



The American Arachnological Society

35th Annual A.A.S. Meeting

July 8 -12, 2011

Portland, Oregon

A, B and C

Dispersal biogeography: the role of dispersal in the generation of biodiversity

Authors

Institution

Ingi Agnarsson

University of Puerto Rico, Biology, San Juan, Puerto Rico

Matjaž Kuntner

Institute of Biology Slovenian Academy of Arts and Sciences, Ljubljana, Slovenia

Oceanic islands are convenient models for studying dispersal and understanding how dispersal ability relates to speciation. We discuss recent studies of three nephilid lineages in the Indian Ocean (*Clitaetra*, *Nephilengys*, *Nephila*), representing poor, intermediate, and excellent dispersers, respectively. Based on these lineages, and empirical examples from other clades, we present a simple conceptual model of dispersal biogeography predicting that species richness of lineages across archipelagos should peak at intermediate dispersal ability. We also discuss likely skew towards high richness of intermediate-poor dispersers on Wallacean (fragment) islands such as the Greater Antilles in the Caribbean, and a skew towards high richness of intermediate-excellent dispersers on Darwinian ('de novo') islands, such as Hawaii. We conclude that although the processes underlying contemporary patterns of diversity on islands are many and complex, some broad patterns can be predicted by very simple models.

The depths of divergence: A phylogenetic analysis of troglomorphic spiders in the genus *Usofila* (Araneae, Telemidae)

Authors

Institution

Tracy Audisio

Joel Ledford

Charles Griswold

California Academy of Sciences, Entomology, San Francisco, CA

Spiders in the genus *Usofila* thrive in cold, moist, dark microhabitats and are exapted for life in caves. Cave obligate, or troglomorphic, *Usofila* exhibit a suite of troglomorphic characters, however, species delimitation is problematic due to a high degree of morphological homogeneity. Although these taxa lack traditional diagnostic characters, they have evolved deep molecular divergence. The evolution of troglobionts can be explained either by the Climatic Relict Hypothesis (CRH) or by the Adaptive Shift Hypothesis (ASH). According to the CRH, troglobionts are relicts of a previously widespread fauna. A climatic shift occurred which pushed these species into caves. Alternatively, the ASH predicts a shift to the troglomorphic lifestyle prompted by resource availability. We used a combination of morphological and molecular data to assess species limits within *Usofila* and to test hypotheses for the evolution of troglobionts. Scanning electron microscopy and automontage were used to assess morphological variation, including both somatic and genitalic characters. Our molecular data is based on 28S rDNA and CO1 mtDNA from a sample of 51 individuals. Parsimony, Maximum Likelihood, and Bayesian analyses were used to estimate phylogenetic relationships and trait data were mapped on the resulting trees. Independent analysis of CO1 resulted in strong support for several terminal groups but was unable to resolve the deeper relationships. A concatenated analysis resolved the deeper relationships and

suggested that there are eight new species of *Usofila* in California and that troglobionts have evolved independently on three occasions, which is consistent with the ASH hypothesis.

High-throughput expression profiling of silk glands in the Western black widow, *Latrodectus hesperus* (Theridiidae)

Authors	Institution
Nadia A Ayoub	Washington and Lee University, Biology, Lexington, VA USA
Jessica E Garb	University of Massachusetts Lowell, Biological Sciences, Lowell, MA
Alex K Lancaster	Whitehead Institute for Biomedical Research, , Cambridge, MA USA
Cheryl Y Hayashi	University of California Riverside, Biology, Riverside, CA USA

Among silk producing organisms, spiders are unparalleled in their reliance on silk and the diversity of silk functions found both within and among species. Most spiders have multiple silk gland types with each type synthesizing a high-performance, task specific fiber or glue. For example, dragline silk, which originates in the major ampullate glands, has a tensile strength comparable to steel, and prey wrapping silk, which originates in the aciniform glands, is incredibly tough. Molecular studies of spider silks have almost entirely focused on the sequences of the component structural proteins (fibroins) and, hence, virtually all models of spider silk evolution and mechanical function are based solely on the attributes of fibroins. However, the spider silk system must involve fibroin as well as non-fibroin genes. Furthermore, the relative expression level of each of these genes, which should contribute to the diversity of spider silks, is largely unknown. We are using high-throughput sequencing to identify the major elements and their putative functions within the gene repertoire underlying silk synthesis in cob-web weaving spiders (Theridiidae), focusing on Western black widows, *Latrodectus hesperus*, and two closely related species. Preliminary results identified the fibroins and non-fibroins that are significantly more abundant in major ampullate glands compared to non-silk tissues. Furthermore, we found notable variation in the relative proportions of fibroin genes between two individuals commensurate with their readiness to build eggsacs. We will expand profiling to each of the silk gland types, and to other species, to further understand the diversification of silk functions.

The goblin spider genus *Opopaea* and its distribution pattern on the Caribbean and the Pacific Islands (Araneae: Oonopidae).

Authors	Institution
Barbara C Baehr	

The goblin spider genus *Opopaea* is a pantropical genus but only four species are widely distributed. *O. deserticola* Simon, 1891 and *O. concolor* (Blackwall, 1859) have their major distribution in Middle America especially on the Caribbean Islands whereas *O. foveolata* Roewer, 1963 and *E. apicalis* Simon, 1893 occur primarily on the Pacific Islands. *E. apicalis* is in fact an *Opopaea* species but not synonymised yet. Three new *Opopaea* species may be short range endemics and were found only on certain Pacific Islands. *O. BB127* is recorded from Fiji together with *O. foveolata* and *O. BB134* occurs on Hawaii, sympatric with *E. apicalis*. *O. BB135* closely related to *E. apicalis* is reported from the Caroline Islands sympatric with *E. apicalis* and *O. foveolata*. All Caribbean and Pacific Islands are populated by not more than three *Opopaea* species with the exception of New Caledonia which has an extremely rich *Opopaea* fauna with 15 species of which 13 species are new to science.

Reproductive output under threat of predation in the wolf spider, *Schizocosa ocreata* (Hentz)

Authors	Institution
Zeynep Benderlioglu George Keeney Andrew Roberts	The Ohio State University, Evolution Ecology and Organismal Biology, Newark, OH USA

Exposure to environmental and genetic stressors during development has adverse consequences on physical growth, physiology, and behavior of individuals. One common environmental stressor is exposure to predators. Nonhuman animals have evolved adaptive mechanisms to avoid being eaten while optimizing reproductive function during predation risk. The current project investigates maternal

exposure to predation risk and reproductive outcome in the wolf spider, *Schizocosa ocreata* (Araneae: Lycosidae). Mature *S. ocreata* females were either maintained in standard laboratory conditions (Non-Stressed; NS), or with exposure to silk and chemical cues from the generalist wolf spider predator *Hogna helluo* (Araneae: Lycosidae) for 12 days after mating (*Hogna*-Stressed; HS). Reproductive behaviors were assessed regarding eggsac production and clutch size. Results show that HS females had less variability in clutch size compared to NS females and that clutch size increased marginally. Whereas none of the HS females produced an eggsac during the 12-day stress period, NS females did so as early as 2 days after mating. Similarly, none of the HS females dropped an eggsac before reaching the minimum incubation period (28 days), whereas 50% of NS females did. All but one female in each group produced at least a second eggsac from the single mating trial. However, only those from HS females resulted in surviving offspring. Our results suggest that exposure to predation risk during egg development increases reproductive performance in *S. ocreata* and is associated with enhanced fitness as evidenced by increased clutch size and offspring survival.

Messing with morphogenesis in early spider development

Authors	Institution
Steve Black Christine Bates Kay Larkin Molly Radany Crystal Chaw	Reed College, Biology, Portland, OR USA

Two large-scale cell migrations occur during early spider development, and only spider embryos do them both. The first is the migration of a small cluster of cells, the cumulus, from the center to the edge of the germ disc. We labeled the cumulus cells with fluorescent dye and determined that their fate is opisthosomal, probably gut diverticula. Next, we experimentally tested whether or not the cumulus is required for normal development by surgically removing the cumulus cells in *Zygiella x-notata* embryos. The operated embryos develop grossly defective germ bands, confirming an important signaling role for the cumulus cells. The second large-scale cell migration occurs days later, at the germ band stage, and is called inversion. Inversion occurs when the germ band splits down the ventral midline and the left and right halves migrate away from each other. We find that inversion proceeds normally in *Z. x-notata* embryos if the yolk cell is poisoned, suggesting that the 'motor' for inversion is in the germ band itself. We think that cell division is part of the motor, because experimentally inhibiting cell division blocks inversion.

Protein intake as a constraint on spider silk expression.

Authors	Institution
Sean J Blamires Chun-Lin Wu I-Min Tso	Tunghai University, Life Science, Taichung, Taiwan

An understanding of the various constraints on spider silk synthesis would assist in devising mechanisms for producing high performance silk analogues. The spidroins that make up spider major ampullate (MA) silk, MaSp1 and MaSp2, differ in proline content. Proline is energetically expensive to synthesize so it might be preferential for spiders that express high proline MaSp2 predominant silk to get most of their proline from food and switch MaSp expression when protein intake is low.

We fed three orb spiders; *Argiope aetherea*, *Cyrtophora moluccensis* and *Leucauge blanda*, high protein (HP), low protein (LP) or no protein (NP) solutions. *A. aetherea* and *L. blanda* MA silks predominantly are principally comprised of the high proline MaSp2, while *C. moluccensis* MA silks are low in proline. After 10 days of feeding, silk amino acid compositions and mechanics were analyzed. The proline and glutamine compositions of *A. aetherea* and *L. blanda* silks decreased with protein intake, while amino acid compositions were less affected by protein intake in *C. moluccensis* silks. The expression of MaSp2 silks thus is constrained by protein intake. Protein intake indirectly affected silk strength and extensibility via proline content.

The switch from expressing silks of predominantly MaSp2 to expressing silks of predominantly MaSp1 by *A. aetherea* and *L. blanda* when protein intake was reduced is indicative of a protein intake constraint over silk expression. The low proline silks of *C. moluccensis* are however relinquished of this protein intake constraint. Most orb web spiders have MA silks of a high proline composition because expressing MaSp2 endows their webs extensibility. Spiders that build three dimensional webs however express MaSp1 predominant silk and are free of the protein constraint. We propose that alleviation of the protein constraint may be an evolutionary force driving spider web three-dimensionality.

Variation among individuals and life stages of *Araneus diadematus* in ultraviolet-induced fluorescence

Authors

Institution

Erin E Brandt

Portland State University, Biology, Portland, OR USA

Susan E Masta

Spiders have previously been shown to possess externally-expressed fluorescence. Different species of spiders were found to vary in the degree to which adult females fluoresced under ultraviolet light. However, it is not known whether fluorescence expression varies over the course of a spider's life, or among individuals within a species. We developed new equipment and techniques to more precisely induce and quantify fluorescence intensity. We are currently quantifying ultraviolet-induced fluorescence of *Araneus diadematus* across each of its life stages. Spiders from different clutches and different molt stages were illuminated with different wavelengths of ultraviolet light. We chose wavelengths that are present in the sun's spectrum and to which *A. diadematus* is commonly exposed. Images were captured with a digital camera, and pixel intensity was analyzed. We discuss the variation in fluorescence intensity within a molt stage among different clutches, and between molt stages.

How spiders avoid sticking to their own webs: clever leg movements, branched drip-tip setae, and anti-adhesives

Authors

Institution

Daniel Briceo

Smithsonian Univ Costa Rica, Biologia, San Jose, Costa Rica

William G Eberhard

Orb-weaving spiders construct webs with adhesive silk, but are not trapped by it. Previous studies have attributed this immunity to an oily coating on their legs that protects against adhesion or, more recently, to behavioral avoidance of sticky lines. But behavioral avoidance is not an explanation, because an orb-weaver pushes with its hind legs against sticky lines hundreds or thousands of times during the construction of a single orb and is not trapped. Video analyses of behavior and experimental observations of isolated legs contacting and pulling away from sticky lines showed that the spider reduces adhesion with an anti-adhesion chemical coating, a dense array of branched setae on the legs that reduce the area of contact with adhesive material, and careful engagement and withdrawal movements of its legs that minimize contact area with the adhesive, and avoid pulling against the line itself.

Phylogeny-based comparative analyses of sex-specific reproductive characters in the North American leiobunine harvestmen (Opiliones: Sclerosomatidae)

Authors

Institution

Mercedes Burns

University of Maryland, Entomology, College Park, MD USA

Jeffrey W Shultz

Marshal Hedin

San Diego State University, Biology, San Diego, CA USA

Sexual conflict is frequently put forth as an alternative to female choice in explaining genitalic diversity, but such proposals rarely include the historical information necessary to identify sexual arms races. We hypothesize that sexual arms races in the eastern North American leiobunine harvestmen are initiated when males alter their mating strategy from one dominated by enticement (nuptial-gift-bearing sacculate penes) to one dominated by coercion (non-sacculate penes); females then respond by evolving a defensive pre-genital barricade. Here we use parsimony and likelihood-based methods to assess whether the probability of the co-occurrence of the lanceolate penis and female barricade is significantly greater than chance and whether evolution of lanceolate penes before female barricades is more likely than alternatives. Our results show that the lanceolate male penis type is tightly correlated to the presence of a female pregenital barrier. However, because the relevant state changes always occur along the same branches and are currently represented by discrete characters, these methods cannot determine the order in which these two traits evolved. We conclude by discussing our results in terms of their implications for phylogeny-based comparative analysis of sexual arms races.

Evidence for the role of experience and social density on eavesdropping and social facilitation of courtship in male *Schizocosa ocreata* wolf spiders (Lycosidae)

Authors

Institution

David L Clark

Alma College, Biology, Alma, MI

Andrew Roberts
Corrina Kizer
Shira Gordan
George W Uetz

The Ohio State University, Evolution Ecology and Organismal Biology, Newark, OH USA

University of Cincinnati, Biological Sciences, Cincinnati, OH USA

Male spiders might reduce costs of finding females by “eavesdropping” and initiating sexual displays whenever male courtship is detected (i.e., social facilitation). A previous study found no evidence for eavesdropping in *Schizocosa ocreata* (Hentz), but involved spiders that matured in lab isolation (without exposure to behavior of adult conspecifics). In this study, males collected from the field as adults demonstrated behavior consistent with eavesdropping, i.e. increased interactive and courtship behaviors during and after video playback of a courting male stimulus. In contrast to previous findings, field-collected males showed a significantly longer duration of interactive behaviors and significantly more bouts of courtship activity when the video male stimulus was present on the video screen. Courtship rates of focal males were positively correlated with rates of courtship in video stimuli. Choice tests with two video screens showed that males recognize differences in male behavior, and respond to video stimuli of courting male wolf spiders more often and for a longer time than walking males or an empty leaf litter background (no spider). Additional studies with both live males and video playback showed that males exhibited significantly more time in courtship displays when presented with 2-3 additional males or male video stimuli simultaneously. Male responses to vibration signals from other males also varied with the presence/absence of female silk. Together, these findings suggest that experience arising from field exposure to adult conspecifics, along with additional variables such as competitor density and female chemical cues may impact male eavesdropping behavior and social facilitation.

Paternity patterns in the giant wood spider *Nephila pilipes* (Araneae: Nephilidae)

Authors	Institution
Nina Cole	University of Michigan Dearborn, Biology Discipline Natural Sciences Dept, Dearborn, MI USA
ChuehEmma Hou I-Min Tso	Tunghai University, Life Science, Taichung, Taiwan
Anne Danielson-Francois	University of Michigan Dearborn, Biology Discipline Natural Sciences Dept, Dearborn, MI USA

Sperm competition occurs when females mate with multiple males and rival sperm compete to fertilize ova. In spiders, the outcome of sperm competition is thought to be influenced by female reproductive anatomy, such that haplogyne species favor the last male to mate and entelegyne species favor the first male to mate. We studied the entelegyne spider *Nephila pilipes* (Fabricius) in the field and the laboratory to determine its mating behavior and paternity pattern. Due to the reproductive structure of the female, we expected that the first male to mate would have the highest paternity. Approximately one hundred female and two hundred male *Nephila pilipes* were collected in secondary forests in Taiwan. Controlled matings took place at Tunghai University, Taiwan where females were randomly mated to two males, one of which was irradiated using the sterile-male technique. Mated females were transported to the University of Michigan and were cared for until eggs were laid. Our findings indicate that the first male to mate will not sire the most offspring as predicted, instead the amount of sperm transferred is a better predictor of paternity patterns in this species.

Transcriptomics of exuberantly color polymorphic *Theridion* species (Araneae: Theridiidae).

Authors	Institution
Peter J Croucher Geoff S Oxford Rosemary G Gillespie	University of California Berkeley, Environmental Science Policy and Management, Berkeley, CA USA

Parallel evolution of complex traits provides some of the most remarkable examples of evolution through natural selection. Among spiders, an interesting example of this phenomenon is provided by the demonstration among distantly related members of the Theridiidae of complex color polymorphisms consisting of multiple combinations of yellow, red and black dorso-abdominal pigmentation that are considered to consist of ommochromes. In all studied species evidence suggests that the polymorphism is maintained by balancing selection. Given the similarity among phenotypes, and the presumed role of selection, the question is: How and to what extent is the similarity due to independent evolution on non-homologous pathways, versus differential expression of homologous pathways. In order to understand the molecular basis of this parallel evolution of color polymorphism and generate a battery of spider genomic resources, we have used Illumina next-generation sequencing technology to reconstruct the transcriptomes of the two highly polymorphic spiders *T. californicum* and *T. grallator* and the genome of *T. grallator*. Here we focus on the assembly and annotation of tens of thousands of *T.*

californicum gene transcripts and the identification of expressed color-pigment metabolic pathways. Results to date have given intriguing insights into numerous homologies across the genome, as well as allowing characterization of a surprisingly rich endo-symbiotic/parasitic community including nematodes and bacteria. Most importantly, we have identified key enzymes in a variety of pigment pathways, including ommochrome, pteridine, papiliochrome, heme and possibly melanin; suggesting that the potential array of pigments available to these spiders may be far greater than previously believed.

Solifugae: exploring the systematics and biology of a little known order of arachnids

Authors	Institution
Paula E Cushing	Denver Museum of Nature and Science, Zoology, Denver, CO USA
Tharina L Bird	Texas AM University, Entomology, College Station, TX
Robert Wharton	American Museum of Natural History, Division of Invertebrate Zoology, New York, NY USA
Jack O Brookhart	
Warren Savary	
Lorenzo Prendini	

Solifugae, the sixth most diverse order of arachnids, are dominant predators in arid ecosystems on most major terrestrial landmasses. Despite their diversity, worldwide distribution, ecological importance, and fascinating morphology, behavior and life history, research on these arachnids has advanced little in 50 years. Many aspects of solifuge biology remain unknown, their taxonomy is in disarray, and an average of only five publications on the order appears annually.

In 2007, Paula Cushing (Denver Museum of Nature & Science) and Lorenzo Prendini (American Museum of Natural History) were awarded a 5-year Biodiversity Surveys and Inventories grant from the U.S. National Science Foundation to study Solifugae. The objectives of this grant were to: 1) conduct a phylogenetic analysis and revise the suprageneric classification of the order based on morphological and DNA sequence data; 2) conduct several family-level taxonomic revisions within the order, also based on morphology and DNA; 3) survey, discover and describe species in the regions of highest solifuge diversity; 4) create a collaborative network of solifuge specialists; 5) train new specialists; and 6) develop a website with an online specimen database, bibliography and information about Solifugae and solifuge researchers.

During this presentation we will provide a report on the project including: a preliminary molecular phylogeny of the order supporting the monophyly of many currently recognized families; a discussion of morphological character systems identified as phylogenetically informative for Solifugae; an update on revisions of the North American Eremobatidae and the African Solpugidae; a summary of results from projects exploring the diversity, internal and external morphology, biology, and behavior of solifuges; and an overview of the web-resources developed at www.solpugid.com.

D,E and F

Genetic diversification without obvious genitalic morphological divergence in harvestmen (Opiliones, Laniatores, *Sclerobunus robustus*) from montane sky islands of western North America

Authors	Institution
Shahan Derkarabetian	Portland State University, Biology, Portland, OR USA
Joel Ledford	California Academy of Sciences, Entomology, San Francisco, CA
Marshal Hedin	San Diego State University, Biology, San Diego, CA USA

The harvestmen *Sclerobunus robustus* is a cryophilic species, composed of two subspecies, restricted to the montane forests distributed discontinuously across southwestern North America. Given the topological complexity and extensive geologic activity of this area, regional taxa are expected to show some degree of morphological and genetic divergence, especially if found on the southern montane 'sky islands'. Here we examine the phylogeographic history and diversification of *Sclerobunus robustus* using a combination of genetic and morphological data. The most widespread subspecies, *S. robustus robustus*, is recovered as six genetically distinct, geographically cohesive mitochondrial phylogroups. Gene tree data for a single nuclear gene reveals congruent, albeit slightly more conservative, patterns of genetic divergence. Divergence time estimates indicate that much of the diversification within and between major phylogroups predate the Pleistocene glacial cycles. Despite high levels of genetic divergence throughout their distribution, phylogroups show extreme conservation in somatic morphology and electron microscopy reveals no differentiation in male reproductive morphology. This uncoupling of morphological and genetic differentiation may be caused by morphological conservatism associated with a conserved microhabitat preference. Based on these data, it is obvious that *S. robustus* has undergone some level of cryptic diversification.

Developing an optimal Rapid Assessment Protocol for ground-accessible macro-invertebrates.

Authors

Institution

Michael L Draney

University of Wisconsin-Green Bay, Department of Natural Applied Sciences, Green Bay, Wisconsin

Development of a Rapid Assessment Protocol (RAP) is an exercise in optimizing two antagonistic goals: Efficiency and statistical rigor. RAP's in wide use by arachnologists today are highly efficient means of accumulating species records at a site, but comparison of data between sites or over time is problematic for at least three reasons. First, lack of randomized replication, which allows statistical comparisons of response variables across sites or over time. Second, lack of a standard sampling effort and standardized area sampled, both of which may have a large effect on total assemblage richness. Third, lack of a standard plot size sufficient to integrate microhabitat variation but small enough to ensure intensive sample effort. I have been developing an RAP that incorporates these critical experimental design features while sacrificing as little efficiency as possible. The protocol is designed so that two or more collectors, including inexperienced collectors, can take a standardized set of samples for one site in one reasonable work day. The ground-accessible fauna of any trail-accessible, walkable site of at least 50 x 50 m (0.25 ha) is sampled by intensive collection of at least three circular 0.01 ha plots randomly located on an easily surveyed grid plan. Each plot is sampled by two time-constrained methods: one hour of vegetation sampling and two hours of rapid field sieving of leaf litter. This RAP was specifically developed to enable one-day comparative sampling of tropical forest sites, but is also being tested in a variety of temperate habitat types.

Demographic influences on dispersal in the newly dominant cellar spider, *Pholcus manueli* (Pholcidae)

Authors

Institution

Jonathan D Edwards

Miami University, Zoology, Oxford, OH USA

Ann L Rypstra

Miami University, Zoology, Hamilton, OH USA

The cellar spider, *Pholcus manueli* (Araneae, Pholcidae), has recently expanded its range in North America and is now abundant and successful throughout the Midwest. However, little is known about its biology and especially factors that might influence its dispersal. In laboratory and field manipulations, we explored the effects of sex ratio and density on dispersal of both males and females. In a laboratory experiment we manipulated the perceived sex ratio by placing six uninhabited recently constructed webs in the center of a large terrarium. Webs in each treatment were constructed either by all females or all males. A spider was placed in the center and allowed 24 hrs to either stay in the center of the arena (remain) or occupy the peripheral area (disperse). Using a logistic regression to analyze these data, both males and females reacted in a similar way to the webs based on the sex of the web builders with a significant avoidance of the male webs ($p=0.005$). In a field study, we established populations with two densities and with contrasting in enclosures and then removed the enclosure and monitored their dispersal. After running a proportional hazards analysis on these data neither sex ratios nor density had an effect on the proportion of each sex dispersing. However, by using a log linear analysis, the sex bias of the treatment did affect dispersal frequency of each sex. Therefore, movement of these spiders between patches is caused, at least in part, by the demography of the population, which may help explain why these animals are expanding their range into areas recently held by a congeneric, *Pholcus phalangioides* (Araneae, Pholcidae).

The first North American records of the synanthropic spider *Cithaeron praedonius* O. P.-Cambridge (Araneae: Gnaphosoidea: Cithaeronidae), with notes on its biology

Authors	Institution
G B Edwards	Florida State Collection of Arthropods, Division of Plant Industry, Gainesville, Florida, USA
Joe T Stiles	Saint Leo University, Information Technologies, Saint Leo, Florida, USA

Cithaeron praedonius O. P.-Cambridge 1872 is an Old World species with a distribution from Libya and Greece to Malaysia and Australia. In the New World, it was recently found in Brazil, and is now reported for the first time in North America, in the United States, State of Florida. Multiple individuals of both sexes and various life stages, including multiple eggsacs, have been found in a home in Port Richey, Pasco County. An adult female was found on the outside wall of the house feeding on another spider, suggesting that *C. praedonius* are no longer contained as a spot introduction in this one house. Observations in captivity indicate that this species may prefer feeding on other spiders. The eggsac and molting nest are described for the first time, and records on fecundity reported.

Adaptive foraging in orb-weaving spiders: predicting adaptive changes in web structure in response to change in hunger level using a computer simulation model.

Authors	Institution
Samuel C Evans Todd A Blackledge	University of Akron, Biology, Akron, OH USA

Orb-weaving spiders rebuild their webs daily using a finite volume of silk, which scales positively with spider body mass, as does the energy absorption potential of the silk threads. The "large, rare prey hypothesis" dictates that spiders build webs that maximize the probability of securing large-but-rarely-encountered prey, which are essential to the spider's reproductive success. However, this likely involves concentrating the allotment of silk in a web of smaller planar area, which lowers the prey-web encounter rate. Therefore, there is an apparent trade-off between prey-web encounter rate and web performance. Spiders that have not recently secured a sizeable meal, and are therefore close to starving, might benefit from a "bet-hedging" strategy of increasing web size to increase prey-web encounter rate, while spiders that are further away from starvation benefit more from gambling with a smaller web that is more effective at securing a large prey item. Therefore, we hypothesize that spiders can adaptively alter web size in response to change in proximity to starvation ("hunger level"). To generate predictions based on this hypothesis, we have constructed a computer simulation model. Prey capture is a three-step process: the web must 1) contact, 2) stop, and 3) retain the prey item. Our model calculates a probability of success in each of these three steps; the product of these probabilities is the probability of prey capture. This process is repeated over thirty days, or until the spider starves, and the growth rates and survival frequencies are compared among spiders using different strategies. Model predictions and planned empirical tests will be discussed.

Arachnid Recovery of Mount St. Helens

Authors	Institution
Katherine M Fiedler Greta J Binford Charlie M Crisafulli	Lewis & Clark College, Biology, Portland, OR USA

The 1980 eruption of Mount St. Helens has served as a living ecological laboratory to examine the recovery of different communities and entire ecosystems. A comparison of arachnid species diversity and community composition over time (1990, 2000, and 2010) and across a scale of disturbance sites (reference forest, tephra forest, blowdown forest, and pumice plain) shows different trajectories of recovery. These comparisons can be made through species identification of individuals collected in pitfall trap samples, as well as feeding guild and habitat distinctions. Disturbed sites have provided ecological niches unavailable in the pre-eruption old growth forests. Furthermore, non-native desert species (e.g. *Xysticus cunctator*) and invasives (e.g. *Phalangium opilio*) have been able to take advantage of early successional landscapes. This examination of arachnid recovery can contribute to an understanding of the overall recovery of these ecosystems.

[Go to the top of the page](#)

G,H and I

Sperm release patterns in two species of funnel-weaving spiders (Agelenidae)

Authors	Institution
Sabah Gagnon Samaa Lutfi Anne Danielson-Francois	University of Michigan Dearborn, Biology Discipline Natural Sciences Dept, Dearborn, MI USA

Sperm competition can occur when females mate with more than one male. Males that transfer more sperm than their rivals are more likely to father more offspring when sperm competition is present. We studied the sperm release patterns of two species of funnel-weaving spiders, *Agelenopsis pennsylvanica* and *Agelenopsis longistyla* (Agelenidae). Penultimates were collected and reared in the laboratory. To observe sperm transfer, staged matings between virgins were conducted in the laboratory. Males were frozen immediately after mating. The amount of sperm remaining in pedipalps and the amount transferred to the female were measured. We found the two species had different patterns of sperm transfer. In general larger males had more sperm than smaller males, suggesting that larger males have an advantage in sperm competition.

A preliminary investigation of the black widow spider venom transcriptome using next-generation sequencing.

Authors	Institution
Jessica E Garb	University of Massachusetts Lowell, Biological Sciences, Lowell, MA
Nadia A Ayoub	Washington and Lee University, Biology, Lexington, VA USA
Alexander K Lancaster	Whitehead Institute for Biomedical Research, , Cambridge, MA USA
Cheryl Y Hayashi	University of California Riverside, Biology, Riverside, CA USA

Animal venoms play a central role in deciphering vertebrate physiology and are essential resources for the development of novel pharmaceuticals and lifesaving antivenoms. Venoms also have significance for understanding biochemical variability as they exhibit many textbook cases of molecular evolution, including unusually high mutation rates, radiation of multi-gene families, molecular convergence, lateral gene transfer and gene-level co-evolutionary arms races. Despite the tremendous biological importance of animal venoms, knowledge of their molecular composition is surprisingly limited in relation to the variety of venoms in nature. We are using next-generation sequencing technology to examine the composition, diversity and evolution of black widow spider venom. To catalog venom gland expressed genes, we have generated an Illumina RNA-seq library from venom glands of the Western black widow spider (*Latrodectus hesperus*), resulting in many thousands of novel sequences. The Illumina sequence assembly will be compared to sequences from traditional venom cDNA libraries, in addition to Illumina RNA-seq libraries from other *L. hesperus* tissues to investigate venom transcriptome complexity, as well as to identify genes exhibiting venom-specific patterns of expression. Our preliminary results will be expanded across related species to identify key changes in venom composition associated with the evolution of the highly potent black widow spider venom.

Adaptive radiation on remote islands: Comparison of diversification across the remote archipelagos of Polynesia

Authors	Institution
Rosemary G Gillespie	University of California Berkeley, Environmental Science Policy and Management, Berkeley, CA USA

The Pacific Ocean contains more islands than the rest of the world's oceans combined. The most remote high islands are those of Polynesia, notably the Hawaiian Islands, and the three archipelagos of French Polynesia: the Society, Marquesas, and Australs. Each of these archipelagos is a hotspot, with islands arranged chronologically from the south east. While patterns of adaptive radiation are relatively well known in Hawaii, comparable patterns in the other archipelagos of Polynesia are less well known. Here I will compare patterns of diversification of spider lineages across the archipelagos to assess the similarity in species, pattern and rate of diversification, and dynamics of community assembly. The Societies show high endemism, in particular on the youngest high island of Tahiti, with the genus *Tetragnatha* a prominent element of the spider biota at both high and middle elevations; relationships appear to be horizontal, with cloud forest species closely related to each other. The Marquesas show high endemism, with *Tetragnatha* again a prominent element, the highest diversity being on the older islands. The Austral Islands are an older, smaller, and lower archipelago; here, the dominant lineages are *Tangaroa tahitiensis* (Uloboridae) and *Misumenops rapaensis* (Thomisidae). These taxa are endemic to the archipelago rather than an individual island, yet there are large genetic distances between island populations, with sequential colonization of islands. Compared to Hawaii, diversification is less pronounced, and community assembly on the youngest island matches to the second youngest island of the Hawaiian chain.

Comparative phylogeography of three Great Basin scorpions: further insight into the biotic assembly of North America's cold desert

Authors	Institution
Matthew R Graham Jef R Jaeger Brett R Riddle	University of Nevada Las Vegas, School of Life Sciences, Las Vegas, NV USA
Lorenzo Prendini	American Museum of Natural History, Division of Invertebrate Zoology, New York, NY USA

The biotas of the Great Basin Desert of western North America were continuously altered by Pleistocene climate cycles. Since the Last Glacial Maximum (LGM) about 21 kya, Great Basin climates have warmed considerably, resulting in expansions of arid environments and contractions of cooler shrub-steppe habitats. Distributions of terrestrial taxa within these habitats are typically thought to have shifted accordingly, but recent evidence from vertebrates (reptiles, mammals) suggests that responses to historical climate change in the Great Basin were not always congruent across co-distributed taxa. We first constructed current and Late Glacial species distribution models (SDMs) for three distantly related scorpion species (*Anuroctonus phaidactylus*, *Hadrurus spadix* and *Paruroctonus becki*) to model their distributional responses to the LGM to Holocene climate transition. Model results were largely congruent, predicting northward expansion from southern areas of warmer climate following the LGM. We then tested this hypothesis by analyzing genetic and morphological data. In accordance with SDM predictions, all species depicted high genetic and morphological diversity in southern areas and lower diversity in northern areas. The patterns, however, indicated that these scorpions may have expanded their ranges from populations within the Great Basin (in the Lahontan and Bonneville basins), as well as from more southern populations as predicted by the SDMs. These preliminary results add scorpions to a growing array of vertebrate and invertebrate Great Basin species whose gene diversity demonstrates a more complex response to the LGM to Holocene climate transition than is revealed by SDMs.

On a fascinating new haplogyne spider from Southern Oregon caves

Authors	Institution
Charles Griswold Joel Ledford Tracy Audisio	California Academy of Sciences, Entomology, San Francisco, CA

A recent survey of caves in Southern Oregon has discovered a fascinating new haplogyne spider that cannot be confidently assigned to any known family. We provide an overview of this spider's unique morphology and discuss alternatives for its phylogenetic placement.

Chthonioid pseudoscorpions: a phylogenetic analysis based on morphology

Authors	Institution
---------	-------------

Mark S Harvey

Western Australian Museum, Terrestrial Zoology, Perth, Western Australia, Australia

The pseudoscorpion superfamily Chthonioidea is well defined and seemingly monophyletic based on previously published morphological and molecular datasets using multiple markers. However, the higher classification is not settled with several alterations over the past two decades. To assist resolve these issues, a phylogenetic analysis was performed using 150 chthonioid species placed in 38 of the 48 recognised genera. Parsimony analyses under equal weights provided little phylogenetic resolution. Implied weights analyses drastically improved the resolution of the trees and, in all analyses, Pseudotyranochthoniidae were sister to the remaining chthonioids. In both equal and implied weights analyses, the taxa currently included in the families Tridenchthoniidae and Lechtyiidae grouped strongly with the chthoniid genera *Sathrochthonius* and *Sathrochthoniella*. Of the remaining taxa, low concavity functions distinguished three other clades, Chthoniini, Tyrannochthoniini and the "apochthoniines" (Apochthonius + Kleptochthonius). Higher concavity functions retained Tyrannochthoniini and the "apochthoniines", but divided Chthoniini into multiple clades. Proposed changes to the classification of the Chthonioidea are discussed.

Enigmatic ornamentation eases male reliance on courtship performance for mating success

Authors

Institution

Eileen A Hebets

Jay A Stafstrom

Rafael L Rodriguez

Dustin J Wilgers

University of Nebraska, School of Biological Sciences, Lincoln, NE USA

Female preferences are frequently invoked to explain the widespread occurrence of elaborate male ornaments, yet empirical data demonstrating such preferences are sometimes equivocal or even contradictory. In the wolf spider, *Schizocosa stridulans*, despite evidence of strong female choice, prior research has been unable to link the conspicuous sexually dimorphic foreleg ornamentation of males to their mating success. We conducted three experiments aimed at determining the function of this previously enigmatic ornamentation. Our first two experiments used males with phenotypically modified foreleg phenotypes in simple and complex mating environments in order to examine the relationship between the presence/absence of ornamentation and male mating success. In both experiments, we found no relationship - courtship rate was the sole predictor of mating success. In a third experiment, we used males with naturally varying foreleg ornamentation in mating trials. Ornamentation was subsequently quantified and we again examined the factors influencing male mating success. As in our first two experiments, we found courtship rate to be a good predictor of mating success. Additionally, we discovered that foreleg ornamentation and courtship rate interact to influence male mating success. At low courtship rates, males with more foreleg ornamentation have a mating advantage, while at high courtship rates males with less foreleg ornamentation have a mating advantage. We discuss several potential explanations for these results. In summary, we provide the first evidence of a benefit of foreleg ornamentation in male *S. stridulans* and suggest that this benefit is realized by the interaction between ornamentation and courtship rate.

Harvestmen Transcriptomics

Authors

Institution

Marshal Hedin

Axel Schoenhofer

Sajia Akhter

James Starrett

Jeffrey W Shultz

San Diego State University, Biology, San Diego, CA USA

San Diego State University, Computer Science, San Diego, CA

University of California Riverside, Biology, Riverside, CA USA

University of Maryland, Entomology, College Park, MD USA

Next generation sequencing (NGS) technology can now be used to efficiently characterize previously unknown genomes from non-model taxa. This flood of data, in combination with new multigenic analytical methods, is transforming the field of molecular systematics. We have collected transcriptome data (NGS characterization of the transcribed portion of the genome from mRNA) for multiple Opiliones species representing three of four major harvestmen lineages. For each taxon we generated gigabase quantities of data using Illumina short-read NGS technology, and successfully conducted de novo assemblies of these data. The comparative assembled data have multiple possible uses – our initial focus centers on the development of PCR primers for multigenic phylogenetics. For relatively ancient divergences we have targeted protein-coding genes that are "single copy, single exon" genes in *Ixodes* (only available annotated arachnid genome). The harvestmen transcriptomes include hundreds of such genes (most nearly full-length with high coverage); we report on primer design and testing for a subset of these genes. For more recent divergences we are developing EPIC (exon-primed intron-crossing) primers, targeting genes known to have introns with conserved position in other arthropod taxa. Again, hundreds of suitable candidates are found in our comparative Opiliones transcriptomes.

Morphological analysis of montane scorpions (*Vaejovis*) in Arizona

Authors	Institution
Garrett B Hughes	University of Arizona, Entomology and Insect Science, Tucson, Arizona, USA

Several scorpions of the genus *Vaejovis* in Arizona are restricted in range to mountain top forests. These scorpions, informally referred to as the “*vorhiesi* complex” are very similar morphologically, but their geographic distribution has attracted the attention of several researchers, resulting in the description of a few new species in recent years. However, these species were described from small sample sizes and were diagnosed with questionable characters that were not sufficiently analyzed. This study evaluates the morphology of scorpions of the “*vorhiesi* complex” from seven regions in Arizona to verify the validity of the species and their accompanying diagnoses. Morphological characters examined include morphometrics, hemispermatophores, size and shape of subaculear tubercles of the telson vessicle, pectinal tooth counts, pedipalp chela denticle counts, metasomal setal counts, development of metasomal carinae, and tarsal spinule counts. New diagnoses are given for previously described species (*V. vorhiesi* Stahnke 1940; *V. lapidicola* Stahnke 1940; *V. paysonensis* Soleglad 1973; *V. cashi* Graham 2007; and *V. deboerae* Ayrey 2009), which are considered valid, based on the morphological evidence gathered. A new species of *Vaejovis* is described from the Piñaleno Mountains in Arizona.

J,K and L

Evolutionary dynamics of social structure in the polyphenic spider *Anelosimus studiosus* (Araneae: Theridiidae)

Authors	Institution
Thomas C Jones Nathan O Weber Brent J Linville	East Tennessee State University, Biological Sciences, Johnson City, TN

In east Tennessee *Anelosimus studiosus* occur in both solitary and social colonies. Solitary colonies are predominant, with social colonies tending to be found in isolated clusters around the range. Previous work demonstrates that social tendency is a heritable trait, and that in cooler microclimates there is a selective advantage to females in small colonies. A remaining question is: if there is an advantage to the social phenotype, why are social colonies rare in the population. One hypothesis is that social colonies are a recently evolved phenomenon, perhaps coinciding with water impoundments over the last century. Another hypothesis is that negative frequency-dependent selection selects against the social phenotype when colonies grow too large for the environment to support. We present molecular results suggesting that local clusters of social colonies evolved independently several times, and demographic data that are consistent with frequency-dependent (boom/bust) dynamics.

Evidence for biological control of the Russian wheat aphid with spiders in winter wheat

Authors	Institution
Lauren M Kerzicnik Eric C Chapman James D Harwood	University of Kentucky, Department of Entomology, Lexington, KY USA
Frank B Peairs	Colorado State University, Department of Bioagricultural Sciences and Pest Management, Fort Collins, CO USA
Paula E Cushing³	Denver Museum of Nature and Science, Zoology, Denver, CO USA

The Russian wheat aphid, *Diuraphis noxia* (Hemiptera: Aphididae) is a significant pest of wheat agroecosystems in the United States. Establishing appropriate predator-prey linkages is important for the conservation biological control of pests within these systems. We used gut-content analysis through PCR as a minimally disruptive technique to describe the connection between two spider species, *Tetragnatha laboriosa* and *Pardosa sternalis*, and *D. noxia*. A partial 1146 bp sequence from the mitochondrial cytochrome oxidase I (COI) gene was used to amplify a species-specific 227 bp fragment of *D. noxia* DNA. We tested the hypotheses that both *T. laboriosa* and *P. sternalis* densities and predation on *D. noxia* would be highest at the highest aphid infestation level in the aphid-resistant wheat cultivar plots. Over 92% of *T. laboriosa* were collected at the 1x or 10x *D. noxia* infestation levels combined, demonstrating that *T. laboriosa* was tracking *D. noxia* densities. Additionally, *P. sternalis* predation on *D. noxia* increased with increasing aphid infestation levels. Feeding trials indicated that *T. laboriosa* and *P. sternalis* molecular half-lives for *D. noxia* DNA were 4.0 h and 2.0 h, respectively. 32% and 48% of field-collected *T. laboriosa* and *P. sternalis* spiders screened positive for the presence of *D. noxia* DNA, respectively. These results suggest that both *T. laboriosa* and *P. sternalis* are essential natural enemies for reducing *D. noxia* densities.

The effect of habitat manipulation on spider distribution and predation of viruliferous aphids

Authors

Institution

Katelyn A Kowles
Douglas W Johnson
James D Harwood

University of Kentucky, Department of Entomology, Lexington, KY USA

Aphids are pests of multiple cropping systems, due to the viruses they vector and the staggering populations they can build within a single season. In Kentucky winter wheat, grain aphids (*Rhopalosiphum padi*, *Sitobion avenae*) cause substantial yield loss as vectors of Barley Yellow Dwarf virus (BYDV), prompting multiple insecticide applications. They transfer the virus from infected to healthy plants as they feed, causing discoloration, stunted growth and sterility. Importantly, these aphids are preyed upon by foliage dwelling predators and, when they fall to the ground, epigeal spiders which play a major role in preventing re-colonization of the plant. This project examines the effect of habitat manipulations, specifically weed strips, on spider distribution and predation in winter wheat fields. Four fields, approximately one acre each, were divided into two treatments: one with two weed strips on opposing sides, and one with no weed strips. Aphids, spiders, generalist predators and plants were sampled over the course of the season, and enzyme linked immunosorbent assay (ELISA) was used to test for BYDV throughout this food web. Additionally, spatial analysis was undertaken to observe the distribution of the spiders in the fields and also relative to the weed strips. The results are discussed in the context of conservation biological control, as this project aims to use spiders and other generalist predators as more sustainable management approaches for pest control.

Firefly Flashing and Jumping Spider Behavior

Authors

Institution

Skye M Long
Sara Lewis
Leo Jean-Louis
George Ramos
Jamie Richmond

University of Massachusetts Amherst, Organismic Evolutionary Biology, Amherst, MA USA

Elizabeth Jakob

University of Massachusetts, Psychology, Amherst, MA USA

Bioluminescent flashing in fireflies, which is primarily a sexual signal, is known to deter some predators while attracting others. We tested whether flashing serves an antipredator function against the jumping spider, *Phidippus princeps*. Because spiders are likely to encounter resting fireflies during the day, we first documented that disturbed adult fireflies (*Photuris* sp.) flash in daylight. We then conducted three experiments to examine the influence of flashing on spider behaviour. (1) We tested whether attacking spiders were startled by the sudden onset of a flashing light by securing crickets next to an LED. Spiders attacked crickets regardless of whether the light flashed or not. (2) Using choice tests we determined whether flashing lights attracted or deterred spiders from attacking prey. Spiders more often attacked crickets next to a flashing LED versus an LED that was either off or glowed steadily. (3) Many firefly species are distasteful, and therefore we tested whether flashing lights facilitate avoidance of unpalatable prey with experience. We compared how attack rates changed after seven encounters with unpalatable prey associated with either flashing or unlit LEDs. Spiders in the two treatments were equally likely to attack the prey during their first encounter, but spiders exposed to flashing LEDs were significantly less likely to attack unpalatable prey by their seventh trial. We conclude that bioluminescent flash signals may increase attack rates by predatory jumping spiders, but may also facilitate learning about unpalatable prey. Thus, the costs and benefits of flashing will depend on the prevalence of firefly palatability.

Diversity in Darkness: Phylogeography of the troglobiotic millipede *Tetracion* Hoffman (Callipodida, Abacionidae)

Authors

Institution

Stephanie F Loria

Sewanee The University of the South, Biology, Sewanee, TN

Kirk S Zigler

J Lewis and Associates Biological Consulting, , Clarksville, IN, USA

Julian J Lewis

Millipedes are an understudied group. Little is known about their ecology, life history, and genetic diversity. Particularly neglected are the cave millipedes of eastern North America. Understanding the patterns and processes that determine their distribution in this region is an area of recent research. Here, we present a phylogeographic study of the cave-obligate (troglobiotic) millipede *Tetracion* (Callipodida: Abacionidae). This genus inhabits caves on the Cumberland Plateau in Tennessee and Alabama, a hotspot for cave biodiversity. Three species have been described: *T. jonesi* from Alabama, *T. antraeum* from northern Alabama and southern Tennessee, and *T. tennesseensis* from south-central Tennessee. To examine genetic divergence within and between species in this genus we sequenced part of the mitochondrial cytochrome oxidase 1 gene from 53 specimens from 11 caves across the ranges of *T. antraeum* and *T. tennesseensis*. We

found: (1) 7.9-8.6% genetic divergence between *T. tennesseensis* and *T. antraeum*, (2) little genetic variation within each species, and (3) a total of ten haplotypes (six in *T. tennesseensis* and four in *T. antraeum*) that were either restricted to individual caves or found in geographically nearby caves. Our results are consistent with previous morphology-based species definitions showing *T. tennesseensis* and *T. antraeum* belonging to distinct taxa. They also suggest that gene flow is limited between caves as the majority of haplotypes are restricted to a single cave. Our research contributes to the growing body of phylogeographic information about cave species on the Cumberland Plateau, and provides a point of comparison for future studies of troglobionts.

Timing of sperm activation in a funnel-weaving spider (Agelenidae)

Authors	Institution
Samaa Lutfi Sabah Gagnon Anne Danielson-Francois	University of Michigan Dearborn, Biology Discipline Natural Sciences Dept, Dearborn, MI USA

Spiders have an unusual reproductive system because unlike most organisms that transfer actively swimming sperm, spider sperm remains encysted (immobile) until activated in the female spermathecae. We examined the timing of sperm activation in the funnel-weaver *Agelenopsis pennsylvanica* (Agelenidae). Penultimate spiders were collected from the natural areas surrounding the University of Michigan-Dearborn. To observe the timing of sperm activation, staged matings between virgin spiders were conducted in the laboratory and females were frozen at different time increments after mating. The sperm stored in the spermathecae was found to be in different morphological states. We found that females frozen immediately after mating had higher percentages of encysted sperm compared to females frozen hours or days later. A more thorough understanding of sperm activation will help shed light on the unique and understudied reproductive system of spiders.

M, N and O

When eating your young isn't a bad thing: Context-dependent eggsac abandonment and filial cannibalism in the wolf spider, *Pardosa milvina*

Authors	Institution
Megan F Marchetti Matthew H Persons	Susquehanna University, Biology, Selinsgrove, PA

Parent-offspring conflict theory predicts that animals should allocate parental effort to maximize lifetime reproductive success. Iteroparous animals should be sensitive to offspring quality and withhold parental care for poor quality current offspring if it jeopardizes future reproduction. Animals should therefore be less sensitive to offspring quality when future reproduction is unlikely and maximize allocation of parental care late in life. The wolf spider, *Pardosa milvina*, demonstrates extensive parental care; however they also occasionally abandon or cannibalize their eggsacs. In this study we tested the effects of eggsac damage and production of a previous eggsac on eggsac abandonment and cannibalism. Treatment groups were randomly assigned for first eggsacs based on damaged or undamaged, and second eggsacs based on treatment of the previous eggsac (N=204). After assigning treatments, we monitored daily eggsac production, eggsac abandonment, cannibalism, protection and repairing behavior for first and second eggsacs. We found that younger females with first eggsacs were significantly more likely to abandon and cannibalize damaged eggsacs compared to unmanipulated eggsacs, however females with second eggsacs were insensitive to eggsac damage. Females also spent significantly more time protecting but not repairing or searching for second eggsacs compared to first and did not vary eggsac protective or repairing behavior based on damage. These results largely support the predictions of parent-offspring conflict theory that indicate that investment should increase and parents should be less sensitive to offspring quality late in life.

Pseudoscorpions break all the rules. Part 1: Drastic reductions in size of mitochondrial RNA genes

Authors	Institution
Susan E Masta Sergey Ovchinnikov	Portland State University, Biology, Portland, OR USA

We have found that pseudoscorpions possess mitochondrial genomes that differ drastically from those of most other arthropods. Although protein-coding gene arrangement is broadly conserved among arthropods, some lineages of pseudoscorpions show rearranged genomes. They also possess extremely short RNA-coding genes. We have inferred the secondary structures for all of their RNA genes (transfer RNA and ribosomal RNA). We find that, compared with other chelicerates (and arthropods in general), these structures have lost entire helices in some regions and have greatly reduced helices in other regions. We use mitogenomic data to determine the evolutionary position of pseudoscorpions, and find surprising, but very well supported, relationships.

Humidity affects the extensibility of an orb-weaving spider's viscous thread droplets

Authors

Institution

Brent D Opell

Shannon E Karinshak

Mary A Sigler

Virginia Tech, Biological Sciences, Blacksburg, Virginia

The prey capture threads found in most spider orb-webs rely on viscous droplets for their stickiness. Each droplet is formed of a central mass of viscoelastic glycoprotein glue surrounded by an aqueous covering, both of which incorporate hydrophilic components. We found that the extensibility of droplets on *Larinioides cornutus* threads increased as humidity increased. However, the deflection of the droplets' supporting axial lines did not change, indicating that atmospheric water uptake increases glycoprotein plasticity, but not glycoprotein adhesion. The extensibility of droplets, along with that of the thread's supporting axial fibers, is responsible for summing the adhesion of multiple thread droplets. Therefore, daily changes in humidity have the potential to significantly alter the performance of viscous threads and orb-webs.

Pseudoscorpions break all the rules. Part 2: Mitochondrial protein-coding genes relax the rules of amino acid use

Authors

Institution

Sergey Ovchinnikov

Susan E Masta

Portland State University, Biology, Portland, OR USA

The mitochondrial genomes of the pseudoscorpions we have sequenced possess many mutational changes compared to other arthropods. Our analyses reveal that these genomes possess a cytosine and adenine bias on their major coding strand, which is the typical condition found in other arthropods. However, their patterns of amino acid use differ dramatically from other arthropods and most chelicerates. We find very high levels of amino acid interchangeability in pseudoscorpion mitochondrial genes. Most surprisingly, we find high levels of interchangeability between functional groups. We compare and contrast the amino acid use patterns of pseudoscorpions with other arthropods, and discuss how amino acid use may influence phylogenetic reconstruction.

P, Q and R

Comparing two trapping methods for capturing wandering spiders: pitfall vs. ramp traps.

Authors

Institution

L Brian Patrick

Ashton Walter

Dakota Wesleyan University, Department of Biological Sciences, Mitchell, SD USA

Mount Marty College, Department of Biology, Yankton, SD

Pitfall traps are a common sampling method used to collect wandering spiders in a variety of habitats, and these traps require soil disturbance to properly set the trap with the top of the trap at the level of the soil surface. However, not all sampling locations are amenable to soil disturbance, either because there is no soil in which to dig (e.g., rock surfaces), or because soil disturbance is not allowed or it is very difficult to obtain permits for soil disturbance (e.g., US national parks). We tested the efficacy of a new trap design called ramp traps and developed by researchers in Canada, against traditional pitfall traps. In two fields of the Fort Pierre National Grasslands, SD, we ran parallel transects of pitfall and ramp traps for two sampling periods of two weeks each, then counted the number of species and the number

of individuals of each species in each trap. Ramp traps captured significantly more species and more individuals, resulting in higher species diversity compared to pitfall traps. However, the species composition caught in ramp and pitfall traps varied, with a small number of species captured only in pitfall traps, and a very small number of species captured only in ramp traps. Despite these subtle differences, ramp traps generally outperformed pitfall traps and may be easily moved to different locations with little or no soil disturbance. Our results indicate that ramp traps would be a viable trapping method, particularly in areas where soil disturbance is not allowed.

Interactions of transgenic *Bacillus thuringiensis* insecticidal crops with spiders (Araneae)

Authors

Institution

Julie A Peterson

Jonathan G Lundgren

James D Harwood

University of Kentucky, Department of Entomology, Lexington, KY USA

Genetically modified crops expressing insecticidal proteins from *Bacillus thuringiensis* (Bt) have dramatically increased in acreage since their introduction in the mid-1990's. Although the insecticidal mechanisms of Bt target specific pests, concerns persist regarding direct and indirect effects on non-target organisms. In the field, spiders may be exposed to Bt toxins via multiple routes, including phytophagy and pollenivory, consumption of Bt-containing prey, and soil exudates in the detrital food web. Beyond direct toxicity, Bt crops may also have indirect impacts, including pleiotropic and prey-mediated effects. Here, we comprehensively review the literature and use meta-analyses to reveal that foliar spider abundance is unaffected by Bt corn and eggplant, while cotton and rice revealed minor negative effects and there were positive effects from potato. Moreover, the soil-dwelling community of spiders was unaffected by Bt corn and cotton, while positively impacted in potato. However, Bt crops had higher populations of both foliar and epigeal spiders compared to insecticide-treated non-Bt crops. The current risk-assessment literature has several caveats that could limit interpretations of the data, including lack of taxonomic resolution and sampling methods that bias the results in favor of certain spiders. These families responded differently to Bt crops and spider responses to insecticides are species- and toxin-specific, thus highlighting the need for greater taxonomic resolution. Bt crops have become a prominent, and increasingly dominant, part of the agricultural landscape; understanding their interactions with spiders, a diverse and integral component of agroecosystems, is therefore essential.

The personality compositions of social spider groups determine the nature of interspecific interactions within their webs

Authors

Institution

Jonathan N Pruitt

Maud Ferrari

Susan E Riechert

University of California Davis, Center for Population Biology, Davis

Although the study of ecological interactions often takes into account functional variation between species, intraspecific variation is commonly ignored. Here, we investigate the importance of an intraspecific polymorphism in shaping interspecific interactions in a habitat-building species. Colonies of the social spider *Anelosimus studiosus* provide habitat for dozens of arthropod species, and colony members exhibit markedly polymorphic behavioural tendencies (BT – “aggressive” or “docile”). We manipulated the phenotypic compositions of colonies (100% aggressive, 50% aggressive 50% docile, 100% docile) and measured the nature and magnitude of interactions between *A. studiosus* and two heterospecific web associates, *Larinioides cornutus* and *Agelenopsis emertoni*. We found that BT composition significantly affected the outcome of interspecific interactions: changing the relationship between *A. studiosus* and its web associates from an ammensalism (where *A. studiosus* experiences reduced fecundity and survival) to a commensalism or mutualism. Although BTs have received much attention in recent years, our study is the first to demonstrate the importance of BTs in mediating the nature of species interactions. Implications for adaptive social group composition and eco-evolutionary dynamics are discussed.

Feeding preferences of solifuges (Arachnida: Solifugae) and their trophic position in desert communities.

Authors

Institution

Kristie Reddick

Robert Wharton

Texas AM University, Entomology, College Station, TX

It is widely recognized that solifuges are important inter- and intraguild predators in arid and semi-arid ecosystems, but their role as a prey animal is not well understood. This talk will be an overview of feeding and prey studies designed to determine trophic position of solifuge arachnids in desert communities. This work was part of a larger study focused on the diversity and distribution of the solifuges of Kenya. It has been demonstrated that at least some solifuges have rejected prey items that were either too large, too heavily sclerotized, or which may have been protected by defensive chemicals. We present a feeding study that provides baseline data on solifuge ability to consume hard and toxic prey and possible preference between the two. Tenebrionid beetles, polydesmid millipedes, *Danaus sp.* pupae and *Pachycondyla sp.* were offered to 17 solifuges. All solifuges in the feeding study ate the termites that were used as a behavioral control, but only three individuals were able to eat both hard and toxic prey items repeatedly. Solifuges were more willing or able to eat toxic prey than hard. Additionally, by quantifying arthropod remains from burrowing owl pellets in the southwestern United States, we were able to determine owl prey preference among six orders of arthropods, including solifuges. Solifuges were the third most frequently encountered

arthropod in the pellets, after caterpillars and beetles, and were also the third most abundant.

Australian Assassins: phylogeny, diversity and biogeography of the Australian assassin spiders (Araneae: Archaeidae)

Authors	Institution
Michael G Rix	Western Australian Museum, Terrestrial Zoology, Perth, Western Australia, Australia
Mark S Harvey	

The 'assassin spiders' of the family Archaeidae are an ancient and iconic lineage of basal araneomorph spiders, remarkable for their extraordinary appearance, specialised ecology, evolutionary antiquity and endemism on the southern continents. The Australian archaeid fauna is newly revised taxonomically and phylogenetically, revealing a diverse and highly endemic fauna characterised by mostly short-range endemic, reciprocally allopatric species. Molecular phylogenetic analyses provide strong evidence for a monophyletic clade of Australian Archaeidae and for the presence of three major endemic lineages, each with non-overlapping distributions in north-eastern Queensland, mid-eastern Australia and southern Australia, respectively. Phylogeographic results highlight the mode and tempo of archaeid speciation in Australia during the Miocene, and provide compelling evidence for the diversification of clades due to the Tertiary contraction and fragmentation of Australia's mesic biomes. Assassin spiders are among the most useful animal models for exploring biogeographic processes in mesic Australia, with the potential to provide new and significant insights into the evolution of the continent's remaining rainforests, wet sclerophyll forests and southern-temperate heathlands.

S, T, U and V

Inferring species trees from gene trees in a radiation of California trapdoor spiders (Araneae, Antrodiaetidae, *Aliatypus*)

Authors	Institution
Jordan Satler	San Diego State University, Biology, San Diego, CA USA
James Starrett	University of California Riverside, Biology, Riverside, CA USA
Cheryl Hayashi	
Marshal Hedin	San Diego State University, Biology, San Diego, CA USA

The trapdoor spider genus *Aliatypus* (Mygalomorphae, Antrodiaetidae) encompasses twelve described species, eleven of which are endemic to California. Several *Aliatypus* species show disjunct distributional patterns in California (some are found on both sides of the vast Central Valley), and the genus as a whole occupies an impressive variety of habitats. DNA sequence data were collected from seven gene regions, including two newly developed for spider systematics. Bayesian inference (in individual gene tree and species tree approaches) recovered a general "3 clade" structure for the genus (*A. gulosus*, californicus group, erebus group), with three other phylogenetically isolated species differing slightly in position across different phylogenetic analyses. For multiple species spanning the Central Valley, explicit hypothesis testing suggests a lack of monophyly for regional populations (e.g., western Coast Range populations). In addition, phylogenetic evidence clearly shows that syntopy is restricted to distant phylogenetic relatives, consistent with ecological niche conservatism. Overall, this study provides fundamental insight into a radiation of trapdoor spiders found in the biodiversity hotspot of California.

New fossil palpimanoids from the early Cretaceous of Spain, with a combined extant/fossil phylogenetic analysis of the superfamily Palpimanoidea

Authors	Institution
Erin E Saupe	University of Kansas, Geology, Lawrence, KS USA
Ricardo Perez-delaFuente	University of Kansas, Paleontological Institute, Lawrence, KS USA
Paul A Selden	

Three palpimanoid fossils were recently discovered from early Albian (110 Mya) amber of Peñacerrada I (Burgos, Spain). These specimens present unique combinations of characters that ally them most closely with the Huttoniidae and Archaeidae/Mecysmaucheniidae. The fossil finds, with their distinctive amalgamation of palpimanoid characteristics, prompted a reevaluation of fossil and extant taxa traditionally assigned to Palpimanoidea. A parsimony-based phylogenetic analysis was conducted using an additional six fossil taxa previously described within the Archaeidae, †Lacunaucheniinae, Mecysmaucheniidae, †Micropalpimanidae, and †Spatiatoridae, and seven extant representatives from the families Archaeidae, Huttoniidae, Mecysmaucheniidae, Palpimanidae, and Stenochilidae. Results from the phylogenetic analysis will be discussed, including the placement and description of the new fossils and their paleobiogeographic significance.

Deep phylogenetic divergences in the harvestman genus *Sabacon* (Opiliones, Dyspnoi), with insights into Holarctic biogeography.

Authors	Institution
Axel L Schoenhofer	San Diego State University, Evolutionary Biology, San Diego, CA, San Diego County
Maureen McCormack Jochen Martens Nobuo Tsurusaki Marshal Hedin	San Diego State University, Biology, San Diego, CA USA

Within the harvestman clade Dyspnoi, Nemastomatidae and Sabaconidae are present on all northern continents (i.e., north America, northern Asia and Europe), while other Dyspnoi families are restricted to two or fewer northern continents. Geographically widespread genera are rare in Dyspnoi, reflecting their poor dispersal abilities - an exception is the genus *Sabacon*, which is present on all three northern continents. A multigenic molecular phylogenetic analysis of *Sabacon* reveals several strongly supported biogeographic connections. For example, species from the eastern United States show connections to both Asia and Europe. Western US species only display Asian affinities, but on different time scales, pointing to repeated vicariance events over time. Taxonomic literature indicates that genetic clades correspond to morphologically distinct lineages that differ especially in genital morphology. At the regional level (e.g., western US, eastern US), our data suggests the presence of many cryptic species; denser geographic sampling and the collection of adult males is needed to further explore this diversity.

Review of fossil Nephilidae

Authors	Institution
Paul A Selden	University of Kansas, Paleontological Institute, Lawrence, KS USA

The recent discovery of a female *Nephila* (*N. jurassica*) in middle Jurassic (c. 165 Ma) rocks of China has prompted a survey of all fossil Nephilidae. The nephilid fossil record consists of three extinct genera in Paleogene (c. 40 Ma) Baltic and Bitterfeld ambers, five *Nephila* species from Neogene (c. 16 Ma) Dominican amber and *Nephila pennatipes* from the Eocene (c. 34 Ma) of Florissant, Colorado. The Mesozoic record consists of *Cretaraneus vilaltae* from the Cretaceous (c. 130 Ma) of Spain. Supposed *Cretaraneus* from the Cretaceous of Brazil and China do not show the characters of the genus, and *Archaeometa nephilina* from the Carboniferous of England, described as resembling a *Nephila*, is probably not a spider. All fossil nephilids apart from *N. pennatipes* and *N. jurassica* are adult males. Restudy of *N. pennatipes* from Florissant confirms its identification. *Nephila* is renowned for its extreme sexual size dimorphism, and there has been debate concerning whether this is due to male dwarfism or female gigantism. *Nephila jurassica* is as large as many Recent *Nephila* females, but a male of this species had not been found until recently (May 2011). The talk will conclude with discussion of what, if anything, the male of *N. jurassica* tells us about the evolution of sexual size dimorphism in the golden orb-weaver spiders.

Silk biomechanics and energy absorption in spider orb webs

Authors	Institution
Andrew Sensenig	Tabor College, Biology, Hillsboro, KS USA
Sean Kelly Kimberly Lorentz Todd A Blackledge	University of Akron, Biology, Akron, OH USA

The kinetic energy of flying insect prey represents a formidable challenge for orb weaving spiders who rely on their webs to first absorb the kinetic energy of flight and then to adhere to insects. While spider silks are renowned for their exceptional material properties, the micron-sized diameters of threads also results in a low Reynolds number and hence viscous interactions with air. This led to the aerodynamic dissipation hypothesis that suggests that drag of silk threads moving through air plays a dominant role in how orb webs stop flying insects. However, evidence for the aerodynamic dissipation hypothesis is derived primarily from studies of single silk threads from *Araneus*. Here, we present a comprehensive study of how orb webs deform under prey impact for several species of Araneidae. We calculate energy dissipation budgets using data derived from high speed images of web deformation in conjunction with material tensile testing. Our findings emphasize the importance of the intrinsic work performed by silk molecules within radial threads, and downplay the role of aerodynamic dissipation and capture spiral deformations in many webs.

Activity of male tarantulas (*Brachypelma vagans*) during the mating season

Authors	Institution
Cara Shillington	Eastern Michigan University, Biology, Ypsilanti, MI

Male tarantulas abandon their permanent retreat on reaching sexual maturity and search actively for reproductive females. To date, three studies have tracked male movement at field sites in Texas, but this is the first radio-telemetry study in Mexico. I tracked 16 male *Brachypelma vagans* in the state of Puebla during the mating season. Males were most active between 8pm and 2am which corresponded with times when females were near the entrance of their burrows. Average distance traveled was 33.4 m / day but there was a lot of variability among the males and several males remained in the same location for several days. Mortality rates were >50% and an additional 18% of males were lost due to equipment issues. Five males were seen in with or in close proximity to female burrows, but no actual mating was observed. In comparing rates of movement with radio-tracked male *Aphonopelma anax* in Texas, *B. vagans* had significantly lower rates but female burrows in Mexico were much more numerous.

Multiple predator effects on the survival of *Pardosa milvina* (Araneae: Lycosidae)

Authors	Institution
Michael I Sitvarin	Miami University, Zoology, Oxford, OH USA
Ann L Rypstra	Miami University, Zoology, Hamilton, OH USA

The role of predation in food webs has frequently been investigated, but systems with multiple predators at the same trophic level have received less attention. Furthermore, multiple predator effects (MPEs) have traditionally been investigated with a non-predatory species as shared prey between predators. Here, we take advantage of the prevalence of intraguild predation among wolf spiders and a carabid beetle to evaluate how a predator responds to multiple predator risks. We first characterized the habitat domain and hunting mode of three predators (*Hogna helluo*, *Rabidosia rabida*, and *Scarites quadriceps*) and their shared prey, *Pardosa milvina*, in laboratory mesocosms. Habitat domain and hunting mode were then used to predict multiple predator effects (i.e., risk enhancement, risk reduction, and substitutability), which were evaluated by recording *Pardosa* survival in the presence of all combinations of the three predators. Predator combinations showed evidence of substitutability, risk enhancement, and risk reduction, though not all MPEs matched predictions based on habitat domain and hunting mode. Specifically, the treatment with *Rabidosia* and *Scarites* resulted in risk enhancement when substitutability was expected. Additionally, the MPE of *Hogna* and *Scarites* showed substitutability when risk reduction was predicted. Deviations from expected MPEs may be attributable to a lack of predation on *Scarites* by *Hogna*, and the possibility that habitat domain and hunting mode are not sufficient predictors of MPEs. This study provides insight into how multiple intraguild predators affect their prey, and raises interesting questions about the role of multiple predator effects in food webs.

Early events in the evolution of spider silk genes

Authors	Institution
James Starrett	University of California Riverside, Biology, Riverside, CA USA
Jessica E Garb	University of Massachusetts Lowell, Biological Sciences, Lowell, MA
Cheryl Hayashi	University of California Riverside, Biology, Riverside, CA USA

Silk spinning is essential to spider ecology and has had a key role in the enormous diversification of spiders. Silk is composed primarily of proteins and studies on the genes encoding silk proteins have largely focused on the derived clade, Orbiculariae (orb-weavers), from the suborder Araneomorphae ('true spiders'). Orb-weavers secrete multiple types of functionally distinct silks from a suite of silk fibroin genes. Underlying this extensive repertoire of silks is a history of duplication and subsequent divergence of silk genes. However, much of the phylogenetic diversity of spiders has yet to be sampled for their silk genes, leaving questions as to when silk gene duplications occurred and how these duplications allowed silks to take on new functions. In contrast to their distant orbicularian relatives, spiders of the suborders Mesothelae (segmented spiders) and Mygalomorphae (tarantulas, trapdoor spiders) have morphologically uniform silk glands and more generalized uses of silk. Given their simpler silk biology, these spiders are hypothesized to have less diversity of silk genes. Here, we report the results of constructing expression libraries from the silk glands of multiple mygalomorph species, a mesothele, and a non-orbicularian araneomorph, to uncover their surprisingly rich silk gene diversity. We relate the attributes of the newly discovered silk sequences to the ecological functions of the spiders. Furthermore, by performing gene-tree and species-tree analyses, we document the numerous silk gene duplications that occurred after the split between the Mesothelae and Opisthothelae (Mygalomorphae plus Araneomorphae).

Retreat construction by *Clubiona riparia*: reality vs. presumption

Authors

Institution

Robert B Suter

Vassar College, Biology, Poughkeepsie, New York USA

Female *Clubiona riparia* (Araneae: Clubionidae) build three-sided retreats in which they enclose both themselves and their eggs. A retreat is constructed by bending a single plant leaf twice, each time causing a fold that is roughly perpendicular to the long axis of the leaf, and joining the edges with silk. To assess the energetic costs involved in assembling a retreat (presuming that the actual method of construction could be ignored), I measured the work that had to be expended in bending and sealing the leaves of a grass, a cattail, an iris, and a willow, all leaves that are normally used by the spiders in retreat construction. The calculated costs of construction (excluding silk expenditure) were very small, the equivalent of about 0.05% of the energy content of single egg of *C. riparia*. Reality intruded, however, in the form of data on the actual behaviors used by these spiders in retreat construction: to bend the leaves, the female makes hundreds to thousands of excursions, shuttling between leaf edges that will ultimately be sealed together. Because of the large number of excursions, most of which have a vertical component and thus involve work against gravity, the work of moving the gravid spider herself is far more extensive than the work done against leaf stiffness. For the construction of a retreat on an Iris blade, for example, the spider must expend roughly 15 times more energy in overcoming gravity than it does in overcoming the blade's resistance to being deformed.

The role of acoustic and seismic communication in *Gladicosa gulosa*: complex vibration signals in a wolf spider.

Authors

Institution

**Alexander L Sweger
George W Uetz**

University of Cincinnati, Biological Sciences, Cincinnati, OH USA

Many wolf spiders produce complex multimodal signals, making them excellent models for testing hypotheses about the evolution of signaling behavior. This research examines acoustic/vibratory communication in the "purring" wolf spider *Gladicosa gulosa* (Walckenaer, 1837). Only minimal research has been conducted on *G. gulosa*, but early studies describe the loud volume of its acoustic/vibratory courtship. This suggests that signaling in this species may be energetically costly, as well as vulnerable to eavesdropping by conspecifics and/or predators. Our objectives were to characterize the signals of courting male *G. gulosa*, and examine various components of courtship as a basis for future studies. Using Laser Doppler Vibrometry and sensitive microphones, we recorded and characterized the components of male courtship. Preliminary analyses suggest that courtship displays by males of this species produce both airborne (acoustic) and seismic (vibration) signals, and incorporate both stridulation and percussion. The components of courtship signals may be affected differently by male size or varying ecological conditions, including the type of substrate utilized for signaling. These results suggest the potential for eavesdropping, and male competitive behavior in the form of social facilitation of courtship.

Behavioral evidence of pheromonal signaling in desert grassland scorpions

Authors

Institution

**Matthew S Taylor
Douglas D Gaffin
Caleb R Cosper**

University of Oklahoma, Department of Zoology, Norman, Oklahoma USA

Behavioral evidence suggests that, in some scorpion species, females deposit a pheromone that attracts mates, but no pheromone has been identified. The goal of our study was to isolate a pheromone from female desert grassland scorpions (*Paruroctonus utahensis*). We made *in situ* whole-body extracts of female *P. utahensis* in a chloroform-methanol solution; the extract stratified into aqueous and organic layers. In controlled laboratory experiments, most males exposed to female extract (aqueous and organic fractions combined) exhibited pre-courtship behavior, whereas those exposed to a control solution of chloroform-methanol showed no change in behavior. When the two extract fractions were separately tested, males initiated pre-courtship behavior when exposed to the organic fraction but not when exposed to the aqueous fraction. These data are the first experimental evidence of a female pheromone in this species and mark the first steps toward chemically characterizing a pheromone in any scorpion species.

The role of visual cues in species and sex recognition in the jumping spider *Lyssomanes viridis*

Authors

Institution

Cynthia A Tedore
Sonke Johnsen

Duke University, Biology, Durham, NC USA

Few visually-apparent features, when viewed in isolation, are unique to any one species of terrestrial arthropod, even in sympatry. Misidentifying and displaying at the wrong species or sex of arthropod predator is dangerous. Thus, in taxa that identify conspecifics visually, selection should favor individuals capable of analyzing multiple features holistically. We tested the specificity of species and sex recognition in the jumping spider *Lyssomanes viridis* by presenting mature males with various images in the presence of female silk. Spider images having a conspecific face and/or legs elicited the expected threat and courtship displays. When a male face was combined with female legs and vice versa, roughly half of males courted and half threatened. Significantly fewer males displayed at a spider image that completely lacked the conspecific color pattern but had conspecific-shaped legs. Most males courted a female *Thiodina sylvana* image and were split between threatening and courting a male *Hentzia palmarum* image. Males did not display at a black circle. Results suggest males can assess multiple isolated features, but do not synthesize and evaluate features holistically, at least not in the presence of female silk.

Food abundance, group foraging and territorial interaction in the California orb weaving spider *Metepeira spinipes*

Authors

Institution

Mark L Tiemeier
George W Uetz

University of Cincinnati, Biological Sciences, Cincinnati, OH USA

Spiders tend to be solitary and aggressive, thus species which exhibit social behaviors offer opportunities to explore the evolution of sociality. *Metepeira spinipes* is a facultatively colonial orb-weaver from Mexico and California, and occurs in groups as well as solitarily, depending on environmental conditions. It appears to exhibit risk-sensitivity, as colonial foraging reduces variance in the amount of prey captured and the frequency and size of colonies is correlated with food availability. However, colonial aggregation is likely the consequence of both individual foraging decisions and specific interactions between spiders. In field experiments, we manipulated the food intake of spiders and found that well fed individuals (ad lib feeding) are significantly more likely to join a nearby colony than starved spiders. Additionally, we examined the interactions between spiders residing within colonies and diet-manipulated spiders which we added to their webs, and found that size rather than condition is the major factor influencing whether intruding spiders escalate encounters and overtake webs. The role of these factors in colony formation will be discussed.

The goblin spiders (Oonopidae) of Madagascar: a morphological comparison of three genera.

Authors

Institution

Darrell Ubick
Charles Griswold

California Academy of Sciences, Entomology, San Francisco, CA

Madagascar has a rich oonopid fauna of over 100 species representing about 24 genera. Most of the species and about 60% of the genera are new and apparently endemic to the island. Here we report on three of these endemic genera.

Genus 1 includes species with large contiguous eyes (eye ring), prominent leg spines, reduced scutes in females and fused scutes in males, all characteristic of the *Ischnothyreus* complex. Genital characters of both the male and female suggest a close relationship to the Asian genus *Camptoscapbiella*.

Genus 2 resembles the many Malagasy species of the *Silhouettella* complex in several somatic characters, such as body form, eye arrangement, body sculpturing and leg spination, but differs in genitalic features. The male embolar region has few broad lobes, as opposed to several slender lobes in silhouettelloids, and the female genitalia lack a large oval receptaculum characteristic of silhouettelloids. Apart from that difference, the female genitalia are typically silhouettelloid and suggest that the genus belongs in this

complex.

Genus 3 includes small spiders with reduced eyes and scutes, and with an unusual character combination. The genus resembles silhouetteloids in body form, leg spination and eye arrangement, but also ischnothyroids in that males have fused abdominal scutes. The female genitalia likewise include characteristics of both groups. The placement of this genus is speculated but remains unresolved.

Chemical communication in *Schizocosa ocreata* (Hentz): a reassessment.

Authors

Institution

George W Uetz

University of Cincinnati, Biological Sciences, Cincinnati, OH USA

Andrea Orton

Trisha Myers

Andrew Roberts

The Ohio State University, Evolution Ecology and Organismal Biology, Newark, OH USA

Chemical communication is an important part of the mating process in the wolf spider *Schizocosa ocreata* (Hentz 1844), as cues associated with female silk are sufficient to elicit courtship from males. However, several questions arise about the role of chemical cues and the nature of chemical communication, which have not been studied in depth. We examined how both male and female *S. ocreata* wolf spiders respond to silk-borne, airborne and cuticular hydrocarbon (CHC) cues from members of either sex. Not surprisingly, males spent significantly more time on female silk. Females spent significantly less time on female silk. However, there were no significant differences for either sex between time on male silk vs. a control (filter paper, no silk). Males and females showed no significant directional response to airborne (olfactory) chemical cues from either sex, but males displayed courtship behaviors more often and at higher rates in the presence of airborne cues from females. Males responded with courtship to filter paper impregnated with cuticular hydrocarbon (CHC) cues of adult females, as well as female exuviae. Comparison of rates of male courtship behaviors exhibited in response to chemical cues from females suggest that silk-borne and CHC cues elicit higher rates of male signaling than airborne cues, but the latter may stimulate courtship at a distance. These data suggest that chemical communication in this species is unidirectional and female-originated, but more complex than previously believed, as multiple sources of chemical cues may be involved in stimulating male courtship.

Scavenging behavior in spiders

Authors

Institution

Richard S Vetter

Historically, spiders are considered to be obligatory predators of live, animate prey. A 2003 study promoted the notion that brown recluse spiders preferentially scavenged rather than attack live prey. In contrast, a 2005 study showed that brown recluse scavenging rate was only 10% to 42% when spider satiation, prey size and prey age was manipulated. The 2003 study also proffered that brown recluse scavenging was due to high intraspecific competition in homes. Spider scavenging is not well documented in the literature. Is scavenging a rare behavior exhibited by brown recluses and possibly a few other species? This study addressed spider scavenging in general. Freeze-killed crickets were offered to 100 non-*Loxosceles* spiders (11 families, 24 genera, 29 species) from a variety of spider hunting guilds. Also included were web-spinners that can secure prey dorsum up (i.e., Agelenidae, Filistatidae, Amphinectidae but not Theridiidae, Araneidae, Pholcidae); webspinners should almost never have the chance to scavenge in nature. Crickets were also offered to 20 brown recluse spiders. Spiders were offered dead crickets at one-week intervals for three consecutive weeks; this compensated for satiation due to pre-trial feeding and pre-molt feeding cessation. Of the 100 non-*Loxosceles* spiders, 99 scavenged dead crickets, 89 in the first trial. All 20 brown recluses scavenged. Therefore, scavenging in spiders is not rare, just rarely studied. Given the opportunity, many families of spiders exhibit scavenging; it is not a special behavior expressed by the brown recluse. However, the extent to which scavenging occurs in nature is still debatable.

A Brief History of the Beginning of The American Arachnological Society

Authors

Institution

Beatrice R Vogel

In 1968 the first issue of the newsletter American Arachnology was published. In 1972 the organizational meeting of the American Arachnological Society was held in Rustler's Park campground in the Chiricahua National Forest. In 1975 the 4th annual meeting and first international meeting of AAS was held at Warrensburg, Missouri.

W, X, Y and Z

The behavioral mechanisms of site selection by web-building spiders

Authors	Institution
Kelton D Welch Kenneth F Haynes James D Harwood	University of Kentucky, Department of Entomology, Lexington, KY USA

The placement of spider webs is an excellent model system for the study of habitat utilization by animals. Patterns of site utilization have been found to correlate with the availability of potential prey and with the distribution of suitable support structures. However, the behavioral mechanisms driving the foraging-site selection by spiders are not fully understood. Previous research suggests that web-building spiders respond directly to habitat structures, which can serve as indirect indicators of prey availability, and that spiders only monitor direct cues from the prey after web construction, to evaluate the profitability of the site and to decide whether or not to remain in it. The role of prey cues in the initial selection of foraging sites by web-building spiders has received very little attention. In this study, a combination of field and laboratory techniques was used to determine how web-building spiders select and utilize foraging sites. In field collections, we uncovered interspecific differences in habitat structure utilization that correlated with differences in activity density of a major prey group, Collembola, supporting the hypothesis that habitat structures indirectly indicate prey availability. However, two-choice experiments were run in laboratory arenas, giving spiders a choice between structurally identical sites with and without prey. In these experiments, spiders showed significant preference for the site with prey. These data combined indicate that both structural and prey cues are involved in the initial selection of foraging sites by web-building spiders. The implications of these findings for spider trophic ecology and biological control potential are discussed.

Evolution of a complex, novel structure, the trap-jaw mechanism, in spiders (Mecysmaucheniidae, Araneae)

Authors	Institution
Hannah M Wood Rosemary G Gillespie	University of California Berkeley, Environmental Science Policy and Management, Berkeley, CA USA
Charles Griswold	California Academy of Sciences, Entomology, San Francisco, CA
Damian O Elias	

Trap jaw mechanisms have been described for the ant genus *Odontomachus* but is virtually unknown in one of the largest arthropod classes, the arachnids. The trap jaw mechanism has evolved twice independently in spiders, once in the family Pararchaeidae and once in the family Mecysmaucheniidae. The underlying structural mechanism for employing a trap jaw is unique in both families, with Mecysmaucheniids achieving the fastest known movements in arachnids. Within the mecysmaucheniids there is variation in both carapace and jaw shape and in the speeds of the jaws closing. Phylogenetic analyses of molecular data results in a mecysmaucheniid phylogeny that can be used to examine the evolution of this trait among lineages from New Zealand and Chile as well as to examine how this trait relates to distribution patterns. The biomechanical properties of this complex trait are examined among different lineages.

Magnetic Resonance Imaging and Spectroscopy of Spiders

Authors	Institution
Jeffery L Yarger Brian R Cherry	Arizona State University, Chemistry Biochemistry and Physics, Tempe, AZ

Our group at Arizona State University is interested in how spiders produce silk with the goal of reproducing this process in the laboratory. Many of the secrets in silk production come from our lack of molecular level understanding of how silk proteins are produced, stored and secreted from glands, through ducts and out spinnerets. We are using magnetic resonance imaging (MRI) and spectroscopy (MRS) to

better elucidate this process. We are able to obtain micro-MR images and spectra from live spiders and use this data to help us better understand protein structure and dynamics at the molecular level.

Intersexual coevolution of genitalia in euophryine jumping spiders (Araneae: Salticidae): sexual selection or “lock-and-key”?

Authors

Institution

Junxia Zhang

University of British Columbia, Zoology, Vancouver, BC Canada

Wayne P Maddison

A long-standing question in spider evolution is the extent to which genitalia are sexually selected or serve as species recognition mechanism (“lock-and-key”). We investigated the lengths of the male embolus and female copulatory duct of euophryine jumping spiders, and found they are positively correlated among species. This correlation confirms an interaction, but it does not indicate the selective mechanism involved. Intra-specific variation of these traits in ‘*Sidusa*’ *recondita* and ‘*Cobanus*’ *cambridgei* shows negative allometry. While this may appear to favor the “lock-and-key” scenario, it could also occur via post-copulatory sexual selection. The size-corrected intra-specific variation is high for genitalia, which has been argued to indicate sexual selection, but could also arise through developmental mechanisms to achieve negative allometry. However, if high intra-specific variation is indicative of sexual selection, there remains the question of the mechanism: cryptic female choice or sexual antagonistic coevolution. An antagonistic arms race of ever-increasing embolus and CD length can be rejected, as decreases appear to occur as often as increases on the phylogeny. Unlike the genitalic traits, the pre-copulatory sexually-selected traits (male chelicerae) tend to show positive intra-specific allometry, and thus may have evolved under strong directional selection. The fact that the species with stronger somatic sexual dimorphism (‘*Cobanus*’ *cambridgei*) has the lower intra-specific variation in genitalia may imply a trade-off between pre- and post-copulatory sexual selection. The mechanisms underlying the variability of euophryine genitalia remain unclear, and in fact sexual selection and species isolation mechanisms in principle could coexist.

The Phylogenetic Scale of Venom Variation in Sicariid Spiders

Authors

Institution

Pamela A Zobel-Thropp

Lewis & Clark College, Biology, Portland, OR USA

Miles M Dale

Greta J Binford

The spider family Sicariidae includes two genera, *Loxosceles* (including the brown recluse) and *Sicarius* (6-eyed sand spiders). Members of this family has been evolving for over 100 million years in the context of being generalist, ground-dwelling predators of arthropods. They are best known for the ability of their venoms to cause dermonecrotic lesions in mammals, an effect that is caused by the toxic venom enzyme sphingomyelinase D. We are characterizing the venomes of a broad phylogenetic representation of species in the sicariid family. With these comparative data we are analyzing the evolution of the full venom cocktail in a lineage with remarkably little evident evolutionary change in feeding biology. We will discuss patterns of presence and absence of multiple venom toxin lineages evolving within this group, and patterns of positive selection within select toxin lineages. Together these data help illuminate the evolutionary dynamics that have shaped venom diversity.