

AAS Virtual Summer Symposium

Oral Presentation Abstracts

Arranged by first author's last name
Asterisk (*) indicates contestant in student competition
Presenter underlined

Chemical species recognition in an adaptive radiation of a Hawaiian spider

Seira A. Adams, Moritz Gerbault, Stefan Schulz, Rosemary G. Gillespie

University of California Berkeley
seira.adams@berkeley.edu

The mechanisms by which reproductive isolation evolves and is maintained in adaptive radiations is central to fundamental processes such as reinforcement, sensory drive, and hybridization. Particularly important are situations where ecologically distinct incipient sister species co-occur geographically, resulting in frequent encounters between diverging species and necessitating finely tuned recognition mechanisms for species to maintain reproductive isolation. This is seen in adaptive radiations of Anolis lizards, cichlid fish, and Hawaiian *Drosophila*. In these systems however, much of the work has been done within the domain of human perception – visual and auditory cues. Chemical cues are one of the most ancient and widespread modalities of communication, yet their importance in species recognition and reproductive isolation remains to be studied in the context of adaptive radiations. This study focuses on the role of chemical species recognition cues in reproductive isolation and speciation within a well- studied adaptive radiation of Hawaiian Tetragnatha spiders in which ecologically distinct sister species co-occur, and visual and auditory cues appear to play little or no role in species recognition prior to mating.

Testing adaptive radiation in Dionychan spiders using morphological and genomic data

Guilherme H. F. Azevedo, Tierney Bougie, Marshal Hedin, Martín J. Ramírez

San Diego State University
ghfazevedo@gmail.com

Adaptive radiation can happen when ecological opportunity is followed by selection-driven divergence of species filling a variety of habitats. *Dionycha* is a relatively recent

clade of spiders, presents extensive taxonomical, ecological and phenotypic diversity, and family-level phylogenetic relationships have proven difficult to resolve. All these suggest possible adaptative radiation following ecological opportunity. We test predictions of this hypothesis using UCE, transcriptome, Sanger sequencing of target genes and morphology. Divergence dating analysis suggests that all families of *Dionycha* emerged over a span of 50 My. Model testing of morphological evolution reveals a higher rate near the base of *Dionycha* followed by a decrease through time. Also, results of Ornstein–Uhlenbeck model of phenotypic evolution suggest different adaptative optima in the three early diverging clades of the group. Estimation of population sizes through time suggests a population expansion early in *Dionycha* evolution compared to its sister clade. These results are expected under adaptative radiation following ecological opportunity. We discuss this hypothesis and alternative processes that also could explain the radiation of *Dionycha* spiders. We also discuss the importance of morphology in inferring phylogenies in cases of adaptative radiations.

Taxonomic revision of the genus *Ammotrechula* (Solifugae: Ammotrechidae)

Diana Laura Batista Perales, Paula Cushing, Jack O. Brookhart, Edmudo González Santillán

Laboratorio de Aracnología, Departamento de Biología, Facultad de Ciencias, UNAM
dbatista@gmail.com

Solifugae is an order of cursorial, mesodiverse, and poorly studied arachnids. The family Ammotrechidae is one of four New World families, distributed from the Southwest United States through Central America and South America. Ammotrechidae has received little taxonomic attention, and the North American taxa have been effectively untouched since the late 1980s. This work presents the first taxonomic revision of the genus *Ammotrechula*, which includes 12 species. This genus suffers from species descriptions that are based on female holotypes only, and also on lumping multiple putative morphospecies into one widely distributed taxon. We've detected that at least two species complexes of species within the genus: *A. borregoensis* and *A. peninsulana*, and the rest of the species require an adequate definition and delimitation of species. Up to this moment, we've identified 16 putative morphospecies based on the comparison of dentition of the Chelicerae, flagellum shape, distribution, and other morphological characteristics. This taxonomic revision based in morphology will inform hypotheses for further testing via molecular techniques.

Transgenerational effects of predator stress on the growth and behavior of *Pardosa milvina*

Alexander Berry*, Ann L Rypstra

Miami University
berryad2@miamioh.edu

The environment plays an important role in the phenotypes of animals. So too does the parental environment through transgenerational plasticity. For instance, predator stress in one generation can alter multiple phenotypes of the next. Here, we tested the hypothesis that maternal exposure to predator cues, would alter the growth and behavior of offspring in the small wolf spider *P. milvina*. We began by exposing immature *P. milvina* to chemotactile cues from predators twice per week until adulthood. *Pardosa milvina* is known to be sensitive to such cues. When spiders reached adulthood, we mated the females with predator naive males and allowed them to produce offspring. These offspring were then run through a series of tests at the 3rd instar and adult stages to look for changes in behavior, growth, and survival. Tests included a feeding trial, a movement trial, and a predator exposure trial. Offspring of predator exposed mothers ate less, at the 3rd instar stage, took longer to reach adulthood, and survived better in the presence of predators, at all ages, than did those of control mothers. Maternal exposure altered both the behavior and life history of *P. milvina*.

Unexpected diversity in the widespread tiger tarantula *Davus pentaloris* (Araneae: Theraphosidae: Theraphosinae)

Daniela T. Candia-Ramírez*, Oscar F. Francke

Colección Nacional de Arácnidos, Instituto de Biología, Universidad Nacional Autónoma de México
brachypelma_boehmei04@hotmail.com

Integrative taxonomy has taken great relevance in the discovery and delimitation of cryptic species by incorporating different sources of evidence to construct rigorous species hypotheses. The genus *Davus* was recently revised and it was found that *Davus pentaloris* presents high morphological variation through its widespread distribution, however, tarantulas usually present low dispersal capabilities that occasionally produce local endemism. In order to evaluate the species boundaries within this taxon, we examine the morphological variation and additionally employ four strategies based on mtDNA data (COI): two distance-based (ABGD and Neighbor-Joining) and two tree-based methods (GMYC and bPTP). Available morphological evidence recovers 13 putative species; but the different methods based on molecular data recover a variable number of candidate species (16–18). Based on the congruence across all analyses and the available morphological data, we recognize 13 clearly diagnosable species, 12 of them new to science. We conclude that the underestimation of the diversity in *D. pentaloris* was mainly caused by bad practices in taxonomy instead of the presence of cryptic diversity. We recommend combining multiple sources of

evidence and strategies in the future to construct better species delimitation hypotheses. This contribution represents the first results on the doctoral project of the first author.

Sex differences of self-derived chemical cue use for shelter recognition in the whip spider *Phrynus marginemaculatus* (Amblypygi: Phrynidae)

Patrick Casto*, Verner P. Bingman, Eileen A. Hebets, Daniel D. Wiegmann

Bowling Green State University
pcasto@bgsu.edu

Previous research has shown whip spiders (*Phrynus marginemaculatus*) are capable of using self-derived chemical cues to recognize their home shelter. Based on field studies that have shown sex differences in refuge fidelity, the current study tested for sex differences in the use of self-derived chemical cues for shelter recognition. Eight female and eight male *P. marginemaculatus* were individually placed in a 1.8 m circular arena containing a single circular shelter at center. Subjects underwent eight nights of testing with alternating nights having the shelter present or removed. For half of the subjects of each sex the arena was cleaned every night (control), while for the remaining subjects the arena was cleaned after each shelter-removed night (treatment). An overhead camera tracked movement of subjects throughout the night and the proportion of time spent in the center of the arena during shelter-removed nights was used as a metric for shelter recognition. Treatment females spent significantly more time in the center of the arena compared to treatment males, as well as male and female controls. These results suggest that, in the absence of a shelter, females, but not males, use self-derived chemical cues to recognize a previously occupied shelter location.

Phylogeography of the widespread Caribbean spiny orb weaver *Gasteracantha cancriformis*

Lisa Chamberland*, Fabian C. Salgado-Roa, Alma Basco, Amanda Crastz-Flores, Greta J. Binford, and Ingi Agnarsson

University of Vermont
chamberlandlisa8@gmail.com

Among Caribbean spiders, widespread species are relatively few compared to the prevalence of single island endemics. The taxonomic hypothesis *Gasteracantha cancriformis* circumscribes a species with profuse variation in size, color, and body form. Distributed throughout the Neotropics, *G. cancriformis* is the only morphological species of *Gasteracantha* in the New World in this globally distributed genus. We

inferred phylogenetic relationships across Neotropical populations of Gasteracantha using three target genes. Within the Caribbean, we estimated genetic diversity, population structure, and gene flow among island populations. Our findings revealed a single widespread species of Gasteracantha throughout the Caribbean, *G. cancriformis*, while suggesting two recently divergent mainland populations that may represent separate species, diverging lineages, or geographically isolated demes. The concatenated and COI (Cytochrome c oxidase subunit 1) phylogeny supported a Caribbean clade nested within the New World. Genetic variability was high between island populations for our COI dataset; however, gene flow was also high, especially between large, adjacent islands. We found structured genetic and morphological variation within *G. cancriformis* island populations; however, this variation does not reflect genealogical relationships. Rather, isolation by distance and local morphological adaptation may explain the observed variation.

Pseudoscorpion sociality: nest architecture and microbial symbionts

Kenneth Chapin, Karly Mae Garrett, Anna Kittle, Anna Dornhaus

University of Arizona
chapinkj@gmail.com

The highly social pseudoscorpion *Paratemnoides elongatus* constructs elaborate nests with connected chambers housing dozens of individuals. Pseudoscorpions use nests as protection for juveniles, eggs (a behavior unique to *Paratemnoides spp.*), and during molting. We present studies testing two hypotheses: That social nest architecture reduces overall silk-use relative to solitary nests or nests of alternative structures; and that the silk of social nests harbor symbiotic microorganisms that protect unsclerotized pseudoscorpions from infection. We found that microorganisms associated with social nest silk can outcompete several other microorganisms in inhibition assays. In particular, the silk microbial isolate outcompeted the entomopathogenic *Bacillus thuringiensis*, and did so much more than the innocuous congeneric *B. subtilis*. Regarding nest architecture, we found that social pseudoscorpions use less silk than if solitary in > 95% of 34 wild-collected nests. We also found pseudoscorpion nest architecture rivals that of the theoretical Honey Bee Conjecture (a mathematical proof that hexagons are the most efficient way to divide 2-dimensional space), but are more flexible in dealing with the varied topography in which the species naturally occurs. We present future directions and natural history findings.

Molecular evolution of inhibitor cystine knot toxins in spiders

T. Jeffrey Cole*, Michael S. Brewer

East Carolina University
coleti16@students.ecu.edu

The inhibitor cystine-knot (ICK) scaffold appears in peptides expressed by viruses, fungi, plants, and animals. The ubiquity of ICK toxins, being among the most widely recruited peptide folds in animal venoms, is likely attributable to the fold's ultra-stability and plasticity. This is particularly evident in the largest group of venomous animals, spiders, whose venom arsenal is largely composed of a rich cocktail of ICK toxins. Despite the prevalence of these toxins, the evolutionary origin of ICKs remains elusive. In spiders, ICK toxins are thought to have originated via several rounds of gene duplication of an ancestral ICK peptide followed by weaponization and diversification of paralogs. Under the birth-and-death model, these rounds of tandem duplication would form multi-copy gene cassettes with some duplicates becoming nonfunctionalized. In this study, we implement an approach to identify ICK peptides in all publicly available spider genome assemblies to highlight two key points. The first of which is the current state of spider genome assemblies and their annotations, the second of which are preliminary insights into the genomic architecture and patterns of molecular evolution of ICK toxins in spiders

Phylogenomics of Triaenonychoidea and biogeography of the Gondwanan family Triaenonychidae (Opiliones: *Laniatores*)

Shahan Derkarabetian, Caitlin M. Baker, Marshal Hedin, Carlos E. Prieto, Gonzalo Giribet

Harvard University
sderkarabetian@gmail.com

The Triaenonychoidea are a group of laniatorean Opiliones with ~500 species/subspecies and ~108 genera currently described in two families: Synthetonychiidae and Triaenonychidae. This project aims to reconstruct the phylogenetic relationships among Triaenonychoidea genera using sequence capture of ultraconserved elements for two main goals: classification and biogeography. First, I will discuss the systematics of Triaenonychoidea, highlighting our current taxonomic revision of this lineage including description of two new families. Next, I will discuss our ongoing research on the biogeographic history of Triaenonychidae, which are entirely restricted to the temperate forests of the former Gondwanan landmasses including southern South America, South Africa, Madagascar, Australia, New Zealand, New Caledonia, and Crozet Islands. Within this family we sequenced 84/108 of the currently described genera. Using a combination of a highly-supported phylogeny, divergence dating, biogeographic reconstructions, and paleoclimate reconstructions I will show that this family's biogeographic history can be explained by divergences pre-dating

Gondwanan breakup, paleoclimatic gradients, and a pattern of common vicariance and rare dispersal.

Multimodal and multifunctional signaling? – Web reduction courtship behavior in a North American population of the false black widow spider

Andreas Fischer*, Xiang Hao Goh, Jamie-Lynne S. Varney, Adam J. Blake, Stephen Takács, Gerhard Gries

Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada
afischer@sfu.ca

Male courtship of many widow spiders consists of web-reduction which entails excising sections of the female's web and bundling them up with their silk. Males of *Steatoda grossa* in European populations also produce stridulatory courtship sound which has not yet been studied in their invaded North American (NA) range. Working with a NA population, we tested the hypotheses that (H1) web reduction renders webs less attractive to rival males; (H2) the deposition of silk has a male-female aphrodisiac function; and (H3) stridulatory sound is a courtship signal of NA males. Testing pheromone-based attraction of males in Y-tube olfactometer experiments revealed that reduced webs (indicative of a mated female) and intact webs (indicative of a virgin female) were equally attractive to males. Recording courtship of males with either functional (silk-releasing) spinnerets or spinnerets experimentally occluded on the web of females showed that males with functional spinnerets were more likely to copulate. Although males possess the stridulatory apparatus to produce courtship sound, they did not produce sounds. In conclusion, web-reduction behavior of *S. grossa* males in their invaded NA range has no long-range effect on rival males but has an inter-sexual signaling function, and apparently no longer entailing sound signals.

How spiders make their eyes: Systemic paralogy and function of retinal determination network homologs in arachnids

Guilherme Gainett, Jesús A. Ballesteros, Charlotte R. Kanzler, Jakob T. Zehms, John M. Zern, Shlomi Aharon, Efrat Gavish-Regev, Prashant P. Sharma

University of Wisconsin-Madison, Integrative Biology, Sharma Lab
guilherme.gainett@wisc.edu

Arachnids are important components of cave ecosystems and display many examples of troglomorphisms, such as blindness. Little is known about how the eyes of arachnids are specified genetically, let alone the mechanisms for eye reduction and loss in troglomorphic arachnids. Here, we investigated a sister species pair of Israeli cave whip

spiders (Amblypygi, *Charinus*) of which one species has reduced eyes. We generated the first embryonic transcriptomes for Amblypygi, and discovered that several Retinal Determination Gene Network (RDGN) homologs exhibit duplications. We show that paralogy of RDGN homologs is systemic across arachnoplumonates, rather than being a spider-specific phenomenon. A differential gene expression (DGE) analysis comparing the expression of RDGN genes in field-collected embryos of both species identified candidate genes involved in the formation and reduction of eyes in whip spiders. We interrogated the function of three candidate RDGN genes identified from DGE, using RNAi in the spider *Parasteatoda tepidariorum*. We provide functional evidence that one of these paralogs, *sine oculis/Six1A (soA)*, is necessary for the development of all arachnid eye types. Our results support the conservation of at least one RDGN component across Arthropoda and establish a framework for investigating the role of gene duplications in arachnid eye diversity.

Fitness implications of nonlethal injuries in scorpions: females, but not males pay reproductive costs

Solimary García-Hernández and Glaucio Machado

University of Sao Paulo
solimarygarcia@gmail.com

The ability to detach a body part in response to a predation attempt is known as autotomy. Although autotomy enhances survival, it may impose reproductive costs to males and females. We experimentally investigated how autotomy affects the reproductive success of males and females in the scorpion *Ananteris balzani*. Individuals of *Ananteris* autotomize the last abdominal segments (“tail”), losing the anus and leading to lifelong constipation since regeneration does not occur. Although male “tail” is used during both courtship and sperm transfer, we found that autotomy had no effect on male mating success. The combined effect of increased mortality and reduced fecundity resulted in autotomized females producing 48% less offspring than intact females. Autotomy is highly advantageous for males because it provides the benefit of scaping alive and allows them to mate before death. For females, autotomy provides an immediate survival benefit, but also imposes a future reduction in fecundity. We suggest that the accumulation of feces inside autotomized females during pregnancy leaves little space for embryo development, thus reducing offspring number. In conclusion, the negative effects of “tail” autotomy are clearly sex-dependent, probably because the factors that influence reproductive success in males and females are markedly different.

River noise alters orb-weaving spider abundance, web size, and prey capture

Dylan Gomes

Boise State University
dylangomes@u.boisestate.edu

Novel anthropogenic noise has received considerable attention in behavioral ecology, but natural acoustic environments have largely been ignored as ecological niche axes. In riparian sites, within an arid sagebrush steppe ecosystem, we use a natural range of acoustic environments along with experimentally broadcasted whitewater river noise to test our hypothesis that river noise is an important niche axis. We show that orb-weaving spiders (Araneidae and Tetragnathidae) are more abundant in high sound level environments, but do not seem to be affected by the background noise spectrum. We explore multiple hypotheses for these patterns, such as loss of vertebrate predators and increased prey capture, and then assess how web-building behavior and body condition may be altered. Here, we demonstrate that river noise has the potential to alter spider abundance and behavior.

Utility of Minibarcodes in Revisionary Systematics

Aaron Goodman*, Lauren Esposito

California Academy of Sciences
agoodman@calacademy.org

Fragmentation and degradation of genetic material hinders broader use of museum specimens for molecular-based research, including molecular-based methods of species identification and its applications for taxonomic discovery and species description. 'Minibarcodes', a short 200-300bp fragment of more commonly used DNA barcodes like Cox1, have proven effective in other groups at species-level resolution for degraded specimens where full length barcode data may be challenging to obtain. We tested the effectiveness of minibarcodes in resolving species diversity within the 'thorelli' clade of *Centruroides* Max, 1890 (Scorpiones: Buthidae), an enigmatic and taxonomically problematic group of tree-dwelling scorpions. This small clade has been plagued with inaccurate taxonomy resulting from their rarity in collections, morphological convergence, under-sampling, and often damaged museum material. Through a paired approach of: 1) minibarcode sequencing to determine phylogenetic associations among disparate localities of singleton museum specimens, we were able to 2) aggregate sufficient material for morphological analysis and delineation of species. Our results support the monophyly of the group, which is now comprised of six new putative species in addition to the three previously described, thereby increasing the diversity of the clade by 60%. This study highlights the utility of minibarcodes for older museum material to infer previously unknown cryptic species, and for the aggregation of specimens which may be sparse within museum collections, of variable age, or preservation method.

The evolution of huntsman spiders (Araneae: Sparassidae): insights into life-history

Jacob A. Gorneau*, Linda S. Rayor, Corrie Moreau

Cornell University
jag482@cornell.edu

Huntsman spiders (Araneae: Sparassidae) are among the most speciose families of spiders and have a near-worldwide distribution. Despite a myriad of unique behaviors, life histories, and physiological adaptations exhibited by this family, some subfamilies and genera are known to be paraphyletic and a synthesis of existing phylogenetic work on sparassids is lacking. In this study, a phylogeny of huntsman spiders is inferred using two mitochondrial (COI, 16S rRNA) and two nuclear (H3, 28S rRNA) genes for 145 ingroup taxa, and the phylogenetic and taxonomic implications of these results are discussed. Insights into the social evolution of some sparassids are analyzed using ancestral state reconstructions (ASR) based on data collected from 18 years of field and lab work in social and solitary huntsman by Dr. Linda S. Rayor (LSR). Furthermore, these maximum likelihood ancestral state reconstructions (ASR) are performed to explore the evolution of egg sac structure, retreat biology, habitat preference, and other life-history characteristics. A more comprehensive and synthetic phylogeny of the Sparassidae is presented to provide groundwork for additional study of this family in an evolutionary context.

Evaluation of traditional and new taxonomic characters of North American Solifugae in a multilocus phylogenetic context (Solifugae: Eremobatidae)

R. Ryan Jones*, Jack O. Brookhart, Patrick Casto, Paula E. Cushing

University of Colorado Denver/Denver Museum of Nature & Science
richjones327@gmail.com

Solifuge taxonomy is relatively underdeveloped, reflecting the relatively few researchers actively engaged with this order. Among the twelve families of Solifugae, North American Eremobatidae is the only family to have received a family-level molecular analysis to date. This multilocus analysis, published by Cushing et al. (2015), provides a context in which to evaluate traditionally used characters and derive new characters to revise genera and species groups demonstrated to be problematic by the Cushing et al. analysis. With the Cushing et al. phylogenetic hypothesis serving as a phylogenetic context, over 70 morphological characters were evaluated using parsimony and ancestral state reconstruction in both Mesquite and R. The systematic utility of multiple

cheliceral characteristics, body length ratios, and setal patterns are validated by the detection of strong phylogenetic signal. Combinations of multiple characters are considered for more adequate definitions of genera and species groups rendered poly/paraphyletic by the Cushing et al. phylogenetic hypothesis.

A transient, diet-driven gut microbiome in the gray house spider *Badumna longinqua*

Susan R. Kennedy, Sophia Tsau, Rosemary Gillespie, Henrik Krehenwinkel

Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University
susanrkennedy@gmail.com

Stable, tightly associated gut microbiomes have been described in many animals including several arthropod species. However, little is yet known about the importance of gut microbes in spiders. Here, we test for effects of diet on gut microbial community composition in the gray house spider *Badumna longinqua*. Using amplicon sequencing and qPCR, we characterize both the gut microbiota and the prey composition of spiders collected from the field. We then test for effects of specific prey types on the microbiome by feeding spiders either tropical house crickets (*Gryllodes sigillatus*) or fruit flies (*Drosophila hydei*). We find a clear correlation between microbial community and prey composition in the field-caught spiders. Furthermore, we find a strong effect of both cricket and fruit fly prey on the gut microbiome. In the cricket-fed spiders, the microbiome resembles that of the cricket for up to several weeks post-feeding. In contrast, the fruit fly-fed spiders show few prey-associated microbes, yet nevertheless show a radical remodeling of the gut microbiome. Our results suggest that *B. longinqua* lacks tightly associated gut microbes and that its gut microbiome is instead determined by diet, but that different prey taxa influence the microbiome in different ways.

Strategic sampling and novel analyses suggest new relationships and multiple orb web origins in the spider tree of life

Robert J. Kallal

Siddharth Kulkarni, Dimitar Dimitrov, Ligia Benavides, Miquel Arnedo, Gonzalo Giribet, Gustavo Hormiga

Smithsonian Institution - National Museum of Natural History
kallalr@si.edu

High throughput sequencing and phylogenomic analyses focusing on relationships among spiders have both reinforced and upturned long-standing hypotheses. Similarly,

the evolution of spider webs – perhaps their most emblematic attribute – is being understood in new ways. With a matrix including 272 spiders and close arachnid relatives, we analyze and evaluate the relationships among these lineages using a variety of orthology assessment methods, occupancy thresholds, tree inference methods, and support metrics. Our analyses include families not previously sampled in transcriptomic analyses, namely Symphytognathidae, the only araneoid family absent in prior such works. We find support for the major established spider lineages, including Mygalomorphae, Araneomorphae, Synspermiata, Palpimanoidea, Araneoidea, and the RTA Clade. Concordance factors, a relatively new node support metric, are implemented and discussed. Using the novel structured Markov model method to assess the evolution of spider webs while accounting for hierarchically nested traits, we find multiple convergent occurrences of the orb web across the spider tree of life. Overall, we provide a comprehensive spider tree of life using transcriptomic data and use new methods to explore controversial issues of web evolution, including the multiple origins and losses of the orb web.

Chronoecology of the Diurnal Orb-weaving Spider, *Micrathena gracilis* (Aranaeae: Araneidae)

Mitchell D. Long*, Dr. Thomas C. Jones, Dr. Darrell Moore

East Tennessee State University
mitch.long.1@gmail.com

Micrathena gracilis, a diurnal orb-weaver, forages exclusively during the day on flying insects. Despite the presence of abundant, suitable prey during the evenings, these spiders cease foraging at night. We investigated, using three different approaches, potential factors influencing the temporal phasing of daily rhythmic behaviors, especially web construction, in this species. First, temporal distributions of prey occurrences were investigated by using sticky traps for prey collection at a local field site (a deciduous woodlot). Spider activity and web captures in the field were also used to confirm natural behavioral patterns and capture success throughout the day. Second, under controlled laboratory light:dark cycles followed by constant dark conditions, locomotor activity patterns were monitored in individual spiders to determine if the temporal activity patterns observed in the field were innate and, if so, under control of the circadian clock system. Third, a wariness assay was performed under laboratory light:dark cycles to measure changes in spider boldness and wariness throughout the 24-hour day, a reflection of the fact that spiders are both predators and prey. Our data strongly suggest that the activity patterns observed in the field are under circadian clock control and are temporally programmed to optimize prey availability and predator avoidance.

Taxonomic revision of fossil Psilodercidae and Ochyroceratidae spiders (Araneae: Synspermiata), with a new species of *Priscaleclercera* from Burmese amber

Ivan L. F. Magalhaes, Andrés O. Porta, Jörg Wunderlich, Daniel N. Proud, Martín J. Ramírez, Abel Pérez-González

Museo Argentino de Ciencias Naturales "Bernardino Rivadavia"—CONICET
ilf.magalhaes@gmail.com

Psilodercidae contains ~200 known extant species of small spiders that live in tropical rainforests and caves. The family is mainly restricted to the Oriental biogeographic realm. Interestingly, at least ten different fossil species have been described from inclusions in Late Cretaceous Burmese amber. This suggests the family has been diversifying in the region for ~100 million years. We revise the taxonomy of fossils of this family and its close relative, the Ochyroceratidae, basing on the re-examination of type specimens. We find that ten Cretaceous species described in the psilodercid genera *Priscaleclercera* and *Aculeatosoma* are valid, and present new illustrations of their type material. The genus *Propterpsiloderces* apparently does not belong to Psilodercidae, but rather to a stem lineage of one of the Scytodoidea families. Ochyroceratidae is represented by a single ochyroceratine genus from Miocene Dominican amber, *Arachnolithulus*. Finally, we present the description of a hitherto unknown species of *Priscaleclercera* from Burmese amber, bringing the total of congeners to ten. By studying its morphological features, we argue that *Priscaleclercera* is a crown Psilodercidae in the *Althepus–Leclercera* lineage. The high species diversity of *Priscaleclercera* indicates that Psilodercidae were already a diverse component of the Oriental tropical forests since the Cretaceous.

Links between circadian rhythms, light environments and courtship success in *Schizocosa* wolf spiders

Rowan H McGinley, Jason E. Bond, James R. Starrett, Eileen A. Hebets

University of Nebraska-Lincoln
rowan.mcginley@gmail.com

Communication requires transmission of signals, from sender to receiver, through the signaling environment. Therefore, the signaling environment may play an important role in signal evolution; some signals may evolve to function under specific conditions, while others may evolve to function across multiple signaling environments. Courtship displays within the wolf spider genus *Schizocosa* vary widely in the use and types of different signal elements – males produce species-specific substrate borne vibrations, in some species males possess brushes or pigmentation on the first pair of legs, and some species also incorporate movements of the body and legs as visual signals. To

assess the influence of the light environment on the evolution of courtship displays in *Schizocosa*, we 1) examined daily activity patterns and 2) ran mating trials under three different levels of light intensity. Diurnal species were more likely to copulate in the light, while species that were active throughout the light-dark cycle were likely to copulate across all light levels, suggesting that *Schizocosa* courtship displays have evolved for effective communication in the light environments in which courtship takes place.

Is navigation by scene familiarity feasible using scorpion pectines? Computer simulations say yes.

Albert Musaelian*, Douglas D. Gaffin

Department of Mathematics, University of Oklahoma; Department of Biology, University of Oklahoma.
Albert.Musaelian-1@ou.edu

Scorpion pectines are intricate, chemo-tactile sensory appendages that brush the ground as the animal walks. Depending on the species, each pair of pectines may have ~100,000 sensory neurons arranged among ~10,000 sensilla. Pectines are involved in detecting pheromones, but their exquisite complexity argues for additional functions. One hypothesis is Navigation by Scene Familiarity, first proposed for the compound eyes of bees and ants: to return home, the navigating insect visually scans a range of orientations, compares them to scenes learned along a training path, and selects the direction that maximizes familiarity. We propose that the pectines support a similar method of navigation but by sensing local chemical and textural information instead of looking outwards. We crafted simulated agents based on known morphological and physiological parameters of the pectines and tested their navigational performance in virtual versions of the animals' sand habitat. Using a supercomputer, we varied nine environmental, sensory, and situational properties and ran a total of 51,840 trials of simulated navigation. We showed that navigation by familiarity with a local sensor is feasible and that — surprisingly — a more informationally dense landscape and sensor are not necessarily optimal for it.

Mitochondrial barcode leads to drastic overestimation of species diversity in an Iberian ant-eating spider: Insights from genomic evidence

David Ortiz, Stano Pekar, Julia Bilat, Nadir Alvarez

Masaryk University, Brno, Czech Republic
davidomartinez@yahoo.es

Genomic data provide unprecedented power for species delimitation. However, current implementations are still time and resources consuming. Also, choice during bioinformatic processing is contentious and its impact on downstream analyses is insufficiently understood. Here we employ ddRAD sequencing and a thorough sampling for species delimitation in *Zodarion styliferum*, a widespread Iberian ant-eating spider. We explore the influence of loci filtering on the downstream phylogenetic analyses, genomic clustering and coalescent species delimitation. We also assess the utility of one mitochondrial (COI) barcode for convenient species delineation in the group. Our genomic data strongly support two morphologically cryptic but ecologically divergent lineages, mainly occurring in the central-eastern and western of the Iberian Peninsula, respectively. Moderate loci filtering gave the best results across analyses: although bigger matrices returned phylogenies with higher support, middle-sized matrices performed better in genetic structure analyses. COI displayed high diversity and a conspicuous barcode gap, revealing 13 mitochondrial lineages. Mito-nuclear discordance is consistent with ancestral isolation in multiple groups, probably in glacial refugia, followed by range expansion, and secondary contact that produced genomic homogenization. Several apparently introgressed specimens further challenge the accuracy of species identification through mitochondrial barcodes in the group. We conclude that barcode gaps are not necessarily good indicators of species limits.

From the Andean páramos to the tropical rain forest: Orb-weaving spiders diversity patterns in Southwestern Colombia

Bryan Ospina-Jara*, Charlotte Hopfe, Carlos Valderrama, Jimmy Cabra-García

Universidad del Valle. Biology, Ecology and Evolution of Arthropods Lab
bryan.ospina@correounivalle.edu.co

The orb-weaving spiders stand out as a promising biological research model due to the relationship of their diversity with vegetation structure, and potential biotechnological uses of their silk. This work aims to estimate alpha and beta diversity patterns of the orb-weaving spider assemblage of Valle del Cauca department, southwestern Colombia, and carry out a cyber-taxonomic approach, the first of its kind in the country. A standardized sampling protocol including three sampling methods was carried out covering eight localities in an altitude range between 0 and 3780 masl. A total of 946 adults belonging to 120 species, 33 genera and 4 families were collected. Araneidae was the richest and the most abundant family. The most diverse locality was a mangrove forest (0 masl) with 42 species and the least diverse was an Andean páramo (3780 masl) with 6 species. Species turnover between localities was the most important component of beta diversity followed by differences in richness. The data suggests a negative relationship between diversity and altitude. Furthermore, it is suggested that spider diversity could be determined by habitat heterogeneity. This study shows partial

results of an ongoing research project and our conclusions should be considered as preliminary.

Elemental examination of the whip spider cuticle

Dragoslav Radosavljevic

University of Massachusetts Lowell
radodrag@icloud.com

Many groups of arthropods contain metals in their cuticle. Among arachnids, the elemental composition of the cuticle has most extensively been researched on spiders and scorpions. This study focused on the elemental examination of the whip spider cuticle, specifically on *Damon diadema* (Simon 1876). The analysis was conducted by Scanning Electron Microscopy (SEM) and Energy Dispersive X-ray Spectroscopy (EDS). Our results revealed significant presence of calcium, zinc and chlorine in prosoma, chelicerae, pedipalp tibia and tarsus, and leg tarsal claws. The presence of calcium may signify an evolutionary trait of Pedipalpi or even Tetrapulmonata. The fact that many different arthropod groups enrich their cuticle with zinc may represent a synapomorphic feature. The discovery of chlorine correlates with the results of previous studies of arthropod elemental enrichment, as it usually accompanies zinc in cuticle biomineralization.

Mobilizing data from taxonomic literature: process, tools and applications

F. Andres Rivera-Quiroz, Jeremy Miller

Naturalis Biodiversity Center/ Leiden University
andres.riveraquiros@naturalis.nl

In recent years, great effort has been dedicated to digitizing data from collections and museum specimens, and integrating them into the global biodiversity knowledge space. Similarly, entire libraries of taxonomic and biodiversity literature have been digitized and transformed to PDF files making them easy to share and greatly improving access to this knowledge. However, there is still great potential on the specimen data contained in these text files. When properly extracted, information can be integrated with biodiversity databases, contribute to taxonomic catalogs, reconcile museum specimens with their literature and research, and help identify biodiversity patterns and knowledge gaps. Here we used taxonomic literature on liocranid spiders from the *Teutamus* group to test the process and applications of these tools. We show examples of data extraction, visualization, integration with GBIF, and future perspectives for the use of these data. Also, we show its application on fieldwork optimization using it to infer the best times

and places to collect adult specimens of these spiders. Our results illustrate the relevance of making data contained in taxonomic treatments accessible and reusable allowing it to fill knowledge gaps and generate more robust biodiversity documentation in support of science, policy, and conservation.

Pervasive and persistent: a survey of symbiotypes in regional populations of *Mermessus fradeorum* (Linyphiidae)

Laura C. Rosenwald, Jen A. White

University of Kentucky
laura.rosenwald@uky.edu

Mermessus fradeorum (Linyphiidae) can be infected with up to five maternally-inherited endosymbiotic bacteria that manipulate host reproduction, including strains of *Wolbachia*, *Rickettsia*, and *Rickettsiella*. In a previous field survey from a single location, we found spiders with several different symbiont combinations, which resulted in two competing reproductive manipulation phenotypes. In the present study, we expanded our survey to include nine locations across four counties of Kentucky to explore variation in symbiont community composition and presumable phenotype among host populations. *Rickettsiella*, which causes cytoplasmic incompatibility (CI), was nearly universal across all spiders at all sites, which is consistent with expectations of a CI-causing symbiont. At all sites except two we also found spiders co-infected with all five symbionts, a symbiotype that produced a feminized phenotype in the original population. The strength of this phenotype appeared to fluctuate in the other populations, as only 55% of propagated matriline with 5-fold infection were strongly female-biased, suggesting that other factors may influence phenotype expression. While there is some variation in symbiotype prevalence across geographic populations, overall there are substantial similarities. Reproductive manipulators likely play a large role in the reproductive success of their hosts, and are pervasive throughout regional populations of *M. fradeorum*.

Bite or flight: Antipredator responses as a function of web architecture

Yi Lin Zhou*, Jessica Schmidt*, Andrea Haberkern, Luis Camacho, Leticia Aviles.

University of British Columbia
jessicaschmidtsp@gmail.com

Animals have numerous strategies to avoid predation; spiders are no exception. Here, we ask what morphological and behavioural antipredator strategies web-building spiders exhibit and whether these presumed adaptations trade off with the degree of

protection offered by the spiders' webs. Spiders build webs with refuges present or absent, of three different types: the potentially more protected 3D tangles and 3D sheet-and-tangles, and the more exposed 2D orbs. We hypothesize that spiders whose webs offer greater protection—a 3D architecture or a web with a refuge, will be less likely to be armoured or aposematic when compared to spiders without these protections. We show that 2D web-builders with no refuges tended to be aposematic and spiny, whereas those with refuges tended to be camouflaged and smooth. As predicted, 3D web-builders were neither cryptic nor brightly coloured, nor armoured, but were also more likely to drop out of the web upon simulated predator contact. These results support the hypothesis that web-building spiders tend to be protected either through the architecture of their webs or their morphology and behaviour, suggesting a trade-off between different types of antipredator strategies.

Population genetics and biogeography of montane Atlantic Forest amblypygids

Gustavo Silva de Miranda

NMNH, Smithsonian Institution
smiranda.gustavo@gmail.com

The amblypygid family Charinidae is widely distributed being found in all tropical continents. Despite its widespread distribution, most species of the family are thought to be poor dispersers or short-range endemics. The Brazilian Atlantic forest in particular has 23 species of *Charinus*, this biome alone richer than any country. The process of origin of this diversity, however, is still unknown and presence and/or degree of gene flow among *Charinus* populations was never studied. In this work, we sequenced genomic ultraconserved elements (UCE) of five species of *Charinus* (*C. asturius*, *C. brasiliensis*, *C. montanus*, *C. potiguar* and *C. ruschii*) from nine populations at the Brazilian Atlantic Forest and studied their population genetics and biogeography. 172 UCE sequences were used for phylogenetic reconstruction and 2098 binary SNPs were called for population genetic analysis. Despite sympatric, *C. ruschii* and *C. montanus* were not recovered as sister species, the first being more closely related to *C. brasiliensis* and the second, to *C. asturius*. A large degree of genetic structure was found among all the different species and one population of *C. montanus*. Different dating strategies were tested. Results and discussion are further developed in the presentation.

Net-casting spider foraging behavior

Jay A. Stafstrom, Eileen A. Hebets

Cornell University
JS2627@cornell.edu

The net-casting spider genus *Deinopis* is a truly fascinating group of animals. These spiders possess an extraordinary visual system, employ an impressive form of diurnal crypsis, and hunt prey using a unique foraging strategy for which they are named – “net-casting”. Though enigmatic, the nocturnality of *Deinopis* has made observations of their natural behavior quite difficult, nearly impossible prior to the advent of infrared video recording technology. As such, records of *Deinopis* behavior are sparse, leaving much to be understood about these eight-legged wonders. Here, I will discuss and display novel behavioral observations of the Costa Rican net-casting spider species, *Deinopis longipes*, focusing on aspects of foraging behavior. Highlights and summaries from remotely recorded field observations will be presented. Beyond the novelty of witnessing never-before-seen behavior, the value of natural field observations regarding hypothesis-driven research will also be discussed.

Long term monitoring of canopy associated spider communities by eDNA metabarcoding from leaves

Sven Weber, Anja Melcher, Rieke Broekmann, Susan Kennedy, Henrik Krehenwinkel

University of Trier (Germany)
webersv@uni-trier.de

Improving the repertoire of methods for biodiversity assessments is a crucial step on the way to quantify population changes on a large scale and understanding the reasons behind them. Arachnids, mostly spiders, are a well-established marker organism to assess terrestrial ecosystems. In this regard, the lack of alternatives to using pitfall traps limits most assessments to ground-dwelling spiders. However, spiders are known to populate a much more diverse spectrum of habitats than just the ground. In this study, we developed a molecular method to monitor arthropod communities, using environmental DNA and high throughput sequencing. The samples were provided by the German Environmental Specimen Bank (GESB) and consist of canopy leaves of the most abundant tree species of Germany, collected nationwide for 30 years along a land-use gradient. We can clearly see that there are unique arthropod and spider communities on each tree species. Our first analyses do not show a general species decline but instead heavy community changes and species turnovers. Not only can we retrace the population changes over time but the method can also be used to detect extremely rare species.

Effect of cadmium and zinc on the activity of antioxidant enzymes of *Oxyopes javanus* via food chain

Muhammad Xaaceph Khan*, Abida Butt, Farah Kausar

IPM Lab, Department of Zoology, University of the Punjab, Lahore
xaaceph@gmail.com

Metals are naturally occurring element and through anthropogenic sources pollute the vast areas of agricultural land. Metals have a potential to accumulate in Organism and damage the cell by generating reactive Oxygen species (ROS). Among metals, Cd is phytotoxic and biologically non-essential metal. Cd is massively used in fertilizers, pesticides, insecticides that have long lasting detrimental effect on agricultural soil, plant and arthropods body. Zinc is microessential element, impacts positively on organism growth and development, if its concentration in an organism does not exceeds the physiological limits, especially in insects. The Objective of present study was to estimate the detoxifying and antioxidative enzymes in *Oxyopes javanus* (Thorell 1887) against different concentrations of Cd, Zn and Cd+Zn. Spider collected from the University of Punjab, maintained in lab and retained on wheat plants grown in metal polluted soil in greenhouse. Sample collected for the purpose of study were feed *Rhopalosiphum padi* L. that reared on contaminated wheat plants. Experiment was performed to estimate the total protein content and antioxidant enzymes Cyt P450, GST, CarE, AChE, SOD, CAT and GPx. All analyses were done by using minitab 18 software. Results showed that Cd has adverse effect on the total protein content and major detoxifying and antioxidant enzymes. Major phase I or defense line antioxidant enzymes decreased gradually with increase treatments of Cd. There is no contrary effect of Zn on detoxifying and antioxidant enzymes activity of *Oxyopes javanus*. Antioxidant enzymes increased at all concentration of Zn. Present study also suggests that moderate ratio of Zn in the presence of Cd can simultaneously decrease the adverse effect of Cd on inhibition of detoxifying and antioxidant enzymes.