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Brian Peck

### Oral Presentation Abstracts

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### **Comparative biogeography of two 'widespread species' in the Caribbean**

Ingi Agnarsson<sup>1</sup>, Matjaz Kuntner<sup>2</sup>, Austin Dziki<sup>1</sup>, Stephanie LeQuier<sup>1</sup>, Greta Binford<sup>3</sup>

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The Caribbean islands harbor rich biodiversity with high single island endemism. Stretches of ocean among islands represent barriers to gene-flow enhancing endemism. Yet some native species are widespread, indicating that such barriers can be ineffective even in wingless organisms like spiders. We compare and contrast the phylogeographic history of two putatively widespread and codistributed species *Argiope argentata* (Fabricius, 1775) and *Spintharus flavidus* Hentz, 1850 in the Caribbean. These differ in dispersal abilities predicting different degrees of diversification in each lineage. Indeed, phylogenetic and biogeographical analyses indicate sharp differences among these lineages where only the better disperser (*Argiope*) can truly be considered widespread while the poorer disperser instead represents an ancient and previously undocumented radiation in the Caribbean. Our findings highlight the value of comparative biogeography and underscore that dispersal ability determines the effectiveness of oceanic barriers and thus has direct consequences for patterns of diversification and endemism.

### **Property variation in spider silks: ecology, evolution and biomimic implications**

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The unique combination of high stiffness, strength and extensibility make spider major ampullate silk desirable for biomimetic applications. The unique properties of spider gluey silks, likewise, render them desirable materials for biomimetics. Intensive research of the genetics, biochemistry and biomechanics of these materials has facilitated a thorough understanding of their properties at various levels. Nevertheless, methods such as cloning, recombination and electro-spinning have so far failed to successfully produce materials with similar properties as spider silk. We suggest that it is imperative to learn more about the ecology and evolution of spider silk variability if the creating of spider silk analogues is to be realized. Here we assimilate the research done and techniques utilized to determine spider silk variability in ecological and evolutionary contexts. We suggest that future research would benefit by focusing on hypotheses that explain spider silk property variations across broader contexts.

### **Near yet far: four families of spiders in adjacent conifer forest sites in northern New Mexico**

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In 2011 I began working on spiders at the Valles Caldera National Preserve, which is adjacent to Bandelier National Monument where I have been working on spider communities for almost 20 years. There were a number of species from the Caldera that I had never collected from Bandelier, although the habitats were similar: mostly conifer forest between and 2500 and 2700m in elevation and with similar temperature and precipitation patterns. Some of the Caldera species were range extensions from areas to the north and east; was the basin topography providing a more mesic habitat for species that might otherwise not occur in the region? I compared species richness and abundance

for 4 ground-dwelling spider families between the two locations. The 4 families (142 species) varied in size and vagility. Habitat specificity ranged from the greatest in the Linyphiidae and Thomisidae, followed by the Gnaphosidae, and Lycosidae with the least; only 7 species were collected at all sampling sites. I found a number of state records for species in the Caldera but many common regional species as well, so that the location is not as much of a refuge as I expected. These records add habitat information for species whose distributions are poorly known and also suggest species at risk of losing habitat as the predicted climate by the end of the century favors pinon-juniper woodland at the expense of mixed-conifer forest, which has greater spider species richness.

**Adaptive radiation and mate recognition: investigating the potential dual roles of venom evolution in the genus *Tetragnatha* (Araneae: Araneomorphae: Tetragnathidae)**

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Venom is considered a key innovation that allowed ecological diversification in a number of lineages including snakes, anguimorph and iguanian lizards, and cone snails. Venoms are complex cocktails of bioactive compounds that serve multiple functions, with components typically having high target specificity. Commonly, venom is employed as a means for predation and defense but is also involved in intraspecific conflict and mate recognition. A recent intriguing insight into the dynamics of venom evolution involves the observation of sexual dimorphism in venoms of some taxa, indicating a potential role in mate recognition. This sets up a possible dual role of venoms in both ecological divergence and mate choice that could influence reproductive isolation of populations through local adaptation. Though disparities in venoms between sexes can sometimes be explained by differences in feeding behavior, evidence also suggests that venom can play a role in intraspecific communication. Our work on *Tetragnatha* venoms, namely transcriptomics and proteomics, shows most species display sexual dimorphisms; males express high molecular mass venom components that are expressed at much lower levels or not at all in females. Additionally, a Hawaiian clade has undergone an adaptive radiation with concomitant evolution of venom peptides. Given the unusual mating behavior (cheliceral locking) in many tetragnathids, it may be that these dimorphic venom components play a role in mate recognition while other components have evolved in response to dietary niche partitioning. Here we present the current state of our ongoing tetragnathid venom research.

**A new species of myrmecophilic spiders from Big Bend, Texas**

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In 1999, a new species of spider was discovered by Midwestern State University graduate student, Greg Broussard in Big Bend, Texas. This spider was collected in the vicinity of the seed harvesting ant, *Pogonomyrmex rugosus* and its range extends at least into northern Mexico since it was also collected in 2011 by Sandra Brantley and David Lightfoot at Cuatrociénegas, Mexico. In June 2015, a team from Midwestern State University and the Denver Museum of Nature & Science visited Big Bend and excavated nests of *P. rugosus* in order to find spiders living inside. We also carried out behavioral bioassays to test the hypothesis that the spiders are chemical mimics of the host ants.

**Failure to launch: Apparent local extinction of a newly established population of a non-native spider, *Clubiona pallidula* (Araneae: Clubionidae)**

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During a 2002 survey of arthropods in invasive common reed (*Phragmites*) and non-invasive cattail (*Typha*) coastal wetlands on Lake Michigan's Green Bay, a Eurasian sac spider never before reported in the Great Lakes region, *Clubiona pallidula* (Clerck), was documented from all three sampled *Phragmites* sites, where it made up 28.9% (11 of 38) of the sampled adult spiders. In June and July 2010, we resurveyed the original *Phragmites* sites as well as 15 other *Phragmites* sites (13 coastal, 2 within 6 km of the coast), ranging 60 km north and south of the original sites, in order to document the spread of the invading species and look for any effects of its presence on the spider communities. In all, we sampled 963 adult spiders belonging to 12 families and 86 species. 11.8% belonged to seven species of *Clubiona*, but no *Clubiona pallidula* were sampled. Based on 2002 data, we would predict the original site samples to include about 54 *C. pallidula*, and if the species had successfully occupied the other sites at the same rate, we would expect about 278 individuals. Thus, a non-native species that established a population including at least thousands of individuals along over 4 km of shoreline has failed to thrive, becoming at least two orders of magnitude less abundant in eight years. This is probably a common outcome of introduced populations, but one that is rarely documented. 2015 re-surveys of the three original sites are underway.

### **Systematics of the scorpion subfamily Rhopalurusinae (Scorpiones: Buthidae)**

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Buthid scorpions are represented in the New World by 13 genera and 403 species. However, the phylogenetic relationships both within and among the two proposed subfamilies, Tityinae Bücherl, 1971 and Rhopalurusinae Bücherl, 1971, have never been tested. Furthermore, the monophyly of the disjunctly distributed genus of stridulating club-tailed scorpions, *Rhopalurus* Thorell, 1876, has never been tested. Molecular data and morphological characters analyzed separately and in combination were used to test relationships among the genera. Results support the monophyly of both subfamilies, recover a paraphyletic *Rhopalurus* that is congruent with its disjunct distributions, and a monophyletic *Centruroides* Marx, 1890 sister to the clade of *Rhopalurus* endemic to the Greater Antilles.

### **A genome-wide phylogeny of the jumping spiders (Araneae: Salticidae) using anchored enrichment**

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The past 15 years have seen extensive progress in resolving relationships among the Salticidae via molecular phylogenetics. However, even the most recent salticid phylogeny, from six nuclear and two mitochondrial gene regions, still leaves major relationships unresolved. We have yet to confidently discern the relationships among the "lyssomanines", both the agoriines and Eupoa remain particularly difficult to place, and several deep uncertainties persist among large clades within the speciose Saltafresia. To attempt to resolve the backbone of salticid phylogeny, we used anchored hybrid enrichment (AE), a cost-effective, high-throughput, probe-based genomics technique capable of capturing hundreds of phylogenetically informative nuclear loci per organism — much more than is tractably obtainable via traditional PCR-based methods. AE is generalizable across non-model taxa, with reliable

probe sets designed for a variety of large vertebrate and invertebrate clades spanning over 500 million years' divergence, including a probe set specific to the Araneae. Therefore, AE has promise to resolve deep phylogenetic relationships within the Salticidae. Here, we report our first attempt at constructing a genome-wide molecular phylogeny of the Salticidae, using AE sequence data from 33 species representing all major salticid groups plus one philodromid outgroup.

### **Submersion tolerance of the coastal dune-dwelling spider *Arctosa sanctaerosae***

Drew Hataway<sup>1</sup>

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Evidence supports the existence of behavioral and physiological adaptations in arthropods that allow for persistence in periodically submerged habitats. One such adaptation recently found in Lycosidae is the ability to shift to an anaerobic metabolism. In the present study we determined whether the adaptation for hypoxic coma is conserved in a dune-dwelling coastal spider *Arctosa sanctaerosae* (Araneae: Lycosidae). The burrows of this species receive stochastic inundation in the form of storm surge associated with severe tropical storms. To assess tolerance to being submerged in seawater for periods approximating the effects of storm surge, 89 adult individuals were submerged for 4 hours. Ninety-four percent of these individuals became unresponsive in this time and 36 percent of these unresponsive individuals resumed activity. Current research is focused on measuring true respiration in individuals for 24-hour periods prior to inundation as well during the recovery period to illustrate changes from baseline.

### **Boom-bust colony dynamics in the socially polymorphic spider *Anelosimus studiosus* (Araneae: Theridiidae)**

Thomas C. Jones<sup>1</sup>

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*Anelosimus studiosus* is an arboreal cobweb weaver common along waterways in the southeastern US. This species is unusual in that it varies in its social structure forming both social and solitary webs. Colonies of a single adult female and her maturing offspring are predominant throughout their range. However, in more northern latitudes, and associated with cooler microhabitats, clusters colonies consisting of multiple adult females which cooperate in foraging, web maintenance, and brood care. Colony structure is an emergent property of individual aggressiveness, with docile individuals tending to form social colonies, and aggressive individuals more often defending solitary webs. Models and empirical data suggest that in cooler habitats females living in small colonies have the highest individual fitness, but that in larger colonies individual fitness drops below that of females in solitary webs. It is hypothesized that such a fitness function would drive frequency-dependent selection on individual aggressiveness, which would create local boom-bust cycles in the relative abundance of social colonies. Results of a spatially-explicit simulation and of a multi-year demographic study are presented in support this hypothesis.

### **Systematics of the Australian leaf-curling spiders *Phonognatha* and *Deliochus* (Araneae, Araneidae)**

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The relationships of taxa at the base of the araneid phylogeny are relatively poorly known. Two of these early diverging taxa are *Phonognatha* Simon 1894 and *Deliochus* Simon 1894, which have been classified at various times in the families Tetragnathidae, Nephilidae, and most recently Araneidae based on morphological, molecular, and behavioral evidence. Neither genus has been revised since their initial description over a century ago despite their phylogenetic relevance to these three families, their relative commonness in their native habitats of Australia

and New Caledonia, or leaf-rolling behavior that all taxa in these genera apparently exhibit. We provide a progress report on the work thus far on these taxa. Morphology of specimens examined so far suggests one undescribed *Phonognatha* and two undescribed *Deliochus* species, one *Phonognatha* species to be synonymized, one *Phonognatha* subspecies to be elevated to species rank, and two tetragnathid species currently misclassified as *Deliochus*. Results of our preliminary analyses of 75 taxa using 6 genetic markers supports the placement of these genera as sister taxa in a clade at the base of the araneid tree.

### **Evidence for sexual selection on spider fangs and behavioral cost**

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Unusual among spiders, males of the long-jawed orb-weaver *Tetragnatha elongata* live approximately as long as females do and frequently consume prey as adults—by stealing boluses of prey from females after mating with them. One striking feature of male *T. elongata* is that their fangs appear to be relatively elongated with respect to the length of their chelicerae. Longer fangs could benefit the male if they are used in agnostic displays with conspecifics and may also aid in stealing immobilized prey from female webs. But for these males that feed frequently, longer fangs may also come at the cost of being able to catch moving prey efficiently. Here, we tested for sexual dimorphism in chelicerae and fang length in *T. elongata* and one potential cost of elongated fangs: feeding efficiency. We compared the cheliceral and fang lengths of spiders in the penultimate and adult stages as well as their prey-catching efficiency when live insects were released in a test chamber. There were no significant differences among male and female penultimate spiders. But adult males were sexually dimorphic for fang length and were significantly slower at catching live prey. Elongated male fangs could be a result of selection for stealing prey and/or as a display/defense against other males. If male fangs are adapted for prey stealing (i.e., taking captured prey from a female's web) rather than prey catching (i.e., attacking flying prey) elongated fangs would enable males to steal a hanging food bolus from a greater distance away from cannibalistic females.

### **Multilocus sequence data reveal dozens of putative cryptic species in a radiation of endemic Californian mygalomorph spiders (Araneae, Mygalomorphae, Nemesiidae)**

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We use mitochondrial and multi-locus nuclear DNA sequence data to infer both species boundaries and species relationships within California nemesiid spiders. Higher-level phylogenetic data show that the California radiation is monophyletic, and distantly related to European members of the genus *Brachythele*. As such, we consider all California nemesiid taxa to belong to the genus *Calisoga* Chamberlin, 1937. Rather than find support for one or two taxa as previously hypothesized, genetic data reveal *Calisoga* to be a species-rich radiation of spiders, including perhaps dozens of species. This conclusion is supported by multiple mitochondrial barcoding analyses, and also independent analyses of nuclear data that reveal general genealogical congruence. We discovered three instances of sympatry, and genetic data indicate reproductive isolation when in sympatry. An examination of female reproductive morphology does not reveal species-specific characters, and observed male morphological differences for a subset of putative species are subtle. Our coalescent species tree analysis of putative species lays the groundwork for future research on the taxonomy and biogeographic history of this remarkable endemic radiation.

### **Phylogenetic resolution of *Habronattus* jumping spiders using transcriptomes (Araneae: Salticidae)**

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*Habronattus* includes about 100 species of jumping spiders notable for their complex and colourful courtship displays. A well-resolved species phylogeny would provide an important framework to study their evolution, but has not yet been achieved because of weak and conflicting signals from the few genes available. While deep coalescence in the recently diverged group could generate conflicting gene trees, previous work has suggested that some conflict is due to hybridization between species. To infer *Habronattus* phylogenetic relationships and to investigate the cause of gene tree discordance, we assembled transcriptomes for 34 *Habronattus* species and 2 outgroups. A concatenated phylogenetic analysis using maximum likelihood for 2.5 Mb of nuclear data yields a strongly supported phylogeny concordant with previous studies, but much better resolved. The tree from 12.5 kb of mitochondrial data is largely in agreement, but disagrees strongly in placing *H. clypeatus* within the *coecatus* group, suggesting introgression from the latter into the former. We analyzed 430 nuclear loci longer than 1 kb with Bayesian concordance analysis and ABBA-BABA tests to explore signals of nuclear introgression. These show little or no introgression, indicating that *clypeatus-coecatus* group introgression was mostly limited to the mitochondrion.

### **Courtship in *Tengella perfuga* Dahl: strumming, stroking, stilting**

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*Tengella perfuga* Dahl (1901) are Nicaraguan cribellate zoropsids found in cloud forest habitat bordering coffee plantations. They spin funnel webs with several knockdown lines placed between buttress roots of strangler figs, outcroppings over streams, between fallen logs and in some cases retreating back into the stonework or woodwork of various buildings. Females are dedicated to their webs, while males abandon their webs upon adulthood and wander to look for females. In the field males were typically collected in situ with the female in her web, or else freshly molted to adulthood prior to abandoning their webs. Here I'll describe and demonstrate for the first time, the courtship behavior and copulation of *T. perfuga*, as well as egg sac production. These natural history observations stem from field observations, as well as laboratory reared spiders as part of a larger project exploring the metabolic trade-offs between silk use and fecundity, as well as silk spigot ontogeny in various lycosoid spiders.

### **A new species of *Liocranoides* (Tengellidae) from Alabama**

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The genus *Liocranoides* Keyserling 1881 (Araneae: Tengellidae) contains five species of mostly cave-dwelling, medium-sized (6 – 9 mm) spiders. Late last year, on a collecting trip in caves throughout northern Alabama, we discovered a cohabiting male and female in Ingram Cave in Blount County, AL. These spiders were determined to be a new species based on morphological differences in the reproductive structures. Here we give an abbreviated description of this new species along with its proposed taxonomic placement in relation to the other species in the genus. Moreover, we also describe tentative plans for a collection trip throughout Appalachia to gather all six species and to develop a molecular phylogeny of the genus using this collected material.

## **Evolutionary and environmental plasticity in the material properties of orb-weaving spider glue droplets**

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Glue droplets of araneoid orb-web viscous prey capture thread differ in hygroscopicity, adapting a species' threads to the humidity of its habitat. As humidity changes, so too does the viscosity and extensibility of the glycoprotein core within each droplet. In this study we characterized the material properties of three species' glycoproteins at five humidities ranging from 20 – 90%: *Argiope aurantia* (*Aa*), a diurnal species found in exposed habitats, *Verrucosa arenata* (*Va*), a diurnal species found in humid forests, and *Neoscona crucifera* (*Nc*), a nocturnal species found along forest edges. We used the Young's modulus and diameters of the axial fibers that support each species' viscous thread in conjunction with the measured angular deflection of these support lines and a droplet's glycoprotein volume to compute the stress on extending droplets. When combined with droplet extension this generated stress-strain curves, from which we determined the Young's modulus and toughness of each species' glycoprotein. Both values peaked at 37% RH in *Aa*, 72% RH in *Nc*, and 90% RH in *Va*. The maximum toughness of *Va* glycoprotein was 15 times that of *Nc* and 215 times that of *Aa*. At 90% RH the energy required to extend the droplets in a mm span of *Va* thread was 48 times greater than at 20% RH, 48 times greater than the maximum value for *Aa*, and 11 times greater than the maximum value for *Nc*. This broad range of performance documents the tremendous evolutionary and environmental plasticity of spider glue and its potential for biomimicry.

## **Ancient colonization of North America via Caribbean islands by recluse spiders, and evidence for cryptic radiation**

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The Caribbean archipelago is a global hotspot of biodiversity, and the region has had historical potential to provide colonization corridors between the biota of North and South America. The recluse spiders (*Loxosceles*) are a medically important taxon widely known for venom that may cause dermonecrotic lesions in humans. There are six described Caribbean *Loxosceles* and 43 in North and Central America. Previous work with limited sampling in the Caribbean has supported monophyly of North American taxa with a sister relationship to Caribbean taxa. Here we use molecular phylogenetic analyses with deep sampling of *Loxosceles* within the Caribbean and broader sampling of worldwide exemplars to (1) test the relationships of this fauna to taxa on North and South America, (2) analyze patterns of relationships within and among islands and infer influences on genetic structure within this group, and (3) test the genetic depth of the currently described species within the Caribbean. We find strong support of a single, old, diverse monophyletic Caribbean clade that is sister to a radiation of species in North and Central America. Our results are consistent with colonization of North America and the Caribbean via the GAARlandia landbridge, far preceding the Panamanian isthmus. The genus shows strong geographic genetic structure within and among islands, and among caves within islands. We find evidence for minimally 18 distinct genetic lineages, triple the known Caribbean diversity. Caribbean *Loxosceles* emerge as a diverse lineage that may reflect ancient geological events and thus help understand the biogeographical history of the Caribbean region.

## **Do the proportions of the spinning duct influence the material properties of major ampullate fibers?**

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Spider major ampullate fibers exhibit high strength, and exceptional toughness. High performance of this material is

based on both the chemical composition and the configuration of molecules given by the conditions inside the spinning duct. The spinning duct secures reabsorption of water from silk precursor, and, by means of shear forces, it elongates the silk protein molecules and aligns them parallel to the fiber axis. The length of the duct determines duration of elongation and alignment and the tapering of the duct determines its intensity. When protein molecules are more elongated and better aligned, more regions can come close to each other and zip into the beta sheet crystals, the structures that make fibers stronger. When the molecules are more elongated, there is no more potential to elongate further, which make fibers stiffer. In this study we tested the hypothesis that the glands with longer, more tapering and narrower ducts should produce stronger and stiffer fibers. In order to minimize the chemical variation of studied silk we chose a group of phylogenetically related species from the families Araneidae and Tetragnathidae. These spiders produce high performance major ampullate silk used for construction of orb webs, dragline or ballooning fibers. We expected various selection pressures in this group, which might have initiated differentiation of duct morphology. To ascertain the morphology of the ducts, we dissected and analyzed the glands under the light microscope. In particular, we measured the length of the duct (each of the three limbs separately), initial and final width of the funnel and the final width of the duct. Then we looked for correlations between these morphological parameters, and the quality of the silk.

### **Short-term impacts of prescribed burning on the spider community (Order: Araneae) in a small Ohio prairie**

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Prescribed burning is a management tool that is widely accepted for prairie management and restoration, yet little is known how burning may impact the spider community. Although it is generally thought that prescribed burning may alter the spider community composition and structure, few studies have examined these shifts in a controlled manner with both a burned prairie and a nearby unburned control. On October 25th, 2014, a prescribed burn of a tallgrass prairie was conducted at the Gwynne Conservation Area, London, Ohio. Spiders were sampled using pitfall traps for four weeks pre-burn and six weeks post-burn in both the treatment prairie and an adjacent unburned control prairie. A total of 298 spiders were collected from 16 families, over 60% of which were in the family Lycosidae. Overall, we found the prescribed burn did not significantly negatively alter the abundance of spiders collected. This trend was seen in the overall spider abundance, as well as for the family Lycosidae. Anecdotal observations also suggest that some spiders are capable of surviving the fire *in situ*. As we continue to study these communities, we will develop a better understanding of role that prescribed burning plays in regulating the structure and composition of the spider communities. Such information is important to develop process-based restoration and management practices in grassland ecosystems.

### **LinEpig: developing a taxonomic reference using collections-management systems**

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LinEpig is an online tool designed to aid in the identification of linyphiid specimens, particularly females in the speciose subfamily Erigoninae, the only nearctic spiders that lack a key to genus. Originally created as a gallery of epigynal images on Google's free "Picasa" photo-sharing platform in 2007, this resource is now being migrated into the Field Museum's KE EMu database. EMu will enable development of taxonomically-meaningful functionality – features that previously had to be accommodated via Facebook-like commenting functions, if at all – as well as incorporation of habitus and palp images. The move also represents an opportunity to scope out, model, and test the functionality most useful to research collections working with problem taxa. Unlike the primarily collections-based resources that have resulted from the growing adoption of collections-management software, the current project presents a taxon vertically across collections rather than a wide range of taxa horizontally across an institution; the goal is for all reliably identified erigonine species held in Nearctic collections to be represented. I present the EMu-

based project, currently in development, to solicit input on the functionality and features that would best serve the principal users of such a taxonomy-based data set. I also give a brief account of the logistical and rights issues involved in obtaining and maintaining such data.

### **Ancient spiders in salt lakes**

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The Green River Formation crops out over 25,000 square miles of Wyoming, Colorado, and Utah, averages 2000' in thickness, and represents one of the world's longest-lived Great Lakes systems, lasting approximately 17 million years. Spider fossils are abundant in some horizons but, until recently, only a single specimen (*Linyphia byrami* Cockerell, 1925) had been described. In the first part of this talk, a sample of spiders from the families Uloboridae, Hersiliidae, Selenopidae, and Thomisidae are described. Such diversity represents a variety of life modes, and habitats; it is suggested that storms and flash flooding were the likely mechanisms for transporting the spiders into the lake. In the second part of this talk, we compare the spider fauna of Green River with those of two other paleolake deposits, and demonstrate how spider leg flexure can serve as a proxy for the paleosalinity of ancient lakes.

### **Spiders (Araneae) of the Everglades National Park, Florida: changes in species composition, 1960s-2000s**

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The Florida Everglades is a large, unique wetland system in southern Florida that has lost 40% of its historic area, with the remaining habitats under threat. Spiders (Araneae) are an understudied organism in this region. It is expected that spider assemblages have changed over time between the two time periods due to restoration, climate change, and non-native spider species. Spiders were sampled in three major Everglades habitats, sawgrass, hardwood hammock, and willowhead, during 1967-1968 and resurveyed in 2008-2009 with the addition of pinelands. Over 10,000 spiders in over 230 species and 27 families have been identified. The 2000s collection contains the greater species diversity with 103 species, compared to the 1960s collection with 53 species. This difference is primarily due to the inclusion of the pineland sample sites in 2008-09 that added 41 species to the records. Sixty-two species are shared between collections. Comparing hardwood hammock samples from both collections revealed an increase in species diversity and a change in the most abundant species. The hardwood hammock sites are the most diverse with 133 species sampled, followed by the pinelands with 88 species. Sawgrass and willowhead habitats are less diverse with 53 and 51 species respectively. The greatest species overlap is found between hardwood hammock and pineland (43%), and willowhead and sawgrass (46%), while pinelands and sawgrass are the most dissimilar (26%). This follows the pattern of vegetal complexity correlating with species diversity observed in other studies and suggests that the variety of habitats are necessary to maintain species diversity.

### **Revision of the genus *Cryptomaster* (Travunioidea, Laniatores) using molecular and morphological data**

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The monotypic genus *Cryptomaster* Briggs 1969 was described based on individuals from a single location in southern Oregon. Despite its large body size compared to most travunioid Laniatores, *Cryptomaster leviathan*, is notoriously difficult to find and thus few subsequent collections have been recorded for this species. The full distribution of *C. leviathan* is unknown, and levels of genetic and morphological variation within this species have gone unstudied. Here, we increase sampling of *Cryptomaster* to 14 total known localities from both coastal mountains and the Cascade Mountains in southern Oregon. Phylogenetic analyses of mitochondrial and nuclear DNA sequence data sampled from individuals from all localities reveal deep phylogenetic breaks that indicate *C. leviathan* is a species complex. We use coalescent species delimitation methods to test hypotheses of new species, and use SEM to assess diagnostic morphological characters for these putative species. Although *C. leviathan* is restricted to a small relictual distribution, this taxon is consistent with other short range endemic taxa in having deep phylogenetic breaks indicative of species level divergence.

### **Intra-orb-web capture spiral adhesive droplet distributions**

\*Sarah D. Stellwagen<sup>1</sup>, Brent D. Opell<sup>1</sup>, Mary E. Clouse<sup>1</sup>

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Orb-weaving spiders complete their webs by spinning a sticky capture spiral that will retain insects that strike the web. Many species exhibit top-bottom asymmetry with the lower half of the web presenting more capture area, which a spider is able to use effectively, as running speeds are faster when spiders move downwards. This study expands the understanding of web asymmetry by examining differences in the characteristics and distributions of the adhesive capture spiral droplets in the upper and lower portions of *Argiope trifasciata* orb webs. These spiders construct webs in low vegetation, where the lower portion of webs experience a combination of higher humidity and lower temperature due to moisture retention from vegetation and less air movement. To determine differences in droplet properties, performance, and distribution across webs, and their relationship to microhabitat conditions characterized in this study, we examined droplets collected from the top, top middle, inner, bottom middle, and bottom of webs. The total and glycoprotein volumes of droplets deposited on the bottom-most threads were the largest, and twice as large as those from the top, despite being deposited at similar times. Droplets from all areas of the web extended for a similar length of time, except bottom droplets, which extended twice as long as the others. However, droplets from the middle of the top and bottom sections absorbed the most energy during extension. This demonstrated that droplets are deposited differentially across the web in a way that suggests that spiders regulate resource allocation to maximize prey capture.

### **Female wolf spiders evaluate males based on multimodal signal quality**

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Theory predicts that females should exhibit ordered preferences for size or expression of male quality-indicating traits, although recent work suggests some species employ comparative rather than absolute evaluation of mates. We tested comparative assessment of differences in male quality by female *Schizocosa ocreata* (Hentz) wolf spiders with unimodal and multimodal video and vibratory/seismic playback choice tests. Females show ordered directional preferences for male quality indicators (leg tuft size, vibration amplitude) in both individual sensory modes and multimodal (combined) signals. Unimodal and multimodal tests show that quality of either signal mode affects mate choice outcome. Females exhibited transitivity of preference, consistently choosing males with higher quality relative to a rival opponent. Multimodal choice tests showed that females made predicted choices when male traits covaried positively, but in negative covariance (cue-conflict) choice tests, females showed a bias for higher male quality in visual signals. Female wolf spiders therefore appear to exhibit comparative mate evaluation of individual signal modes in multimodal signals, and assess male quality relative to that of rivals.

**Do spiders transmit bacteria when they bite? The evidence suggests otherwise**Richard S. Vetter<sup>1</sup><sup>1</sup>Department of Entomology, University of California Riverside, Riverside, CA, USA

Much of my research over the years has been overturning misconceptions and falsehoods that are well established in the medical community in regard to spider bites. Quite often no scientific evidence exists to support their platitudes. One such platitude is that spiders can vector bacteria when they bite and are plausible etiologies of bacteria infections in humans. Several researchers have swabbed spider mouthparts and plated the swabbings on agar with resultant bacterial growth. From this, the extrapolation was then promoted that spider fangs and mouthparts are sources for skin infections including one study, which incriminated *Latrodectus* spiders, which have never been associated with skin lesions despite centuries of bite reports. However, these authors never took their speculation to the proper conclusion: if spiders do vector bacteria, then the spider bite literature should be plastered with spider-bacteria associations. Therefore, I data-mined the literature to address this premise which included widow, recluse, wandering, wolf, Sydney funnel-web spiders as well as verified bites from random spiders. When examining over 20 studies that encompassed over 4,000 verified or diagnosed cases of spider bite, there is typically no mention of bacterial infection whatsoever. Several studies list a multitude of bite symptoms with bacterial infection being conspicuously absent. Therefore, the evidence is deficient that spiders are bacterial vectors in human skin maladies. In part, one reason for the lack of bacterial transfer is that venoms from all animals have antibacterial properties, which may be an evolutionary adaptation to clear bacteria from prey before ingestion.

**Diel patterns of courtship in the subsocial spider *Anelosimus studiosus* (Araneae: Theridiidae) may not be driven by female aggression**\*J. Colton Watts<sup>1,2</sup>, Nathaniel Hancock<sup>2</sup>, Ashley Herrig<sup>2</sup>, Madeleine Miller<sup>2</sup>, Sara Normark<sup>2</sup>, Rebecca Wilson<sup>2</sup>, Thomas C. Jones<sup>2</sup><sup>1</sup>School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA<sup>2</sup>Department of Biological Sciences, East Tennessee State University, Johnson City, TN, USA

Male *Anelosimus studiosus* (Araneae: Theridiidae) prefer to court females with a social behavioral phenotype characterized by decreased boldness and aggression, including decreased frequency of sexual cannibalism. However, female *A. studiosus* also show a predictable diel pattern of boldness. To determine if variation in courtship also reflects diel changes in female behavior, we assayed male courtship behavior in the presence of females from multifemale and singleton webs during simulated dusk and dawn. We further investigated whether variation in male behavior was driven by female cues by pairing males with females that were maintained on the same light cycle or a diametrically opposed light cycle. Males paired with females from multifemale webs took longer to court at dusk and generally took longer to court females maintained on the opposite light cycle, but the time of day effect did not depend on female light cycle. No such pattern was observed for trials with females collected from singleton webs. We then assessed the effect of time of day and light cycle manipulation on female behavior by assaying patterns of foraging behavior and locomotor activity. Females from multifemale webs tended to be less aggressive toward prey at dusk, a diel change in behavior not seen in females from single female webs. These findings suggest that variation in male courtship correlates with temporal shifts in female behavior in addition to differences among females, but the adaptive value of temporal shifts in male behavior remains unclear.

**The ecology of RNAi: what do spiders have to do with it?**Kelton D. Welch<sup>1</sup>, Jonathan G. Lundgren<sup>1</sup><sup>1</sup>USDA-ARS, North Central Agricultural Research Service, Brookings, SD, USA

Insecticide science has graduated from the age of simple toxins into join the genomics revolution. The latest insecticidal products, exemplified by RNA interference (or RNAi) technology, interface directly with the pest's genome to manipulate gene expression with ostensibly species-specific precision. Unfortunately, risk-assessment science has not kept pace with insecticide developments, and it is essential that scientists and agriculturalists recognize and account for the unique ecological considerations of genomic insecticides. For example, RNAi works by silencing messenger RNA's (mRNA's), and its insecticidal applications involve silencing mRNA's with critical regulatory functions inside a pest insect's cells, with an ultimately lethal effect on the pest insect. Some organisms can amplify the RNAi effect using proteins called RNA-dependent RNA polymerases (RdRp's). Phylogenetic analyses have shown that insects lack these proteins, and it is thus commonly believed that amplification of RNAi is not an important concern. However, several arachnid genomes have been found to contain gene sequences for RdRp's, and the hypothetical potential to produce unpredictable secondary RNAi effects. Despite the very unique considerations arising from these findings, and despite the great abundance, diversity and functional significance of spiders and mites in agricultural ecosystems, arachnids have not yet been featured in RNAi risk-assessment protocols. Here, we use field collections, laboratory assays and genomic databases to aid in characterizing and understanding the unique risks posed by insecticidal RNAi products for arachnids.

### **Micronutrient consumption by female *Argiope bruennichi* affects offspring survival**

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Sexual cannibalism, when females kill and consume males, is often hypothesized to be a foraging behavior driven by female hunger. Consumption of a male has rarely been documented to increase female fecundity, which is not surprising given the small size of males in many species. Yet, recent studies have shown more subtle effects of cannibalism on hatching success and offspring performance, which could result from consumption of essential nutrients from the male body. We tested the effects of dietary essential nutrients on egg production, hatching success and offspring survival of *Argiope bruennichi*. Essential nutrients had no effect on the timing or mass of the first or second egg sac produced nor on hatching success of eggs. Yet, females provided with a small supplement of dietary essential amino acids had offspring that survived starvation longer than control females. In our study, cannibalism had no effect on offspring survival. However, the current study used lab-raised males while a previous study that found an effect of cannibalism on offspring survival used males collected in the field. Our results suggest that micronutrient consumption can have important consequences for female spider fitness. Hence, even in species with high sexual size dimorphism, small male bodies may still be a valuable nutritional resource if they provide females with dietary essential nutrients.

### **Need for speed: extremely rapid predatory strikes evolved repeatedly in trap-jaw spiders (Araneae, Mecysmaucheniidae)**

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Small animals have devised intriguing morphological and behavioral traits that allow them to capture prey, including innovative mechanisms that allow for extremely rapid movements that overcome biological constraints on muscle speed. The current study describes a trap-jaw prey capture system among tiny ground-dwelling spiders, which parallels that of some of the fastest animal movements known. Kinematic data from high-speed video reveals that there is a great variety of cheliceral ("jaw") speed within the spider family Mecysmaucheniidae, with the fastest

species being two orders of magnitude faster than the slowest species, and the fastest species attaining peak speeds of 26.5 m/s in less than 0.18 milliseconds. Molecular phylogenetic analysis reveals that extremely rapid cheliceral speeds may have evolved four times independently within the family. Using light microscopy, synchrotron-based tomography, and high-speed video, we identify the following traits as being unique to all mecysmaucheniid species, compared to the majority of spiders: trap-jaw predatory behaviors; a highly modified carapace where the chelicerae muscles are oriented horizontally; clypeal apodemes; modification of an inter-cheliceral sclerite; and trigger hairs. We also identify the structural changes unique to the four lineages that evolved extreme speeds: the clypeal apodemes and clypeus are greatly thickened and enlarged. This suite of structural and behavioral innovations may have set the stage for the parallel evolution of an extremely rapid innovative predatory strike.

### **The effects of autotomy on male-female interactions in *Pholcus phalangioides***

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Cellar spiders are frequently found living in close proximity to one another, often as male-female pairs. This could make mating more efficient, but could lead to increased competition for resources. Autotomy of a leg could further complicate intersex interactions in these pairs. We studied the effects of autotomy of a front leg on the behavior of paired *Pholcus phalangioides*. We collected spiders from basements around Janesville, WI and recorded living condition (paired or single) and instances of autotomy. Living as part of a male-female pair was common (47% of spiders) as was autotomy (18% of spiders), but only 4.5% of spiders were part of a pair and missing a leg. Intact spiders were collected and assigned to one of the following treatments: 1) both spiders intact, 2) male intact, female autotomized, or 3) male autotomized, female intact. For each trial, a pair of spiders and three crickets were placed together in a three gallon tank for twenty-four hours. Trials were digitally recorded during daylight hours. We measured change in weight, number of prey captured, activity levels and interactions between pairs. Neither weight change of males and females nor number of crickets killed by a pair differed between treatments. Highly aggressive interactions between individuals were rare, but included autotomy in two trials with one of those spiders later cannibalized. Although these results indicate that missing a leg might not have serious effects on competition between paired spiders, further analyses may tease apart more subtle variations in behavior for the different treatments.