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[1] The British Arachnological Society

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The **British Arachnological Society** was founded in 1968 from the British Spider Study Group. It has about 500 members around the world. The British Arachnological Society publishes a Newsletter and the *Bulletin of the British Arachnological Society*. In addition to receiving these publications, members enjoy indoor and field meetings, access to the Society's extensive reprint and slide libraries, an exclusive web site which is a major online resource for arachnologists, and an email discussion group. In the near future, members will also have access to the *Bulletin* online. Overseas membership costs £18 (£19 via PayPal), and institutions can subscribe to publications for £30 (£32 by PayPal). Go to <http://wiki.britishtspiders.org.uk> for further information. First published in 1969, the *Bulletin* is a quality, peer-reviewed publication covering all aspects of arachnology (except works primarily on Acari); it has three issues per year. Prospective authors are invited to submit their manuscripts through the online system at <http://bas.msubmit.net>.

[2] SPIDA: Using expert systems on the web to identify spiders:

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For all researchers who study spiders and their kin it becomes our contractual obligation to identify spiders for homeowners in our community. Frequently we are forced to make these identifications, sight unseen, based solely on narrative descriptions offered by the apprehensive layperson. Over the years I have been interested in using a web-based computer program and the internet to simulate the thought processes we use when making identifications not by sight but by narrative description. In this identification process we frequently ask questions concerning the behavior or ecology of the spider in addition to physical descriptions of the spider. As we collect these answers, we assign them relative weights and rank them in terms of their strength of correlative association and predictive value. For example, being told the spider could climb on the vertical glass window may be more informative than being told the spider is brown. Ultimately our identification is based upon the associated suite of traits (morphological, behavioral, ecological) given. Computer software engineers have attempted to mimic this process by developing Expert System software. Using these systems as a model, we developed SPIDA an internet based interactive key designed to identify spiders common around, and in, buildings in Kentucky. SPIDA avoids using technical terms or dichotomous keys to identify spiders, but instead simulates the types of questions arachnologist use to make best guess identifications without actually seeing the specimen.

[3] Integrating and Sharing Biodiversity Data Online: Museum Science and International Collaboration in the Age of Cybertaxonomy

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In the Natural History museum setting, missions include building and sharing collections, training students, and accumulating data for publications in taxonomy, phylogenetics, and biodiversity. Collecting expeditions designed around structured sampling can reveal critical information about the World's most diverse communities of plants and animals while generating raw material for studies in taxonomy and phylogenetics. New developments in communication and technology are revolutionizing the way we collect, organize, and share information. Synergies among all these activities can lead to a holistically integrated research program that confronts the taxonomic impediment in an era of biodiversity loss and democratizes access to scientific data. I report on the results of a recent collecting expedition to Vietnam.

[4] Molecular and mechanical comparisons of cob-web weaver spiders (Theridiidae) dragline silk.

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Spider dragline silk is one of the strongest biological materials, approaching the tensile strength of steel. However, mechanical properties of dragline silks vary significantly among the different species measured thus far. In this study, we compared the molecular and mechanical properties of dragline silk of three cob-web weaving species (Theridiidae): *Latrodectus hesperus*, *L. geometricus*, and *Steatoda grossa*. We found that the *Latrodectus* species produce dragline silk twice the tensile strength of *S. grossa* dragline, which spans the range of measured tensile strengths for all spiders (Araneae). The close relationship of these species offers the opportunity to identify molecular changes associated with this dramatic shift in tensile strength. Thus, we constructed a cDNA library for *S. grossa* in order to characterize genes that encode the protein components of dragline silk. We will compare these protein sequences to previously published sequences for *Latrodectus* dragline.

[5] Spider Glue Silk Proteins: Molecules with Novel Biomimetic Potential

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Spider silks have been under natural selection for millions of years, resulting in diversity of function along with unique mechanical properties. Because it is impractical to farm and harvest spider silk for various reasons, the ability to produce synthetic fibers from recombinant spider silk proteins allows for the potential to develop a new unique class of biomimetic materials. Here we investigate the structural and mechanical properties of pyriform silks from the golden orb-weaver, *Nephila clavipes*. Nanoscale indentation measurements using atomic force microscopy on natural pyriform silk suggests this biomaterial has high toughness that may be suitable for dissipating high amounts of mechanical energy, possibly due to the occurrence of highly organized nanocrystals. In contrast to dragline silks, amino acid sequence analysis reveals that the glue silk protein, Pyriform Spidroin 2 (PySp2), does not contain the traditional poly-(Gly-Ala) and poly-Ala repeats that have been shown to contribute to strength and extensibility. We hypothesized that PySp2 contains new protein motifs sufficient to polymerize into functional structures. To investigate the functional contributions of these novel motifs during pyriform fiber assembly, we expressed and spun different recombinant PySp2 proteins with various portions spanning its block repeat units into fibers. In addition, we demonstrate recombinant PySp2 proteins that contain single block repeat units can self-assemble into foam-like nanostructures. Taken together, our findings suggest glue silk proteins can be used for a wide range of biomimetic materials with morphologies ranging from fibers to porous structures.

[6] Does spider silk hold a "memory" of the spinning process?

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Hydration of major ampullate (MA) silk leads to an increase in fiber diameter and a decrease in fiber length. This change is known as supercontraction. Previous studies have shown that supercontraction disrupts intra/intermolecular hydrogen bonding leading to a rearrangement of spidroin motifs. When MA silk from the spider, *Nephila clavipes*, undergoes supercontraction in 8M urea, the silk takes on a distinct banded appearance. While the pattern of banding is variable, at any point along the length of the silk the two individual MA fibers that make up the spider's dragline are identical. We propose that some factor (or factors) are acting in concert on the fibers as they are being drawn from the individual silk glands of the spider. We have examined the influence of reeling speed on the banding pattern of supercontracted silk. MA silk was collected from *N. clavipes* at different reeling speeds. Silk was supercontracted using either distilled water or 8M urea. Diameters of control or water hydrated silk fibers did not change with reeling speed. In contrast, the diameter of the urea-hydrated silk did show a statistically significant change with increasing reeling speed. The pattern of banding was only found in the urea-hydrated silk samples. The complexity of the banding pattern also increased with increasing reeling speed. These results suggest that the pattern of banding found in 8M urea supercontracted MA silk may represent a 'memory' of the physiological forces applied to the silk fibers during the spinning process.

[7] Ovarian Development in the Western Black Widow Spider, *Latrodectus hesperus*

Wendy Ouriel, Merri L Casem1*

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Black widow spiders (*Latrodectus hesperus* Chamberlin & Ivie (1935)) have the potential to generate multiple egg sacs containing hundreds of eggs over a period of several months, often from a single copulation. This feat can only be accomplished if there is a steady supply of oocytes. In this study, ovarian tissue was isolated from black widow spiders at different stages of ovarian development and examined by light and electron microscopy. Oocytes at varying stages co-exist as clusters on the spider's ovary where they attach to the muscular ovarian wall by way of a multicellular stem-like structure and project into the abdominal cavity. Pre-vitellogenic oocytes are characterized by a homogeneous cytoplasm with numerous mitochondria. During vitellogenesis, the oocytes increase in size accompanied by the accumulation of yolk granules. The number, size, and organization of the yolk granules change over time. In the gravid spider, the oocytes separate from the ovary wall and are loosely aggregated within the abdomen of the spider. Following oviposition, the fertilized eggs become surrounded by a hardened chorion composed of small spherical granules. Overall, the pattern of ovarian development in the black widow spider is similar to that documented in other spiders. We are seeking to determine the cellular processes involved in the accumulation of yolk material, the possible role of apoptosis in the separation of the oocytes from the stem, the origins of the chorion material and the mechanism that moves mature oocytes from the abdominal cavity to the gonopore.

[8] Microstructure of the Nerve Cell Clusters in the Wolf Spider *Arctosa ngreungensis* (Araneae: Lycosidae)

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Research on the central nervous system (CNS) of arachnids is still an unexplored field compared to insects or crustaceans. Here, we have investigated the microstructure of the nerve cell clusters in the wandering spider, *Arctosa kwangreungensis* using various visualization techniques. For image processing and reconstruction, serially sectioned paraffin blocks were scanned with research complex microscopy, and 3D images were reconstructed from the brain sections. The image stacks of the central complex and surrounding neuropils obtained from the brain sections were processed using Amira 5.3.2 software. In *A. kwangreungensis*, the supraesophageal ganglion (brain) of an adult spider is made up of a protocerebral and tritocerebral ganglion, whereas the subesophageal ganglionic mass is composed of a single pair of pedipalpal ganglia, four pairs of appendage ganglia, and a fused mass of abdominal neuromeres. The only nerves arising from the protocerebrum are the optic nerves, and the neuropiles of the principal eyes are the most thick and abundant. In the supraesophageal ganglion. Complex neuropile masses are located in the protocerebrum including optic ganglia, the mushroom bodies and the central body.

[9] Biochemical Investigation into the Presence of Golgi Apparatus in Spider Silk Glands

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Spider silk is a large multi-protein polymer that is synthesized by cells that form silk producing glands in the abdomen of the spider. One would predict that silk, like all secretory proteins would be synthesized on the rough endoplasmic reticulum (rER), processed by the Golgi apparatus and secreted from cells into the lumen of the glands. Interestingly, the Golgi apparatus is not apparent in transmission electron micrographs of silk-producing cells. A biochemical assay was conducted to detect the presence of the Golgi in tissues of the black widow spider, *Latrodectus hesperus*, using a glycoprotein western detection kit. I combined glycoprotein detection with an assay for EndoH sensitivity to determine whether glycoproteins present in the spider's tissues have been modified by the Golgi apparatus; causing them to become EndoH resistant. Results indicate that the glycoproteins are EndoH sensitive, supporting the idea that the proteins only go through core glycosylation in the rER and do not enter the Golgi apparatus.

[10] Does Hawaiian *Tetragnatha* venom composition vary with feeding strategy?

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Spider venoms are a rich source of largely unexplored biodiversity, and we have much to learn about the evolutionary mechanisms that generate this stunning diversity. The Hawaiian radiation of *Tetragnatha* offers a unique system with which to address this question. The majority of the 35 Hawaiian *Tetragnatha* species are orb-weaving spiders, however, a recently derived lineage has abandoned this ancestral state to adopt a cursorial feeding strategy, and have become obligate wanderers (Gillespie 1999). Binford (2001) demonstrates some differences between the venoms of these two species, but was unable to specifically identify venom components. In this study, I apply transcriptomic methods to 1) characterize the venom of two species of Hawaiian *Tetragnatha* (one orb-weaving and one wandering) and 2) analyze differences and similarities between them. After screening cDNA libraries for both species I identified a total of 5 distinct putative toxins including homologs of theraphotoxins and lycotoxins, none of which were common to both species. However, the vast majority of cDNAs that I identified were ribosomal or other 'housekeeping' sequences. This study demonstrates that after methodological optimization, the venom of Hawaiian *Tetragnatha* can be successfully characterized and will be useful to address questions regarding the evolution of chemical biodiversity.

[11] East is east and west is west: Defensive chemistry of North American travunioid harvestmen

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North American opilionids of the taxon Travunioidea are the subject of much recent systematic and phylogeographic research. Here we report on an apparent dichotomy in defensive chemistry between the eastern and western genera. *Erebomaster* and *Theromaster* species of the eastern US secrete a mixture of alkaloids dominated by anabaseine, while the western US genera, including *Sclerobonus*, *Cryptomaster*, *Speleomaster*, *Metanonychus*, *Paranonychus* and *Speleononychus* secrete N,N-dimethylphenylethylamine (pseudephedrine) as the major component. Preliminary results on southern hemisphere (New Zealand) triaenonychids (usually taken as the phylogenetic outgroup to travunioidea) are preliminary, but they appear to secrete various alcohols and aldehydes, so are not of present help in polarizing this character on cladograms. At present we suggest that anabaseine secretion arose once, in the clade that consists of *Erebomaster* and *Theromaster*. Studies on European and east Asian travunioidea are needed to complete the picture.

[12] **Intercontinental ecomorph convergence and community evolution in jumping spiders (Araneae: Salticidae)**

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Adaptive radiations contribute to diversification of life on earth, yet the question remains as to whether patterns of species differentiation are a result of predictable evolutionary processes or historical contingencies. My research asks whether phylogenetically independent communities of jumping spiders (Salticidae) predictably converge in morphospace or whether they are influenced by historical contingencies. To achieve samples not biased by selective species description and to isolate a single ecological context I propose to intensely sample salticids at single sites in comparable tropical rainforests in South America and Australasia (4 sites total) while recording microhabitat data (foliage, litter, tree trunks). I will combine geometric morphometric data with molecular phylogeny and habitat specificity to show whether different sites show independent but similar diversifications in morphology correlated with ecology ("ecomorphs"). This would demonstrate quantitatively that large scale continental diversifications can behave as predictably as smaller diversifications. On the other hand, if strong differences among sites imply contingencies, I will use the dated phylogeny to explore whether relative clade youth could explain lesser diversification. My research will provide a rare example of a large scale study of intercontinental community-level patterns to distinguish convergence and contingency using a comparative phylogenetic framework.

[13] **Fine Structural Aspects on the Ganglionic Neurons in the Golden Silk Spider, *Nephila clavata* (Araneae: Nephilidae)**

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Since arachnids are distinguished from insects by the fact they have eight legs and have no antennae or wings, the spider's CNS is made up of two relatively simple ganglia, or nerve cell clusters, connected to nerves leading to various muscles and sensory systems. The central nervous system (CNS) of the golden silk spider, *Nephila clavata* consists of a dorsal supraesophageal ganglion and a ventral subesophageal mass. A number of nerves arise from these ganglia and spread out to the body, making up the peripheral nervous system. In *N. clavata*, the nerve cells in the supraesophageal ganglion are packed in frontal and dorsal and lateral regions, but the nerve cells of the subesophageal mass are only restricted to the ventral and ventrolateral regions. The central body, which is recognized as an important association center for web building, is isolated at the rear of the protocerebrum and two types of cells are identified on the basis of fine structural characteristics. The globuli cell (Type-A cell) has a large nucleus and poorly stained cytoplasm, whereas the Type-B cell has a granular chromatin and clear cytoplasm.

[14] **Fine Structural Aspects of Dragline Silk Processing in the Valve and Nozzle of the Ampullate Gland of the Spider *Nephila clavata***

Myung-Jin Moon^{1*}, Hoon Kim¹, Jong-Gu Park¹
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As the feedstock flows through the funnel of the ampullate duct, the droplets coalesce and are progressively stretched out by elongation flow to form silk filaments, and finally the polymerized dragline silk fibers are produced at the spigot on the anterior spinneret. Spiders can easily modify the spinning conditions by moving speed, and the diameter of the silk can be controlled by the valve located at the end of the duct. Here we investigate fine structural characteristics of dragline silk processing in the valve and nozzle of the major ampullate gland in *Nephila clavata* using various electron microscopic visualizations. The numerous cuticular cavities are distributed from the middle part of the third limb to the valve, and flask-shaped cells in the epithelium extend to the exocuticle of the duct through these cavities. In addition, we could find detailed cuticular grooves on apical surface of the third limb which are distributed with helical pattern of rifling. Accordingly, the major procedure for the conversion of the liquid feedstocks into insoluble dragline silk seems to be accomplished at the third limb near the valve, and both of the cuticular cavities and rifling grooves seem to contribute to facilitate the rapid conversion of the liquid feedstocks into an insoluble silk thread.

[15] **Microstructure of the Dragline Spinning Duct in the Spider *Nephila clavata* (Araneae: Nephilidae)**

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Silk spinning by araneid spiders are the most complicated and differentiated thread-producing procedures in animals. Recently, spider's dragline silks has been a major goal of biomimetic research for mass-production of artificial silks because of their outstanding tensile strength and toughness. Morphologically, the duct of ampullate gland for producing the dragline silk loops back on itself to form an S-shape and thereby is divided into three limbs of duct sections. As the feedstock passes through the long duct of the large ampullate glands, the polymerized dragline silk fibers are finally produced at the end of its spinning nozzle. Although the importance of this extra length is still not fully understood, our microstructural observations suggest that each limb of the duct may have distinctive functions in the dragline production because each limb seems to be containing different phases of silk, and its cuticular layers or cell types are combined with radical decrease of diameter. Thus, we demonstrate here some microstructural properties of the dragline processing system of the major ampullate gland in *Nephila clavata* using various visualizations including light and electron microscopy.

[16] **Sex but not prey availability drives seasonal variation in body condition in the wolf spider, *Pardosa milvina***

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The physiological state of an organism likely varies in relation to environmental conditions. In particular, availability of food resources should have profound effects on the physiological state of animals. Predatory arthropods such as spiders are considered food limited and extremely polyphagous, which means they should eat any prey available to increase their chance of survival and reproduction. Therefore, we predicted that body condition should be correlated with increased encounter rates with prey. We conducted a field survey of the wolf spider, *Pardosa milvina*. Spiders were collected between May and October in two habitat types, corn and soybean fields. To assess changes in spider condition, we used the residual index from a regression of measurements of size of spiders, carapace width, and mass. Prey abundance was monitored in these same fields to track fluctuations in abundance within fields and between months sampled. Males were on average in poor condition as compared to females. Although body condition declined over the growing season, availability of potential prey increased. These results are consistent with previous characterizations of the sex roles of male and female *Pardosa*, where males forage less than females but are more active as they search for mates. From an ecological perspective, these results suggest that prey abundance is less important than other factors in this system in determining foraging success.

[17] **Trap design choice of *Loxosceles reclusa***

Jennifer L Parks*, William V Stoecker

Pest control without the use of chemicals leaves a consumer with limited options. Glue traps are normally used in circumstances where pesticide use is being avoided. Three-dimensional shape preferences of the brown recluse spider, *Loxosceles reclusa*, were investigated using 4 different glue trap shape designs. These four shape designs were tested using pairwise shape comparisons. The leading trap design was a flat glue trap, which can pose risks in homes with children and pets. Cardboard, a material that brown recluses are known to prefer were used to make the traps more alluring.

[18] **Captive rearing of the orb-weaving spider *Araneus diadematus***

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Previous studies have reported difficulties raising orb-weaving spiders in captivity. We experimented with different methods of rearing *Araneus diadematus* (Clerck 1757) in captivity. We collected spider egg sacs from the wild and maintained them in vials in the lab, then raised spiders from hatching until maturity. To assess life-history characteristics, we recorded the length of time between molts and the number of days to adulthood, for both males and females. We also compared survival rates of early instars for spiders kept in groups versus spiders kept in individual vials. We found that spiders spent significantly longer in the second instar relative to other instars. Spiders took an average of 115.88 ± 13.60 days to reach adulthood. More males reached adulthood than females. Spiders kept in groups tended to mature earlier than those kept in individual vials.

[19] **Scorpion fluorescence and reaction to light**

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Scorpion fluorescence is a mystery. These largely solitary, nocturnal arachnids glow a bright cyan-green under UV light. Interestingly, previous studies of four species from three families have shown that scorpion lateral and medial eyes are maximally sensitive to green light (around 500 nm) and secondarily to UV (350 to 400 nm). We used light-avoidance behavior to assay the responses of desert grassland scorpions, *Paruroctonus utahensis*, to 395 nm UV light, 505 nm cyan-green light, 565 nm green light, and no light within small, circular arenas. Based on the eye sensitivity data, we predicted maximal response to 505 nm, followed by lower responses to 395 and 565 nm. In our experiments, however, scorpions responded most intensely to 395 nm and 505 nm. In field observations, we often spot *P. utahensis* beneath isolated twigs amid open sand. Other studies indicate that photosensitive elements in scorpion tails are sensitive to green light. We therefore propose that the cuticle may function as a whole-body photon collector, transducing UV light to cyan-green before relaying this information to the CNS. The animal may use this information to detect shelter, as blocking any part of the cuticle could diminish the signal. We are conducting behavioral trials on scorpions with their eyes blocked or fluorescence diminished by sunscreen. We predict that scorpions with eyes blocked will respond to UV but display diminished response to green, whereas sunscreen-treated scorpions will show the opposite result. If confirmed, these results would suggest an active role for fluorescence in scorpion light detection.

[20] **UV reflectance in crab spiders (Thomisidae) is derived from guanine crystals**

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The diversity of colours in animals reflects the variety of selection pressures that animal colouration are subjected to. Despite the remarkable number of studies on the function of animal colouration, the full understating of the adaptive significance of colouration can only be complete when the mechanism of colour production is known. Crab spiders (Thomisidae) are a diverse family of sit-and-wait predators. Some crab spiders that ambush prey on flowers are UV-reflective, creating a colour contrast against the flowers that is attractive for pollinators. These spiders are also known by their ability of changing colour, including the UV component, over a few days. Here we investigated the mechanism of colour variation in Thomisidae species, with emphasis in the UV. The analyses showed that high UV colouration is achieved by exposing UV-reflective guanine crystals, present in storage cells bellow the hypodermis, through an UV-transmitting hypodermis and cuticle. White non-UV and yellow colouration are achieved by the presence of ommochrome pigments in different stages in the hypodermic cells, filtering the UV-reflective guanine crystals. Furthermore, the cuticle of spiders are not transparent to light (300-700 nm) as previously argued and therefore it is an important component on the formation of spider colours.

[21] **Setal and sensory structures on the pedipalps of Solifugae**

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Solifuges, or camel spiders (order Solifugae) keep their pedipalps extended when moving through the environment and males use them during copulation. The pedipalps are covered with sensory setae and it is assumed that they are used for chemo- and mechanoreception. However, little work has been done to test this hypothesis. We used scanning electron microscopy (SEM) to examine the surface morphology of the pedipalps of solifuges representing the 12 families. Although similar sensory setae are found throughout the order, several unique setae are found only in particular families, suggesting that the patterns and structures of these setae may be phylogenetically informative.

[22] **A potential morphological indicator of sperm competition in spiders**

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Sperm competition has been studied in a small fraction of spider species. One potential indicator of mating systems and sperm competition would be to compare the relative sizes of the male pedipalp sperm reservoir and the female sperm storage organs (spermathecae) within a species. For example, if the comparison resulted in a 1:1 ratio, one might expect a monogamous mating system. If the ratio of male to female sperm storage amount was 1:3, one would expect polyandry and a higher amount of sperm competition. Given that the mating systems of many species of spiders are unknown, this morphological indicator might provide hypotheses to test concerning species' behavior. In our experiment, we collected orb-weaving species concentrating mainly on the spider families Araneidae and Tetragnathidae with some outgroup entelegyne and haplogyne species for comparison. We measured body and leg length as well as the size of the male pedipalp sperm reservoir and the female spermathecae. To examine male pedipalps, we first expanded the pedipalp and then measured the width, height, and length of the sperm reservoir in millimeters. To examine female spermathecae, we dissected the spermathecae and cleared them with 10% KOH making the spermatheca bulb and duct more visible before measurement. Spider species with known mating systems and levels of sperm competition were used to determine the effectiveness of the morphological comparisons.

[23] Chromosome mapping of dragline silk genes in the genomes of widow spiders (Araneae, Theridiidae)

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Western black widow (*Latrodectus hesperus*) and brown widow (*L. geometricus*) spiders are in the cob-web weaver family, Theridiidae (Araneae). We determined karyotypes and sex chromosome organization for these two species. We then used fluorescent *in situ* hybridization to map the genomic locations of the genes for the silk proteins that compose the remarkable spider dragline. These genes included three loci for the MaSp1 protein and a single locus for the MaSp2 protein. In addition, we mapped a MaSp1 pseudogene. All the MaSp1 gene copies and pseudogene localized to a single region of chromosome 1 while MaSp2 was located on chromosome 8 in *L. hesperus*. Using probes derived from *L. hesperus*, we comparatively mapped all three MaSp1 loci to a single region of chromosome 4 in *L. geometricus*. As with *L. hesperus*, MaSp2 was found on a separate *L. geometricus* chromosome, chromosome 2. These results indicate orthology of the corresponding chromosomal regions in the two widow genomes. Moreover, the occurrence of multiple MaSp1 loci in a conserved gene cluster across species suggests that MaSp1 proliferated by tandem duplication in a common ancestor of *L. geometricus* and *L. hesperus*.

[24] Building the silk gland transcriptome for the Western black widow (Araneae, Theridiidae, *Latrodectus hesperus*)

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Orb-weaving spiders and their relatives synthesize up to seven functionally distinct high-performance silk fibers in specialized abdominal glands. These fibers are primarily composed of structural proteins termed spidroins (spider fibroins). Some of the genes encoding spidroins have been described for a select number of spider species, and virtually all molecular models of silk properties rely on the sequences of spidroins alone. However, non-spidroin genes must also play important roles in silk synthesis. We are using high-throughput sequencing to describe the entire suite of genes expressed in the silk glands of three cob-web weaving spider species (Theridiidae). We constructed a preliminary database of genes expressed in the silk glands of the Western black widow, *Latrodectus hesperus*, using *de novo* assembly of 34 million 75 base pair sequences. This initially resulted in 18,000 contiguous sequences (contigs) greater than 200 base pairs long. Here, we focused on improving the quality and contiguity of a subset of 175 contigs, which based on homology searches were predicted to represent only 27 unique genes. We reduced the number of contigs to 143 and added over 7000 base pairs of sequence data. This resulted in at least 22 complete, high quality black widow genes. We additionally identified 70 non-identical contigs that nevertheless displayed homology to each other and thus likely represent paralogous gene copies. These genes were specifically chosen for their high rate of expression in silk glands and thus offer important insights into regulation of silk synthesis.

[25] Morphological and molecular homology and repurposing of the spider silk spinning apparatus.

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Spiders are unparalleled in the diversity of functionally distinct silks they spin, including silks for egg-case construction, different web elements, and adhesion. The production of silk has been best characterized in araneoid (orb-weaving) spiders, a derived lineage typically possessing seven categories of morphologically distinctive silk glands, each expressing unique silk proteins that compose silk fibers. The majority of these proteins belong to the spidroin (spider fibroin) gene family. The phylogenetic distribution of these seven gland types and their functional roles is poorly known outside of araneoids, because silk glands exhibit great diversity in their morphology and numbers across spider families. In this study, we conducted a comparative analysis of the spinning organs and spidroin proteins involved in egg-case silk production in distantly related spiders. Specifically, we identified glands in the haplogyne spider *Diguetia canities* involved in egg-case silk synthesis, based on amino acid composition of their silk glands and egg-case silk fibers. We also identified the primary spidroin composing *D. canities* egg-case fibers from silk gland cDNA libraries. *D. canities* synthesizes egg-case silk from glands that are morphologically dissimilar to araneoid tubuliform (egg-case) silk glands. Moreover, the egg-case silk of *D. canities* is composed of a spidroin that is extremely divergent from the araneoid tubuliform spidroin (TuSp1) in its repetitive architecture and sequence. We inferred the phylogenetic position of the *D. canities* egg-case spidroin relative to TuSp1 and consider the distribution of egg-case silk glands and spigots across families to examine the evolution of the machinery involved in silk production.

[26] Genes expressed in venom glands of *Loxosceles rufescens*

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Spider venoms are diverse chemical concoctions that evolved for the capture and digestion of prey. Venoms of sicariid spiders cause dermonecrotic lesions in humans, but outside of the dermonecrotic toxin sphingomyelinase D, little is known about the chemical components in their venoms. We have conducted a study to characterize the “Venome” (full set of venom components) of the sicariid spider *Loxosceles rufescens*. *L. rufescens* venom composition is of interest because they are cosmopolitan and thus have potential to be a wide ranging risk and they are members of the divergent and poorly studied North West African clade of *Loxosceles*. To characterize the venome we used transcriptomic (cDNA) and proteomic (MuDPIT) approaches. We identified genes with homology to SicTox gene family toxins (sphingomyelinase D), Sicaritoxins, Ctenitoxins, Lycotoxins, Theraphotoxins, Latroinsectoxins, Astacins, and various housekeeping transcripts. We isolated *L. rufescens* transcripts with homology to nearly all of the toxins found in other sicariid venoms. We were able to identify various evolutionary mechanisms acting on sicariid venom toxins, such as gene recruitment and duplication events. From these data we are able to better predict whether the venom gene families are conserved across the entire sicariid family.

[27] Evolutionary analysis of venom gland gene expression in brown and black widow spiders.

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Venoms have evolved as a means for an animal to quickly disable a victim for feeding and for defensive purposes. The venoms of widow spiders (genus *Latrodectus*) are composed of complex mixtures of proteins, several of which possess potent neurotoxic activity. Despite their biomedical significance, the composition, diversity and evolutionary origins of these toxins remains largely unstudied. We constructed a cDNA library from venom gland tissue of the brown widow spider, *Latrodectus geometricus*, in order to identify Expressed Sequence Tags (ESTs) that code for toxin proteins. In addition, we performed a comparative analysis of toxins and venom-specific proteins from related species, including the black widow spider (*Latrodectus hesperus*). With our data we constructed phylogenetic trees to understand the evolution of these proteins. Our results demonstrate the molecular diversity of spider venom as well as identifying toxins with relevant medical functions.

[28] Investigating the genetic basis of the color polymorphism in *Theridion californicum*

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The leaf-dwelling spider *Theridion californicum* displays a remarkable polymorphism in abdominal color pattern, exhibiting more than 12 color morphs. The evolutionary history and ecological significance of this polymorphism is a topic of ongoing research. A recent population genetic study using AFLPs has demonstrated that, similar to *T. californicum*'s congener the Hawaiian Happy Face spider *T. grallator*, the polymorphism is maintained by frequency-dependent (balancing) selection. A next important step in the investigation of the evolutionary basis of this polymorphism is the identification of genes involved in color expression and patterning. Ommochrome pigment genes, such as vermilion and cinnabar, belong to a widely conserved pathway that has previously been demonstrated to contribute to color patterning in many arthropods including *Heliconius* butterflies, *Drosophila melanogaster* and *Tribolium castaneum*. We show that several ommochrome genes are expressed in the abdominal epidermis of *T. californicum*, making them likely candidates for the genetic basis underlying the color polymorphism. By performing in situ hybridization experiments on the abdominal epidermis, we are comparing spatial expression patterns of the aforementioned ommochrome pathway genes to the different color morphs to investigate the individual significance of those genes in *T. californicum* for color pattern development. Differentially expressed genes could be suitable candidates for further population genetic and phylogenetic investigations into the molecular basis and role of natural selection in shaping the independent evolution of remarkably similar color polymorphisms in multiple representatives across the family Theridiidae.

[29] Molecular and mechanical characterization of minor ampullate silks from cob-web weaving spiders (Araneae: Theridiidae)

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Orb-weaving spiders and their relatives (Orbiculariae) make at least five different types of task-specific silks that are synthesized in unique abdominal glands. These proteinaceous fibers are all high performing materials in terms of strength and extensibility. Relating molecular sequences to mechanical properties has focused on dragline (major ampullate) silk due to its high tensile strength. However, minor ampullate silk shows a unique combination of extensibility and strength that would be desirable for a synthetically engineered material. We have thus obtained sequences of minor ampullate silk encoding genes (*MiSp*) from four cob-web weaving species (Theridiidae), including two complete copies (six total) from *Latrodectus hesperus*, *L. geometricus*, and *L. tredecimguttatus* as well as a partial sequence from *Steatoda grossa*. There are substantial differences in the proportions of amino acid motifs found in *MiSp* both between different loci in the same species and across species. For instance, one copy of *L. geometricus* *MiSp* has a high proportion of Proline-rich motifs, which likely form elastic beta-spirals, but the other copy is almost entirely composed of Alanine-rich motifs that should form beta-sheets. In contrast, *L. hesperus* and *L. tredecimguttatus* *MiSp* have no Proline-rich motifs and a high proportion of Alanine-rich motifs. Mechanical testing will be performed to test hypotheses that relate amino acid motifs to mechanical properties. We predict that *L. geometricus* minor ampullate silk, with its high Proline content, will be the most extensible, but that *L. hesperus* and *L. tredecimguttatus* silks, which are Alanine-rich, will be stronger.

[30] Population genomics in a changing landscape: Area effects and natural selection in the exuberantly polymorphic spider *Theridion californicum* (Araneae: Theridiidae).

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The spider *Theridion californicum* exhibits a dramatic dorso-abdominal color polymorphism comprising at least 12 color morphs. Using nuclear (AFLP) and mitochondrial genetic markers (CO1) we explore the population genetic structure of this species in the San Francisco Bay area. Focusing on Charles

Lee Tilden Park, an area, like many in the region, that has experienced a return to a 'natural' (forested) landscape following centuries of human management (rangeland), we demonstrate a lack of isolation-by-distance in this species, instead revealing a pattern of 'area effects' indicating recent expansion of populations from scattered refugial pockets of native vegetation. Comparisons among AFLP markers and the color locus indicate that many AFLP loci, together with the color polymorphism itself, are likely to be maintained by balancing selection. As would be predicted, these markers show little of the population genetic structuring revealed by the neutral AFLP and mtDNA loci.

[31] Advancing molecular systematics of spiders (*Araneae*) with expressed sequence tags and gene tree parsimony

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Spiders (*Araneae*) belong to one of the most diverse orders of animals, comprising 110 recognized families, 3821 genera, and 42,055 species. Much of this diversity is likely ancient, with fossils representing modern families dating to well over 100 million years ago. Thus, identifying shared derived characters and determining the evolutionary relationships among families has been challenging for both morphological and molecular systematists. Molecular systematics of spiders has additionally been hampered by limited genetic information. However, there is a growing database for numerous species of short sequences (less than 800 base pairs) that represent portions of expressed genes (expressed sequence tags, ESTs). We compiled ESTs for 35 species, representing 26 families, by combining publically available sequences with our own database of genes expressed in silk glands. We assembled ESTs for each species separately to create non-redundant sets of contiguous sequences (contigs), resulting in a total of 16,141 contigs. Basic Local Alignment Search Tool (BLAST) identified all potential homologs among spider contigs. We wrote a complex clustering algorithm in Python to construct non-overlapping groups of homologous ESTs. Clusters typically contained both orthologs and paralogs. We then performed global alignments and determined maximum parsimony gene trees for each cluster individually. We will use gene tree parsimony to infer a species tree that minimizes the number of gene duplication events across the final set of maximum parsimony gene trees.

[32] Species discovery of millipeds in the Pacific Northwest with molecular analyses of *Chelojulus* (*Julida*, *Chelojulidae*) supporting yet another new species.

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Ongoing faunal surveys of Diplopoda in the Pacific Northwest since 2000 have resulted in the discovery of approximately 70 new species. Of these, a handful have been described and published including a new family, three new genera, and half a dozen new species. Among these discoveries was a 500 km range extension of the morphologically unique Julida genus *Chelojulus sculpturatus* from northern Idaho into the Willapa Hills of western Washington. Morphological discrimination of this species was not possible using standard gonopodal differentiation. Though the taxonomic absolute of gonopodal differences are not tested here using morphometric analyses, the newly discovered population as a unique species is tested using molecular analyses. The mitochondrial 16S and nuclear ribosomal 28S genes are used to test species limits in the genus *Chelojulus*. These gene trees support unique species for this group, with vicariance likely coinciding with orogeny of the Cascade Mountains around 5 MYA. Natural history of the group, as well as distribution in the mesic forests of the northern Rocky Mountains, including first state records for Montana, are also reported.

[33] Not so banal after all; latest evidence on *Loxosceles* diversity in Canary Islands and Northwestern Africa

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The venomous spider genus *Loxosceles* has a widespread distribution, and the vast majority of its species are concentrated in North and South America. The cosmopolitan *Loxosceles rufescens* (Dufour, 1820) has its original distribution range in the Mediterranean basin, and has been the only valid representative of the genus in this area until the recently discovered *Loxosceles mrazig* Ribera & Planas, 2009 from Tunisia. Recent collecting trips carried out in Morocco and Canaries provided us with abundant material of *Loxosceles*. In this poster, we present the preliminary results on biogeography and taxonomy of this genus in the Mediterranean and Canary Islands, based on morphology and molecular data. Canary Islands harbor an endemic group of *Loxosceles* species. Until now we have identified 5 endemic species: 1 from Fuerteventura and Lanzarote, 2 from Tenerife and 2 from Gran Canaria. Our data suggest a single colonization event to the eastern Canary Islands (Fuerteventura and Lanzarote) and a posterior interinsular colonization to Gran Canaria and Tenerife. Within the *L. rufescens* lineage, preliminary results, including individuals from the type locality and a large number of specimens from the Mediterranean Basin, show several independent evolutionary lineages that could suggest a cryptic speciation.

[34] Molecular and biomechanical insights into the parallel origin of orb-like webs in spiders

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The evolutionary origin of the spider orb web in Orbiculaeae was accompanied by new spinning behaviors and significant changes in the material properties of silk. In particular, the major ampullate silk that forms the backbones of most webs is stronger and stiffer among orb-weaving spiders, possibly

facilitating the capture of flying insect prey. However, the little known *Fecenia* also constructs a two-dimensional aerial web that is strikingly similar to an orb web. Here, we first test the evolutionary affinity of the pseudo orb versus genuine orb webs and then compare the material properties of their silks. We sample two *Fecenia* and one *Psecchus* species (both in *Psecchridae*) and sequence partial fragments of mitochondrial (16S, COI) and nuclear (18S, 28S, H3, wingless) markers, adding these data to the published orbicularian and RTA matrices to infer their phylogenetic affinities using Bayesian inference. We also perform tensile tests on the radii from both types of webs to compare their material properties in a broader evolutionary context.

[35] Archaeid spiders and their relatives (Araneae, Archaeidae): fossil placement, biogeography and evolution of the carapace morphology

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Molecular and morphological phylogenetic analyses are performed for living and extinct archaeids and for outgroup taxa representing 20 different spider families sampling throughout the Araneomorphae. Fossil archaeids are examined using X-ray Computed Tomography in order to understand phylogenetic placement of extinct lineages. Additionally, a molecular phylogenetic analysis of living archaeids is performed to elucidate relationships among extant species from Australia, Madagascar and South Africa. Biogeographic findings within different continents as well as between continents are discussed. The limits of the superfamily Palpimanoidea is examined. Furthermore, evolution of the carapace shape is examined from a phylogenetic context.

[36] A new trapdoor spider species from the southern Coast Ranges of California (Mygalomorphae, Antrodiaetidae, *Aliatypus coylei*, nov sp), including consideration of mitochondrial phylogeographic structuring.

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The trapdoor spider genus *Aliatypus* (Araneae, Mygalomorphae, Antrodiaetidae) includes eleven described species, ten of which are endemic to California. *Aliatypus* species are known from most physiographic provinces in California, with the noticeable absence of described species from the southern Coast Ranges. Here we describe a new species (*Aliatypus coylei*, novsp) that is shown to occur at more than 20 locations, the majority of which are in the southern Coast Ranges. This species is morphologically most similar to members of the *A. erebus* species group (*A. erebus* Coyle and *A. torridus* Coyle), but differs from these latter species in several male features. Female specimens are more difficult to distinguish from *A. erebus* and *A. torridus*, but can be easily separated using DNA characters. Collection of mitochondrial DNA sequence data from 21 sites shows that *A. coylei* is genetically very divergent from all described *Aliatypus* species, and also reveals extreme population subdivision across the fragmented southern Coast Range landscape.

[37] Jumping spider phylogeny, continued: more genes, more species, more resolution (Araneae: Salticidae)

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New molecular data from more species and more genes continues to resolve salticid phylogeny. Previous studies have used the genes 28s, Actin 5C, 16sND1, 18s, CO1, Histone 3, and Efl-alpha, with 28s showing the clearest phylogenetic signal. To these we add the wingless gene, wnt-8 and myosin. Preliminary analyses shows wingless results are strongly concordant with those of 28s; myosin is promising but sequenced from only a few species to date. Together these confirm many of the previous results, and add some deep salticoid resolution, including an apparent clade of plexippoids, aelurilloids, salticines, leptorchestines and euophryines. Well-supported placements are found for cocalodines and the ant-like Eburneana. Most problematic are the strange Agorius and Synagelides, whose placements differ among genes.

[38] Fossil spiders from the Lower Cretaceous Crato Lagerstätte, Brazil

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At present three spider species have been described from the Crato Formation of Brazil, a single araneomorph (*Cretaraneus matinsnetoi*) and two mygalomorphs (*Cretadiplura ceara* and *Dinoplura ambulacra*), known from a total of five published specimens. Preliminary study of almost a hundred undescribed Crato spider specimens reveals two more mygalomorphs, and at least three araneomorph species. The mygalomorphs are probably assignable to *Cretadiplura ceara* and display details of the coxosternal region that are not observable in the type specimens. The most common araneomorph is probably congeneric (if not conspecific) with *Cretaraneus matinsnetoi*, however neither this nor the original material displays the characteristics of *Cretaraneus* and its assignment needs revision. Two large specimens resemble nephilids, while a single small specimen may represent a palpimanid. Further work is required to accurately identify these specimens. Many of the Crato spiders are preserved in an uncompressed, three-dimensional state, and it is hoped that CT-scanning may reveal further details of their morphology preserved within the matrix that will assist in their identification.

[39] A multifaceted taxonomic assessment of the tarantula *Aphonopelmaanax* (Araneae: Theraphosidae) and its close relatives from South Texas

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The tarantula genus *Aphonopelma* comprises at least 90 species throughout the United States, Mexico, and portions of Central America. Despite this putative diversity, however, very few non-type specimens can be confidently identified using available taxonomic keys or species descriptions; consequently, species boundaries in this interesting group of spiders remain obscure and problematic. Of particular interest is the species *A. anax* and its close relatives *A. harlingenum* and *A. breenei* from South Texas. These spiders have been described on the basis of only a few individuals, resulting in poorly defined limits of intraspecific and interspecific variation. In order to assess species boundaries in this group, we employed a multifaceted taxonomic approach utilizing genetic and geospatial data. Our results demonstrate that these three nominal species are genetically and ecologically “cohesive” and should no longer be recognized as three distinct species; instead, our data support the synonymy of *A. harlingenum* and *A. breenei* under the name *A. anax*. Our results further show that *A. anax*-like specimens from some western localities belong to a genetically divergent lineage; however, geospatial analyses do not demonstrate concomitant ecological divergence between western and eastern populations. As such, we argue that *A. anax* is the only “large brown” tarantula species in South Texas, but it possesses substantial genetic diversity that appears roughly structured along the boundary between the following Level III Ecoregions: the Southern Texas Plains and the Western Gulf Coastal Plain.

[40] First steps towards a world monograph of the spider family Leptonetidae

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Recent revisionary work has dramatically improved our understanding of species level diversity in the Leptonetidae, particularly in East Asia and North America. However, most leptonetid genera remain poorly characterized and phylogenetic relationships within the family are unexplored. As the rate of species discovery accelerates, there is a need to better define leptonetid genera in order to provide a taxonomic foundation for future studies and produce a scaffold for evaluating biogeographic and evolutionary patterns. Here we present the first assessment of leptonetid relationships based on a combination of molecular and morphological data including exemplars for most described genera worldwide. Morphological characters supporting major clades are discussed and an overview of leptonetid biogeography is provided.

[41] Several new species of silhouetteloid goblin spiders of Madagascar (Araneae, Oonopidae).

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Currently goblin spiders are subject to considerable taxonomic research by a large group of colleagues in many countries as part of the Planetary Biodiversity Inventory (PBI). The work presented here contributes to this effort to document and describe oonopid diversity world wide. We describe a total of nine species from Madagascar and the Seychelles documented with ca. 390 compound digital images and 670 scanning electron microscope pictures. These species represent two genera: *Silhouettella* Benoit, 1979 characterized by the absence of leg spines, eyes well developed occupying three quarters of the cephalothorax width and abdomen completely covered with scuta, and the new genus characterized by a gradual reduction of eyes, presence of leg spines and abdominal scuta. All species are new except *Silhouettella curieusei* the type of this genus which is only known from the Seychelles. The core of the taxonomic descriptions was done automatically by coding character observations to the PBI website using only a Internet browser and based mainly on the images mentioned above. The geographic distribution for all specimens was added to the PBI Database for Entering Collection Data (DEC) web interface. All of this information will be available online through the species pages of the PBI goblin spider website after the species descriptions are published. In addition, we used a novel feature of this taxonomic descriptive data base to export a phylogenetic data matrix of 1,173 taxa and 450 characters. A phylogenetic analysis with a subset of 543 taxa and 361 non redundant characters between sexes recovered these nine Malagasy species as two different clades: the former including *S. curieusei* plus two new species, and the latter including six new species. We emphasize that the character scoring for this 1,100+ species data set represents a collaborative effort of the PBI team of researchers, postdoctoral fellows and graduate students.

[42] Antimicrobial properties using egg cases for Theridiidae spiders *Latrodectus hesperus* and *Latrodectus geometricus*

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Spider egg cases function to protect developing spiderlings. Among its many characteristics, the silk that makes up the egg case appears to have antimicrobial properties. We report here on a preliminary analysis of the antimicrobial properties of egg case silk from the Theridiidae spiders *Latrodectus hesperus* and *Latrodectus geometricus*. Egg cases were collected from spiders that were housed in the lab. Egg cases were frozen to arrest development. Eggs or spiderlings were removed and separated from the silk. To test for the presence of bacterial floral small samples of the egg case silk were aseptically transferred to test tubes containing tryptic soy broth. Bacterial growth was monitored for a period of a week using optical density measurements. The majority of egg case samples from *L. hesperus* did not show any evidence of bacterial growth. In contrast the majority of samples from *L. geometricus* did give rise to bacterial growth. The presence of bacteria on the silk surface was also examined by repeatedly touching a silk sample to the surface of a tryptic soy agar plate. Colony formation did not occur after 48 hours for both type of species with a much greater rate of colony formation for *geometricus* vs. *hesperus*. Silks from Araneidae spiders have been shown to have multiple surfaces layers. We hope to identify the factors responsible for the antimicrobial properties we have observed.

[43] Accumulation of toxic heavy metals in urban spider webs

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Spiders in urban environments are impacted by many variables: the quality of the habitat, type of prey available, and urban pollution from anthropogenic sources. Although some urban ecological studies have focused on insects, such as ants, no studies have focused on a key arthropod predator: spiders. Spiders may be especially affected by poor air quality in ways that insects are not because spiders build webs that may act as environmental filters. In urban environments air quality may be poor, particularly near industrial sites. Spiders that build webs may be especially affected by air pollution in the form of ultra-fine particles (such as are released from motor vehicles and also some industries) that are caught and contained in their webs. We sampled spider webs from an urban neighborhood in Detroit near an industrial area by the Detroit River for three consecutive weeks in July 2009 and July 2010. We found that detectable levels of toxic heavy metals were trapped in spider webs. This result could help to make direct connections between humans and their effects on the environment, as well as bringing to light some potential health hazards in urban settings for people as well as spiders.

[44] Seasonal Dynamics and Biomass of Spiders and Other Soil Invertebrates in Oak Forests of Black Rock Forest, NY

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The Black Rock Forest (BRF) is located in New York State about 60 miles north of New York City. Our study is part of a large, multistage BRF project: "Ecosystem Consequences of Dominant Taxon Loss: the Future of Oak Forests." Spiders and other soil invertebrates studied on two already designated sets of plots: a pilot project area and a main project area. A pilot project includes two areas: fenced and unfenced. The fenced area protects vegetation against different wild animals, mostly deer. We collected in the oak forest 210 species of spiders and also representatives of different orders of invertebrates. Preliminary data shows that spider's biomass has an interesting correlation between fenced territory and area outside the fence, hence the spider's biomass outside of the fenced area in June is reaching its maximum and is slightly higher than the spider's biomass inside of the fenced area. This data suggests that ground inhabiting spider's community is not significantly affected by herbivorous mammals, such as deer. In June the spider's biomass outside of the fenced area shows a very strong correlation with the type of experimental plots: the lowest spider's biomass was on the plot with all oak trees girdled, the next spider's biomass was on the plot with all oak trees girdled on 50%, next all non-oaks trees girdled and the maximum spider's biomass was recorded on the control plot. This data definitely shows that the state of dominant trees health plays important role on the species diversity and the spider's biomass.

[45] Orb-weaving spiders accumulate toxic heavy metals in southeastern Michigan

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Spiders are top invertebrate predators in terrestrial food webs and yet little is known about whether they bio-accumulate significant levels of anthropogenic pollutants such as heavy metals. In this study we collected orb-weaving spiders and environmental samples from 10 sites along the lower branch of the Rouge River as well as from two more pristine sites near the start of the middle Rouge River: Johnson Creek in Northville and the Huron River in Pinckney. The Rouge River sites were sampled from June to August to observe any short and long-term changes in the soil and water quality. The spiders and environmental samples were analyzed for toxic heavy metals using inductively coupled plasma mass spectrometry (ICP-MS). We found detectable levels of toxic heavy metals in both spiders and environmental samples collected along the Rouge River in southeastern Michigan. This result suggests that orb-weaving spiders may be sensitive to anthropogenic pollution and they should be considered when restoring wetland ecosystems.

[46] Diel periodicity in activity and location in the web of the common house spider (*Achaearanea tepidariorum*)

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Circadian rhythm is a type of endogenous clock that controls daily behavioral patterns in most organisms. Spiders have been shown to exhibit both circadian and non-circadian rhythms in their behaviors. This rhythmicity may allow spiders to cope with diel changes in environmental conditions. Both diurnal and nocturnal behavior have different sets of costs and benefits to a species' survival. *Achaearanea tepidariorum* is one species in which potential circadian rhythmicity has never been studied. Due to its foraging behavior, it was predicted that its daily activity would be arrhythmic. We recorded the positions within the web of forty individuals throughout the day, and then observed their daily activity via use of an infrared activity monitor. Analysis of the resulting actograms and web position data revealed a significant nocturnal periodicity in the spiders' activity, as well as possible anticipation of the daily cycle. This nocturnal periodicity, coupled with specific web-building behavior, may be the result of this species balancing the costs and benefits of predation and foraging. More studies are needed to provide more information about the circadian behavioral patterns of *A. tepidariorum*.

[47] The effect of reproductive status on the predatory efficiency of female Arizona Bark Scorpions (*Centruroides sculpturatus*)

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Acquiring resources is crucial for an organism's survival, and therefore animals spend a considerable amount of time foraging for food. Studies have shown that the foraging and feeding rates of predators can be influenced by their reproductive state. Changes in the feeding rates of female predators during pregnancy can influence maternal energy reserves, as well as the amount of resources allocated to offspring development during gestation. Although changes in the feeding rates of gravid (pregnant) female predators have been documented, the efficiency with which gravid females capture prey has received much less attention. We investigated how predatory efficiency may be influenced by reproductive state in female Arizona Bark Scorpions (*Centruroides sculpturatus*). Prey-handling trials were conducted, and the times taken to pursue and subdue prey were compared among females of

different reproductive states. Our results suggest that gravid females do not experience decreases in predatory efficiency, suggesting that they are able to mechanically cope with increases in body mass and physiologically handle the metabolic cost of developing offspring during gestation. Further, prey-handling times increased significantly for females exhibiting maternal care (carrying offspring on their backs) compared to non-reproductive and gravid females. Following offspring dispersal, females did not exhibit faster prey-handling times than females still carrying offspring possibly due to physiological exhaustion following maternal care. These results suggest that the cost of reproduction in terms of reduced prey-handling efficiency for female Arizona Bark Scorpions is experienced during and subsequent to the maternal care period.

[48] Sex amongst cannibals: the reproductive behavior of a mimetid spider.

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Spiders of the family Mimetidae, commonly known as the pirate spiders, are some of the most intriguing and lesser-known araneophagic spiders. Despite their reasonably high population density, only a few researchers have studied their predatory behavior and the reproductive behavior of pirate spiders is unknown. How these spider-eating cannibals mate has been an intriguing theoretical question until now. This study is the first description of reproductive behavior of any pirate spider species. We describe the mating behavior of a fairly common species found in southeastern Michigan and surrounding areas.

[49] Cooperative kleptoparasitism? Living in groups increases foraging efficiency in *Argyrodes miniaceus* (Argyrodivinae, Theridiidae).

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Kleptoparasitic spiders conduct foraging primarily in the webs of larger spiders. Their foraging strategies include araneophagy, scavenging, sharing prey with host, and silk-eating, and may be flexible and interchangeable within one species. About 20 out of 220 species in Argyrodinae are group-living in the webs of their hosts: multiple individuals forage in one host web and show strong conspecific tolerance, especially when sharing prey items directly with their host. The properties of this group-living behavior have never been examined. We test whether group-living behavior increases foraging success in *Argyrodes miniaceus*, a species that shares prey directly with the host. *Argyrodes miniaceus* and its host, *Nephila pilipes*, were raised in the lab in 2 X2 X 2 ft cages. For each experimental trial, a ~0.3 g cricket was provided to the host spider. We used average feeding duration as the indicator of foraging success and tested kleptoparasite group sizes from 1 to 7, with total replications ranging from 20 to 42 individuals in each group size treatment. ANOVA results show per capita feeding duration is highest in groups of two or three individuals. Time series analyses show that when group size is larger than four, *A. miniaceus* individuals take turns to feed, so that usually only two or three kleptoparasites feed with the host at one time. Several behaviors are associated with higher foraging duration in groups. We conclude that group-living behavior in *A. miniaceus* is a type of cooperative foraging.

[50] Shifts in female silk deposition in the presence of composite silk from conspecifics in the wolf spider *Pardosa milvina* (Araneae; Lycosidae)

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Males and females of the wolf spider, *Pardosa milvina* (Hentz, 1844), produce silk draglines to attract prospective mates. Silk is energetically costly to produce so females may benefit by selectively investing in silk advertisements based on mate availability and the presence of other female silk. Females may also benefit by discriminating among silk from two different males or silk from a female vs. a male. Information about spider sex or individual identity through draglines could allow females to use silk to attract specific males, assess local sex ratios, or minimize silk deployment by exploiting the advertisements of other females. Females may also benefit by assessing the order of silk deposition by conspecific males and females. Using silk, females could assess whether males are currently pursuing a female or if females were in the area last. We measured female silk deposition over a 30-minute period in the presence of silk from seven different combinations of conspecific males and females that deposited silk over different time periods and in different sequences. Females deposited significantly more silk on blank substrates and reduced silk deposition when encountering silk from other spiders. Females showed more silk deposition in the presence of silk from a single female rather than multiple females or males and did not discriminate between the order of silk deposition for males and females. Females mediate silk deposition based on the different combinations of conspecific silk but females varied in the quantity of different silk types depending on the context.

[51] Can spiders recognize their own silk?: Variation in silk deposition in response to self and conspecific silk in the wolf spider, *Pardosa milvina* (Araneae; Lycosidae)

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Silk is an important communication medium for the wolf spider *Pardosa milvina* (Hentz 1844). Both sexes produce silk as they move through the environment. This silk may function in species recognition, sex identification, mating status assessment or to convey information about body condition. Silk is also energetically costly; therefore, males and females may benefit by selectively depositing silk to maximize communication efficacy but minimize cost. Spiders may also benefit by discriminating between their own or another conspecific's silk. Silk-mediated self-recognition could allow spiders to identify areas that they have previously visited, competitively block silk advertisements from sexual rivals, or minimize redundant signaling in an area. We tested if male and female *P. milvina* wolf spiders can discriminate between their own silk and the silk of another spider of the same sex. Using a paired design, we quantified male and female deposition of three silk types: draglines, cord silk, and attachment disks on substrates containing either their own silk or the silk of a conspecific (N = 51). Both males and females significantly increased dragline and cord silk deposition on substrates containing same-sex conspecific rather than their own silk with males producing more cord silk than females. Males increased attachment disk deposition on conspecific male silk compared to their own while females showed the opposite response, decreasing attachment disk deposition on conspecific female silk. Wolf

spiders can recognize their own silk with small but significant qualitative and quantitative differences in silk deposition by males and females.

[52] Experience with chemotactile cues indicating female feeding history impacts male courtship investment in the wolf spider *Schizocosa ocreata*

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Male fitness is often determined by the ability of the male to gain access to multiple mates, although in spider species that exhibit sexual cannibalism, males might increase their likelihood of being cannibalized with each encounter. The risk of cannibalism should therefore create selection for males who are able to perceive potential risks associated with mating encounters. We studied male *Schizocosa ocreata* wolf spiders to determine whether they use chemotactile cues (silk, excreta) of females as indicators of potential risks, and how these cues affected subsequent male courtship behaviors. Female treatments included satiated females vs. starved females, as well as a treatment where females had recently cannibalized a male *S. ocreata*. We performed experiments to assess if males: 1) alter courtship investment in response to female chemotactile cues indicating potential risks associated with different female feeding treatments; and 2) how male experience with female chemotactile cues affected courtship investment in subsequent female encounters. Results indicate that at a first encounter, males do not vary courtship investment (number of bouts, duration and vigor) with different female feeding treatments. However, during subsequent encounters with female chemotactile cues, male behaviors varied, depending on female feeding treatment and experience with chemosensory cues previously encountered.

[53] Some die that others live: death by Ichneumonid

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The larvae of ichneumonid parasitoids are infrequently attached to the upper, anterior parts of the abdomen of *Araneus* species (Araneae: Araneidae) and other immature spiders. Very rarely are these parasitoids reared from the larval stages to the pupa to the adult. *Araneus gemmoides* Chamberlin & Ivie immatures (2nd or 3rd instar), with an ichneumonid parasitoid larva attached, were photographed at extreme close-up distances starting in April. The spiders are about 3 mm long or less. Normally, this spider would hatch from the egg the previous June (2-year life cycle here), and would be at least 6-9 mm in body length. Chemicals issued by either the larva, and/or the mother wasp, inhibit ecdysis. A series of photos shows the larva growing larger, killing and abandoning the spider's shrivelled body, the parasitoid pupa in a cocoon, through to the adult of *Polysphincta koebelei* Howard. *Araneus gemmoides* is a new host for this parasitoid, and this is the first record for *Polysphincta koebelei* in Canada.

[54] Effects of food limitation on locomotory behavior in tarantulas (*Brachypelma albopilosum*)

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Tarantulas are typically considered sit-and-wait predators. During periods of extreme prey scarcity however, they can either increase activity levels to find more prey or decrease activity levels and possibly metabolic rates to save energy. We examined changes in locomotory activity in tarantulas (*Brachypelma albopilosum*) in response to prey scarcity. Initially all tarantulas were fed 20-25% of their body mass and activity levels were recorded over a 6-hour period. Tarantulas were then separated randomly into two groups and over a three month period were fed a cricket diet of either 20-25% body mass or 3-6% body mass and activity levels of the two groups were again compared. No differences were found in activity levels in the initial trial. However, after 3-months of differential feeding between groups, tarantulas in the food-limited group had significantly more bouts of movement even though they did not necessarily travel greater distances. Our findings suggest that prey scarcity can reach low enough levels that *B. albopilosum* will alter its sit-and-wait foraging strategy to pursue a more active foraging strategy. A more active foraging strategy increases the likelihood that *B. albopilosum* will encounter potential prey items and thus may affect survival and lifetime fitness.

[55] Nuptial thief: male spiders steal food from mating partners

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Adult male spiders do not build webs. Once males molt to maturity, they wander in search of females to mate. For orb-weaving spiders, not building a web means that no prey can be captured and hence males cannot feed themselves. In some sexually dimorphic orb-weaving species with extremely tiny males, such as *Nephila*, the males are kleptoparasitic and subsist on the leftover remains of prey not eaten by females. No spider species has been observed to have males that steal prey items caught by females. Here, we report for the first time that males of at least one orb-weaving species, *Tetragnatha elongata*, are able to feed as adults by actively stealing food from their female partners after mating. We collected adult *T. elongata* in southeastern Michigan and performed 165 staged matings in the laboratory. We found that male food-stealing behavior was significantly influenced by the relative body masses of males and females. When the difference in body mass was minimal, males were able to steal prey. This finding suggests that males may have a trade-off between acquiring food resources and achieving greater reproductive success with larger more fecund females.

[56] The effect of chemotactile cues from multiple predators on the condition and survival of the wolf spider *Pardosa milvina* (Araneae: Lycosidae)

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Predation risk can have strong effects on the ecology and behavior of potential prey. Many arthropods detect chemical cues (excreta, feces and, for spiders, silk) from their predators. Two wolf spiders, *Pardosa milvina* (Araneae: Lycosidae) and *Hogna helluo*, and a ground-dwelling beetle, *Scarites quadriceps* (Coleoptera: Carabidae), coexist in agricultural fields. The spider, *Pardosa*, detects cues from both of the large species but responds differently to them. We studied the effect of exposure to the chemotactile cues of the larger predators as an immature on body condition and ultimately survival time of *Pardosa*. We placed the *Pardosa* in a container previously occupied by one of two predators for a period of 24 or 72 hours. Body measurements were taken before and after exposure to quantify feeding success. Spiders were then maintained in normal laboratory conditions and lifespan was recorded. Although exposure to predator chemical information had no effect on feeding success of *Pardosa*, there were sex differences in lifespan contingent on predator and length of exposure. Both sexes survived less time if they were exposed for 72 hrs as compared to 24 hrs. Interestingly, females that were exposed to *Scarites* chemical information lived longer than unexposed controls and those that were exposed to *Hogna* died more quickly. Males survived less time after exposure to cues from either predator than when exposed to blank substrate. The results reveal interesting indirect effects of predators on their prey and these effects likely impact the fitness of *Pardosa* in the field.

[57] Social Interactions in the colonial Mygalomorph Heterothele villosella (Strand 1907)

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Spiders are normally solitary animals, infrequently engaging in contact with conspecifics. In rare circumstances, species abandon their solitary tendencies and remain in a group. Extreme inbreeding, reduced genetic diversity, high colony turnover rates and high rates of extinction potentially account for the rarity of this phenomenon. A potentially useful subject for addressing the evolution of spider (Mygalomorph) sociality is the Ischnocolid tarantula species *Heterothele villosella*. The social lifestyle of this species is not unique among its congeners but not all of them have been documented for sociality. Herein, we aim to examine fundamental social interactions and how environmental conditions influence this species' sociality. This understanding will contribute to the growing body of knowledge pertaining to the evolution of spider sociality and how the assembly of these communities affects the evolution of competition and social living in an otherwise solitary animal.

Initial observations suggest that cannibalism increases directly with incidences of contact when there are no established territories. We can postulate that dispersal, either natural or stochastic, may lead to increased rates of cannibalism in nature. After a brief acclimation period, individuals were observed to establish individual retreats/territories. During this phase, we observed social tolerance among individuals living in adjacent and shared retreats, greatly reducing the instances of cannibalism. Therefore, the observed colonial nature of the species may be impacted by familiarity/residency duration and overall environmental stability.

[58] In pursuit of the forces that drive sexual display divergence in closely related jumping spiders

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Sexual display traits often comprise the greatest phenotypic differences among even closely related species. This indicates the forces shaping sexual displays are a rich source of biological diversity and may play a role in speciation. Describing these forces at the earliest stages of display divergence is key to understanding how they affect diversification. We take up this challenge in a set of *H. americanus* jumping spider populations that are diverging in male sexual display morphology. We document generally weak genetic differentiation among populations and a regional pattern of increasing genetic isolation by geographic distance. These results suggest that selection in the face of gene flow, rather than genetic drift among isolated demes, underlies display divergence in this system. We also observe surprisingly low genetic differentiation between the *H. americanus* populations and that of a nearby congener, *H. sansonii*, raising the possibility that this second species provides a source of divergent selection or genetic variation for *H. americanus*.