegian-Patagonian population sample. Future analyses include additional ancient DNA sequencing to expand this dataset for examining loci related to both arsenic and iodine metabolism, as well as genome-wide selection scans to determine if other loci have shown significant changes over time in this geographic area.

E-01

Regulatory Divergence Is Structured by Genetic Distance

Ashutosh Sharma, Purdue University
Brian Metzger, Purdue University

Abstract:

Variation in gene expression is a major source of phenotypic diversity, adaptation, and species divergence. A central question in evolutionary genetics is how regulatory differences accumulate through time and whether expression divergence is driven primarily by cis-regulatory variants, trans-regulatory factors, or both. Allele-specific expression analysis in F1 hybrids estimates regulatory divergence by directly measuring cis effects, while trans effects are inferred from parental and hybrid expression. However, hybridization becomes increasingly difficult with greater genetic divergence, restricting most ASE studies to closely related taxa and limiting inference across broader phylogenetic scales. To address this gap, we reanalyzed cis- and trans-regulatory divergence across eukaryotes. Our objectives were to develop a bias-aware ASE framework that minimizes technical artifacts in cis-trans estimation, evaluate how biological and technical factors influence inferred regulatory patterns, and quantify regulatory divergence across evolutionary distances. We compiled ASE datasets from 47 intra- and interspecific studies spanning diverse eukaryotic lineages. To place these comparisons within a common evolutionary framework, we estimated pairwise genetic distances from whole-genome sequencing data using an alignment-free k-mer approach. Applying a standardized analytical pipeline across all datasets revealed that biological and technical factors influence regulatory divergence estimates. Sequencing depth affected detection of regulatory classes, highlighting the importance of accounting for technical variation in comparative ASE analyses. Biologically, conserved regulatory patterns declined with increasing genetic distance, consistent with progressive divergence of regulatory architecture among lineages. Trans-regulatory divergence was common at short evolutionary distances but declined with increasing divergence, whereas cis-regulatory divergence exhibited a gradual positive relationship with genetic distance, suggesting long-term accumulation and persistence of cis-regulatory changes. This study advances our understanding of how regulatory divergence evolves across eukaryotes and provides a comparative framework for future research on gene regulation, evolutionary genomics, phenotypic diversification, and the molecular mechanisms underlying adaptation and species divergence.

E-02
Reproductive Isolation between Two Populations of Creeping Voles (Microtus oregoni)

Emma Knoles, University of California
Polly Campbell, University of California Riverside

Abstract:

In the creeping vole, Microtus oregoni, non-disjunction in the male germline results in sex-specific transmission of both sex chromosomes. This species is unusual in having two X chromosomes and no canonical Y chromosome. The paternal X chromosome (Xp) is only present in males whereas the maternal X (Xm) is present in the somatic cells of both sexes but is only transmitted through females. Although female somatic cells have only one X chromosome (XmO), selective mitotic nondisjunction in the germline results in all eggs carrying Xm. Sperm, in contrast, carry Xp or no sex chromosome at all. Dramatic differences in sex chromosome length were recorded between M. oregoni populations in Oregon (OR) and Washington (WA). The WA Xp chromosome is much larger than that in the OR population, whereas the Xm is larger in OR than in WA. This contrast indicates independent evolution of the sex chromosome system in OR and WA voles. Preliminary lab crosses between WA- and OR-derived voles uncovered partial sterility in F1 hybrids. We paired F1 males and females from reciprocal interpopulation crosses with tester individuals from the OR population, evaluated reproductive output, and assessed relative testis size, sperm count and sperm motility in F1 males. To date, 2/6 F1 females produced litters and 1/10 males sired a litter. Reproductive assays on F1 males revealed sterility phenotypes ranging from reduced relative testis size and low sperm count with no sperm motility, to normal testis size and sperm count but no sperm motility. These preliminary results suggest that early-acting Bateson-Dobzhansky-Muller incompatibilities are polymorphic in OR/WA crosses whereas late-acting incompatibilities affecting sperm motility may be fixed. Evaluating the contribution of the sex chromosome polymorphism to these incompatibilities is an important next step.

E-03
Microbes as manipulators of egg size and developmental evolution

Matthew Kustra, University of California
Tyler Carrier, University of North Carolina at Charlotte

Abstract:

Marine invertebrates mainly reproduce by energy-poor eggs that develop into feeding larvae or energy-rich eggs that develop into non-feeding larvae. The factor(s) responsible for driving transitions in reproductive strategy and developmental mode remain elusive despite having been studied in detail. Microbes may be one such factor, as they are functionally beneficial to animal reproduction and have evolved mechanisms to override components of this host program. We identify the first suspected reproductive manipulator in the ocean and then presents theoretical

models that support the premise that this type of microbe could serve as the selective agent of these developmental transitions. Specifically, these models outline the predicted circumstances by which these microbes may spread within populations. They then predict that microbial manipulators would create a sperm-limited environment that selects for larger eggs by shifting the host's sex ratio towards female dominance and, as a result, serve as an evolutionary driver of transitions in the developmental mode for marine invertebrates. Lastly, we suggest candidate marine invertebrate genera from throughout the world's oceans that fit the framework of a microbe-induced switch between these predominate reproductive strategies.

E-04
A quantitative genetic simulation of the missing fraction under phenotypic plasticity and viability selection

Olivia Brown, Auburn University
Matthew Wolak, Auburn University

Abstract:

Phenotypic plasticity and viability selection can both cause large shifts in the means and variances of key ecological traits within populations. Inherently, reaction norms exclude individuals who die prior to expressing the focal trait, thus ignoring changes in trait distributions caused by viability selection. When the environmental gradient along which plasticity is being quantified is also a source of viability selection removing individuals with certain phenotypes prior to measurement, reaction norms exclude non-random portions of the trait distribution. This missing fraction has the potential to bias estimates taken from these distributions. To assess the potential implications of the missing fraction, we simulated four scenarios (plasticity and viability selection, no plasticity and no viability selection, no plasticity and viability selection, and plasticity and no viability selection). For each scenario, we fit quantitative genetic generalized linear mixed models with mass and juvenile survival in two environments as the four response variables and estimated genetic correlations between mass and juvenile survival for each sex. We compared the posterior distributions of the estimated genetic variances and correlations of G-matrix with the true values to evaluate how the missing fraction introduces biases across the four scenarios, and in doing so, we demonstrate how to identify these cases and suggest ways to separate viability selection from plastic responses when estimating reaction norms.

E-05
Quantifying and Understanding Trichome Variation in Medicago spp. with a Trained Machine Learning Model

Michelle Artiga Rivera, University of Pennsylvania

Abstract:

Plants have developed a variety of traits to increase their fitness in the face of constant exposure to abiotic and biotic stress. Among these adaptations are anatomical structures known as trichomes, which are hair-like defense structures on their epidermis. While trichomes can provide vital protection from herbivory, water loss, and high temperatures, the presence of these structures varies greatly within and across species in the Medicago genus. Hence, this study sought to understand what factors contribute to the expression and evolution of trichome density in the Medicago genus. Trichomes were quantified utilizing a newly developed automated machine learning model. Our results showed that rhizobia mutualism only significantly affected trichome density in one of the nine species, while climate at ancestral sites significantly affected trichome expression in multiple species, but the direction of some of these effects varied between species. These results suggest that trichome expression is heavily driven by genetic elements that likely arose from local adaptation to climatic factors.

E-06
Nuclear and Mitochondrial Discordance Reveals Complex Hybridization Dynamics in a Philippine Hybrid Zone

Alexandra Files, University of Kansas
Robert Moyle, University of Kansas

Abstract:

Island hybrid zones are underappreciated and often overlooked, despite the novel insights they could provide into reproductive isolation and speciation. Two species of tailorbirds (Aves: Cisticolidae), Orthotomus chloronotus and O. derbianus, hybridize in a broad contact zone across central Luzon, an island of the Philippines. Previous research using a limited number of nuclear and mitochondrial loci hinted at the complexity of this hybrid zone; mitochondrial haplotypes were strongly differentiated between species, nuclear loci showed moderate population structure, and phenotypes appeared uncorrelated with either mitochondrial or nuclear markers. To investigate these contrasting patterns, we generated whole-genome sequences for 40 birds sampled across Luzon. We found that all central Luzon samples were hybrids, with varying levels of backcrossing with O. chloronotus, and clustered with northern, allopatric O. chloronotus during genetic analyses. In contrast, the southern allopatric population of O. derbianus were consistently recovered as a distinct lineage. These allopatric O. derbianus possessed highly divergent mitochondrial genomes but showed relatively low autosomal differentiation from hybrids and allopatric O. chloronotus. Furthermore, loci on the Z chromosome and three neo-Z chromosomes

exhibited moderate population structure. Together with the distinctive mitochondrial haplotypes, these data suggest sex-biased gene flow within this insular hybrid zone.

E-07
Chromosome Scale Assembly of three novel Caenorhabditis species

Lara Arbex Herden, FIU
Michelle McCauley, Florida International University
Tori Eggers, Florida International University
Karolina Willicott, FIU
Janna Fierst, Florida International University

Abstract:

Much of what is currently known about nematode biology comes from a small number of model species, particularly Caenorhabditis elegans. This species has been indispensable for understanding development, genetics, and genome evolution, but C. elegans represent only a small fraction of nematode diversity. Expanding genomic representation beyond established model organisms is essential for studying the evolution of this clade and reconstructing a more complete picture. To address this gap, we present three novel genome assembly and annotations of Caenorhabditis species #59 (strain JU3778), C. species #61 (JU4110) and C. species #65 (JU4118). Unlike C. elegans, these species are dioecious, with distinct male and female sexes, reflecting a reproductive strategy that is likely ancestral within the genus. Using Hi-C and PacBio HiFi long-read sequencing, we generated high-quality, chromosome-level assemblies with comprehensive gene annotations. These resources will expand the comparative genomic foundation within the genus and strengthen the phylogenomic framework for Caenorhabditis, supporting future studies of reproductive mode evolution, species divergence, and the breadth of biological diversity that remains unexplored even within well-studied groups.

E-08
Male frequency does not predict inbreeding depression or recovery across diverse C. elegans strains

Jasbelle Sosa, Florida International University
Steve Abraham, Florida International University
Gabriel Blanco, Florida International University
Rohit Kapila, Florida International University
Janna Fierst, Florida International University

E-09
Investigating the relationship between variation in rDNA copy number and life history traits

Elizabeth Doty, University of Iowa

Abstract:

Asexual lineages experience little to no recombination relative to sexual counterparts, a feature of their biology that is often assumed to explain why these lineages are not more widely successful. We here evaluate whether structural variation in the copy number of an important class of genes, rDNA, that does not rely on recombination could generate meaningful and heritable phenotypic variation. We leverage striking across-asexual lineage variation in rDNA copy number in the New Zealand freshwater snail Potamopyrgus antipodarum to ask whether these differences in rDNA copy numbers are (1) associated with rDNA gene expression levels, and (2) variation in life-history traits known to be linked to rDNA abundance, like individual growth rate and time to reproductive maturity. We will be quantifying ribosomal DNA transcriptional output with Droplet Digital PCR (ddPCR) to measure rRNA abundance across a diverse range of asexual P. antipodarum lineages that vary as much as sixfold in rDNA copy number. These expression data will be paired with growth rate and age at maturity estimates from each lineage to evaluate potential relationships between genomic variation and fitness-related traits. Together, these data will provide information relevant to understanding the generation and maintenance of genomic variation in the absence of sex, with potential relevance to the maintenance of sex in nature.

E-10
Phylogenetic Estimation of Diversity-Dependent Biogeographic Rates using Deep Learning

Albert Soewongsono, Washington University in St. Louis
Michael Landis, Washington University in St. Louis

Abstract:

Ecological theory predicts that local species richness can influence biogeographic rates of speciation, extinction, and dispersal. For instance, increasing the number of competing species within a region may cause local speciation and dispersal rates to decrease but local extinction rates to increase, inducing a carrying capacity for local species richness. In this article, we introduce a fully generative, event-based phylogenetic diversification model, called DDGeoSSE, that allows diversity-dependent effects of local species richness to modulate biogeographic rates of diversification and range evolution. DDGeoSSE can accommodate and test a variety of alternative diversification scenarios that involve positive, negative, and neutral interactions among sympatric species for speciation, extinction, and dispersal. We derive mathematical and statistical properties of biogeographic outcomes generated by this model, such as the carrying capacity for a clade at equilibrium, which we validate through simulation. Because diversity-dependent phylogenetic models typically do not have tractable likelihood functions, we use deep learning with phyddle to perform parameter inference and model selection. Separately applying DDGeoSSE to Caribbean Anolis lizards and cloud forest-dwelling Viburnum plants, we find evidence that local species richness plays a significant role in shaping diversification dynamics for both clades.

F-01

Molecular identification of bacteria with potential influence on the anhydrobiotic capacity of Paramacrobiotus fairbanksi Schill, Förster, Dandekar & Wolf, 2010 (Tardigrada)

Dr. Pushpalata Kayastha, Florida International University
Kacper Socha, University of Gdansk
Magdalena M. Bartylak, Adam Mickiewicz University in Poznań
Edyta Konecka, Adam Mickiewicz University in Poznań
Łukasz Kaczmarek, Adam Mickiewicz University in Poznań
Aleksandra Naczk, University of Gdansk
Jason Pienaar, Florida International University
Monika Mioduchowska, University of Gdansk

Abstract:

The microbiome of invertebrates, including tardigrades (Tardigrada), has attracted increasing attention because of its potential influence on host physiology and stress tolerance. However, the mechanisms underlying anhydrobiosis, which enables tardigrades to survive extreme dehydration, remain incompletely understood. In this study, the microbiome composition of Paramacrobiotus fairbanksi was investigated across developmental and physiological stages associated with short-term (7-day) and long-term (120-day) anhydrobiosis to determine whether anhydrobiotic ability is linked to a specific microbiome structure.

Individuals representing different developmental and physiological stages were subjected to DNA isolation followed by amplification of the bacterial 16S rRNA V3–V4 region and next-generation sequencing (NGS). Bioinformatic and statistical analyses were used to compare microbiome diversity and composition among stages.

Relative abundance analyses of the ten most prevalent bacterial genera revealed shifts among developmental and anhydrobiotic stages, although these differences were not statistically significant. In contrast, alpha diversity analyses based on Shannon–Wiener and Simpson indices demonstrated significant differences among samples. Taxonomic classification identified 16 bacterial genera shared across all analyzed microbiomes, while each stage possessed a distinct set of bacterial taxa. Similarity analyses revealed clear microbiome differentiation between early physiological stages and prolonged anhydrobiotic stages, which was further supported by SIMPER analyses.

Several identified bacterial taxa included thermophilic bacteria and bacteria associated with trehalose synthesis and biofilm formation, traits potentially linked to desiccation survival and rehydration. These findings demonstrate dynamic microbiome restructuring during anhydrobiosis and suggest that specific bacterial communities may contribute to the anhydrobiotic capacity of P. fairbanksi.

F-02

A Coalescent Framework for Inferring the Timing of Unfixed Gene Duplications

Hongxi Li, Indiana University Bloomington
Matthew Hahn, Indiana University

F-03

Fast or accurate: comparing steppingstone and model averaging for model selection

Kaitlin Languirand, Southeastern Louisiana University

F-04

Acoustic responses in a Neotropical treefrog: Testing for population-level differences

Pedro Aguiar, Federal University of Juiz de Fora
Renato Nali, Universidade Federal de Juiz de For a

F-05

Resolving Taxonomic Boundaries and Hybridization in the Genus Ellipsoptera

Skylar Godwin, Rice University
Scott Egan, Rice university
Daniel Duran, Rowan University

Abstract:

The genus Ellipsoptera represents a diverse clade of tiger beetles with 13 historically described species and 28 subspecies. However, the evolutionary relationships and taxonomic boundaries within this highly variable and broadly distributed genus remain unresolved. This study will use population genomics and phylogenetic reconstruction of the Ellipsoptera clade to address this taxonomic uncertainty. In addition, we will test a long hypothesized hybrid zone between two closely related Ellipsoptera distributed across the eastern or western sides of the U.S. Gulf coast that overlap in the panhandle of Florida, where morphological "hybrids" have been reported. This collective work will make important contributions to evolutionary biology, taxonomy, and conservation.

F-06

Evaluating conflicting signal on an Andean clade — the case of the Neotropical blueberry genus Cavendishia (Ericaceae)

Katherin Arango-Gomez, Louisiana State University
Laura Lagomarsino, Louisiana State University

F-07
Culturing Tidal Tardigrades

Evan Reid, Florida International University
Dr. Pushpalata Kayastha, Florida International University
Alexis Mas, Florida International University
Kevin Murillo, FIU
Jason Pienaar, Florida International University

Abstract:

Tardigrades inhabiting marine intertidal zones represent an understudied yet ecologically significant group, and establishing long-term cultures of these organisms presents unique challenges, but equally unique benefits. This study presents original culturing methodology, life history documentation, and reproductive characterization for three marine tardigrade species from South Florida, including two species new to science.

Specimens were sourced through systematic field sampling of intertidal substrates at two Miami-Dade County sites: Archechiniscus biscaynei and Echiniscoides sp. D (Deering Estate) were collected from Deering Estate, while Echiniscoides sp. M (Matheson Hammock) was collected from Matheson Hammock Park. Culturing experiments were conducted to identify optimal conditions for each species, including substrate composition, salinity, temperature, and food source availability. A critical component of the long-term cultures was the establishment of algal cultures both from supplier bought Nannochloropsis strain and from algae isolated directly from the original field samples, both of which are now maintained continuously in the lab and the latter undergoing identification.

All three cultures remain active to date. A. biscaynei has been maintained continuously since September 17, 2025, while Echiniscoides sp. D have been in culture since Nov. 29th, and sp. M since Dec. 7th respectively, representing some of the longest sustained cultures documented for marine heterotardigrades. Reproductive mechanisms were documented for all three species, with photographic and video footage captured of eggs, juveniles, and all subsequent life stages, providing a comprehensive developmental record that will serve as foundational data for forthcoming species descriptions. A formal life history table compiling developmental data across all three species is in progress.

Additionally, preliminary results are presented for culturing attempts of Stygarctus sp. from Key Biscayne, including culture conditions employed. Together, these findings contribute foundational methodology for marine tardigrade husbandry and pave the way for future experimental work on marine and intertidal tardigrade ecology and evolution.

F-08
Gene duplications and deletions: functional analysis of a prostate-specific protease in hominoid primates

Neil Rossman, Duquesne University

Abstract:

Primates utilize a wide range of mating strategies, resulting in vastly different pre- and post-copulatory selective pressures. For example, gorillas (Gorilla gorilla) live in single-male multi-female social units, whereby the male controls mating access through threats and fighting with other males. Conversely, chimpanzees (Pan troglodytes) live in multi-male multi-female social groups, with female chimpanzees commonly mating with multiple males, resulting in intense sperm competition. This variation in the mode and intensity of sexual selection is reflected in the differential evolution of primate male reproductive genes. One example is Kallikrein-like peptidase 3 (KLK3), a prostate-specific serine protease. KLK3 is a relatively young gene, having arisen from a gene duplication of KLK2 in the ancestor of Old World monkeys and apes, and subsequently neofunctionalized through substitutions that switched the substrate preference from a trypsin-like protease to chymotrypsin-like. In humans, KLK3 cleaves cross-linked semenogelin proteins following ejaculation, freeing entrapped sperm. Previous research has identified significant differences in KLK3 enzyme kinetics between primate species, with chimpanzees showing elevated KLK3 catalytic efficiency relative to humans. Interestingly, both the gorilla and gibbon (Hylobates spp.) lineages have independently experienced a genomic deletion event involving KLK2 and KLK3, resulting in a merged reading frame and a subsequently translated "chimeric" KLK (cKLK). To determine whether these chimeric enzymes have reverted to a broad substrate specificity, or have retained the specificity of one or the other "parent" genes, we expressed and purified them as recombinant proteins in a mammalian cell culture system and tested their enzyme activity through in vitro assays against a variety of substrates. Our results demonstrate that both cKLKs are KLK3-like (i.e., chymotrypsin-like) in their substrate specificity, showing little to no activity against KLK2 substrates. Additionally, we found that these cKLKs have relatively low catalytic efficiency, consistent with the low intensity of sperm competition facing these species.

F-09
The Effect of Urbanization on Tardigrade Species Composition

Ana Perezsanchez, Florida International University
Pushpalata Kayastha, Florida International University
Evelyn Vides-Argueta, Florida International University
Georgina Ale, Florida International University
Kevin Murillo, Florida International University
Jason Pienaar, Florida International University

Abstract:

Limnoterrestrial tardigrades are aquatic micro animals that live in the water pockets of mosses and lichens. They are best known for their tolerance to extreme environments that include extreme radiation, cold and hot temperatures, desiccation, and even the vacuum of space. More recently, tardigrades have become the subject of interest as potential model systems due to these anhydrobiotic capabilities. However, diversity patterns of tardigrade communities are still

unknown, where only a handful of species' distributions are well characterized. Larger scale sampling efforts across US regions are still needed, and more importantly the consideration of urban areas as habitats, since not only have tardigrades been persistently found in such areas, but their distribution can also vary. The objective of this study will be to explore the ecological association between tardigrades and environmental human intervention. As well as whether their community composition is affected across an urbanization gradient. Thus, this study aims to address two questions. The first being an ecological question: Does community composition change across an urbanization gradient? Thus, I hypothesize that diversity increases the lower the degree of urbanization goes (urban, suburban, rural, and wilderness), where some species of tardigrades may show specificity to urbanized areas. This question will be addressed by 1) establishing an urbanization gradient sampling scheme, from most urbanized to least urbanized areas (urban, suburban areas, agricultural, wilderness areas), across Alabama. As well as 2) Using an integrative taxonomical approach, including morphological traits, and molecular analysis of barcodes species differentiation. Further understanding tardigrade species patterns could give us a better insight into how different tardigrade species interact and adapt to altered environments, especially manmade environments. And whether these distribution patterns are the result of species variability in extremotolerance abilities.

F-10
Using Satellite-Derived Census Size to Predict Genomic Inbreeding in Giant Kelp (Macrocystis pyrifera)

Defne Clarke, University of California Santa Cruz

Abstract:

The effects of small effective population size on genetic health are well established. Small population problems, such as increased magnitude of genetic drift and inbreeding, can erode genetic diversity and increase mutation load over time, leading to smaller and smaller population sizes. Genomic information can be expensive and time-consuming to obtain, so the ability to predict genetic health metrics using existing data sources is a conservation priority. Here, we ask if census population size, estimated from satellite imagery, can reliably predict genetic health metrics of giant kelp (Macrocystis pyrifera) along the California coast. Using low-coverage whole-genome sequencing data from the California Conservation Genomics Project (CCGP), we estimated Watterson's theta and inbreeding coefficients for M. pyrifera populations distributed along the California coast, then tested for correlations with 40-year mean canopy biomass derived from satellite imagery. This information will help managers evaluate the genetic health of kelp populations and more effectively assign conservation resources, as well as inform our understanding of how genetic diversity scales with population size estimates in this system.

G-01
Diversification of growth strategies as antipredator adaptations among closely related land snails

Yuta Morii, Hirosaki Univ

Abstract:

Predators may cause diversification of life-history traits between closely related prey species or between ecotypes within a species. Several possible instances of the diversification of life-history traits have been demonstrated between predator- and predator-free environments. Although divergence of life-history traits might result in speciation, evidence on this idea—the predator-driven speciation hypothesis—is insufficient both theoretically and experimentally, and there is also no information on the sympatric divergence patterns of life-history traits in prey species. Recent research proposed that two land snails, Karaftohelix editha and K. gainesi (Camaenidae, Stylommatophora), and their shared predators, malacophagous carabid ground beetles, distributed in northern Japan, can be an excellent model to explore the prey divergence via antipredator adaptations for some reasons. Although these two species were indistinguishable using several neutral DNA markers and shared their distribution area and habitats almost completely, there were vast inter-specific differences in various phenotypic traits, and almost all of them appeared to function as antipredator strategies. In this study, the ontogenetic growth patterns of K. editha and K. gainesi and their candidate ancestral species K. blakeana were investigated, which revealed several inter-specific differences in growth strategies. For instance, K. editha and K. blakeana, linearly increased their shell thickness throughout the entire growing stages, whereas K. gainesi drastically changed the growth rate of shell thickness along with each growing stage. All inter-specific differences discovered in this study may function efficiently as species-specific antipredator strategies for each species.

G-02
Evaluating cryobiosis across tardigrade taxa and tackling the anhydrobiotic carryover hypothesis

Neil Hinduja, Florida International University
Pushpalata Kayastha, Florida International University
Evan Reid, Florida International University
Jason Pienaar, Florida International University

Abstract:

Microscopic ecdysozoans of the phylum Tardigrada, commonly referred to as tardigrades, are known to exhibit remarkable tolerance to a vast array of environmental stressors. Among the most documented are their robust capability to survive complete dehydration, ionizing radiation, and extreme temperatures. While desiccation tolerance has been explored extensively, freeze tolerance in hydrated tardigrades (cryobiosis) remains comparatively understudied, and even less understood

is its evolutionary emergence. Some hypothesize that cryobiotic functionalities are co-opted from anhydrobiosis, while others posit it an independently-evolved mechanism. The present study evaluates the freeze-tolerance capabilities of Hypsibius exemplaris (freshwater), Paramacrobiotus experimentalis (limnoterrestrial), and Archechiniscus biscaynei (tidal) in the hydrated state to assess variation across an ecological and desiccation-prone environmental gradient. Additionally, measured expression of Cytoplasmic Abundant Heat Soluble (CAHS) proteins and conferred viability during cold exposure are utilized to further evaluate the possibility of cryobiotic mechanisms being evolutionary carryover from desiccation tolerance. By integrating survivorship assays with molecular analysis across species occupying different habitats, this study aims to provide insight into both the diversity and cross-tolerance relationships of cryobiotic capabilities in tardigrades.

G-03

How do homologous transcription factors diverge in regulatory function across species

Shunxin Zhou, Purdue University

Abstract:

Transcription factors are master regulators that coordinate large downstream gene programs, placing them under strong pleiotropic constraint, yet homologous transcription factors can produce detectably different regulatory outputs across species. Whether this divergence is widespread or rare, and whether it arises through changes in transcription factor dosage or protein function, remains poorly understood. This project asks: do homologous transcription factors diverge in regulatory function at the repertoire level, and what constrains them?

To address this question, an interspecific hybrid between Saccharomyces cerevisiae and Saccharomyces eubayanus is used: two lineages that diverged under distinct ecological pressures but can be crossed to produce viable hybrids. By deleting one species' allele at a time while retaining the other in an identical genomic background, I applying reciprocal hemizygosity tests across 170 homologous transcription factor pairs, the downstream regulatory consequence of each allele will be measured independently by RNA-seq, enabling direct allele-resolved comparison across the full transcription factor repertoire.

Two questions will be addressed. First, how often is divergence detectable across the 170 pairs, establishing whether pleiotropic constraint is permissive, allowing frequent divergence or restrictive, limiting it to a small fraction of accessible transcription factors. Second, which molecular route drives divergence: promoter-driven when the transcription factor locus itself shows allele-specific expression, indicating dosage-level change, or coding-driven when downstream divergence occurs without transcription factor locus expression differences, implicating functional change in the protein itself.

Together, this work will establish whether pleiotropic constraint prevents regulatory divergence or instead structures it, determining how often it occurs and channeling it through a limited set of

molecular routes. This work will provide the first repertoire-level test of whether pleiotropic burden predicts transcription factor divergence, moving toward general predictive rules for how gene regulatory networks evolve under constraint.

G-04
Differential Gene Expression Associated with Red Tail Coloration in Xiphophorus variatus

Sashoya Dougan, Stanford University
Paola Fascinetto-Zago, Stanford University
Theresa Gunn, Stanford University
Molly Schumer, Stanford University

Abstract:

In fishes, red pigmentation is often associated with signaling and can arise through specialized pigment cells such as erythrophores and xanthophores. In the swordtail fish Xiphophorus variatus, red coloration is present in the caudal fin of some individuals and, in certain males, is also expressed in the throat region. The developmental and genetic relationship between these two color traits remains unknown.

This study investigates the genetic basis and potential developmental origins of red coloration in X. variatus. To identify genes associated with red pigmentation, we compared gene expression profiles between red and non-red tissues using RNA sequencing and differential gene expression analyses. Functional enrichment analyses were conducted to identify biological processes and pathways associated with pigment development and chromatophore function. We further evaluated whether genes implicated in red coloration are shared between the caudal fin and throat, providing insight into whether these traits may arise through similar genetic mechanisms.

G-05
Sex Evolution in Exaiptasia diaphana

Hannan Shabaan, Pienaar Lab
Victoria Eggers, Florida International University
Jason Pienaar, Florida International University

Abstract:

The sea anemone Exaiptasia diaphana typically serves as a model system for studies in coral symbiosis as it's able to survive bleaching (expulsion of their symbiont). I propose that E. diaphana also serves as a model system for sex evolution. The early divergence of cnidarians within Metazoa offers insights into the evolutionary origins of complex traits, such as its sex determination mechanisms and reproductive strategies. Here I present two de-novo sex-specific assemblies of the E. diaphana clonal lineages H2 (female) and CC7 (male) to uncover genomic sex differentiations.

G-06
Evolutionary patterns in reproductive mode in Madagascar's Mantellid frogs

Anna Wilkinson, Stony Brook University
Pascal Title, Stony Brook University

G-07
Genetic Comparisons of Italian Ryegrass (Lolium multiflorum) Populations in North Carolina

Audrey Fahey, North Carolina State University
Nikolai Hay, North Carolina State University
Leigh Schwinden, North Carolina State University
Emily Hochschild, North Carolina State University
Acer VanWallendael, North Carolina State University

Abstract:

Agricultural weeds adapt and evolve resistance to herbicides in as short as 4 years. When multiple herbicide mode of action resistances are found in the same plant, the complexity of understanding the genetics behind such an evolution increases. Lolium multiflorum, or italian ryegrass, was introduced to the US from Europe as a cover crop. Now it is a weed for row crops such as corn and soybean. Various herbicides were effective against italian ryegrass until they weren't. As a last resort, paraquat was used to kill the weed. In 2020, the first case of paraquat resistance in italian ryegrass in North Carolina was reported. Using pooled sequencing of individuals from paraquat resistant and susceptible populations, an Fst analysis was conducted. The values highlight regions of genetic difference between these two populations. Analysis of nearby genes show regions of difference are near genes involved in abiotic stress response. Future functional analysis can determine whether these genetic differences or changes result in changes in expression levels or functionality in the plants and when.

G-08
Elucidating the Evolution of Olfactory Receptors

Zoya Wani, University of Houston

Abstract:

An organism's ability to sense and adapt to its environments is essential for survival, enabling it to locate food, avoid predators, and find mates. These processes are mediated by sensory systems. Among these sensory systems, olfaction is mediated by olfactory receptors (ORs), which comprise one of the most rapidly evolving gene families in vertebrate genomes. This example of dynamic evolution reflects the strong selective pressures associated with detecting environmental cues. Previous studies of OR evolution in fish and mammals have identified two major receptor

classes: Class I receptors, which primarily detect waterborne compounds, and Class II receptors, which primarily detect airborne compounds. However, little is known about OR evolution in organisms that rely on both aquatic and terrestrial environments.

Anurans provide a unique study system due to having evolved diverged life histories (biphasic, fully aquatic, direct-developing) that allow for an investigation of sensory adaptation across both aquatic and terrestrial habitats. This study examined the distribution of odorant receptor gene across anuran genomes. using a bioinformatics pipeline to identify and classify OR genes across a broad sampling of anuran species, we characterized patterns of OR gene diversity and will compare receptor class representation among taxa.

Our analyses revealed substantial variation in OR gene repertoire size across anuran species. Additionally, species with larger genomes generally had larger OR repertoires, indicating that genome expansion may facilitate sensory gene duplication and retention. The broad variation in OR repertoire size within the same life history strategy suggests that sensory evolution is likely influenced by multiple interacting factors such as ecology, genome architecture, and lineage-specific gene duplication events.

G-09
Patterns of linkage disequilibrium and recombination across 50 generations of laboratory evolution in response to salinity decline in the copepod Eurytemora carolleeae

Jinhui Wang, UW-Madison
Zhenyong Du, University of Wisconsin–Madison
Joshua DeRuyter, University of Wisconsin-Madison
Hayden Woodard, University of Wisconsin - Madison
Carol Lee, University of Wisconsin

G-10
Herbarium genomics of wild radish hybrid weed formation

Julia Harenčár, University of California

Abstract:

Invasive weeds threaten conservation and agriculture, and hybridization between weeds and their crop relatives often exacerbates invasions. I am developing invasive wild radish (Raphanus raphanistrum), which hybridizes with the crop radish (R. sativus), as a model system for uncovering the genetic and climatic drivers of crop-wild hybrid weed formation. The history of California hybrid wild radish evolution and invasion is entirely captured by over 160 years of plant collections stored in Herbaria. I am using ancient DNA techniques to sequence specimens dating back to 1864 and covering a wide diversity of climates. I am pairing this genomic data with climate associated traits like phenology and water use efficiency from isotope analysis to elucidate how selection in

different climates shapes phenotypic and genotypic outcomes of hybrid evolution. Here, I present preliminary sequencing results, phenology analysis, and next steps. I am eager to discuss and hear feedback at this early stage! By analyzing and comparing the genetics of crop-wild hybridization through time and across climates, this research will clarify how climate change influences crop-wild hybridization and how climate-mediated gene flow facilitates invasion.

G-11
Meiotic drivers and their influence on X chromosome exclusion from the male germline in the creeping vole, Microtus oregoni

Kaitlyn Venator, University of California Riverside
Emma Knoles, University of California
Polly Campbell, University of California Riverside

Abstract:

Meiotic drivers are selfish genetic elements that manipulate transmission during meiosis such that the chromosome that carries the driver is transmitted to over 50% to offspring. This can lead to reduced fertility or viability. Most species that display drive in wild populations quickly evolve suppressors, effectively restoring Mendelian inheritance. The creeping vole (Microtus oregoni) has an uncommon sex determination system with no Y chromosome and two distinct X chromosomes: a maternally transmitted X (Xm) and a male-limited X (Xp). Female M. oregoni have a single copy of Xm in somatic cells (Xm0) whereas male somatic cells have both Xm and Xp. However, Xm is excluded from the male germline and males only transmit Xp. The fact that males do not transmit Xm suggests a history of drive on this chromosome, now suppressed by exclusion from the germline. In other systems with drivers, suppression can be incomplete. The goal of this study is to determine whether this is the case in M. oregoni. Specifically, is Xm ever transmitted through males? If so, XmXm individuals should exist. Xm and Xp carry the same genes but multicopy genes are in higher copy numbers on Xp. Therefore, the copy number should be intermediate in XmXm individuals relative to Xm0 and XmXp. I used a qPCR copy number assay to test for XmXm individuals in a M. oregoni colony derived from two geographically isolated populations with distinct sex chromosome size differences. Results suggest that, if XmXm individuals exist, they are very rare. This study contributes to the understanding of a unique mammalian sex chromosome system.

G-12
Investigating the Evolutionary Origins of Copy Number Variation

Madeleine Bartz, Indiana University Bloomington