



49th Annual Meeting – June 15-18, 2025
Golden, Colorado

MEETING ABSTRACTS

Arranged by first author's last name

Presenters underlined

* designates student competition participant

TALKS

SEXUAL SIGNAL DIVERGENCE AND REPRODUCTIVE ISOLATION IN AN ADAPTIVE RADIATION OF A HAWAIIAN SPIDER

Seira Ashley Adams, Rosemary Gillespie, Santiago Ramirez
UC Davis; UC Berkeley

Studies of adaptive radiations have been central in developing our understanding of the processes involved in speciation and diversification. The explosive nature of adaptive radiation that results in exceptionally high levels of diversity over a short time has provided fruitful grounds for biologists to understand how divergence between close relatives is attained and maintained. Shifts in ecological opportunities or pressures arising from the colonization of new habitats have been shown to influence the divergence in ecological traits and are fundamental in adaptive radiations. Likewise, divergence in sexual signaling traits has also been shown to play an essential role in the reproductive isolation of many rapidly radiating lineages. However, many of the sexual signals studied to date are deeply intertwined with ecological factors that power the ecological divergence. When the divergence in sexual signals overlaps with that of ecological traits, it can be difficult to discern the initial axis of variation, whether it is in the ecological traits or sexual traits. This study focuses on how variations in sexual signaling traits are generated and selected upon using a lineage of Hawaiian *Tetragnatha* spiders that has diversified across an age-structured and ecologically similar landscape, allowing the process to

be examined at different slices in time while controlling for divergence in ecological traits. Using genomic tools in conjunction with chemical analysis of mating pheromones and behavioral responses of males to these pheromones, this study investigates the evolutionary processes underlying sexual signal divergence and reproductive isolation in an adaptive radiation of Hawaiian *Tetragnatha* spiders.
Genomics Symposium

TRACTS OF THE CENTRAL NERVOUS SYSTEM OF *ULOBORUS DIVERSUS*

Gregory Artiushin, Rohan Upadhyay, Andrew Gordus
Johns Hopkins University

An understanding of the neural correlates of behavior is predicated upon knowledge of the populations, structures, and connectivity of the nervous system. Both classic and recent studies of spider brain neuroanatomy have focused on major fiber tracts to anchor their descriptions of the nervous system, using techniques such as silver staining. We have previously established a three-dimensional immunofluorescence-based brain atlas for the model species, *Uloborus diversus*, using whole-mounted central nervous system. While describing neuropil structures and their terminal co-expression of neurotransmitter markers, the adjoining major tracts have thus far not been annotated. In the current image volumes, we employ immunostaining for β -Tubulin to trace patterns of tract connectivity throughout the *U. diversus* brain and relate the positioning to features visible with anti-Synapsin immunoreactivity. Our annotations reveal new details of fiber pathways, particularly within the supraesophageal mass, and in respect to the mushroom body, enabling comparative analysis to existing neuroanatomical findings in both cursorial as well as orb and non-orb web-building species.

Session 7: Morphology, Physiology & Development

MAKING UNDERGRADUATE RESEARCH IN ARACHNOLOGY MORE ACCESSIBLE VIA COURSE-BASED UNDERGRADUATE RESEARCH EXPERIENCES (CURES)

Anthony Auletta, Lisa Taylor, Laurel Lietzenmayer
University of Florida

Undergraduate research is a high-impact practice that provides many benefits to both students and their mentors. However, due to limitations of space, time, and funding, traditional 1-on-1 research assistantships not always available to all students who seek them. Furthermore, these barriers to research opportunities can disproportionately impact students from groups underrepresented in STEM. To address this need to make undergraduate research more accessible, we have developed a course-based undergraduate research experience (CURE) that embeds authentic research into the entomology curriculum at the University of Florida and can accommodate up to 36 students / semester. In this course, students work in collaborative teams on a novel research project alongside instructors who also serve as research mentors; students collect publishable data and thus contribute new knowledge to the field. Here we will present lessons learned from a 2024 CURE in which students investigated prey choice and the evolution of color vision in jumping spiders (Araneae: Salticidae). Paired pre- and post-course surveys indicate that students made significant gains in technical skills, critical thinking, science communication, and other metrics. A majority of students had no prior experience in research or spider biology but reported increased interest in pursuing further research opportunities and/or careers in arachnology. These findings suggest that our CURE model can provide the same benefits as traditional research experiences but on a larger scale- thus engaging and recruiting a more diverse array of

students into our discipline. We also present practical strategies for instructors interested in developing CUREs of their own.

Session 5: Education & Outreach

CO-EVOLUTION OF MOLECULAR AND MATERIAL PROPERTIES OF AGGREGATE GLUES

Nadia Ayoub, Richard Baker, Thomas Clarke, Sandra Correa-Garhwal, Cheryl Hayashi, Kyle Friend, Brent Opell

Washington & Lee University; American Museum of Natural History; Suffolk University; Virginia Tech

Orb web and cobweb weaving spiders in the superfamily Araneoidea are distinguished by their ability to make a chemically sticky aqueous glue in specialized aggregate silk glands. Aggregate glue is an environmentally responsive material that has evolved to perform optimally around the humidity at which a spider forages. Composite proteins and their post-translational modifications likely confer stickiness to the glue, but the identities of these proteins have only been described for a few species. Using proteomics, we documented the glue composition in 17 species including 4 cobweb weavers (Theridiidae) and 13 orbweb weavers (Tetragnathidae and Araneidae). Glue composition is more complex than fiber composition with 30-60 proteins found in each species' aggregate-lined prey capture threads. Aggregate spidroins, cysteine-rich proteins, and a few other classes of proteins are consistently found in all species, but the relative composition varies considerably. We will relate this variation in molecular composition to variation in material properties of glue droplets across the araneoid phylogeny.

Session 4: Silks & Venoms

THE OPILIONES OF MEXICO: A COURSE RETROSPECTIVE

Ryan Bacon, Edmundo Gonzáles-Santillán, Mercedes Burns

University of Maryland, Baltimore County; National Autonomous University of Mexico

Opiliones is the third most diverse order of arachnids, with more than 6,600 described species worldwide. An estimated 230 species of Opiliones are thought to occur in Mexico, however, knowledge of Opiliones in this region is comparatively limited. Many of these 230 species are only known from outdated texts, and the majority of these descriptions lack critical information and/or are based on a single individual. This lack of information is reinforced by a dearth of current researchers focused on the region. In 2024, a course funded by the International Society of Arachnology was curated and taught at the National Autonomous University of Mexico (UNAM), with the goal of increasing local knowledge and interest in Opiliones. This goal was successful, with 21 local graduate and undergraduate students enrolling in the course. Participants were introduced to the four suborders of Opiliones that exist in Mexico, including their morphology, physiology, behavior, identification, and evolutionary history. Utilizing material held within the Arachnid biological collection at UNAM, as well as time spent collecting specimens, provided students with significant hands-on training. The Opiliones of Mexico was the first course of its kind in the region and served to expand the study of Opiliones, while simultaneously providing identifications to previously uninvestigated specimens in the Arachnid collection. Improved documentation of material within the National Collection of Arachnids, combined with course revisions driven by elicited student feedback, will help reinvigorate arachnology research in Mexico and forge connections amongst local investigators.

Session 5: Education & Outreach

GENE REGULATORY NETWORKS UNDERLYING MALE WEAPON POLYMORPHISM IN OPILIONES

Jesús A. Ballesteros, Sophie M. Neu, Ethan M. Laumer, Prashant P. Sharma
Kean University; University of Wisconsin-Madison

Sexual selection is an intensively studied process that has yielded some of the most spectacular traits in nature, spanning ornaments, complex behaviors, and weapon. In species that exhibit male weapons used for combat or threat displays, male polymorphism of secondary sexual characteristics commonly occurs as a function of male body condition. How such polymorphisms arise and are maintained across phylogenetic scales is a key question in evolutionary biology. One arthropod group renowned for sexually polymorphic male traits is the arachnid order Opiliones. Multiple lineages of Opiliones have independently evolved exaggerated weapons, which include spines on the legs and body, hypertrophied chelicerae and pedipalps, and enlarged cheliceral horns. One of limitations to exploring the genetic basis of this phenomenon has been the lack of reliable genomic reference, as well as the acquisition of tissues at selected developmental stages that would allow the comparative framework to explore this phenomenon. Here we generated RNA-seq libraries for developing chelicerae of male and female *P. opilio* in stages immediately preceding horn formation. Reads were mapped to a high quality reference genome of this species. Sequencing of cheliceral tissue identified the first candidate genes potentially underlying the expression of the weapon polymorphism in this arachnid. Using an algorithmic approach, we reconstructed gene networks that appear to underlying the horn polymorphism and compared these to counterpart datasets from insect weapons.

Genomics Symposium

SEX DIFFERENCES IN WHIRLING BEHAVIOR IN *PHOLCUS PHALANGIOIDES*

Alexander Berry
Buena Vista University

Predation is a risk for most species. As such anti-predator behaviors are common among many animals. The cellar spider *Pholcus phalangioides* displays a complex antipredator behavior known as whirling, where the spider rapidly spins in its web and is thought to visually confuse the predator. We set out to examine if there were differences in the whirling behavior between males and females. We tested this by using a simulated predator stimulus to trigger whirling and then videoing both males and females. We then analyzed the videos for speed, duration, the shape of the whirling pattern, and other components of the whirling behavior. We found significant differences between males and females in whirling behaviors, such as males whirling faster than females and females whirling in a more elliptical pattern than males. Females were also more likely to whirl in response to our stimulus. Some of these differences may be due to differences in biology or willingness to abandon a web, but others may indicate differences in whirling strategy or differences in the effectiveness of whirling as an anti-predator behavior.

Session 6A: Behavior

THE EFFECTIVENESS OF TACTILE OUTREACH EXPERIENCES FOR NON-CHARISMATIC INVERTEBRATES

Jackie Billotte, Tara Teel, Ruth Hufbauer, Richard R. Reading
Colorado State University

Experience-based outreach can have a stronger impact on a person's attitudes and beliefs than one based on only providing facts. Ambassador animals are commonly used in experience-based public

outreach. The term “ambassador animal” is typically used to refer to an animal housed full-time at a facility and habituated to being around people, such that it can be used for outreach or education. The “Rosie Experience” at the Butterfly Pavilion, in Brighton Colorado allows guests of the zoo the opportunity to hold a live tarantula. Tarantulas, like most spiders, suffer from a “public image” problem and are seen as uncharismatic fauna. Guests of the Rosie Experience exhibit were asked about their beliefs and views regarding spiders before holding Rosie, then again six days and three months after folding Rosie to assess the effectiveness of a tactile, interactive outreach experience with non-charismatic fauna. A hierarchical model of cognition was used to provide a way to understand the public’s views about spiders and how to effectively educate them about invertebrate conservation, and if physical interaction like the one provided by the Rosie exhibit, can be more effective at changing a person’s attitude toward a species than ambassador animal exhibits that allow visitors to only view the animal.

VICARIANCE, RETICULATION AND ECOLOGICAL OPPORTUNITY SHAPED THE DIVERSIFICATION OF IBERIAN SCORPIONS (BUTHIDAE: *BUTHUS*)

Javier Blasco-Aróstegui, Yuri Simone, Octávio S. Paulo, Lorenzo Prendini
University of Lisbon; CIBIO-InBIO; American Museum of Natural History

Cytonuclear (or mito-nuclear) discordance, evolutionary incongruence between the mitochondrial and nuclear genomes, is a widespread but underappreciated phenomenon that may obscure signals of introgression and hybridization important for understanding evolutionary trajectories and species boundaries. The study presented here explored the evolutionary history of *Buthus* Leach, 1815 scorpions in the Iberian Peninsula, a hotspot for cytonuclear discordance, in which complex topography and glacial history facilitated repeated cycles of isolation and secondary contact among populations. Genomic, morphological, and ecological data were leveraged to investigate how vicariance historical biogeography, reticulation and ecological opportunity contributed to the diversification of *Buthus* in the Iberian Peninsula, revealing an intricate evolutionary history, shaped by secondary contact and introgressive hybridization. The results refute recent taxonomic inflation in the genus and highlight the importance of considering cytonuclear conflict in species delimitation. By integrating diverse sources of evidence, a refined perspective on the evolutionary history of *Buthus* was achieved, which underscores the role of cytonuclear discordance in shaping patterns of biodiversity across biogeographically complex regions.

Session 1: Systematics & Evolution

MICROHABITAT DIFFERENCES, SPIDERS IN A RURAL YARD

Richard Bradley
Ohio State University

I have been surveying spider occurrences rural yard and home since 1991. Most observations are vouchered with photographs or specimens. As of this date a total of 201 species have been documented in this small (0.6 ha) yard. A variety of native trees, shrubs, and herbaceous plants have become established. In addition to haphazard sampling, two sets of pitfall traps were installed. One under a pine (*Pinus strobilus*) stand, and one under an oak (*Quercus bicolor* & *Q. palustris*) stand. The pit samples were collected monthly between September 2012 and March 2015. A total of 219

individuals of 38 species were collected in the pitfall traps. Most species were found in both the oak and pine samples. A total of 12 species were found exclusively in oak pits, 8 only in pine pits. It is tempting to attribute these records to microhabitat preferences; but the sample size is too small to be conclusive. From the larger dataset, with 34 years of observations, it is clear that some microhabitats in the yard do attract particular species. For example, five species have been found frequently, but only in open grassy areas.

Session 8: Ecology

ADVANCEMENT FOR MYGALOMORPH GENOMICS: A CHROMOSOMAL GENOME OF *APHONOPELMA MARXI*

Ethan Briggs, Andrea Noble-Stuen, Saoirse Foley, Chris Hamilton
University of Idaho; Marian University

Mygalomorph spiders represent a major infraorder of spiders that includes several evolutionarily and medically significant lineages. Among them, tarantulas (Theraphosidae) are particularly diverse and widespread, with over 1,100 described species. The North American tarantula genus *Aphonopelma* is one of the most extensively studied in this group. However, genomic resources for mygalomorphs remain limited, with only a few chromosomal genomes available, hindering comparative analyses. Here, we present the first chromosomal genome assembly for *Aphonopelma marxi*, and only the second for a tarantula. Using PacBio HiFi long reads and Hi-C scaffolding, we generated a high-quality de novo assembly of the 6.5 Gb haploid genome, comprised of 18 chromosomes that represent 99.7% of the assembly. This resource provides a critical foundation for comparative genomics across spiders and advances our understanding of genome evolution in mygalomorphs.

Session 3A: Evolution, Genetics & Genomics

YOUR FRIENDLY NEIGHBORHOOD COBWEB SPIDERS: WEB AND GLUE PLASTICITY IN THE PRESENCE OF CONSPECIFICS

Tyler A. Brown, Sarah Stellwagen
UNC Charlotte

Organisms must be able to adaptively alter their behavior in response to local mate and prey competition intensity, as this can dictate the optimal strategy for obtaining resources. These behavioral responses may be particularly strong in sessile organisms, such as cobweb (Theridiidae) spiders. Spiders can adjust web structure and silk biomechanical properties in response to the environment, indicating they may be able to similarly respond to other stimuli, such as conspecific presence. We quantified the web phenotype and prey-capture glue biomechanical properties of *Parasteatoda tepidariorum* females both before and after cohabitation with multiple conspecific females. We measured the density of silk threads in the retreat and gumfoot web sections as a proxy for energy investment into either safety or prey capture. We also biomechanically tested the flexural strength of gumfoot prey-capture glue and measured glue droplet volume and number. We hypothesized that, because silk production is energetically costly, spiders would supplement their investment into prey-capture and safety by producing stronger and more glue in lieu of solely increasing the density of safety and gumfoot lines.

Session 2: Behavior

SMALL BUT MIGHTY: EVOLUTION AND BIODIVERSITY OF MICROHEXURIDAE RELICT SPIDERS

Arnau Calatayud-Mascarell, Ethan Briggs, Chris A. Hamilton

University of Idaho

Microhexuridae is a relictual North American spider family comprising two described species, *Microhexura montivaga* and *M. idahoana*, with a disjunct distribution across high-altitude conifer forests in the Blue Ridge Mountains and Pacific Northwest. Despite their evolutionary distinctiveness—having diverged over 200 million years ago—the family remains poorly studied. This project aims to reconstruct the evolutionary history and biogeography of Microhexuridae using a modern integrative approach combining phylogenomics (ultraconserved elements and SNPs), morphometrics, and ecological niche modeling. Preliminary genomic work suggests 1) undescribed diversity in Pacific Northwest populations, 2) the presence of short range endemics that could be threatened by human pressure and 3) a deep and complex evolutionary history. Resolving the taxonomy and evolutionary relationships of Microhexuridae, this research will not only inform conservation strategies for short-range endemics but also enhance our understanding of North American geological and evolutionary history.

Session 1: Systematics & Evolution

GRAZING EFFECTS ON SPIDER COMMUNITIES IN NORTH CENTRAL TEXAS RANGELANDS

Nadia N. Castanon, Heather A. Mathewson, Adam B. Mitchell, James P. Muir, Darrel B. Murray

Tarleton State University; Texas A&M AgriLife Research Center

Spiders (Arachnida: Araneae) contribute services to rangeland ecosystems through top-down regulation of herbivorous arthropod prey that otherwise reduce vegetation used by other wildlife; however, spider assemblages could be negatively affected by unsustainable rangeland practices, such as intensive grazing by domesticated livestock and the introduction of nonnative forage. Our study sought to evaluate the influence of grazing on spider communities in north-central Texas. Specifically, we sought to: 1) quantify changes in vegetation communities in rangelands under different grazing pressures; 2) determine the relationship between grazing pressure, spiders, and their arthropod prey; 3) assess spider guild assemblages on native and nonnative vegetation; and 4) identify the best range management practice to promote occupancy and biodiversity of spider communities. We surveyed ungrazed, previously grazed (0.8–1.0 AUM/ha), and overgrazed (> 1.0 AUM/ha) pastures in Erath Co., Texas and sampled vegetation and arthropods once every two weeks from April to October 2024 along 30-m transects using line point intercept method for vegetation and pitfall traps and vacuum sampling for arthropods. Preliminary results suggest that grazing influenced vegetation cover ($F_{6,24} = 3.11$, $P = 0.02$), where we observed lower densities of spider in overgrazed pastures ($1.6 \text{ individuals/m}^2 \pm 0.34 \text{ SE}$), compared to previously grazed ($3.1 \pm 1.12 \text{ SE}$) and ungrazed ($2.7 \pm 0.92 \text{ SE}$) pastures. Web-building spiders were more common in sites with greater vegetation, meanwhile ground-dwelling spiders dominated overgrazed sites due to reduced vegetation structure. We aim to promote sustainable management practices and enhance spider biodiversity within rangelands.

RANGE SIZE AND EVOLUTIONARY HISTORY OF *PHIDIPPUS* SPECIES

F. Sara **Ceccarelli**, Luis C. Hernández-Salgado, G.B. Edwards, Rodrigo Monjaraz-Ruedas, Marshal Hedin
Center for Scientific Research and Higher Education; Florida State Collection of Arthropods; Natural
History Museum of Los Angeles; San Diego State University

Species range sizes vary due to interactions between biotic and abiotic factors and species-specific needs. A key question is whether range size is heritable, meaning closely related species might have more similar range sizes. Range size can also depend on speciation geography, species turnover, and divergence times. The North American salticid genus *Phidippus* has 61 described species with varying range sizes, from widespread (e.g. *P. audax*) to highly restricted (e.g. *P. pacosauritus*). Using a maximum likelihood (ML) phylogeny of 55 species and time-calibrated Bayesian Inference (BI) of 48 species, along with their known distributions, we addressed two questions: 1) Do species range sizes show phylogenetic signal? and 2) Are species age and range size correlated? Range sizes were quantified by the number of ecoregions occupied and the estimated area based on species distribution models. Phylogenetic signal was assessed using the ML tree and 100 random post-burnin dated BI trees, while correlations between species age and range size were examined on dated trees. Significant phylogenetic signal was found for both the number of ecoregions occupied and the distributional areas. The Pearson correlation coefficient between species age and the number of ecoregions varied from weakly positive to moderately negative, with nearly half being significant. However, no significant correlation was found between species age and estimated area of distribution. Therefore, species range size is likely heritable in *Phidippus*, and while a larger proportion of younger species may be ecological generalists, the size of their distributional area is not linked to evolutionary age.

Session 3A: Evolution, Genetics & Genomics

MOLECULAR INSIGHTS INTO THE EVOLUTION OF SPIDER GLUE

Richard H Baker, **Sandra M Correa-Garhwal**, Nadia A Ayoub, Toby C Clarke, Kyle Friend, Candido Diaz Jr,
Paul B Frandsen, Cheryl Y Hayashi
American Museum of Natural History; Suffolk University; Washington and Lee University; Vassar
College; Brigham Young University

Orb-weaving spiders rely on a sticky, protein-based glue to capture prey in their webs—an adaptation that offers strong adhesion at a low energetic cost. These liquid glue proteins are encoded by aggregate spidroins (AgSps), a group of silk genes that evolved from the same gene family as fibrous spidroins. While previous work has described aspects of these genes in a few species, broader evolutionary trends have remained unclear. Here, we examine the genetic makeup of glue-producing proteins across 14 spider species. Our findings reveal three distinct AgSp genes that are ancestral to orb-weavers but exhibit molecular divergence within the family. Each gene displays unique patterns of expression and sequence organization, suggesting that they may serve different roles related to glue performance. We also identify specific molecular features within these genes that are likely tied to glue function. These insights shed light on how molecular changes have contributed to the innovation and diversification of spider glue.

Genomics Symposium

THE SECRET IS IN THE POSTERIOR MAXILLARY LYRIFISSURE: A REVISED SUPERFAMILY ASSIGNMENT FOR THE PSEUDOSCORPION FAMILY MENTHIDAE

Mark S. Harvey, Ligia R. Benavides, Terrence L. Miller, Juli G. Cosgrove, Gonzalo Giribet, Michael G. Rix
Harvard Museum of Comparative Zoology; Western Australia Museum; Queensland Museum

Menthidae is a species poor pseudoscorpion family (12 species) found in disparate patches of xeric habitats across the globe. Since the description of the family by Chamberlin in 1930, the consensus among systematists has been that Menthidae is the sister group to Olpiidae and that these two families belong to either their own superfamily, Olpioidea, or that both families belong to the superfamily Garypoidea along with Garypidae, Geogarypidae, and Hesperolpiidae. Recent collection of the North American species *Menthus californicus* Chamberlin, 1930 and Australian species *Thenmus aigialites* Harvey, 1990 has led to the first molecular data generated for Menthidae, and subsequently the first molecular phylogenetic analyses including menthids. We analyzed two separate molecular datasets to infer the position of Menthidae within Pseudoscorpiones; one dataset made up of three Sanger sequenced genes and one made up of de novo transcriptome assemblies. In contrast to the historic hypothesis that menthids are garypoids, both molecular phylogenetic analyses recovered Menthidae within the superfamily Neobisioidea, earning the family a revised superfamily assignment. Within the framework of this revised Pseudoscorpiones phylogeny, we were able to identify previously overlooked morphological characters that are shared between menthids and the other neobisioids. This study incorporates the first molecular sequence data for Menthidae in order to robustly infer the family's phylogenetic placement and reassigns Menthidae to the superfamily Neobisioidea.

Session 1: Systematics & Evolution

A NEW SPECIES IN THE SPIDER FAMILY MYRMECICULTORIDAE (ARACHNIDA, ARANEAE) AND EVIDENCE OF MYRMECOPHAGY IN THE FAMILY

Paula E. Cushing, Edmundo González Santillán

Denver Museum of Nature & Science; Universidad Nacional Autónoma de México, Instituto de Biología

A new species in the unusual myrmecophagous family Myrmecicultoridae is described. This new species, *Myrmecicultor pueblaensis* sp. nov. shares several unique morphological features with the one other species in the family, *M. chihuahuensis* Ramírez, Grismado, and Ubick 2019 including two tarsal claws with no claw tufts, a strongly procurved posterior median eye row, distinctly oval shaped posterior median eyes with tapeta, a pronounced clypeus, reduced spinnerets, a serrula on the anterior border of the endites, and a distinctive patch of apparently chemosensory setae on the male cymbium and female pedipalp. A multi-locus phylogenetic analysis of six molecular markers from the mitochondrial (12 S rDNA, 16S rDNA, cytochrome oxidase subunit I) and nuclear (18S rDNA, 28S rDNA, histone H3) genomes places this new species as sister to *M. chihuahuensis*. In addition, the new species is a myrmecophage and shows similar hunting behavior to *M. chihuahuensis* in which a spider bites the rear leg of an ant and backs away waiting for the venom to take effect. We hypothesize that additional species of this unusual family may be distributed throughout the desert ecosystems of southern Mexico in association with various species of ants.

Session 6B: Systematics & Evolution

COMPARISON OF LOWLAND TROPICAL FOREST SPIDER (ARANEAE) ASSEMBLAGES FROM CONGO AND PANAMA USING A RAPID ASSESSMENT PROTOCOL

Michael L. Draney, Mbumba Jean-Louis Juakaly, Petra Sierwald, Marc A. Milne

University of Wisconsin-Green Bay; University of Kisangani (DR Congo); Field Museum of Natural History, Chicago; University of Indianapolis

A Rapid Assessment Protocol (RAP) for non-canopy spiders was used to collect replicate samples from four lowland rainforest sites for a proof-of-concept comparison of spider assemblages from the Democratic Republic of the Congo, and Panama. The samples yielded 350 adult spiders belonging to 29 spider families. The Panama samples yielded more adult spiders (235 vs. 115) and more spider families (24 vs. 14) than the Congo samples. Overall, the dominant five spider families in these non-canopy samples were Theridiidae (24%), Salticidae (15%), Linyphiidae (11%), Oonopidae (10%), and Pholcidae (7%), with the 20 remaining families each making up less than 5% of the total adults. The three most abundant families in Congo were Theridiidae, Oonopidae, and Thomisidae, while the top three in Panama were Salticidae, Theridiidae, and Linyphiidae. An NMDS ordination analysis of the four plots failed to show significant differences between any of the four assemblages, but when the plots were analyzed by region, there was a significant difference in the family-level assemblages between the continents. This paper shows proof-of-concept that this RAP can produce statistically valid data from brief sampling trips by teams with inexperienced collectors and simple, inexpensive sampling equipment.

Session 3B: Ecology

DIRECT EFFECTS OF WETLAND MOSQUITO CONTROL INSECTICIDES ON A DOMINANT SALT MARSH PREDATOR

Matthias Foellmer, Ethan Philip

Adelphi University; Emory University

One of the many anthropogenic impacts on wetlands, such as salt marshes, is the application of insecticides with the aim of controlling mosquitoes to minimize disease transmission risks. Modern approaches to combat mosquitos focus on spraying larvicides designed to act specifically on a narrow range of target species (Bti protoxins), but also commonly involve the application of broad-spectrum larvicides (insect growth regulators such as S-Methoprene), as well as adulticides (mostly pyrethroids). However, direct effects of IGR- and Bti-containing products on non-target species have rarely been tested beyond immediately co-exposed aquatic species and potential interactive effects with pyrethroids are poorly understood. Here we test for the effects of the larvicides VectoBac® (Bti) and VectoPrime® (Bti + S-Methoprene), and of the pyrethroid adulticide Sumithrin on mating and prey capture behaviors in the wolf spider *Pardosa littoralis*, a dominant predator in salt marshes in eastern North America. We applied pesticides at field concentrations sequentially (first larvicides, then adulticides), reflecting their application in the field, and videotaped all trials. First results suggest that exposure to VectoPrime® lowered mating propensity but increased prey capture speed and success, while VectoBac® and Sumithrin had no detectable effects. Valent BioScience's proprietary method to combine the Bti strain and (S)-Methoprene in a specific toxin ratio in VectoPrime® may involve bio-active compounds, which warrants further study.

Session 3B: Ecology

RECENT INSIGHTS INTO IDIOPIDAE RELATIONSHIPS THROUGH A COMBINED MORPHOLOGICAL AND PHYLOGENOMIC APPROACH

Rafael Fonseca-Ferreira, Antonio D. Brescovit, José Paulo L. Guadanucci, Ethan Briggs, Millke J. A.

Morales, Lionel Monod, Peter Schwendinger, Chris Hamilton

University of Idaho; Instituto Butantan; Universidade Estadual de São Paulo; Natural History Museum of Geneva

The family Idiopidae, the second most diverse among mygalomorph spiders, includes 437 species in 23 genera of exclusively trapdoor spiders with a predominantly Gondwanan distribution. It comprises three subfamilies: Arbanitinae, Genysinae, and Idiopinae. Recent phylogenomic analyses using Ultraconserved Elements confirmed the monophyly of Idiopinae, which is divided into two geographically distinct clades: Neotropical and African. However, both the genus *Idiops* and the family Idiopidae were recovered as non-monophyletic, due to the presence of distinct *Idiops* lineages in the Neotropical and Palearctic regions, and the phylogenetically distant position of *Neocteniza* (Genysinae) relative to other Idiopids. In this study, we provide new insights into Idiopid relationships through morphological analysis of Idiopinae type specimens and updated phylogenomic data, including new samples of *Idiops*, *Neocteniza*, and the first representatives of *Prothemienops*, an Asian genus with uncertain taxonomic placement. Our results support previously recovered relationships, with Arbanitinae sister to Idiopinae, and Idiopinae split into two distinct clades. Additionally, the genera *Segregara* and *Ctenolophus* were found to be non-monophyletic. Morphological and genomic evidence corroborates the restriction of *Idiops* to Neotropical species. *Prothemienops* was recovered as a distinct lineage, sister to Arbanitinae and Idiopinae. Finally, *Neocteniza* was placed as an evolutionarily distant lineage, more closely related to Theraphosoidina, suggesting that it may represent a separate family.

Session 6B: Systematics & Evolution

GENOMIC EXPLORATIONS OF SILK PRODUCTION ACROSS THE SPIDER TREE OF LIFE

Jessica Garb

University of Massachusetts Lowell

Silk production has independently evolved in multiple arthropod lineages but has reached its greatest complexity in spiders. Some spiders can simultaneously spin as many as eight silk types, each tailored for a distinct function. The different silks made by a single spider exhibit a range of mechanical properties, such as varying strength, extensibility, and adhesion. Such high-performance silks have enabled the evolution of complex web forms such as the iconic orb-web, slingshots, lassos, and water-adhering traps. In this talk I will discuss the spidroin protein family, the members of which compose different silk types, and how this protein family has co-evolved with the spider's silk-spinning apparatus. Spidroin proteins are highly repetitive and evolvable, explaining their ability to rapidly generate divergent material properties. Here I will present examples of genomic investigations of silk production to understand its evolution at different levels across the spider tree of life. I will also discuss how this information can be translated into the production of synthetic spider silk, an enduring goal of biological engineering.

Monday plenary

BUILDING A CASE FOR DUAL CLOCK CONTROL OF CIRCADIAN LOCOMOTOR ACTIVITY IN A SYNANTHROPIC SPIDER

Joseph Giulian, Caroline N. Cavin, Raven Ragsdale, Autumn Dishman, Heidi Allen, Thomas C. Jones, Darrell Moore
East Tennessee State University

Spiders have recently emerged as a model system for studying variation and extremity in circadian rhythm properties. Prevailing hypotheses suggest their atypical rhythms result from weak molecular clocks, easily influenced by clock gene protein concentrations that realign circadian timing in response to external stimuli like light and temperature cycles. To test this, we exposed a spider, *Pholcus manueli* Gertsch, to a 6-hour delayed light cycle for 5, 7, 9, or 15 consecutive days; following which, spiders were maintained in constant darkness (DD). For the 5- and 7-day shifts, locomotor activity remained largely unshifted in DD compared to controls, and any detectable change opposed the delay. This contradicted expectations that activity onset would delay accordingly. After 9 and 15 days in the phase delay, however, circadian output was dramatically altered-either nearly obliterated or manifesting extreme periodicities approaching the longest and shortest rhythms observed in nature. These findings challenge single weak versus strong clock models. Instead, we propose that two major internal molecular rhythms interact via wave interference to shape circadian outputs.

Session 2: Behavior

PROGRESS ON THE GENOMICS OF *UROCTONUS MORDAX* (SCORPIONES)

Jacob A. Gorneau, Katherine O. Montana, Diana Phan, Damian O. Elias, Rosemary G. Gillespie, Lauren A. Esposito
UC Berkeley, California Academy of Sciences; American Museum of Natural History, City University of New York

The Western forest scorpion (*Uroctonus mordax*) is found in forested regions along the Cascade, Coast, and Sierra Nevada Ranges in the western United States. Previous work employing SNP data from RADSeq discovered a deep divergence among northern (Washington, Oregon, parts of northern California) and southern (California) clades and distinct population structuring within these two clades. In this project, we sought to assemble a high-coverage reference genome from PacBio HiFi and Omni-C reads. While originally estimated to be about 1 Gb, this genome has proven to be much larger, and the trials and tribulations of reference genome sequencing for this scorpion are discussed. Our current estimate for this genome size is about 3.4 Gb. We report progress on this reference genome and existing phylogeographic work on the group with low-coverage resequencing data from over 100 samples distributed throughout the range of this species in California, where the southern clade of this species is located. While the reference genome is still in progress, we attempt to examine the phylogeography of this species with both UCE and mitogenome data. We discuss the success of both of these approaches and the initial results. Our results provide a rationale for a morphological revision of the genus to rectify the existing paraphyly of the type species. While the reference genome is still in progress, these data provide the potential for future landscape genetic analysis to examine the effect of major wildfires as barriers to gene flow, as well as SNPs associated with environmental features.

Genomics Symposium

BUILDING THE OPILIONES (SUPER)TREE OF LIFE: A RESOURCE FOR UNDERSTANDING EVOLUTIONARY PROCESSES

Laís A. Grosse, Daniel S. Caetano
Universidade de São Paulo

Extensive phylogenies are essential to understand evolutionary processes and constitute the first input for comparative analyses. Opiliones are a group with great diversity in species, distribution, morphology, and behavior. Despite the significant efforts to estimate the relationship within some families, we lack an all-encompassing phylogeny tree for the group. Here we produce the largest Opiliones (Super)tree to date to create a resource for the study of trait evolution, diversification, and biogeography. We collected molecular sequences of 7 genes (12S, 16S, 18S, 28S, COI I, Histone H3, and EF1a) for 1069 species from GenBank. We used Maximum Likelihood and Bayesian approaches to estimate the molecular tree and dated the tree using fossils as secondary calibration points. After establishing this backbone, we used matrix representation with parsimony to add 21 topologies from the literature. Finally, we used the node ages of the molecular backbone as secondary calibrations to date the supertree. The resulting supertree has a total of 1388 species across all 64 families of Opiliones (20.3% of the species). We hope this is the first of many attempts to create an all-encompassing Tree of Life for Opiliones and that it will support comparative studies now and in the future.

Session 1: Systematics & Evolution

AN INTEGRATIVE TAXONOMIC REVISION OF THE CAMEL SPIDER GENUS *CHANBRIA*

Quincy G. Hansen, Erika L. Garcia

Denver Museum of Nature and Science; Colorado State University; University of Colorado Denver

This talk summarizes the recent taxonomic revision to the solifuge genus *Chanbria* proposed by Garcia et al. (2024). Utilizing an integrative taxonomic approach combining phylogenetic, biogeographic, and morphological data, two new synonymies are proposed and the species *Eremochelis plicatus* is transferred to *Chanbria*. Two new species, *Chanbria brookharti* sp. nov. and *Chanbria mapemes* sp. nov. are described. Additionally, new synapomorphies which unite the *Chanbria* clade are identified using previously acquired genomic data.

Session 6B: Systematics & Evolution

RELATING POSTCOPULATORY SEXUAL SELECTION TO MATING SYSTEMS ACROSS TWO SPECIES OF NEARCTIC DOLOMEDES

Eileen A. Hebets, Bridget Bickner, Dan Schoenberg, Nick Pace, Mariela Oviedo-Diego
University of Nebraska-Lincoln

Mating systems are traditionally predicted to be influenced by pre-mating sexual selection. Males, with their relatively smaller and assumed cheaper gametes are expected to benefit by mating with multiple females. In contrast, females, with their relatively larger and fewer gametes, are expected to mate less frequently and to be picky about their partner(s). In numerous animals, however, females mate multiply and males mate one. Such single male mating is observed in *Dolomedes tenebrosus*, a species in which every male dies (and gets eaten) following sperm transfer, while their female partners can go on to mate with multiple partners. In their close relative *D. scriptus*, however, females mate with a single male while males mate with multiple females, conforming to more traditional expectations. The

present study explored the relationship between the potential for postcopulatory sexual selection – specifically sperm competition – and mating patterns in these two distinct species. First, we quantified the amount of sperm males of each species produced, the amount of sperm males transferred to females, and the proportion of sperm males transferred. Additionally, we explored the mechanism of sperm transfer by dehydrating males of each species and testing the impact of presumed low hemolymph pressure on sperm transfer. We found that male *D. tenebrosus* produce and transfer significantly more, but a similar proportion, of sperm than *D. scriptus*. We also found that hydration impacts sperm transfer differently between the two species. Our results are consistent with the suggestion that strong postcopulatory selection can influence female and male mating patterns.

Session 6A: Behavior

PREDATORY BEHAVIOR AND BOLDNESS IN *BRACHYPELMA* AND *TILTOCATL*

Yann Henaut, César Raziel Lucio-Palacio

El Colegio de la Frontera Sur, Chetumal, Mexico

The tarantula genera *Brachypelma* and *Tiltocatl* are closely related lineages distributed in México and Central America. The *Brachypelma* species are found in drier regions of Western Mexico, whereas *Tiltocatl* species are distributed in the eastern and southern of México and as far as Central America. These two genera also differ greatly in body coloration, which is brighter for *Brachypelma*, with colors that appear aposematic and duller for *Tiltocatl*. We wanted to know if there were any behavioral differences between these two genera in early stages, and if present, whether these differences modulate their predatory behavior. We observed spiderlings of both genera in the laboratory during 13 feeding events in their rearing boxes, one-third filled with potting soil. To assess a boldness index, we noted for each of the 13 observations whether each individual was visible or hidden in a burrow. Termites were offered during each of those 13 events. We noted whether each tarantula attacks and captures and the time for capture. *Brachypelma* were clearly bolder than *Tiltocatl*, which are more variable in temperament. While shier individuals seem to have more difficulty attacking prey, all tarantulas attacked and captured with comparable success once the prey was been detected. The differences found in terms of boldness could be linked to their antipredator strategy and possibly bolder-related aposematism.

Session 2: Behavior

MULTI-ELEMENTAL NUTRIENT CYCLES DRIVEN BY PREDATOR DIET ACROSS MULTIPLE PREY TYPES

Colton Herzog, Jamie T. Reeves, Yetkin Ipek, Andrea Jilling, Dror Hawlena, Shawn M. Wilder

Oklahoma State University; The Hebrew University of Jerusalem

Predators occupy fundamental roles in cycling nutrients through ecosystems, influencing the quantity and composition of materials—such as waste and uneaten prey—that become available to decomposers. Since prey items differ in elemental composition and predators selectively retain or excrete certain elements, the elemental makeup of predator waste may vary depending on diet. We examined how feeding on different prey types (caterpillars, cockroaches, crickets, and flies) affected the concentrations of 23 elements in wolf spider excreta across two seasons (spring and fall). Compared to unconsumed whole prey carcasses and prey remains, spider excreta had lower concentrations of carbon and higher concentrations of several elements: Al, B, Ba, K, Li, P, S, Si, and Sr. Additionally, while the elemental content of unconsumed prey and prey remains varied among prey species, spider excreta

showed less variation, suggesting a consistent elemental excretion pattern regardless of prey identity. Seasonal differences in excreta elemental content were also observed: in the fall, wolf spider excreta contained higher concentrations of Fe, Mg, Mn, Mo, S, and V, whereas in the spring, concentrations of Al, B, Ba, Ca, Cd, Cu, K, P, Na, Si, Sr, and Zn were greater. These findings emphasize that both prey identity and seasonal context influence how predators contribute to the cycling of multiple elements. Thus, gaining a clearer understanding of these nutritional dynamics is important for identifying how predators influence ecosystems.

Session 8: Ecology

SMALL SPEED DEMONS: RUNNING SPEED IN SE ASIAN AND WEST AFRICAN SPARASSIDS

Sadie Hoefler, Linda S. Rayor
Cornell University

Sparassids are among the fastest known spiders (Hurst & Rayor 2021; Boehm et al 2021). Our previous studies with 26 species of huntsman have shown that the Heteropodinae, containing the genera *Heteropoda*, *Barylestis*, and *Pandercetes*, are among the fastest. Here we measured the maximum velocity (cm/sec) and speed in body lengths per second in six additional small species from Singapore, Thailand, and West Africa. Spiders were run in a 68cm long x 7cm internal diameter acrylic tube. We videotaped their runs and tracked them using DeepLabCut. We compared running speeds among species, sexes, and ages. These relatively small to tiny species were at the fast end of the sparassids in both maximum velocity and body lengths per second. Compared to speeds in the large and extremely fast *Heteropoda* species, such as *H. boiei* or *H. lunula*, the smaller species ran in the same or faster velocity range (up to 122 cm/sec) but traveled almost double the number of body lengths per second. Leg length directly correlated with speed, with species with long legs (legginess = leg 2 length/cephalothorax width) running faster. As in our previous study, speed tended to decrease with spider body mass. Not unexpectedly, males with longer legs and lighter bodies moved faster than females in body lengths per second.

Session 6A: Behavior

DEVELOPING TARANTULA MEDICINE: A PRESENTATION OF FOUR CASE STUDIES

Lacey Jones, Sarah Triplett
Laurel Veterinary Clinic

Tarantulas are becoming an increasingly common pet in addition to representing conservation efforts in zoos. While tarantulas are relatively easy to care for with proper husbandry, veterinary care for these animals is underdeveloped for their complex physiology. In this presentation we will discuss 4 case studies on tarantula medicine: intracardiac fluids to treat dehydration, assisted limb autotomy, euthanasia, and anesthesia to facilitate removal of retained exuvia. Sarah Triplett is an entomologist with 10 years of experience in invertebrate husbandry and Dr. Lacey Jones is a veterinarian with special interest in arachnids, they are both members of the Veterinary Invertebrate Society. Lacey is the veterinarian for the Butterfly Pavilion and works closely with Sarah at Laurel Veterinary Clinic; this collaboration allows for unique exposure to a variety of species and medical problems. Our medical techniques were based on the one veterinary medical text that exists for invertebrates as well as exotic

veterinary forums and experience. Developing tarantula medicine likely increases quality and length of life for captive owned animals as well as supporting species survival plans.

Session 5: Education & Outreach

OUT OF MEXICO: NORTH AMERICAN WARM DESERTS AS THE CRADLE OF EREMOBATID SOLIFUGES

R. Ryan Jones, Erika L. Garcia, Goran Shikak, Jack. O. Brookhart, Matthew R. Graham, Paula E. Cushing
University of Colorado Denver; Denver Museum of Nature & Science; Eastern Connecticut State University; University of Wisconsin-Madison

We present a highly complete phylogenomic analysis of North American solifuge family Eremobatidae, with a focus on the eremobatinae subfamily. Ultra-conserved elements captured from field collected and historical museum material allowed for vastly improved sampling effort for the family, achieving over 350 terminals representing all genera and >70% of the known eremobatid species diversity in addition to several putative new species, the majority of which are distributed in the warm deserts of the southern United States and Mexico. Biogeographic ancestral state reconstructions indicate the majority of the historical and contemporary biodiversity occurs in the Sonoran and Chihuahuan deserts, with more recent, and coincidentally overestimated, species occurring in the northern latitudes of North America, and in some cases to the southern-most latitudes of Mexico. Cladogenesis appears to co-occur with the aridification and development of desert ecosystems in the southwest United States and northwards into dry grasslands and prairies. We also propose new genera to accommodate the para/polyphyly of *Eremobates*, the most speciose genus of the family.

Session 6B: Systematics & Evolution

WEB OF LIFE ARCHITECTS: EDUCATION INITIATIVES INSPIRED BY THE BEAUTY & WONDER OF SPIDERS

Sarah Karikó

Gossamer Labs LLC/Harvard Museum of Comparative Zoology

Education plays a key role cultivating leaders empowered to make decisions to care for our interdependence. Initiatives are needed to address biodiversity knowledge gaps reported by UNESCO in order to address impacts on the health/wellbeing of the living world who sustains us. Knowledge of one of the largest groups of animals, invertebrates, who are key to the critical foundations of life on Earth, is often not included commensurate with their importance. There are few invitations to learn about these amazing animals and the vital roles they play in daily life. To address this, I will share a range of educational initiatives that interweave multiple branches of knowledge with arachnology as the starting point-- integrating arts, indigenous knowledge and negotiation training--that often start with the Beauty & Wonder of Spiders. Some programs are created in collaboration with an orthopedic surgeon, pastry chefs, dancers, and Native American artists, and offered in museums, hospitals, and on public lands. These programs are designed to spark and support participants' natural curiosity, creativity and care, and range from traveling exhibits to spider superhero programs for pediatric oncology and hematology patients and beyond. Methods are creative, science- and place-based, participatory and grounded in field, laboratory, and museum collections research. My boots-on-the-ground observations have spanned decades during this time of dynamically changing environmental and societal conditions on Earth. This conference talk aims to highlight unique educational strategies

and collaborations and spark a larger conversation to better care for our interdependence throughout the web of life.

Session 5: Education & Outreach

SPIDER EGG SACS REVEAL HOW POCKETS OF AIR CAN BE USED TO CONSERVE WATER

Katherine Karkosiak, Ravi Schwartz, Hunter King, Todd Blackledge

The University of Akron; Rutgers University-Camden

Controlling water transport across surfaces is essential for all living organisms. Spider egg sacs are multifunctional membranes that protect eggs and spiderlings from the external environment. Past research gives conflicting results about whether these mats of silk fibers reduce evaporation of water in part because the diffusive resistance of any membrane cannot be measured independently of the system in which it is studied. We develop a model to describe water vapor transport across porous surfaces that includes the important roles of the gap space underneath the membrane and the boundary layer on the outside of the membrane in controlling water vapor flux, in addition to the relative impermeability of the membrane itself. The model accurately predicts diffusive resistance of a variety of synthetic surfaces from empirical studies, as well as the egg sacs of the black widow *Latrodectus hesperus* and the garden spider *Argiope aurantia*. We show that “typical” spider egg sac membranes offer surprisingly low diffusive resistance to water because they are highly porous at microscopic scales. However, silk egg sacs still play key roles in controlling water loss by preserving and defining an internal region of stagnant air that often dominates the diffusive resistance of the whole system. Our model provides a tool to explore diverse spider egg sac geometries but can also be adopted to fit a variety of systems to facilitate comparison and engineering of diffusive resistance across membranes.

Session 7: Morphology, Physiology & Development

A COMPARISON OF THE FLEXURAL STRENGTH OF COBWEB AND ORB WEAVER SPIDER SILKS

Ella Kellner, Sarah Stellwagen

UNC Charlotte

Spider webs are made from several types of silk, some of which are among the strongest biomaterials known. Silks can withstand forces in many directions in order to capture prey, for example, cobweb weavers use gumfoot lines as spring-loaded traps to capture ambulatory prey. Conversely, orb weavers use capture spiral silk to intercept and retain flying prey. The tensile strength, or the parallel forces generated when a silk strand is pulled from both ends, has been tested and is well-characterized for these silks. However, flexural strength, or the force that results when a silk is pushed or deformed perpendicularly, has not been investigated. As silks in nature are warped and distorted from many directions depending on use, it is important to understand the contrasting functional characteristics when alternately stressed. We have begun examining the flexural strength of spider prey-capture silk and found cobweb gumfoot lines sustain higher flexural forces at faster speeds. Comparing prey capture strategies, which are adapted to the habitats in which spiders reside, can provide key insights into how differences in spider silk biomechanics evolve.

Session 4: Silks & Venoms

DISCOVERING THE DEVELOPMENTAL GENETIC MECHANISMS UNDERLYING APPENDAGE INNOVATIONS IN CHELICERATA

Benjamin Klementz, Sophie Neu, Ethan Laumer, Emily Setton, Isaac Hinne, Austen Barnett, Georg Brenneis, Monika Gulia-Nuss, Prashant Sharma
University of Wisconsin-Madison; University of Florida; University of Nevada; DeSales University; Universität Wien

Much of what is known about appendage patterning in arthropods stems from insect models like *Drosophila melanogaster* and *Tribolium castaneum*. Yet insects rarely deviate from the archetypal five-segmented condition of their legs. Chelicerates, however, exhibit numerous innovations in both the number and structure of appendage podomeres. Prominent examples of these taxon-specific innovations include the patellar and metatarsal podomeres, additional coxae in Pycnogonida, and subdivided trochanters or femora in lineages such as Ricinulei and Solifugae. While little is known about the genetic mechanisms that underlie the origins of these traits, recent literature has favored the hypothesis that these novel traits were facilitated by the evolution of new, chelicerate-specific gene copies. Using a comparative approach that explores embryos of multiple chelicerate orders, such as Opiliones, Acariformes, Parasitiformes, and Pycnogonida, we show that the origins of new segment boundaries are instead grounded in changes in the expression domains of ancient transcription factors. Taxon-specific changes in the activity of extradenticle and clawless underlie the origins of the chelicerate patella and tarsus, respectively. In addition, the expression of SoxNeuro substantiates the interpretation of supernumerary coxae in developing nymphs of sea spiders. Our results support the hypothesis that evolutionary novelties in the chelicerate body plan are achieved by changes in the spatiotemporal regulation of ancient and evolutionarily conserved genes.

Genomics Symposium

SPECIES LIMITS OF THE ENDANGERED TOOTH CAVE SPIDER (TAYSHANETA MYOPICA) IN CENTRAL TEXAS

Joel Ledford, Jason Bond
UC Davis

The phylogeny of *Tayshaneta* spiders is inferred using sub genomic data from ultraconserved elements (UCEs). Taxon sampling includes *Tayshaneta* species from across Central Texas, with emphasis on populations of the endangered Tooth Cave Spider (*Tayshaneta myopica*) and its sister species *T. paraconcinna*. Maximum likelihood and coalescence-based inference support the monophyly of *Tayshaneta* but show that the species, *T. myopica* and *T. paraconcinna* need to be reevaluated. Variational autoencoder clustering and STRUCTURE analyses of single nucleotide polymorphisms (SNPs) show evidence of gene flow between some *Tayshaneta* populations, but troglobites are genetically isolated. The distribution of *T. myopica* is expanded North and South of the Colorado River, despite its recognition as a biogeographic barrier for karst-associated fauna. Implications for the conservation of *T. myopica* are discussed and compared to other karst-associated arachnids in the region.

Session 3A: Evolution, Genetics & Genomics

DISTRIBUTION OF *TLILTOCATL VAGANS* AN THREATENED TARANTULA: FROM PAST TO FUTURE

Yann Hénaut, Salima **Machkour-M'Rabet**, Cara Shillington, H Weissenberger, L Legal

El Colegio de la Frontera Sur, Mexico; Eastern Michigan University; Université de Toulouse

It is vital to be aware that change in temperature is having a detrimental effect on many species around the world, increasing the risk of extinction, and that tarantulas are no exception to this. Many species of Mexican tarantulas belonging to the *Tliltocatl* genus are considered threatened, particularly due to human activity. We have been gathering data on the presence of the widely distributed species *Tliltocatl vagans* (Ausserer, 1875). We have developed distribution models using the MAXENT algorithm for past, present and future (RCP 4.5 and RCP 8.5) climate scenarios, and using variables available on Worldclim. The distribution model obtained for the current *T. vagans* period overlaps the general distribution of the *Tliltocatl* genus. Models obtained for past periods suggest an extensive distribution in Central and South America during the last interglacial period (LIG), decreasing considerably during the last glaciation. The current distribution is more concentrated in southern Mexico than it has been in the past. With regard to potential future distributions, rising temperatures are likely to result in a significant reduction in available areas, with the possibility of extinction in some areas of current distribution. Our research indicates that the conservation of Mexican tarantulas is a matter of concern, and that their protection is essential for ensuring their survival.

Session 3B: Ecology

GLOBAL PATTERNS IN SPIDER OCCURRENCE DATA: MONITORING CRYPTIC FAUNA IN AN ERA OF HUMAN OBSERVATIONS NETWORKS AND COMPUTER VISION MODELS

Jeremy Miller

Naturalis Biodiversity Center, Leiden

Monitoring cryptic and highly diverse groups of organisms is particularly critical at a time when our global environment is warming and urbanizing. GBIF, the Global Biodiversity Information Facility, is the largest aggregator of primary biodiversity records, that is the records of which species were observed where and when. Most records in GBIF come from two major source categories. The largest data source category is human observations networks of citizen scientists, which tend to produce huge numbers of records but for relatively few species. Museum collections databases provide a more modest number of records, but these include many species not found in the human observations networks data or other sources. Analysis using trait data demonstrates that for the more than 5 million global records of spiders, data from human observations networks have a significantly larger body size compared to museum collections. This suggests that human observations networks may be dominated by relatively conspicuous species compared to museum collections. Semiautomated taxonomic tools such as DNA barcoding and machine learning applications now complement classical expert-based taxonomy. Computer vision models are a form of artificial intelligence/machine learning that are currently being applied in the domain of taxonomic determination. We show that the computer vision models are capable of reliably distinguishing taxonomically challenging spider species based on both habitus and reproductive structures. We report how available technologies can be used to build learning machines for high throughput biodiversity monitoring.

Session 3B: Ecology

CENTENNIAL REENACTMENT (1923-2023) OF THE CROSBY & BISHOP SOUTHEASTERN SPIDER EXPEDITION

Marc A. Milne, Michael L. Draney, Nina Sandlin

University of Indianapolis; University of Wisconsin - Green Bay; Field Museum of Natural History

In October of 1923, two arachnologists, Cyrus R. Crosby and Sherman C. Bishop, along with their wives, undertook a month-long collecting expedition from Ithaca, NY down the eastern states. Some of the data gathered from this collecting trip were published in ten manuscripts from 1925 – 1938 and included 12 species new to science. One hundred years later, after the 2023 AAS meeting in Ithaca, we re-created part of their trip (excluding NC) in an attempt to recollect several species that are now considered rare or lost since their description by Bishop and Crosby from their journey. Of the 77 species that we know were collected on the original journey, we managed to recollect 12 (16%). However, of the 173 species we collected – including two undescribed species – only 17 were found by Bishop and Crosby (10%). The reasons for these discrepancies in data are likely four-fold: 1) there is no complete list of taxa collected by C&B, we have to depend on published mentions of data, therefore comparisons are incomplete, 2) C&B collected in late October while we collected in late June, 3) C&B likely had different collection techniques than we did, and 4) C&B likely collected in different habitats and sites than we did (there was no list of exact locations). This trip highlights the importance of these two titans of arachnology in our current understanding of American arachnology.

Session 5: Education & Outreach

HIGH DIFFERENTIATION AND ENDEMISM IN THE CALIFORNIA MOUNTAINS: POPULATION GENOMICS AND SPATIAL PHYLOGENETICS OF MYGALOMORPH SPIDERS

Rodrigo Monjaraz-Ruedas, James Starrett, Toby Hays, Emma Jochim, Jason Bond, Marshal Hedin
Natural History Museum of Los Angeles County; UC Davis; San Diego State University

Inclusion of cryptic intraspecific lineage diversity and evolutionary history is crucial for understanding spatial patterns of diversity and the drivers promoting this diversification. Spatial phylogenetics is a tool that incorporates both lineage diversity and phylogenetics, allowing for flexibility in species concepts and ease in comparison of different units. The California Floristic Province (CAFP) is a biodiversity hotspot with high species richness and endemism of plants and vertebrates, but little is known about patterns of endemism in arthropods (including spiders) despite their high species diversity.

Mygalomorph spiders are characterized by extreme cryptic lineage diversity, in part due to their sedentary lifestyle and low dispersal abilities, but the factors promoting such diversity remain uncertain. We first use genome-wide data and apply phylogenetic comparative methods to elucidate the spatiotemporal and ecomorphological determinants of genetic diversity and differentiation. This analysis informs our selection and definition of lineages, which are subsequently used in spatial phylogenetic analyses to estimate centers of paleo- and neo-endemism across the CAFV. We find hotspots of endemism in the CAFV and show that omitting cryptic diversity can drastically undermine estimates of endemism. Finally, we urge for the inclusion of arachnids in future work with spatial phylogenetics to improve our understanding of spatial patterns of biodiversity.

Tuesday Platnick Award Plenary

A BEHAVIORAL AND MORPHOLOGICAL PERSPECTIVE OF OLFACTORY AND GUSTATORY COMMUNICATION IN A *TETRAGNATHA* SPIDER

Kathryn Nagel, Seira A. Adams, Clara Meyer, Rosemary Gillespie
UC Berkeley; UC Davis

Chemical sensing is a critical mode of communication in many organisms, particularly when locating and identifying mates. In arthropods, many insects and arachnids use chemical pheromones to identify conspecific mates, but much is still unknown about the physiological mechanisms of chemosensation. Species-specific chemical compounds (long chain methyl ethers) have been identified in the silk extracts of several species of California and Hawaiian long-jawed orb weavers (Tetragnathidae: *Tetragnatha*). Through behavioral assays, male *Tetragnatha versicolor* preferentially select conspecific, mature females through gustation (silk and silk extracts) and olfaction (airborne chemical cues). However, the chemosensory modes behind this behavior are unclear. In this study, we used scanning electron microscopy (SEM) to identify two distinct classes of chemosensory hairs present on *Tetragnatha*. The first is a tip-pore sensilla consistent with known examples of gustatory hairs and is present on males, females, and juveniles. We also identify and describe a previously undescribed variation of these tip-pore sensilla with scale-like projections along the hair shaft. The second, present only on mature males, shows traits consistent with olfactory hairs recently described in Talukder et al. These short hairs have numerous wall-pores across the length of the hair shaft, and also show the presence of a terminal pore, a trait shared by gustatory hairs but distinctive from the olfactory hairs found previously. The combined behavioral and morphological evidence suggest that *T. versicolor* uses both olfactory and gustatory chemical cues to distinguish both species and life-stage of potential mates, using at least two distinctive chemosensory hairs.

Session 7: Morphology, Physiology & Development

MO' SPIDER, NO PROBLEM: LOW RISK OF AND MINIMAL DISCOMFORT FROM BITES BY THE INVASIVE JORO SPIDER

David R. Nelsen, Angela Chuang, Aaron G. Corbit, Michael I. Sitvarin, Hannah E. Bergmann, Everaldo P. De Araujo, Jr., Sarah R. Hunter, Jared K. Ing, Justin J. Park, Kaitlyn A. Vasquez, Amani S. Wang, David R. Coyle Southern Adventist University; Clemson University, Washington College; Union College

Despite rampant arachnophobia, spider bites are not too common, and only a few species are medically relevant. Orb-weavers (Araneidae) are generally docile and have not been implicated in human health issues. However, several representative species are large and highly visible, none more so than species within the genera *Nephila* and *Trichonephila*. One such species, *Trichonephila clavata*, has recently become well established in the eastern United States. Due to its size and coloration, in addition to its large webs, high population density (in some areas), and its synanthropic nature, human interactions are likely to increase. Thus, there is a need to assess the risk this species poses to humans. In this study, we documented the behaviors performed during increasingly stressful interactions with humans and evaluated the risk and severity of a bite. Most commonly, these spiders attempted to avoid the interactions (moved away or remained motionless), rarely bit unless under extreme duress, and hardly ever injected venom when they bit. Furthermore, bites resulted in mild and localized edema and erythema that were resolving within 30 minutes and were almost entirely resolved within 24 hours. We see little evidence that these spiders pose a direct risk to humans.

Session 4: Silks & Venoms

THE EVOLUTION AND DEVELOPMENT OF TARSOMERES IN OPILIONES

Prashant P. Sharma, Ethan M. Laumer, Sophie M. Neu, Benjamin C. Klementz
University of Wisconsin-Madison

Like many animal groups, Opiliones show marked asymmetry of diversity across their phylogeny. Some clades, such as Cyphophthalmi, are small and morphologically conservative, whereas others, such as Sclerosomatidae and Gonyleptidae, exhibit considerable species richness and body plan disparity. Various hypotheses account for such patterns, such as latitudinal species gradients, clade age, and morphological innovations. One morphological trait that correlates with the species richness of Opiliones is the number of tarsomeres, the articles of the tarsus that confer prehensibility to the Opiliones leg. How the prehensile leg of Opiliones is patterned genetically is virtually unknown. Here, we show that the tarsomeres of the daddy-longlegs *Phalangium opilio* are patterned sequentially from proximal to distal. Using a combination of small molecule inhibitors and gene silencing experiments, we demonstrate a role for Notch-Delta signaling in patterning the tarsomeres. We additionally show that disruption of EGFR signaling results in the truncation of the tarsus and the loss of the distal tarsomeres. Our experiments provide some of the first insights into the developmental genetic basis for tarsomere patterning in a non-insect arthropod and suggest that the genetic mechanism underlying arachnid tarsomere development is markedly different from its insect counterpart.

Session 7: Morphology, Physiology & Development

DETERMINANTS OF ORB WEAVING SPIDER GLUE DROPLET HYGROSCOPICITY

Brent Opell, Mary Hendricks, Sarah Morris, Spence Francis, John Greenhalgh, Bryan Norris
Virginia Tech; The George Washington University

The adhesion of the viscoelastic protein cores within the glue droplets of an araneoid orb web's prey capture thread is ensured by droplet hygroscopicity. Low molecular mass compounds (LMMCs) in the aqueous layer that surrounds these cores attract atmospheric moisture to tune droplet performance to the humidity of a species' habitat. This study, which measured the hygroscopicities of 15 species' glue droplets at 20%, 37%, 55%, 72%, and 90% relative humidity, revealed a wide interspecific range of droplet hygroscopic profiles. This indicates that individual LMMCs contributed independently to droplet hygroscopicity and that their hygroscopic strengths are not simply averaged. A comprehensive model of the determinants of droplet hygroscopicity supported the important role of LMMCs by showing that they were responsible for 44% of droplet hygroscopicity. However, four additional variables also contributed: cube root droplet volume 21%, the ability of core proteins to assimilate water 16%, core volume relative to aqueous volume 14%, and core protein elastic modulus 5%. In each of the 15 species there was good agreement between modeled and measured droplet hygroscopicities. However, interspecific differences in the values of the five contributing variables caused their % droplet hygroscopic contributions to differ greatly in the 15 species. Moreover, values of the five contributing variables differed when species were grouped by foraging humidity as: low-humidity, mid-humidity, high-humidity, and nocturnal. These findings show that the volume and molecular composition of each glue droplet constituent affect droplet hygroscopicity and indicate that these properties are related to the humidity of a species' habitat.

Session 4: Silks & Venoms

THE MITOCHONDRIAL GENOME OF THE SMALLEST AFRICAN WOLF SPIDER, *MINICOSA NEPTUNA* ALDERWEIRLDT & JOCQUÉ, 2007 (ARANEAE, LYCOSIDAE)

L. Brian Patrick

Dakota Wesleyan University

The mitochondrial genome of *Minicosa neptuna* Alderweireldt & Jocqué, 2007 has been sequenced and annotated for the first time. This species, the smallest known wolf spider in Africa, is found primarily in northeastern South Africa and part of Mozambique. DNA was extracted using a Qiagen DNEasy Blood and Tissue kit, then sequenced on an Illumina NovaSeq 6000 for 150 bp paired-end reads. Contigs were assembled in SPAdes and the rough draft mitogenome extracted from the resulting contigs. The rough draft genome was then used in NOVOPlasty for de novo assembly as the reference genome and the COI gene from the rough draft genome as the seed, and then circularized by this same program. The mitogenome was annotated using MITOS2 and by comparing it to other species in the family Lycosidae. The mitogenome is 14,706 base pairs in length, containing 22 transfer RNA (tRNA) genes, 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, and a control region. This is the first complete mitochondrial genome for this species.

Session 6B: Systematics & Evolution

TANGLED IN TIME: UNRAVELING THE MOLECULAR MECHANISMS OF CIRCADIAN RHYTHMS IN SPIDERS

Jessica Petko, Karoul Garas, Justin Cheetham, Nadia Ayoub, Natalia Toporikova, Thomas C. Jones, Darrell Moore

Penn State York; Washington and Lee University; East Tennessee State University

Circadian rhythms regulate daily cycles of behavior and physiology in all animals and are driven by transcription-translation feedback loops that control gene expression within the nervous system. While environmental cues fine-tune these rhythms, spiders exhibit unique properties-including variable free-running periods and resistance to jetlag-that make them an intriguing model for studying circadian regulation. Spiders share a conserved set of clock proteins with other arthropods, yet their function and regulation remain unknown. This study investigates how spider clock gene orthologs contribute to the circadian feedback loop and how their regulation differs from species with conventional rhythms. By introducing spider clock genes individually and in combination within cultured cells, we assess their effects on circadian reporter gene output to determine their role in timekeeping. Additional experiments explore light sensitivity, protein interactions, and broader cellular inputs that influence spider circadian rhythms. Our findings advance understanding of arachnid circadian regulation to offer insights into how biological clocks have evolved.

Session 3A: Evolution, Genetics & Genomics

A PHYLOGENOMIC FRAMEWORK FOR COSMETIDAE (OPILIONES: LANIATORES) REVEALS LOCALIZED ENDEMISM AND SUPPORTS REGIONALLY FOCUSED TAXONOMIC REVISIONS OF GENERA

Daniel N. Proud, Caleb Gunkle, Cielo Disla, Hailey Hoffman, Maria Lubbos, Santoshi Mutyala
Moravian University

Cosmetidae are the most diverse family within the Laniatorid harvesters (Opiliones: Laniatores), comprising 723 described species distributed throughout North and South America, as well as the Caribbean Islands. Systematic revisions of this family have proven difficult due to the absence of clear

synapomorphies that can reliably delimit most genera. Here, we present the first phylogenetic analysis of Cosmetidae based on ultraconserved elements (UCEs), providing a novel framework for understanding relationships within the family. Our dataset includes UCE sequences from 72 cosmetid species from Mesoamerica and the Caribbean Islands. We examine the biogeographic patterns and phylogenetic relationships of several clades within these regions. Our results reveal that monophyletic groups are typically confined to relatively small geographic areas, highlighting a pattern of localized endemism. Our findings underscore the importance of biogeographic context in taxonomic revision, suggesting that genus-level boundaries in Cosmetidae should be re-evaluated within regional frameworks.

Session 3A: Evolution, Genetics & Genomics

HOW DO THE RETREATS, DEMOGRAPHICS, AND BEHAVIOR OF SOCIAL AND SOLITARY HUNTSMAN SPIDERS IN THE GENUS *DELENA* DIFFER: LET ME COUNT THE WAYS.

Linda S. Rayor

Cornell University

There are 9 genera of Delenine huntsman spiders endemic to Australia. The genus *Delena* is the basal lineage with 7 to 11 species. I have studied five *Delena* species and ~46 other huntsman species to determine whether the prolonged subsocial species are exceptionally tolerant or radically different from the solitary species. Unexpectedly, I discovered that besides the well-known social species, *Delena cancerides*, three other *Delena* species (*D. lapidicola*, *D. spenceri*, and *D. melanocheilus*) were also prolonged subsocial living for many months in relatively complex groups of a single adult female and multiple cohorts of older and younger offspring. These prolonged subsocial species share unique developmental and egg sac traits with *D. cancerides*, but not with their solitary congener, *D. gloriosa*. Here I discuss the distinctive differences in the five *Delena* species habitat and retreats, duration of association, clutch size, and behavior.

Session 2: Behavior

FORESTS ADJACENT TO BLUEBERRY CROPS GENERATE SEASONAL STABILITY OF GROUND-DWELLING SPIDER COMMUNITIES

Sarah Rezende, Svoboda Pennisi, Jason Schmidt

University of Georgia, Tifton; University of Georgia, Griffin; University of Georgia Cooperative Extension
Spiders are among the most diverse and abundant predators within agroecosystems that contribute significantly to biological control. Recent studies show that land-use change can alter the functioning of spider food webs, but the composition and dynamics of spider communities are largely unknown in many systems. Here we study how within-farm field positions shape aspects of spider communities in blueberry production. We estimated ground-dwelling spider communities in blueberry fields of southeast Georgia for eight months to include the blooming and fruiting phenological stages. Over two years, we sampled eight commercial farms using pitfall traps among three field positions (interior, edge, and forest border). During the two-year study, we enumerated 3020 adult spiders representing 24 families. Spider communities were primarily included (89%) five families: Lycosidae (45%), Linyphiidae (8%), Gnaphosidae (11%), Phrurolithidae (7%), and Corinnidae (15%). The forest border supported higher diversity and more stable spider assemblages compared to the field interior and edge. Additionally, spiders were more abundant on the field edge and exhibited dissimilarity in community

composition related to field position. Although most families were found in all three field positions, some families such as Corinnidae were only observed within the interior and edge of the blueberry field assemblages, while the family Hahniidae was only observed in the forest border assemblage. Our findings show a diverse ground-dwelling spider community in blueberry fields in Georgia and suggest that forests adjacent to crops play a key role in supporting biodiversity and foresting ground spiders within blueberry systems.

Session 8: Ecology

DEI IN THE AAS: WHERE ARE WE AND WHAT'S NEXT?

J. Andrew Roberts, Nathaniel Swigger, Mercedes Burns

American Arachnological Society & The Ohio State University at Newark; University of Maryland, Baltimore County

The purpose of the American Arachnological Society (AAS) is to “further the study of Arachnids, foster closer cooperation and understanding between amateur and professional arachnologists, and to publish the Journal of Arachnology.” We have a well-established journal and other means of knowledge dissemination (webpage, newsletter, book sales), but society efforts to promote cooperation are less established. Given the strong evidence that a diversified pool of scientists in any field generally leads to more innovative approaches and solutions to complex problems, we recognized a need to do more. In 2021, the Executive Committee established an ad hoc Diversity, Equity, and Inclusion (DEI) committee charged with proposing new initiatives. One such effort was the creation and distribution of a demographic survey to provide a baseline of data on membership identity, research fields, and study organisms upon which to build. Our survey of the AAS community finds that 2/3 of respondents identify as male, and show strong support for, and interest in, DEI initiatives. Nevertheless, we find limited racial diversity among American practitioners, and racial/ethnic minorities were significantly less likely to report feelings of belonging in the community. Minority respondents were more likely to report that they studied arachnology due to encouragement from a mentor but were less likely to report they felt comfortable seeking advice or mentorship within AAS. However, neither race, gender, sexual orientation, nor disability had significant influence on society participation rates (conference attendance, award application, etc.), which suggests that existing attention to DEI may be having a positive effect.

Session 5: Education & Outreach

MURDER IN THEIR HEARTS: SIBLING CANNIBALISM AND ITS CONSEQUENCES FOR CYTOPLASMIC INCOMPATIBILITY IN A SPIDER HOST

Rebecca R. Robertson, Jennifer A. White

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Maternally-inherited bacterial symbionts often spread throughout their host populations via reproductive manipulations. The most common of these is cytoplasmic incompatibility (CI), in which pairings between uninfected females and infected males show reduced hatch rates, disadvantaging these uninfected females relative to infected females in the host population. However, in cannibalistic predators like spiders, unhatched eggs within a CI eggmass may serve as a nutritious resource for surviving siblings, giving them a fitness advantage over families without CI, partially counteracting the CI effect. We evaluated sibling cannibalism in the context of CI using *Mermessus fradeorum*

(Linyphiidae), a common agricultural spider. Like many spiders, *M. fradeorum* spiderlings hatch within an eggmass, then undergo an additional molt and sclerotization before emergence, providing ample opportunity for unobserved pre-emergence cannibalism of unhatched siblings. We evaluated pre-emergence cannibalism in incompatible (CI) versus compatible crosses by dissecting a subset of eggmasses before spider sclerotization and counting hatched versus unhatched eggs. We compared these values to hatched spiderlings and unhatched eggs in unmanipulated eggmasses that were allowed to emerge naturally. In naturally-emerging eggmasses, we observed more evidence of cannibalized eggs in CI crosses compared to other types. Unhatched eggs found in early-dissected eggmasses were missing in naturally-emerged ones, likely due to unseen cannibalism. These findings suggest that spiderlings from CI crosses benefit from increased sibling cannibalism, while non-CI spiderlings do not, indicating that cannibalism could hinder the spread of CI bacteria in a host population. Overall, cannibalism may limit the spread of CI symbionts in hosts with siblicidal tendencies.

Session 2: Behavior

GENOMIC AND TRANSCRIPTOMIC EXPLORATIONS OF ORB-WEAVING AND SEX IN *ULOBORUS DIVERSUS* (AND HER MANY COUSINS)

Calvin Runnels, Luca Rodrigues, Jeremiah Miller, Andrew Gordus

Johns Hopkins University; Baltimore Polytechnic Institute; University of Florida

In the years since molecular studies debunked the assumption that all orb-weaving spiders belong to one clade, two hypotheses have emerged: either the behaviors behind the cribellate (woolly) and ecribellate (sticky) orb webs arose independently and convergently in the distantly related spiders who weave them, or orb-weaving originated with their common ancestor and was lost or transmuted in many other descendants. Evolutionary histories like these leave traces on the genomes of extant species which can be measured computationally. We have tested 4756 orthologous genes from publicly available transcriptomes of 98 spider species for evidence of selection that supports either hypothesis. 790 genes shared by at least 75% of species showed evidence of selection patterns corresponding to orb-weaving, including genes homologous to known silk gland, neuronal, and body-patterning genes. Moreover, orb-weaving is sexually dimorphic: adult males of many species lose the ability upon maturation. It is one of spiders' many fascinating and well-documented sexual phenotypes-from extreme body size differences to sexual cannibalism-yet little is known about the sex determination system(s) producing these dramatic outcomes. Beyond orb-weaving, we are investigating the genetics and evolution of sex in spiders both on the species level-searching for genes showing sex-biased expression/splicing in RNA-seq data from the cribellate orb-weaver *Uloborus diversus*-and on the order level, using genomes across Araneae to trace sex chromosome evolution and find conserved sex-linked genes. The result of these preliminary explorations is an extensive dataset of genes whose role in orb-weaving, sex determination, or both is ripe for experimental validation.

Genomics Symposium

UNLOCKING SCORPION VENOM ORIGINS THROUGH COMPARATIVE GENOMICS

Carlos E. Santibáñez-López, Prashant P. Sharma

Western Connecticut State University; University of Wisconsin

Scorpions, comprising more than 2500 species distributed across every continent (except Antarctica), are an ancient lineage of arachnids renowned for their potent venom and resilience to harsh environments. While scorpion biology research has historically emphasized systematics and venom characterization, genomic studies remain limited, with only five genomes representing two parvorders (Buthida, Iurida) and two families (Buthidae, Hadruridae). To unravel the evolutionary origins of scorpion venom, particularly the transition from less to highly toxic lineages, broader genomic sampling is crucial, especially from phylogenetically pivotal groups like Chaerilidae. Here, we present a draft genome of *Chaerilus stockmannorum* (Chaerilidae), a key species for bridging our understanding of venom evolution between lineages like Buthidae (highly toxic to humans) and Hadruridae (less toxic). We also report a chromosome-level genome for *Centruroides sculpturatus*, a species highly toxic to humans. Our initial analyses underscore the paramount importance of comparative genomics in venomomics to elucidate the mechanisms and patterns underlying toxin gene evolution. Furthermore, expanding genomic resources within Iurida and less toxic Buthida lineages will be essential to illuminate the origins of scorpion toxins targeting mammalian ion channels.

Genomics Symposium

EXPLORING THE ECOLOGY OF THE INTRODUCED JORO SPIDER, *TRICHONEPHILA CLAVATE*, THROUGH DNA METABARCODING

Jason M. Schmidt, Erin E. Grabarczyk

University of Georgia, Tifton Campus; Valdosta State University

Recent news outlets have flared up about the potential of large invasive spiders, *Trichonephila clavate*, ballooning from the sky to rain down havoc on cities and people. While these myths are not easy to silence, we must push forward to better understand the ecology of introduced spider species and what functions or dysfunctions these spiders or other introduced species may generate in introduced habitats. Here we provide an overview of studies implementing DNA metabarcoding to unravel some trophic characteristics of spiders in Georgia at sites determined by iNaturalist to contain active populations of *T. clavate*. Results confirm prior studies on metabarcoding predators that some materials will be swamped out with DNA templates of the predator, and there are some primers available that can aid in detecting more of the prey DNA template targets within spider guts. In addition, prey remains within spider webs of orb web weavers appear to be a valuable source of prey information and potentially a viable minimally invasive tool for monitoring biodiversity. Lastly, results looking at differences in male and female feeding show that we detect a greater variety of prey DNA templates in females as compared to males, and males appear to have less access to the diverse food captured in female webs. Therefore, while *T. clavate* is a large introduced generalist predator species that can occupy and colonize large areas, there is much to be learned using this spider as a model for understanding orb web building spider ecology.

Session 3B: Ecology

GENOMES AND THE EVOLUTION OF THE CHELICERATE BODY PLAN

Nikolaos Papadopoulos, Siddharth Kulkarni, Bastian Fromm, Christian Baranyi, Emily V. W. Setton, Benjamin C. Klementz, Sophie Neu, Ethan Laumer, Guilherme Gainett, Prashant P. Sharma, Andreas Wanninger, Georg Brenneis

University of Vienna; Indian Institute of Science Education and Research; University of Wisconsin-Madison; The Arctic University of Norway; University of Florida; Harvard Medical School

Pycnogonids (sea spiders) are the uncontested marine sister group to the remaining chelicerates. Pycnogonida's phylogenetic position and unique body plan makes these animals a valuable lineage for interrogations of chelicerate phylogeny and evolution. However, realizing the promise of this group is impeded by the absence of high-quality genomic and transcriptomic resources. We utilized long-read sequencing methods, complemented by comprehensive developmental transcriptomes and Iso-seq datasets, to assemble the first chromosome level pycnogonid genome using *Pycnogonum litorale*. Toward elucidating the origins of whole genome duplication (WGD) events in euchelicerate taxa, we identified conserved homeobox gene clusters in the pycnogonid genome and surveyed for duplication events, finding no evidence of a WGD. Intriguingly, we found that *P. litorale* has lost the posterior trunk Hox gene abdominal-A, whose loss is correlated with the loss of segments in groups like tardigrades and acariform mites. Additionally, we re-examined the sea spider proboscis, a suctorial feeding apparatus of unclear developmental origin. Using the new genomic resources for *P. litorale*, we identified orthologs of head patterning genes and performed gene expression assays in embryonic stages. Taking a comparative approach, the same targets were surveyed in the apulmonate arachnid *Phalangium opilio*. We show that the proboscis is exclusively protocerebral in origin and represents a circum-oral outgrowth that expresses limb-patterning genes. The segmental position and the outgrowth of the proboscis are discussed in the context of the arthropod Paleozoic fossil record.

Session 7: Morphology, Physiology & Development

RECIPROCAL ILLUMINATION BETWEEN GENOMES AND PHYLOGENY IN THE EVOLUTION OF THE ARACHNIDS

Prashant P. Sharma

University of Wisconsin-Madison

Arachnids comprise a species-rich group of predatory arthropods that are found in ecosystems spanning most of the Phanerozoic. The discovery of a shared and ancient genome duplication (WGD) event in a subset of arachnid orders (the Arachnoplumonata) has dramatically changed modern understanding of arachnid phylogeny, as well as positioned this clade as a useful system to study the impact of new genes on diversification dynamics. However, much of the higher-level phylogeny of Arachnida remains unresolved. Here, I explore advances in phylogenomic relationships of arachnids using analyses of rare genomic changes. I show that certain classes of rare genomic changes can resolve deeply recalcitrant nodes in the arachnid tree of life.

Genomics Symposium

TWO NEW GENERA OF CAMEL SPIDERS FROM NORTH AMERICA (SOLIFUGAE: EREMOBATIDAE)

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Our work summarizes the taxonomic treatment for a large species group of Solifugae in the family Eremobatidae from North America. In 2015, the first family level phylogeny was produced, revealing that the three most speciose genera were para-polyphyletic and in need of taxonomic revision. The *Eremobates palpisetulosus* species group was created by the late Dr. Martin Muma for 42 described species using a single character but was not supported as a monophyletic group in published and ongoing phylogenetic analyses. Instead, four separate monophyletic clades were recovered across the family phylogeny. We identified two clades from the palpisetulosus species group distributed across the Chihuahuan, Great Plains and Sonoran habitats to review. While these clades overlap in distribution, taxonomic literature from the 1900s suggested there were characteristics that separated these focal taxa. In tandem with the ongoing UCE phylogenetic analyses, we assessed whether we could provide support for elevating these two clades as new genera by exploring the morphology of the chelicera and conducted a series of tests. Traditional and novel trait ratios were used to identify meaningful differences distinguishing the clades. The new genus *Eremobtusus* was proposed for a set of species where both males and females are characterized by darkened, blunt chelicera and the only described palpisetulosus taxa having lost additional dentition. The new genus *Eremodromus* was proposed for a wide-ranging clade that possesses proportionally larger chelicera, larger legs scaled to the body and various additional characters not found in *Eremobtusus*.

Session 6B: Systematics & Evolution

TRACKING MALE TARANTULAS: RADIOTAGGING AND MARK-RECAPTURE OVER THE MATING SEASONS IN THE COLORADO BROWN TARANTULA (*APHONOPELMA HENTZI*)

Cara Shillington

Eastern Michigan University

The mating season for the Colorado Brown Tarantula is well-documented in the popular media, when hundreds of males are found crossing roads in SE Colorado. However, surprising little is known about individual movement and behavior of males during this period. During the 2024 fall mating season, I radiotagged mature males and recorded daily movements at a field site in the Comanche National Grasslands where there is a large number of occupied burrows. Additional males located at the site were captured, weighed and marked individually (bee markers) before being released at their site of capture within 24 hours; GPS locations were recorded. Over the duration of the mating season (late August through early November), males were tracked daily via radiotelemetry and each time marked individuals were encountered, their location was again recorded. Distances travelled for both radiotagged and bee-markered individuals were determined from GPS coordinates. Temperature and precipitation data were also recorded over this time. A total of 279 males were marked individually; of these 177 were never seen again and nine were encountered more than once. Of the 17 radiotagged males, many males spent surprisingly long periods in “found” burrows in-between bouts of locomotory activity. Activity decreased during prolonged periods of hot and dry conditions and the highest levels of locomotory activity occurred during the latter part of the mating season. It is difficult to draw clear

conclusions based on just one reproductive season, but the data suggest environmental conditions impact activity and mortality rates are likely high.

Session 6A: Behavior

WHO'S THE FATHER? INSIGHTS INTO ARTHROPOD PATERNITY AND FUTURE DIRECTIONS WITH *DOLOMEDES* SPIDERS

Gustavo Silva de Miranda, Eileen Hebets
University of Nebraska – Lincoln

Spiders exhibit a unique mode of reproduction characterized by indirect sperm transfer via the male's pedipalps and sperm storage in female spermathecae. While multiple mating is common in many species, the dynamics of sperm competition and cryptic female choice remain poorly understood. Specifically, little is known about the extent of paternity bias, mechanisms of sperm precedence, and the role of female-mediated sperm selection in spiders. This study aims to fill some of these gaps by first conducting a comprehensive review of paternity studies across terrestrial arthropods, focusing on experimental approaches, molecular markers, and analytical tools used to assess paternity outcomes. Building upon this synthesis, we present preliminary results on a novel investigation into paternity patterns in laboratory mating assays of the fishing spider genus *Dolomedes* (Dolomedidae). Using newly generated whole-genome sequences of *Dolomedes tenebrosus* and *Dolomedes vittatus* as reference datasets, we plan to employ genomic paternity analyses to quantify the proportion of offspring sired by each male and explore evidence for sperm competition and cryptic female choice, offering new insights into the evolutionary dynamics of spider reproduction.

Session 6A: Behavior

UNDERSTANDING THE DIVERSITY AND EVOLUTION OF TARANTULAS IN THE MADREAN SKY ISLANDS

Karina Silvestre Bringas, Chris Hamilton
University of Idaho

The Madrean Sky Islands are an important biodiversity hotspot housing several endemic species of the southwestern United States and northern México. These mountain ranges are characterized by the unique Madrean Pine-Oak woodlands and the stacking of biomes created by their dramatic change in altitude and complex climactic conditions. Since the last glaciation, these mountain ranges have become increasingly isolated from each other, limiting genetic interchange between populations creating ideal conditions for diversification. *Aphonopelma* is the only tarantula genus residing within the United States and are found throughout a variety of habitats including the Madrean Sky Islands where *Aphonopelma marxi* species group resides. We infer a phylogeny of the Marxi group using 1300 ultra conserved elements (UCE) loci from populations across >40 MSI from USA and, for the first time, Mexico. This work is the first representation of the many populations of Sky Island tarantulas and creates a framework for determining species diversity of the group bringing further understanding of one of the most ecologically diverse regions in the country.

Session 1: Systematics & Evolution

RAPID EVOLUTION OF PREZYGOTIC REPRODUCTIVE ISOLATING MECHANISMS IN THE *SCHIZOCOSA OCREATA* AND *S. ROVNERI* SPECIES COMPLEX

James Starrett, Rowan McGinley, Eileen Hebets, Jason Bond

UC Davis; Smithsonian Tropical Research Institute; University of Nebraska-Lincoln

Testing hypotheses of the role of multi-modal traits in driving speciation requires robust inference of evolutionary relationships. *Schizocosa* is a model for the study of multi-modal courtship behavior and reproductive isolation. *Schizocosa ocreata* and its hypothesized sibling species *S. rovneri* have received considerable attention regarding vibratory and visual signaling and their role in maintaining species boundaries. *Schizocosa ocreata* and *S. rovneri* contrast in male secondary sexual ornamentation and signal complexity. Females of these species are morphologically indistinguishable; however, females are highly selective for conspecific males, thus maintaining a prezygotic barrier to gene flow. Inference of the evolutionary relationship between *S. ocreata* and *S. rovneri* is unclear despite application of molecular datasets. Mitochondrial and multi-locus nuclear datasets indicate that the two species are not reciprocally monophyletic. Here, we densely sample *S. ocreata* and *S. rovneri* from across their ranges and generate RADseq (3RAD) and ultraconserved element (UCE) datasets. Cluster analyses of SNP data support two geographic-based groups rather than grouping along taxonomic lines. One group consists of *S. ocreata* from the deep southeast of North America and the second group consists of western and northern populations of *S. ocreata* plus *S. rovneri*. Phylogenetic analyses of UCE data indicate high support for the non-genealogical exclusivity of *S. ocreata*, and high support for a derived placement of *S. rovneri* within *S. ocreata*. These results show that *S. rovneri* is a recently derived species associated with rapid evolution of morphological and behavioral characters that maintain a prezygotic reproductive barrier.

Session 3A: Evolution, Genetics & Genomics

NEW INSIGHTS INTO CAMEL SPIDER (SOLIFUGAE) REPRODUCTION: FROM COURTSHIP TO SPERM COMPETITION

David Vrech

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As part of the forthcoming book *The Biology and Natural History of Camel Spiders (Arachnida, Solifugae)*, we are preparing a chapter focused on reproductive biology. This contribution integrates classical and contemporary knowledge with novel data across multiple stages of the reproductive process. In this presentation, I will briefly introduce the book project and highlight three case studies that exemplify the diversity and complexity of solifuge reproductive strategies—all of which will be fully developed and discussed in the book chapter. First, I will present recent findings on precopulatory behavior, showing that male solifuges exposed to female chemical cues modify their exploratory movements, progressively using shorter pulses. This shift suggests a faster detection and response mechanism than previously anticipated. Second, I will share preliminary data from an ongoing study of two sympatric species from central Argentina, focusing on sperm production and copulatory morphology. Our results reveal interspecific differences that may be linked to distinct mating strategies. Lastly, I will address postcopulatory aspects, including the presence of female sperm storage organs and the potential for sperm competition in this group. Together, these examples emphasize the richness of

solifuge reproductive biology and its relevance to broader questions in sexual selection and evolutionary biology. By showcasing this diversity and the value of integrating behavioral, morphological, and physiological data, we hope to stimulate further research on this fascinating but understudied arachnid lineage.

Session 6A: Behavior

SUBSTRATE SPECIFICITIES IN SICTOX VENOM TOXINS FROM SICARIID SPIDERS INFLUENCE CYTOTOXICITY

Finn Watson, Lindy Gewin, Matthew Cordes, Greta Binford
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The family Sicariidae contain SicTox in their venoms, a variant of Phospholipase D (PLD). SicTox is known to cause loxoscelism in humans and fast acting and immobilizing toxicity in insect prey. SicTox variants make up more than 50% of the proteins found in *Loxosceles* and *Sicarius* venom, implying an important role in prey capture. Despite this outsized presence in venom, the effects of SixTox isoforms in prey systems are poorly understood. Notably, different homologues of SicTox show different cleavage specificity towards various phospholipid substrates. The effects of this diverse specificity on prey immobilization remains unknown. One hypothesis is that varying phospholipid substrate specificity could allow toxins to target wider varieties of prey, allowing for the generalist hunting behavior of spiders in this family. To investigate the effects of SicTox on prey we perform in vitro cytotoxicity assays by treating SF9 cells with extant venom toxins and mutants that modify phospholipid binding. We measure cell permeability via a propidium iodide assay in a microplate format. We find that venom toxins with diverse phospholipid specificities result in differing effects on prey cells. Additionally we find that mutations predicted to increase substrate binding to sphingomyelin can cause increased cell permeability. These data are consistent with our hypothesis that varied specificity could broaden the range of physiological effects on prey.

Session 4: Silks & Venoms

TEMPERATURE AS A DRIVER OF SYMBIOTIC POLYMORPHISMS IN AN AGRICULTURAL SPIDER

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Maternally-inherited bacterial symbionts often manipulate the reproduction of their host arthropods, to promote the spread of infection throughout the host population. Theory predicts that symbionts will often spread to near fixation, based on several parameters including penetrance of the manipulative phenotype, fitness costs to the host, and efficiency of vertical transmission from mother to offspring. Host populations that are polymorphic, consisting of individuals with different symbiont complements and phenotypes, have rarely been investigated in nature, and we know relatively little about the mechanisms that maintain such variation. Our group has now been studying the agricultural spider *Mermessus fradeorum* (Linyphiidae) for over a decade, and we have documented that our local population has maintained a mixture of spiders with different symbiotypes and different phenotypes throughout this time. Temperature likely plays a critical role in maintaining this polymorphism, through effects on all the parameters that affect symbiont maintenance and spread. This leads us to several concrete hypotheses about geographic variation in infection that we are currently testing. Our results contribute to the growing body of literature that shows temperature may be a driving but

underappreciated force in determining the distribution and persistence of host-symbiont polymorphisms.

Session 3B: Ecology

THE MICRONUTRITIONAL ECOLOGY OF EGG PRODUCTION IN A WOLF SPIDER AND PHOLCID

Shawn Wilder, Colton Herzog

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The provisioning of eggs, especially with dietary essential nutrients, could have important consequences for the success of offspring. Prey items vary in their elemental content and many spiders are generalists that consume a variety of insects and spiders, including cannibalism. Hence, there may be variation in micronutrient provisioning of eggs by females. We compared the micronutrient content of spider eggs to wolf and pholcid spiders (*Hogna carolinensis* and *Crossopriza lyoni*) and four insect prey to test which prey were a better match for the nutrients found in eggs. Micronutrient content was measured as 17 elements ranging from B to Zn. In both spider species, males and females were similar in micronutrient content while eggs were distinct. Insect prey also differed in micronutrient content compared to spiders and their eggs. These results suggest that cannibalism may not be a perfect match for the micronutrient content of eggs, as the composition of eggs is different from that of both male and female spider bodies. However, cannibalism is still likely to be beneficial, as there are certain nutrients that are in higher concentrations in both spiders and their eggs than in insect prey. Insect prey alone could allow spiders to meet the nutritional needs of egg production but may require female spiders to consume more overall food to gain enough of certain elements. Further work is needed to understand nutritional plasticity in spider egg composition and its consequences for offspring.

Session 7: Morphology, Physiology & Development

A ROBUST GENOME ASSEMBLY WITH TRANSCRIPTOMIC DATA FROM THE STRIPED BARK SCORPION, *CENTRUROIDES VITTATUS*

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Scorpions, a seemingly primitive, stinging arthropod taxa, are known to exhibit marked diversity in their venom components. These venoms are known for their human pathology, but also important as models for therapeutic and drug development applications. We report a high-quality genome assembly and annotation of the striped bark scorpion, *Centruroides vittatus*, created with several shotgun libraries. The final assembly is 760 Mb in size, with a BUSCO score of 97.8%, a 30.85% GC, and a N50 of 2.35 Mb. We estimated 36,189 proteins with 37.32% assigned to GO terms in our GOanna analysis. We mapped venom toxin genes to 18 contigs and two scaffolds. We were also able to identify expression differences between venom gland (telson) and body tissue (carapace) with 19 Sodium toxin and 14 Potassium toxin genes to 18 contigs and two scaffolds. We also provide further data regarding other toxin components and remark on current spider genomic assemblies.

Session 4: Silks & Venoms

LATENT PREFERENCE FOR RED ORNAMENTATION DRIVES INTERSPECIFIC MATING IN NASCENT JUMPING SPIDER SPECIES (*HABRONATTUS AMERICANUS* GROUP, F. SALTICIDAE)

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UC Berkeley; University of Kansas; Columbia University; San Diego State University

Heterospecific interactions between nascent species offer insights into how sexual selection may shape novel traits, potentially illuminating patterns in species interactions and diversification. We tested female preference patterns between two recently diverged, allopatric species of jumping spiders: *Habronattus americanus* PLC, with red-colored males performing short multimodal displays, and *Habronattus sansoni* CC, with brown-colored males performing long multimodal displays. Mate choice experiments showed that females of both species preferred *H. americanus* males. To examine the role of red coloration, we manipulated male coloration in both species. Results indicated that red-painted *H. sansoni* CC males experienced an increase in mating success, whereas brown-painted *H. americanus* males did not show reduced success, suggesting that preferences for red coloration are weaker in populations where the trait is already common (*H. americanus*) than in populations where it is absent (*H. sansoni* CC). Our study suggests that (1) strong latent female preferences for a trait can drive unidirectional introgression across species boundaries potentially leading to genomic homogenization and (2) the strength of that preference may be weaker in populations expressing the trait, potentially setting the stage for future diversification. Overall our study demonstrates the role that mating interactions can play in speciation dynamics.

Session 2: Behavior

POSTERS

COMPOSITION OF SPIDER COMMUNITIES IN PEANUT LANDSCAPES

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Biodiversity of arthropod natural enemies is shown to enhance biological control service in agricultural systems. However, further research is needed on the assemblages that make up the communities within these systems in southern subtropical climates. Our study examines the composition of spider families that occur in peanut (*Arachis hypogaea*) fields in the state of Georgia with a particular focus on Salticidae. Vacuum sampling was done over 2 years across 67 sites during the period of cotton and peanut flowering. We collected approximately 1,850 individual spiders, the majority representing the families Salticidae (~500), Oxyopidae (~400), and Thomisidae (~250) with the remaining (700) consisting of immatures and those not yet identified to family. Being the most abundant family, we began to our analysis with focus on salticids identified to the lowest taxonomic level possible and correlated community composition of salticids to field position (i.e. field edge and interior). Further identification of the collected samples, particularly those not identified to family, is needed to create a clearer picture of the diversity of spider communities in peanut landscapes.

CONSERVED POST-TRANSLATIONAL MODIFICATION TO AGGREGATE SPIDROINS SUGGEST CONTRIBUTIONS TO GLUE STICKINESS IN ARANEOID SPIDER WEB

Karim Abualnaja** , Hallie McMurdie, Ryan Boyd, Richard Baker, Sandra Correa-Garhwal, Thomas Clarke, Brent Opell, Kyle Friend, Nadia Ayoub

Washington and Lee University; American Museum of Natural History; Suffolk University; Virginia Tech
Spiders in the superfamily Araneoidea are defined by the presence of aggregate glands that produce an aqueous chemically sticky glue used to capture prey. Aggregate glue droplets rely on a balance of adhesion, cohesion, and extensibility to maintain attachment to prey items under mechanical stress. These properties arise from aggregate spidroins (AgSp1, AgSp2, and AgSp3) and other specialized proteins embedded within the glue. Post-translational modifications (PTMs)-specifically phosphorylation and glycosylation-may contribute to the functional properties of these proteins. We identified proteins and PTMs using mass spectrometry of capture spiral silks and mapped the site of modification to full length (14 species with whole genomes) or partial length (4 species with transcriptomes) AgSp sequences. We aligned repeats within individual sequences to test if amino acid residues are consistently modified across repeats. We then aligned AgSp1 across all species, including orb-web and cobweb weavers, and identified conserved regions of phosphorylation and glycosylation. Our preliminary findings suggest that glycosylation may contribute to the adhesive properties of spider glue, while phosphorylation may play a role in maintaining cohesion. Conserved PTMs further indicate that modifications are not random but may be essential for fine-tuning the mechanical performance of spider glue. This work advances our understanding of how molecular-level adaptations underlie the exceptional functionality of biological adhesives.

DATA IN THE WILD: A DATA SCIENCE CURRICULUM FOR EARLY UNDERGRADUATE GENERAL EDUCATION

Greta J. Binford, Finn Watson, Jeremy McWilliams
Lewis & Clark College

Empowering students to learn and apply strong quantitative reasoning skills and data science can transform their ability to address questions meaningful to them. Through an NSF-funded initiative at Lewis & Clark College, in collaboration with the University of Arizona, we have created curricular modules that are designed to broaden access to data science skills in early undergraduate education. We introduce data science in a section of our first-year core (“Numbers”) called Data in the Wild (DIW). The course has three parallel narratives: (1) a framing scenario of our class building a settlement on Antarctica where we confront challenges and environmentally-conscience development decisions using data science; (2) building general quantitative reasoning skills including data concepts, key methods of extracting information from data through descriptive statistics, and supporting data-driven decision making with inferential statistics; and (3) teaching data science skills using R programming. DIW is followed by the option of Applied Data Science, taught in partnership with the US Fish & Wildlife service, with students doing current and future niche modeling for species under consideration of changing endangered listing status. Pre and post surveys for DIW indicate nearly 100% increase in understanding the role of data science in addressing problems, over 75% expressed interest in data science and nearly 40% had increased interest in incorporating data science into their careers. Our curricula are freely available and scalable with modules that can be overlain with individual course narratives, datasets and examples.

SUPPLEMENTAL FEEDING ALTERS FORAGING BEHAVIORS OF TARANTULAS IN THEIR NATURAL HABITAT (*APHONOPELMA HENTZI*)

Annalyse Brogan**, Cara Shillington
Eastern Michigan University

Foraging success is a crucial factor in survival and reproductive success for many animals. One mechanism that can improve an organism’s foraging success is foraging plasticity, or the organism’s ability to alter their behavior in response to environmental changes. This study aimed to evaluate if *Aphonopelma hentzi*, the Colorado Brown Tarantula, as a long-lived, sit-and-wait predator would use foraging plasticity in response to increased prey encounters. We conducted a short-term field study on foraging behavior in *A. hentzi* in their natural habitat in the Comanche National Grasslands. We predicted that tarantulas with more prey encounters would have a higher residual body condition index, shorter foraging duration, and shorter distances traveled from their burrows. We compared a group of tarantulas that received supplemental feeding to a non-supplemented control group using video-tracking to capture and score behaviors. As hypothesized, the supplemented tarantulas had increased body conditions, lower foraging duration, and did not travel as far from their burrows. Additional behavioral observations were also scored, including repeated prey capture and novel object interactions. The ability of tarantulas to alter foraging behaviors in response to environmental stimuli could have important implications on how they can tolerate changes in the environment, which could be necessary in the face of habitat disturbances and climate change.

INVESTIGATION OF BEHAVIORAL PATTERNS DURING OLFACTORY-GUIDED HOMING BEHAVIOR IN THE AMBLYPYGID *PHRYNUS MARGINEMACULATUS*

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Effective navigation by some terrestrial arthropods relies on integrating chemical and spatial cues, yet the behavioral mechanisms underlying such navigation remain underexplored. This study investigates whether distinct behavioral sequences emerge during odor-guided navigation in the amblypygid *Phrynus marginemaculatus*. Subjects were first trained to associate a specific odor with the presence of a shelter. Following training, individuals were placed in a linear arena with a gradient of the conditioned odor or no odor and their movements were video recorded and tracked using a custom-trained SLEAP model. Pose trajectories were analyzed with keypoint-MoSeq, an unsupervised machine learning framework that infers discrete behavioral syllables and their transitions using a hierarchical autoregressive hidden Markov model. Behavioral syllable usage and transition structure were compared between odor and no-odor treatments to identify patterns associated with olfactory-guided navigation. Ongoing analyses focus on evaluating whether odor availability modulates behavioral sequence architecture, potentially revealing navigational strategies specific to the use of chemosensory cues. This approach provides a high-resolution behavioral lens to examine how odor guides amblypygid navigation behavior.

ENTRAINED POSITION OF LOCOMOTOR ACTIVITY IN DD IS RESISTANT TO DRASTICALLY ALTERED LIGHT CYCLES, IN A SYNANTHROPIC SPIDER (*PHOLCUS MANUELI*)

Caroline N. Cavin** , Joseph Giulian, Raven Ragsdale, Autumn Dishman, Heidi Allen, Thomas C. Jones, Darrell Moore
East Tennessee State University

Previous research on spiders has found remarkable variation in free-running periods (FRPs) both within and among species. *Pholcus manueli*, a synanthropic species, exhibits behavioral adaptations that may be advantageous to their survival in anthropogenic environments where artificial light at night (ALAN) is common. Preliminary findings suggest that this species retains its original window of entrainment even after several days in a phase shifted light cycle. To further test this, we first exposed spiders to a 12:12 LD cycle for five days similar to their natural environment. Then a 6-hour phase advance was induced for five days; followed by constant darkness (DD) to assess free-running activity. Locomotor activity moved to the shifted phase position in advanced LD, but returned to a stable phase position reflecting the original light cycle while in DD. Another group of spiders were first placed in a 12-hour phase shifted light cycle for five days and then 6-hour phase delayed for five days, again followed by DD. As with the previous experiment, phase position of activity followed the light cycles, but then returned to the original natural phase position in DD. The presence of transients in these and other experiments suggest that this is more than just a simple masking effect. These findings suggest that this synanthropic spider retains a strong entrainment phase position that is resistant to phase shifts while demonstrating rapid resynchronization of nocturnal activity to changing LD cycles. Such resistance to unnatural perturbation of light cycles may contribute to this species' ability to thrive in urban environments.

PROTEIN-PROTEIN INTERACTIONS OF PUTATIVE CIRCADIAN REGULATORS IN THE COMMON HOUSE SPIDER, *PARASTEATODA TEPIDARIORUM*

Justin Cheetham** , Karoul Garas, Jessica Petko

Penn State York

Circadian rhythms drive daily patterns of animal behavior and physiology. The circadian day length of an organism without environmental input, also known as the free-running period, is generally close to 24 hours (± 1 hour). In the presence of time cues such as light, the molecular clockwork can be tweaked to maintain a perfect 24-hour biological rhythm, a process called entrainment. Spiders are unique in that they exhibit extreme free-running periods (18-29 hours). When entrained to a 24-hour light schedule, spiders with extreme free-running periods are jetlagged by as much as 6 hours without physiological consequence. Our lab is interested in the molecular genetics of spider circadian clocks and how they compare to organisms that exhibit normal circadian parameters. One way in which circadian proteins are regulated is through protein-protein interactions. In this study, we map the domains of putative spider clock genes and analyze predicted interactions using a GST-pulldown assay.

FIRST PITFALL TRAPPING SURVEY OF GROUND-DWELLING SPIDERS OF HOOD RIVER VALLEY PEAR ORCHARDS

Sean Counihan** , Christopher Adams

Oregon State University

Pear orchards practicing integrated pest management rely on natural enemies to help control key pests. Orchard managers regularly sample for these natural enemies in an effort to predict their potential contribution to pest control. While some key natural enemies are well known in pear orchards, other predaceous arthropods, such as spiders, are neglected in regular scouting efforts. To investigate the ground dwelling spider community within managed pear orchards, we placed pitfall traps under the canopy of pear trees in 20 orchards across the Hood River Valley. Trapping data was collected weekly from June through August. Spiders were identified to the most precise possible taxonomic level using *Spiders of North America* (second edition). In total, 168 spiders from 7 families were collected. The majority of specimens belonged to the families Gnaphosidae, Lycosidae, and Linyphiidae. *Zodarion rubidum*, an introduced species to North America and obligate predator of ants, is noted for the first time from the Hood River Valley and North American pear orchards overall.

BIOLOGY AND NATURAL HISTORY OF CAMEL SPIDERS (ARACHNIDA, SOLIFUGAE): NEW TEXT BOOK

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Denver Museum of Nature & Science; National Research Council (Conicet Argentina); National University of Córdoba, Argentina; University of Wisconsin, Madison

Camel spiders (arachnids in the order Solifugae) are major desert-dwelling predators of insects and other arthropods throughout the world and are, themselves, an important food resource for other desert-adapted predators. In other words, camel spiders are major components of desert communities. In recent years, research has advanced our understanding of this enigmatic group of arachnids. *Biology and Natural History of Camel Spiders (Arachnida, Solifugae)* will present our current understanding of the anatomy, systematics, taxonomy, behavior, physiology, genetics, and natural history of these

animals. In addition, this book includes an overview of the extraordinary mythology surrounding them. This text draws upon the expertise of researchers throughout the world who are exploring various aspects of the biology of Solifugae. It is the hope of the editors and chapter authors that it will serve to both inform and inspire all those interested in desert ecosystems and the animals that call these habitats home.

TIMING OF SPRING EMERGENCE AND MATING BEHAVIOR OF THE ORCHARD SPIDER (*LEUCAUGE VENUSTA*)

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Leucauge venusta (Walckenaer 1841) is a common but understudied orbweaver in the midwest and eastern United States. Here, we described the timing of *L. venusta* spring emergence and operational sex ratio (OSR) in southeast Michigan and conducted a laboratory study on its mating behavior. From May to June 2024, we collected 108 *L. venusta* from the forested 120 acre environmental study area of the University of Michigan-Dearborn. We surveyed our study area and collected all male and female penultimate stage spiders as they emerged in the early spring. We confirmed sex once they reached adulthood to estimate OSR. In the laboratory, individually housed *L. venusta* were fed *Drosophila*. After molting to the adult stage, females were transferred to larger tanks to spin webs. In staged mating trials, virgin females were mated to either one virgin male only or two virgin males in succession. Immediately after mating (or cannibalism) males were collected and frozen at -80 °C for later sperm counting. We found that the OSR was initially male-biased but shifted to female-biased in mid-May. In the 41 staged mating trials we found that first males transferred more sperm to females than second males and 51% of staged matings were successful (i.e., palps inserted long enough for sperm transfer). Antagonistic behavior of females toward males occurred in both mating types and the overall frequency of attack and/or cannibalism was 20%. Older females were more likely to attack males. Future research will include a detailed analysis of sperm release behavior.

SPIDERS OF THE COAST: BUILDING THE TREE OF LIFE FOR ARACHNIDS IN MAGIC: THE GATHERING

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Science communication is an important part of being a scientist and can take on many forms. This article combines our love for our science, arachnid taxonomy and evolution, and one of our hobbies, the Magic: The Gathering card game. We introduce both the hobby and the science, then we take our roles as scientists and naturalists into the realm of Magic: The Gathering (MTG). Here we conducted the first systematic analysis of creatures within the MTG multiverse, focusing on those that are considered arachnids in our plane of existence. We downloaded card photos of all spider (and other arachnid) creature cards and used the illustrations to create a data matrix of characteristics that was used to create a “tree of life” (phylogeny) for all creatures examined. Based on these results we propose the first taxonomic classification for arachnids of MTG, focusing on spiders. We then discuss some aspects of spider evolution in the MTG universe.

APHONOPELMA HENTZI SPRING BURROW OPENING IN COMANCHE NATIONAL GRASSLAND

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Otero College; Eastern Michigan University

Aphonopelma hentzi, commonly known as the Colorado Brown Tarantula, has large populations in the Comanche National Grasslands (CNG) in southeast Colorado. As large, long-lived fossorial tarantulas, juveniles and females live in burrows for the majority of their lives. At the start of their mating season, males leave their burrows in search of mates; males likely die during this period. Once the mating season ends in mid-November, juvenile and female tarantulas plug their burrow entrances to avoid the cold temperatures of Colorado winters and reopen them the following spring. Surprisingly, we know little about the timing or triggers for these events. Thus, the goal of our study was to determine when *A. hentzi* reopen their burrows and the correlating temperatures. To document the reopening events, camera traps were placed above marked entrances in mid-March. Every 2-3 weeks, photos were retrieved and reviewed. Local temperature and precipitation data were obtained around this same time period. In early March, while some burrows were already opened, very little webbing covered the entrances. With concurrent checks, more burrows were opened, and the webbing became more visible. Maximum temperatures around the first check reached 26 °C, while average low temperatures were still below freezing (-0.9 °C). By the third visit, average maximum temperatures were 21.9 °C and average minimums above freezing (3.8 °C). Precipitation amounts were very low. Additional data on burrow temperatures and prey availability would provide additional insight to the timing of these events.

FUTURE FOCUS: INVESTIGATING THE EFFECTS OF CIRCADIAN RHYTHM DISRUPTION ON THE BIOMATERIAL PROPERTIES OF SPIDER SILK AND GLUE

Hannah Faye, Sarah Stellwagen
UNC Charlotte

Circadian rhythms are integral to many physiological and molecular processes including metabolism, immunity, gene transcription, behavior, etc. Despite the growing breadth of literature describing circadian connections and control on new processes, there has been little to no research exploring the relationship between invertebrate biomaterials and circadian rhythms. Research in mammalian models such as mice have shown that biomaterial strength and functionality are reduced when an organism is suffering circadian induced stress. In *Larinioides sclopetarius* (Araneidae), circadian stress due to artificial light at night (ALAN) resulted in reduced web size. These findings support a probable connection between invertebrate biomaterials and their circadian rhythms. We plan to establish baseline spider prey capture silk and glue strength and then induce circadian stress in *Uloborus glomosus* (Araneidae), *Argiope aurantia* (Araneidae), and *Parasteatoda tepidariorum* (Theridiidae). We will then measure silk strength and glue adhesion to establish the effects of circadian stress on these materials. This research will further the understanding of the true scope of circadian control in invertebrate organisms and may also show more tractable characteristics of prey capture glues and silks that can be targeted for biomimetics.

SPIDER WEB INCLINATION AFFECTS PREY AND DEBRIS ACCUMULATION IN FOREST UNDERSTORY

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Trade-offs in web structure and function (e.g., prey capture rates vs. construction and maintenance costs) likely contribute to variation in web characteristics among orb-weaving spiders. *Leucauge venusta* (Walckenaer) is a habitat generalist that exhibits high intraspecific variation in the angle of web inclination relative to the ground. We investigated the effect of web angle on prey interception and debris accumulation in artificial *L. venusta* webs in forest understory in Kentucky, USA. In May, July, and September 2024 we placed circular, clear plastic sticky traps at three inclinations (vertical, 45 degrees, or horizontal) along three 100m transects. We measured abundance, identity, and body length of captured prey. Most captured prey (96%) were small insects (<5mm body length) and most (61%) were true flies, mainly fungus gnats (Diptera: Mycetophilidae). The average body length of prey tended to be higher in horizontal and 45° traps than in vertical traps. Prey abundance was significantly lower in September than in May or July and was not affected by trap inclination. Horizontal and tilted traps accumulated significantly more debris than vertical traps in all months. The results suggest that web inclination affects the types of prey captured and the likelihood of web damage or spoilage from falling debris in forest understory. Collectively, these results suggest that the relatively horizontal orb webs of *L. venusta* reflect an evolutionary balance between prey capture and damage risk.

NAVIGATION BY DÉJÀ GOÛTÉ: HOW SCORPIONS FIND THEIR WAY HOME

Douglas D. Gaffin, Mariëlle H. Hoefnagels

University of Oklahoma

Scorpions have arguably the most elaborate “tongues” on the planet: their pectines. The paired pectines, which sweep the ground as the animal walks, support thousands of peg-shaped sensilla, each richly supplied with chemosensory and mechanosensory neurons. Males use their pectines to detect female pheromones during the mating season, but females have pectines too. We have long wondered what additional roles the pectines could play; in particular, why are there so many pegs? We have assimilated all we know about pectine biology to test the hypothesis that scorpions use their pectines to navigate by chemo-textural familiarity. The premise is that the peg arrangement enables scorpions to acquire memories of chemo-tactile information matrices during early journeys toward their burrow. Then, during subsequent walks, the animal steps in a direction that minimizes the difference between its current pectinal “taste” and the matrices it has in memory. In essence, the animal moves toward what “tastes and feels” most familiar at any time. Since déjà vu means “already seen,” we opted for déjà goûté (“already tasted”). We first showed that this form of familiarity navigation is consistent with behaviors we observed during scorpion homing excursions. We then developed a computer simulation to analyze navigation success using multiple combinations of sensor sensitivity levels, sensor resolutions, and landscape characteristics. We also assessed the effects of additional sensory channels and of landscape disruption. Finally, we showed that the simulated agent can navigate across a landscape the size of a typical sand scorpion’s home range.

LOCOMOTORY EFFECT OF REVERSIBLY RESTRAINING THE PECTINES OF SCORPIONS

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University of Oklahoma

Scorpions possess unique, ornate mid-ventral sensory organs called pectines. The pectines are used to process chemo- and mechanosensory information acquired from the ground as the animal walks, and they are implicated in a variety of behaviors including navigation and detection of mates and prey. Many previous researchers have investigated pecten function by cutting the organs from the animals (full ablation) and comparing their behaviors with those of intact scorpions. This drastic approach is likely to not only cause enormous stress to the ablated animals but also change their behavior. Here, we have developed a method for gently and reversibly covering the pectines. We fabricated small rectangles of a commercially available lightly adhesive foil tape that we placed across the pectines and secured to the body wall with a thin strip of a more strongly adhesive lab tape. Using a repeated measures design, we monitored the animals' locomotory activity overnight in small behavioral arenas under three conditions: unmodified (intact) control, pectines covered, and sham control. We found that scorpions with their pectines covered had a significant increase in both the distance and duration of movement when compared to unmodified and sham control animals. Our method allows for temporary, reversible compromise of pecten function and should be useful in fully understanding the role of pectines in behavior.

EXPRESSION AND FUNCTIONAL REGULATION OF CIRCADIAN CLOCK PROTEINS IN THE COMMON HOUSE SPIDER, *PARASTEATODA TEPIDARIORUM*

Karoul Garas**, Justin Cheetham, Nadia Ayoub, Natalia Toporikova, Thomas C. Jones, Darrell Moore, Jessica Petko

Penn State York; Washington and Lee University; East Tennessee State University

Circadian rhythms regulate physiological processes across animal species, typically operating on a genetically driven ~24-hour cycle. While disruptions in these rhythms can lead to phenomena such as jet lag, spiders exhibit remarkable circadian variability—some species show significantly shorter or longer periods, and they adjust to light cycle shifts with no detectable signs of jet lag. In all animals, circadian regulation is governed by transcription-translation feedback loops (TTFL), wherein the core CLK/CYC transcription complex is subject to negative feedback, generating oscillations in gene expression. While arthropods share a common set of clock proteins, their functional roles vary across taxa. In monarch butterflies and crustaceans, CRY2 and PER/TIM proteins inhibit transcription, cycling throughout the day to maintain rhythmicity, while light-sensitive CRY1 binds to TIM, triggering degradation upon exposure to light. This study investigates the daily expression patterns and regulatory function of TTFL feedback inhibitors and accessory regulators in the spider *Parasteatoda tepidariorum*. Antibodies were developed against spider clock proteins, and western blotting was used to analyze their circadian expression. Additionally, cultured cells expressing *P. tepidariorum* CRY1 were exposed to varying light conditions to assess its sensitivity and degradation. These findings provide insights into the unique molecular mechanisms underpinning circadian timekeeping in spiders, highlighting evolutionary divergences in clock regulation across arthropods.

SCORPIONS ON A SCALE: MEASURING GROWTH IN JUVENILE *HETEROMETRUS SPINIFER*

Kris Gibbons, Cara Shillington
Eastern Michigan University

Growth rates provide valuable insight into a species' life history, including developmental stages, reproductive maturity, and survival strategies. In this study, we used parthenogenetic Asian Forest Scorpion (*Heterometrus spinifer*) siblings on similar feeding regimes to examine variation in body condition and growth rates over successive molts. Weight and carapace width were used to calculate body condition indices (BCI), which are indicators of individual fitness. Although we are still collecting data as siblings grow to maturity, initial comparisons indicate that the mean intermolt period was significantly shorter for 2-3rd instar than for the transition from 3-4th instar. Preliminary results also suggest surprising variation among the siblings, e.g., the first intermolt period ranges from 54 to 143 days and the second intermolt period ranges from 88 to 227 days. This variation may impact time to reach sexual maturity and maximum body size; both of which, in turn, impact lifetime reproduction.

SEARCHING FOR A BETTER WAY TO DEFINE A GENUS IN COSMETIDAE (OPILIONES: LANIATORES) USING MORPHOLOGY AND PHYLOGENOMICS

Caleb Gunkle, Daniel Proud
Moravian University

We explored two datasets to understand the evolutionary history of Cosmetidae in Central America and the Caribbean Islands. First, we used a multi-locus phylogenetic tree based on Sanger data for 70 terminals, with a primary focus on species from Costa Rica, to reconstruct the ancestral states for 12 traits. We discuss traits that may be helpful in diagnosing cosmetid genera from this region but recognize that these combinations of characters may not apply across all Cosmetidae genera, particularly those from South America. Second, we present the first phylogenetic tree based on ultraconserved elements (UCEs) for the family Cosmetidae containing 72 taxa that are primarily from Mexico and the Caribbean Islands. We recovered at least eight distinct clades of Cosmetidae and detected a strong association between monophyletic groups and their geographic ranges. We intend to build upon this UCE framework by including more species from Costa Rica, Panama and Cuba. We also discuss the difficulty in identifying species based on original descriptions that lack precise locality data. By examining and compiling images of type specimens, we were able to confidently identify some taxa collected during recent field expeditions as well as identify some species from observations on iNaturalist.

MAPPING HEMOLYMPH FLOW CHANNELS IN SCORPION TAILS: MORPHOLOGICAL INSIGHTS FROM HIGH-RESOLUTION X-RAY IMAGING

Sophie E. Hanson, Lin Yan, Elizabeth G. Clark, Damian O. Elias
University of California, Berkeley; Lawrence Berkeley National Laboratory

Scorpions rapidly extend multiple joints in their tail to defensively strike. This dynamic movement is hypothesized to be powered by a combination of muscle actuation and hydraulic pressure. In other arachnids, hydraulic pressure is generated by muscular pumps in the body, which increase hemolymph flow through open channels in the limb, extending the joint, and powering locomotion. Yet, this mechanism remains relatively unexplored in scorpion tails. To investigate hemolymph flow channels in

scorpions' multi-segmented tails, we used high-resolution X-ray imaging of metasomal segments in *Uroctonus mordax* (1.6 μm resolution, Synchrotron ALS Beamline at Lawrence Berkeley National Laboratory). We reconstructed a 3D model of the hypothesized hemolymph flow channel and quantified the morphology and geometry of the channel. Given that the channel's geometry (cross-sectional area, length, and shape) directly mediates flow rate and pressure change, these measurements are key to understanding how hydraulic pressure is controlled. These methods have the potential to validate the use of hydraulic pressure in scorpion joint extension and provide insight into hydraulic mechanisms across a diversity of arachnids.

DIVERSITY OF EPIGEIC SPIDER SPECIES IN DIFFERENT GROUND COVER TYPES IN THE UNC CHARLOTTE BOTANICAL GARDENS

Sarah Stellwagen, Hope Hulse**
UNC Charlotte

Spiders are generalist predators and inhabit nearly all terrestrial habitats. They play a key role in regulating insect populations which contributes to ecological balance. Environmental factors such as type and structure of ground cover can influence their diversity and abundance. Understanding how different ground covers within the UNC Charlotte Botanical Gardens affect spider populations and biodiversity will allow for better implementation of habitat management. We installed pitfall traps within three monoculture ground cover habitats: moss (no cover), virginia creeper (medium cover), and sensitive fern (high cover). Over the course of a full year (September 2024 - September 2025), data on spider biodiversity and abundance is being assessed through a weekly schedule of trapping and identifying specimens. We expect to find a greater amount of diversity within heavier ground covers due to shelter accessibility, foliage that contributes to mating communication and prey habitat, and protection from predators. Current data collected supports the hypothesis for increased spider diversity and abundance in higher ground cover.

OUTSIDER SPIDER: INVESTIGATING COMPETITION BETWEEN THE INVASIVE NON-NATIVE JORO SPIDER AND NATIVE WEB-BUILDERS

Caitlin Jones**, Daniel Simberloff
University of Tennessee-Knoxville

The expansion of the non-native Joro spider *Trichonephila clavata* in the SE US correlates with a decrease in native orb-weaver abundance. A causal relationship has not been established, but competitive displacement is hypothesized. We aim to test aspects of competition between the Joro and native spiders in Tennessee. Visual surveys along 100m line-transects will be conducted over three years in Great Smoky Mountains Park to record potential changes in spider communities. Simultaneously, diet analyses will be conducted on native web-building spiders and *T. clavata* individuals and webs collected from paired sites in Chattanooga, TN. We will use dissected guts, feces, and prey remains from webs to determine prey composition. We expect native spider communities to change with the *T. clavata* invasion, and that *T. clavata* diet should overlap more with similar-sized native web-builders. We also hypothesize that juvenile *T. clavata* compete for web locations with similarly-sized natives, and that as *T. clavata* grows these preferences will change to support heavier

webs and spiders. To address this question, we will start by experimentally releasing one spider into a chamber containing two attachment surfaces that will differ in physical characteristics, giving spiders 24h to build. Two trials will be conducted using the same spider but randomizing the location of the choices to eliminate potential biases for left or right arenas. We will repeat this experiment with field-collected adult and juvenile *T. clavata* and adult female native spiders to compare web attachment preferences.

BENEATH THE SURFACE: A MORPHOLOGICAL DESCRIPTION OF A NEW SPECIES OF *TROGLORAPTOR* (ARANEAE, TROGLORAPTORIDAE)

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We present a morphological description of a new species of spider in the family Trogloraptoridae, recently discovered in caves in the Columbia River Gorge in Northwestern Oregon. This species is genetically distinct and has been collected in four localities within the Gorge. To date, it is known only from female specimens; despite multiple attempts across different seasons, we have not found a mature male. This species retains the key morphological characteristic - subsegmented raptorial tarsi - which is a distinct synapomorphy of the family. It also retains the oblique membranous division of the basal segment of the anterior lateral spinnerets as in *Trogloraptor marchingtoni*, the only described species in the family. This species is distinguished from *T. marchingtoni* by its color pattern and vulvar structure.

NEW INSIGHTS INTO THE FEEDING BEHAVIOR OF *TROGLORAPTOR*

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In 2010, a new family of spiders, Troglorapteridae, was discovered in caves of southern Oregon and described by Griswold et al in 2012. The type species, *Trogloraptor marchingtoni*, has distinctive subsegmented raptorial leg tarsi that are synapomorphic for the family. Though it has been well over a decade since the discovery of *Trogloraptor*, the function of these extraordinary subsegmented raptorial tarsi has been unknown, though they were hypothesized as an adaptation for catching prey. The goal of this project is to document how these raptorial feet are used in prey capture behavior and test that hypothesis. Using field data, we have evidence that a newly discovered *Trogloraptor* species in northern Oregon eats other arachnids. Through high quality video taping, we have recorded a *Trogloraptor* wrapping its tarsi around the legs of arachnid prey (*Calymmaria*). Although these data are preliminary, they suggest that *Trogloraptor* hunt potentially dangerous arachnid prey and use their unique legs to grab prey while they administer venom to incapacitate them.

MANY MASKS OF MALE *HABRONATTUS HIRSUTUS*: SURPRISING CO-OCCURRENCE OF DISCRETE RED AND BLACK FORMS WITHIN A SINGLE POPULATION

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Habronattus is a diverse genus of jumping spiders with males exhibiting vividly colored ornaments used in visual courtship displays towards females. Many species have extensive geographic color variation, but variation within populations is usually continuous. In *Habronattus hirsutus*, male facial coloration is highly variable across their broad geographic range (western US, Canada, and Mexico), yet not all populations exhibit continuous variation. Here, we describe two populations of *H. hirsutus* in Arizona, where males with either bright red or black facial coloration coexist without intermediate forms. We characterized this color variation using reflectance spectrophotometry and observed male courtship behavior to assess whether these two types of males had similar courtship displays. Next, we developed a red–intermediate–black color standard based upon the Arizona populations, which we applied to iNaturalist images across the entire *H. hirsutus* range to assess whether other populations exhibit similarly discrete, coexisting red and black forms (without intermediates). Arizona males showed distinct red and black spectral curves, but preliminary behavioral observations suggest that both male forms utilize similar courtship behaviors when presented to females. From iNaturalist images, we found that facial color largely varies continuously with geography; however, we also identified multiple additional localities in Arizona and California with only discrete red and black forms occurring. To our knowledge, *H. hirsutus* is the first documented example of male dimorphism in *Habronattus*, where discrete male forms coexist within a single population. Future work will explore the functions of these distinct male forms and the mechanisms maintaining them within populations.

BIODIVERSITY AND INSECTICIDE SENSITIVITY OF NANTUCKET BOG SPIDERS

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Spiders are important pest management regulators in agricultural systems, appearing in high biomasses across a variety of niches. Research is limited with respect to system specific biodiversity, as well as population impact from pest management practices. This study compares the diversity of spider populations from an active conventional cranberry agroecosystem (Milestone) to those from a cranberry bog undergoing restoration into a naturally functioning wetland (Windswept) on Nantucket Island, Massachusetts, sampled across a one-month period in August 2023. We identified mature specimens using dichotomous keys and supplemented spider identification was with cytochrome oxidase I (COI) genetic sequencing. We also performed toxicity assays on large Lycosid spider populations from each system type, using the pyrethroid pesticide formulation FanFare (bifenthrin), a chemical applied at Milestone during the growing season in which samples were collected. Results show more diverse taxa present at the Windswept site, with toxicity curves showing greater susceptibility to FanFare. Our results suggest that active management negatively impacts beneficial, non-target spider populations in conventional cranberry production, and provide novel details regarding spider biodiversity in both actively managed and restored wetland systems.

TAXONOMIC CLARITY AND MULTI-YEAR SAMPLING PROVIDES INSIGHT TO LYCOSID SUBSTRATE PREFERENCE

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Biological inventory of Lycosidae spiders was conducted in Summers of 2023 and 2024 within a forested ecosystem at Virginia Commonwealth University's Rice Rivers Center in Charles City County, Virginia. 40 belt transects (2m x 10m) were surveyed through visual census via eye-shine and manual capture of up to three individuals per transect per survey. These transects were evenly divided between maintained lawn grass and deciduous forest leaf litter substrate types. This yielded no significant difference in total abundance between lawn and leaf litter transects ($W = 74.62$, $p = 0.6$); however, there was a significant difference in total abundance across substrates and between survey periods (chi-squared = 60.33, $df = 11$, $p \ll 0.05$). The representative samples of the populations collected during surveys were later identified in the lab. At the genus level of identification there is significant difference in diversity across substrate types (Inverse Simpson; $W = 87.5$ and $p = 0.002$) with higher diversity in lawn plots. Several species had significant associations with lawn or leaf litter substrate (chi-squared = 376.54, $df = 8$, $p \ll 0.05$). Most notably, *Schizocosa ocreata* which is positively associated with deciduous leaf litter and *Tigrosa annexa* which is positively associated with lawn grass. Preliminary understanding of species specific phenological data gathered during these surveys provides a basis for future study into population dynamics.

MALE MOVEMENT PATTERNS IN ARGIOPE TRIFASCIATA

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Arachnids exhibit incredible mating behaviors that provide valuable insights into the evolutionary dynamics of reproduction. Some species exhibit mate guarding to prevent their partners from remating while others break off parts of their genitalia to plug a partner's opening. Still others sacrifice their lives to benefit their offspring. Among these diverse species, *Argiope trifasciata* stands as an excellent model for investigating complex reproductive strategies in both sexes. This species exhibits extreme female-biased sexual size dimorphism, multiple mating by both sexes, and females reportedly show web site fidelity throughout the season. Multiple males will gather around the webs of pre-adult females in the pursuit of opportunistic matings. This study explores these patterns in detail through an in-depth field study using marked individuals and daily transects for continuous monitoring throughout the mating season. Initial findings show that females will leave webs and build new ones meters away significantly more than was described in the literature. We use our collected field data as well as weather data to describe the underlying movement patterns of males and females throughout the field.

GENERATING SYNTHETIC ETHOGRAMS OF SPIDERS WITH LARGE LANGUAGE MODELS: A COMPARISON

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Ethograms are important descriptive tools supporting most behavior studies. For many animals, they are either unavailable or unpublished. In such cases, one approach is to construct an ethogram from behavior descriptions in existing studies, even when such studies do not include an explicit ethogram. One potential shortcut to assembling such synthetic ethograms is to take advantage of large language models (LLMs), which are trained on vast amounts of data, which likely include a large amount of animal behavior literature. I used eight LLMs, including ChatGPT and DeepSeek, to construct ethograms for contrasting species with a lot of published information (*Schizocosa ocreata*) with more limited published information (*Phidippus audex*). I followed the ethogram requests with prompts to list their sources and to compare each species to in related genera (*Lycosa*, *Habronattus*). All models generated recognizable ethograms that were improved by refining the prompts given. Despite this, there were multiple errors and “hallucinations” in some of the ethograms. I will also address whether species with more behavior data accessible allow LLMs to yield more detailed and complete ethograms that exhibit fewer errors and hallucinations.

FUNCTIONAL DATA VALIDATE A CONSERVED ROLE FOR PAX6 IN THE DEVELOPMENT OF CHELICERATE VISUAL SYSTEMS

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Across Metazoa, the paired box transcription factor Pax6 plays a prominent role as a master regulator of the retinal determination gene network, initiating the embryonic development of eyes in distantly related phyla including cnidarians, chordates, and mollusks. Arthropods, however, bear two Pax6 homologs, Pax6A (eyeless) and Pax6B (twin-of-eyeless), with functional data suggesting conservation of this role in eye development across Mandibulata. Pax6 homologs in chelicerates, however, are thought to have lost this role in patterning the lateral visual system as surveys of the expression of both Pax6 homologs in spider embryos demonstrate localization to only the median eyes. The related Pax2 gene is thought to have replaced Pax6 based on expression of a duplicated Pax2 paralog in the lateral eyes of a spider. No functional data yet exist for any Pax homolog in arachnids, however. To redress this gap, we performed gene silencing of Pax2 and Pax6 homologs in the model daddy-longlegs *Phalangium opilio*, given absence of paralogous gene copies in this apulmonate lineage and the presence of both median and vestigial lateral visual systems. Silencing of Pax2 and Pax6A did not affect eye development and produced no discernible phenotypes. Depletion of Pax6B, however, yielded the loss of the median eyes, but not the lateral eyes. A subset of embryos surveyed also exhibited numerous ectopic vestigial eyes, suggesting an earlier role for Pax6B in head patterning. This dataset provides the first functional evidence that a Pax6 homolog plays a conserved role in head and eye patterning in any arachnid model.

CAUGHT IN TIME: COLLECTION TIMING AND SENESCENCE IN MALE TARANTULAS (*APHONOPELMA HENTZI*)

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Sexual dimorphism in longevity represents a striking example of natural selection favoring reproductive success over survival. In the Colorado brown tarantula (*Aphonopelma hentzi*), females live over two decades while males survive only 5-10 years, with rapid physiological decline following sexual maturity. This study investigates how collection timing during the mating season affects metabolic patterns in male tarantulas from southeastern Colorado. Using open-flow respirometry, we measured CO₂ production in males collected at three timepoints (early August, mid-September, and late October; n=28) to track metabolic changes associated with reproductive effort. Log-transformed metabolic rate (MR) data were analyzed across collection periods; we compared maximal and minimal MRs as well as factorial aerobic scope. Results revealed pronounced differences in metabolic variability between collection periods, with males exhibiting an average factorial aerobic scope of 3.11 - demonstrating their capacity to rapidly mobilize energy during mate-searching and competitive activities. This metabolic variability appeared notably reduced in late-season males compared to mid-season animals. While Maximum MRs showed the typical positive correlation with body mass, Minimum MRs showed a negative relationship with mass and were distinctly elevated in late-season males despite their declining maximum capacity. The progressive deterioration of metabolic scope aligns with observational evidence of male senescence during the mating season, providing a physiological mechanism for their post-maturity decline. These findings suggest earlier laboratory collection may prevent metabolic spikes associated with reproductive activity, potentially extending male longevity through reduced oxidative stress while providing novel insights into life-history trade-offs and extreme sexual dimorphism in aging.

CIRCADIAN RESONANCE AND ENTRAINMENT IN *PIRATA SEDENTARIUS*, A LYCOSID

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Agreement between an organism's endogenous clock (circadian clock) and the light/dark (LD) cycle in its environment is termed "circadian resonance" and is typically beneficial for the organism. In most cases, misalignment between an organism's circadian clock and the LD cycle it lives in leads to physiological and metabolic disruptions which ultimately result in a reduced lifespan. This reduction in lifespan is attributed to the metabolic cost of attempting, but failing, to synchronize its activity (entrain) to non-resonance light cycles. Previous work has established that some Araneoid spiders do not experience a reduced lifespan in non-resonant light cycles, even though they successfully entrain to them. This suggests that Araneoid spiders may somehow be released from the metabolic cost of re-entrainment, while still having a highly plastic circadian system. The present study evaluates whether this "cost release" phenomenon persists in *Pirata sedentarius*, a Lycosid. Approximately 50 adult individuals of mixed sex were placed into chambers with periods of 19 (9.5:9.5h LD), 24 (12:12h LD), or 29 hours (14.5:14.5h LD). Contrary to what has been observed in Araneoid spiders, *P. sedentarius* lived significantly longer in the 24h LD cycle than in the 19h or 29h LD cycles. Current work seeks to

investigate if *P. sedentarius* are able to entrain to non-24h light cycles. Overall, this evidence suggests differences in circadian plasticity across spider taxa.

USING 3RAD GENOTYPING BY SEQUENCING TO EVALUATE REPRODUCTIVE MODE IN *BANDONA BONINENSIS* (OPILIONES: ASSAMIIDAE)

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Bandona boninensis (Opiliones: Laniatores), found in East Asian countries, maintains its population through both asexual and sexual reproduction; however, its preference for either method remains unknown. Similar to other species of Opiliones, *B. boninensis* is female-biased and male specimens are rare. Genetic diversity is reliant on sexual reproduction, whereas asexual reproduction limits this characteristic but allows for rapid population growth. To assess the genetic health and evolutionary trajectory of an island population, we examined the genomes of two lineages to determine the frequency of offspring that were a result of asexual and sexual reproduction using a three-restriction endonuclease genotyping-by-sequencing approach (3RAD). This generated a genome-wide set of single nucleotide polymorphisms for two female *B. boninensis*, their daughters, and their granddaughters. The program Colony was used to estimate the coefficient of inbreeding for each lineage, and the clonal probability for each F1 and F2 individual. Genetic analysis is currently ongoing. The findings of this study will contribute to our understanding of *B. boninensis*'s adaptability, clonal reproduction, and the broader reproductive strategies of arthropods.

COMPARING LOCOMOTORY ACTIVITY, GROWTH RATES, AND SEX RATIOS IN MALE AND FEMALE JUVENILE CURLY HAIR TARANTULAS

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Despite its important role in tarantula natural history, little is known about sex ratios from egg sacs or the growth and behavior of male and female spiderlings. Sex ratios can be difficult to determine in tarantulas; there is no genetic marker, morphological differences can't be readily determined in the early instars, and, at later instars, ratios may be skewed due to high mortality rates. One laboratory-based study indicated a relatively even M:F sex ratio and documented increasing size dimorphism with age. This study aimed to document sex ratios in a large sibling group of Curly Hair Tarantulas (*Tiltocat/ albopilosus*); we also measured differences in growth and locomotory activity between juvenile females and males. We predicted even M:F sex ratios with males having faster growth rates and longer legs compared to females. Additionally, we expected no difference in locomotory activity in juveniles, but suggest that higher activity levels would become apparent as males approached sexual maturity. Sex was determined from exoskeletons of 5-7 instar individuals by the presence and development of spermatheca in females and the lack thereof in males. Locomotory activity was measured via video-tracking (Ethovision), and distance and velocity were compared between the sexes. While sex of all siblings in the group is still underway, the current ratio is female-biased. Additionally, juvenile females overall have higher means for both velocity and distance than their male siblings. Juvenile females also have higher weights, but additional size measurements (carapace width and leg length) are still needed.

LOCOMOTOR ACTIVITY IN TARANTULAS: A COMPARISON ACROSS SPECIES AND SEXES

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Pace-of-life Syndrome (PoLS) suggests a correlation between life history, behavior, and physiology along a spectrum from slow to fast. Tarantulas are good model organisms for examining PoLS; from the perspective of different sexes and species. Different tarantula species have different paces of life, including growth rate and longevity. Tarantulas with a faster PoL may have higher activity levels which can be measured as locomotor activity. This activity is poorly documented for tarantulas, especially across a broad range of species. In this study, we recorded locomotory activity in five tarantula species. We predicted activity duration would be greater in males, and greater in tarantulas with a faster PoL. Locomotor activity was video-tracked (Ethovision) during 30-minute trials with animals in circular arenas approximately five body lengths in diameter. Differences in body size can influence distance travelled and velocity, so we compared the duration of locomotor activity during each trial. We also examined the degree of thigmotaxis, i.e., how frequently animals moved away from the arena wall. Across species, females had lower activity levels than corresponding males. Additionally, field-caught *Aphonopelma hentzi* males had the longest duration of locomotory activity. Males of other species were lab raised (probably for multiple generations). With the limited sample species, it is unclear whether differences can be attributed to long-term lab-raising and possible inbreeding. Our sample size was also limited by the availability of sexually mature tarantulas, resulting in very different sample sizes across groups.

COMBINED MATHEMATICAL AND BEHAVIORAL EXPLORATION OF THE DAILY LOCOMOTOR ACTIVITY OF *STEATODA GROSSA*

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In this work, we investigated circadian locomotor activity in the *Steatoda grossa* spider. We used a locomotor activity monitor to collect the spiders activity in three different light-dark conditions: constant dark (DD), constant light (LL), and 12-hour alternation between light and dark (LD 12:12). We found that spiders were entrained under light conditions close to natural and had a free-running period in constant light and dark conditions. The only significant difference in the behavior in LL and DD was an increase in the duration of activity bouts in LL. We used a mathematical model to determine the mechanism for regular cyclicity in constant light. The model predicts that the neural feedback between the eyes and the circadian system in the brain can explain the cyclicity under continuous light.

POPULATION GENETICS OF AN INVASIVE SPIDER SPECIES, *PHOLCUS MANUELI*, ACROSS ITS U.S. INVASION RANGE

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The field of invasion biology seeks to understand the factors that contribute towards a non-native species' spread (Reichard & White, 2003). It is well acknowledged that characteristic differences, such as behavior, are vital during multiple phases of the invasion process. More recent studies have shown

that these characteristics tend to vary throughout the area of invasion, contributing further towards possible success (Bélouard et al., 2019). However, genetic makeup across an invasion area, particularly in arachnids, is still a relatively unexplored factor in this field. In this study, two target genes were used to study *Pholcus manueli* (Gertsch, 1937) from the core and edge of its United States invasion range. Two genes were identified, amplified, and sequenced from 36 specimens. The relative genetic distance between populations of different areas was investigated through various methods of post-run analysis. Results determined that there was not a correlation between genetic and geographic distance, nor was there a significant difference between core and edge invasion areas.

THE SAME STING FOR ALL? PERSONALITY AND PLASTICITY IN A PUBLIC HEALTH-RELEVANT URBAN SCORPION

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Animal personality is defined as the consistency of behaviors within individuals and the differences in those behaviors among individuals over time and across contexts. Variation in behavioral traits (e.g., aggressiveness/docility, boldness/shyness) plays a crucial role in ecological and evolutionary processes. Scorpions represent an ideal model for studying animal personality, as they exhibit ritualized behaviors in various scenarios. This study aims to evaluate behavioral consistency in females of *Tityus carrilloi*, a parthenogenetic and synanthropic scorpion species of public health relevance in Argentina, in response to anthropogenic disturbance. Twenty females were exposed to two artificial stimuli: direct contact (tapping the metasoma with a wooden rod) and substrate vibration. Each experiment was repeated ten times per individual. Behavioral responses were recorded in binary form, indicating presence or absence of movement. Preliminary results indicate that all females responded to the stimuli with movement. However, inter-individual variation was lower than intra-individual variation, suggesting that the behavior is more plastic than consistent. This pattern may reflect a high degree of behavioral flexibility in response to human-like disturbances, potentially contributing to the species' adaptability to urban environments. These findings lay the groundwork for future research on how urbanization and environmental change influence the expression of animal personality and the interaction between wildlife and humans.

HETEROSPECIFIC MATE CHOICE REVEALS HIDDEN AND VARIABLE FEMALE PREFERENCES IN THE *HABRONATTUS clypeatus* group of jumping spiders

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Strong sexual selection is expected to act as a barrier to heterospecific mating by reinforcing species-specific mate preferences. We investigated this hypothesis using two allopatric but closely related species of jumping spiders with complex male courtship displays: *Habronattus formosus* and *H. gilaensis*. Males of both species exhibit courtship behaviors that differ in some respects but not others. Surprisingly, females of both species mated indiscriminately with conspecific and heterospecific males.

However, latency to copulation was significantly longer in heterospecific pairings. Preference function modeling revealed that female preferences were more variable when interacting with heterospecific than with conspecific males. These results suggest that, despite apparent indiscriminate mating behavior, females make quicker mating decisions when interacting with conspecifics, likely due to stable preferences for traits expressed by conspecifics. Our findings highlight the complex role of female preferences in shaping mating outcomes and maintaining “species” boundaries and suggest a behavioral mechanism for diversification even with “leaky” species boundaries.

CHANGES IN BODY CONDITION IN MALE TARANTULAS OVER THE REPRODUCTIVE SEASON

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Energy requirements vary greatly between sexes in mature tarantulas; females seldom travel far from burrows while males engage in active mate-search and can travel long distances in search of receptive females. At maturity, males have higher resting metabolic rates to support their increased locomotory activity compared to sedentary females. In this study, we examined field-caught tarantulas. In lieu of metabolic rates, we used body condition indices (BCI) as a non-invasive measure of quality and fitness of animals where a high BCI suggests higher energy reserves. Measurements of non-reproductives (both juveniles and females) were completed outside of the reproductive season (May). Mature males were collected early (August/September) in the mating season and maintained in the lab. Additional measurements were obtained from males encountered in the field towards the end of the mating season (October). We compared weights and BCIs among these groups. Because of their high energetic costs we predicted males would have lower BCIs than females. Additionally, males maintained in the lab would have higher BCIs than field-encountered males. BCIs were calculated using the residual index based on regression of log-transformed body mass on carapace width. Despite small sample sizes, females generally had higher weights and thus corresponding higher BCIs than males. Males maintained in the lab with constant temperatures and regular feedings, had higher BCIs than field-encountered males. Additional data will be collected during this year’s mating season and correlations between BCI and metabolic rates measured in the lab will be determined.