ABSTRACT BOOK

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International
Congress of
Arachnology

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INVITED SPEAKERS

Plenary talk, day 1

Sensory systems, learning, and communication – insights from amblypygids to humans

Eileen Hebets

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Arachnids encompass tremendous diversity with respect to their morphologies, their sensory systems, their lifestyles, their habitats, their mating rituals, and their interactions with both conspecifics and heterospecifics. As such, this group of often-enigmatic arthropods offers unlimited and sometimes unparalleled opportunities to address fundamental questions in ecology, evolution, physiology, neurobiology, and behaviour (among others). Amblypygids (Order Amblypygi), for example, possess distinctly elongated walking legs covered with sensory hairs capable of detecting both airborne and substrate-borne chemical stimuli, as well as mechanoreceptive information. Simultaneously, they display an extraordinary central nervous system with distinctly large and convoluted higher order processing centres called mushroom bodies. With respect to these under-explored, yet intriguing, animals, I will highlight how studies focused on basic behaviour, natural history, and neuroanatomy can lend insight into fundamental and generalizable scientific understanding. I will do this by discussing my research, conducted in collaboration with colleagues, which pertains to the link between the amblyypygid's unique sensory morphology, nervous system, and complex behaviour, including learned behaviour. Additionally, I will use my research on the North American wolf spider genus *Schizocosa*, and potentially the fishing spider genera *Dolomedes* and *Pisaurina,* to demonstrate how spider reproductive behaviour can help scientists understand basic processes and mechanisms underlying divergence in reproductive tactics and ultimately speciation. Finally, I will show how the wonders of arachnid biology, combined with creative visual aids and active educational techniques, can inspire not only arachnid conservation, but also the next generation of science professionals; including arachnologists.

Young Arachnologist: Oral presentation, day 1

The evolution of diverse animal weapons

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Weapons, exaggerated structures used by males to increase mating opportunities, are among the most elaborate and diverse structures in animals, but we know very little about the mechanisms driving their evolution. Comparative approaches that determine patterns of weapon evolution across a group of closely related species can help us understand why weapons are so diverse. We are investigating the factors driving weapon diversity in a group of endemic New Zealand arachnids, the neopilionid harvestmen. Males bear extremely exaggerated chelicerae, which are correspondingly much reduced in size in females. The degree and form of chelicerae exaggeration varies drastically both within and between species.

As well a striking range of chelicerae size and shape among species, several species also exhibit chelicerae polymorphism, where males can possess reduced female-like chelicerae or one of two exaggerated morphs (long slender or short broad chelicerae). Using a phylogenetic framework coupled micro-CT imaging to quantify 3D shape variation, we elucidate patterns of weapon divergence across this group to determine how these extreme traits have evolved.

Young Arachnologist: Oral presentation, day 1

Evolution of palpimanoid spiders: bizarre morphologies, unusual behaviours, and extreme speeds

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Morphological diversity may be redundant in relation to function, that is, different morphological solutions may evolve to produce similar performances. Thus, in order to understand how morphological diversification occurs it is crucial to first understand the link between form and function. The palpimanoid spiders have restricted distributions, exhibit strikingly deviant morphological, behavioural, and ecological traits, and are an ancient lineage with a fossil record. In particular, in palpimanoids, the novel and unusual modifications of the cephalicarea and chelicerae may allow these spiders to capture prey in innovative ways. They are an excellent group for addressing questions about how a specific trait functions, which in turn, may allow for examination of broader macroevolutionary questions about how these traits (as well as lineages) diversify. My talk will be a discussion of our current understanding of cheliceral function and morphology in palpimanoids, which has been enhanced by Computed-Tomography scanning techniques for visualization of minute internal structures. Additionally, I'll talk about how the extensive fossil record in palpimanoids has allowed for the examination of shifts in morphological diversity over time. Finally, the study of morphological evolution is confounded by distribution patterns, and I'll discuss research about the interplay between trait evolution and biogeography patterns.

Young Arachnologist: Oral presentation, day 1

The promises of next generation sequencing technology for high throughput assessment of spider diversity

Henrik Krehenwinkel

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Next generation sequencing (NGS) technology has revolutionised evolutionary biology and ecology in the past decade and enabled unprecedented insights into the structure of the tree of life and the genetic basis of speciation and local adaptation. NGS based DNA barcoding protocols have also greatly simplified the analysis of species diversity and interactions in biological communities. Using Hawaiian spider communities, we here present different NGS based tools for rapid, cost-efficient and large-scale analysis of taxonomy, biogeography and species interactions. Home to impressive and diverse adaptive radiations, the Hawaiian Archipelago is a biodiversity hotspot of global importance. In conjunction with its geographic isolation and well-known geology, the island chain is also considered a natural laboratory for

the study of island biogeography. Although much of the Hawaiian biodiversity is comprised of arthropods, very little is known about diversification and assembly of Hawaiian arthropod communities. The emerging technologies of next generation sequencing now allow for unprecedented insights into the process of community assembly. Here, we present results from the application NGS to multi-locus phylogenetic and taxonomic analyses of mixed spider community samples. Using metabarcoding protocols, we acquire qualitative and quantitative data of the species composition within and across communities on the Hawaiian Islands. In addition, we introduce novel approaches to study the feeding ecology of spiders in great detail. Combining gut content analysis and microbial community sequencing, we then present results on the effect of diet on the gut microbial communities associated with spiders.

Plenary talk, day 2

Spider phylogenetics and evolution – beyond the trees

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Spider systematics has advanced tremendously in the last years from phylogenetic analyses of sequence data, mainly anonymous in terms of phenotype. For the first time the phylogenies are relatively robust and easy to obtain, yet the evolutionary implications for functional morphology, behaviour and biogeography are only slowly emerging. For those who are not systematists it is difficult to digest the phylogenies that are published year after year, and for systematists it is not easy to understand or elaborate on the evolutionary implications of their discoveries. In this talk I will try to summarise a personal view of some important advances in spider systematics and how they are linked to general questions of functional anatomy and behaviour. Then I will discuss how is it like to investigate the historical biogeography of spiders from a peripheral country far in the southern hemisphere, with access to a peculiar diversity of species, witness of a certain geo-climatic events, temporal scales and adapted to specific habitats. In this presentation I will try to show how evolutionary studies from the south can provide a distinctive and original perspective.

Young Arachnologist: Oral presentation, day 2

Arthropod systematics in the age of “big data” and machine learning

Chris A. Hamilton

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Understanding how Earth's diversity has been shaped by evolution is one of the key objectives in biological research. My research is driven by three major questions: 1) What are the relationships within the arthropod Tree of Life?; 2) How has evolution produced such an astonishing array of form and function?; and 3) Why are particular lineages more diverse than others?. By integrating large amounts of data (morphology, molecular, behavioural, ecological), I work to understand evolutionary relationships and explain patterns across differing landscapes and time, in particular by discovering and describing new diversity. For example, *Aphonopelma*, a widespread genus of North American spider, has long been known as a "taxonomic and nomenclatural nightmare”. Across their distribution, similarly sized species are often frustratingly similar morphologically, leading the genus to be deemed one of the greatest known challenges to species delimitation in spiders. By using an integrative approach, we investigated data from nearly 3,000 specimens to test species hypotheses. Future work will apply machine-learning and data from taxonomic works, like *Aphonopelma*, to differentiate species boundaries and aid in species identification and discovery on a natural history collections scale. Lastly, a fundamental tenant of modern science is to provide methodology that allows for reproducibility. By creating an open-access bioinformatics pipeline for Anchored Hybrid Enrichment phylogenomics, my goal is to provide a mechanism whereby independent researchers can use the same data to answer their questions, but at the same time continue adding to and updating our larger understanding of the spider Tree of Life.

Young Arachnologist: Oral presentation, day 2

Pseudoscorpion research in the 21st century – discovering the great unknown.

Danilo Harms

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Progress in arachnology is driven primarily by the study of spiders. The advent of molecular techniques has revolutionised our understanding of spider evolution, there are new and exciting facets of morphological research, and some spider species have even become important model systems in behavioural ecology. Research on mites, scorpions and harvestmen is also progressing, i.e. biogeographical studies on these groups have provided unique insights into the evolution of Earth’s biota. Much less is known about an order of arachnids that is perhaps equally diverse but largely neglected: the pseudoscorpions. Studies of this group largely focussed on its taxonomy, principally following standard protocols of species description invented almost a century ago. However, the application of molecular techniques is becoming more frequent and indicates that the neglected cousins of spiders and scorpions are extraordinarily diverse, potentially equalling spiders in species numbers, and show complex modes of biogeographical patterning, molecular evolution, and behavioural ecology. Pseudoscorpions are an old lineage with origins in the Devonian and during their long evolutionary history have developed diverse ecologies and adaptive morphologies, despite their concealed life style and comparatively small body size. Here, I will showcase how knowledge about pseudoscorpions could facilitate our understanding of arachnid evolution and biogeography, whilst also pointing out recent developments in the fields of palaeontology, ecology, nature conservation, venom evolution and taxonomy. Please join me in discovering the “great unknown” arachnid order – a hidden world that remains to be explored.

Young Arachnologist: Oral presentation, day 2

Physical optimum in silk anchors as a global driver of spider web evolution

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Spiders are a prime model to study the evolution of building behaviour. Despite continuing efforts to unravel the evolutionary history of spider webs, there is little understanding of the evolutionary drivers and constraints of web building behaviour. Here, we demonstrate that spider web diversification repeatedly followed strikingly similar evolutionary trajectories, channelled by physical constraints. We found that the evolution of aerial webs that intercept flying prey was preceded by small changes in silk anchoring behaviour with considerable effects on the robustness of web attachment. The use of cribellar capture threads conflicts with the behavioural enhancement of web attachment, and the repeated loss of the cribellum has driven the evolution of web anchor structure. These results represent a new twist in the discussion of orb web evolution and the functional significance of cribellum loss.

Plenary talk, day 4

Spider communities in agricultural landscapes – response patterns and consequences for predation services

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Agricultural intensification is amongst the major causes for the global loss of terrestrial biodiversity. More sustainable approaches to agricultural production are needed and spiders can play an important role in such future strategies. Agricultural intensification affects the taxonomic and functional diversity of spider communities across spatial scales ranging from landscape to field-level changes. Spider communities in agricultural landscapes are for example often dominated by agrobiont species which can cope with high levels of agricultural management. The carnivorous diet and prey preferences of these species further contribute to their important role as natural enemies of pests in conservation biological control approaches. After presenting examples for the complex response patterns of spider communities to management in agricultural landscapes, associated consequences for their functional role as natural enemies are highlighted. This overview combines results from ten years of research using literature data, field experiments, community surveys, molecular gut content and stable isotope analyses. The results suggest that habitat manipulations that focus on a “one size fits all” approach to simultaneously conserve high taxonomic diversity and provide high levels of biological control services by spiders may fail. Major constraints for the simultaneous conservation of diversity and pest control services in agricultural landscapes are the limited knowledge about functional consequences of management practices for pest control and the conflicting responses of community properties to such practices. Future strategies for sustainable agriculture need to account for potential trade-offs between diversity components and pest control provision. Ultimately, an evidence base that contributes to more sustainable future approaches to food and energy production is needed. An improved understanding of the effects of agricultural management on spider trait composition, spill-over between semi-natural and agricultural habitats and consequences for predator-prey interactions is crucial to accomplish this goal.

Plenary talk, day 5

The evo-devo spyglass: a promised renaissance for morphology in an era of genomes and functional toolkits

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The rapid progress of sequencing technologies in the past decade has resulted in an accelerated integration of morphological and molecular approaches in organismal biology. One discipline that has benefited greatly from this integration is evolutionary developmental biology (or evo-devo), which addresses the genetic origins of morphological variation. However, developmental biology has been historically underrepresented at past meetings of the International Society of Arachnology, in comparison to such disciplines as systematics, phylogenetics, faunistics, ecology, and behaviour. Here I highlight recent advances in developmental biology, functional genetics, and comparative genomics in multiple chelicerate model systems, which together establish a platform for both exploring evolutionary history of arachnids, and for interrogating macroevolutionary processes. I explore how changes in gene regulatory networks across the arthropod tree of life inform the genetic equipment used to pattern segments in spiders. I demonstrate how new data from developmental genetic approaches are compelling reassessment of long-held homology schema in arachnology. Finally, I examine how paralogy in developmental patterning genes can be leveraged as a phylogenetic data class to redress some of the most daunting challenges in arachnid phylogenomics. The sum of these developments in arachnology spells the dissolution of boundaries between morphological and molecular approaches.

ORAL PRESENTATIONS

Student oral presentation

The Australian ant-slayer: specialised ant hunting behaviour and the use of silk in *Euryopis umbilicata* (Theridiidae)

Alfonso Aceves-Aparicio[1]; Marcelo Christian[2]; Ajay Narendra[1]; Jessica Garb[3]; Marie E. Herberstein[1]

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Most spiders avoid feeding on ants, as they are often dangerous prey. However, *Euryopis umbilicata* spiders seem to feed exclusively on a narrow spectrum of ant species that dwell on tree trunks. *Euryopis umbilicata* do not have obvious morphological adaptations to prey on ants, and do not build a capture web (unlike the majority of myrmecophagic Theridiidae spiders). Instead, *E. umbilicata* shows a particular array of specific behaviours that helps them to capture dangerous ants (e.g., *Camponotus* sp. and *Crematogaster* sp.). From our field surveys, we describe *E. Umbilicata*'s hunting strategy, which involves assuming a flat position on the tree trunk, using silk anchors, a cartwheel-like jump to attach a silk restraint, and fast circular silk spinning. This behavioural sequence results in rapidly subduing ants on a vertical surface. These spiders can produce large amounts of silk during prey capture. The silk is highly adhesive, supporting the capture of their prey. The behaviour and silk use of *E. umbilicata* were experimentally surveyed to assess their capture effectiveness against both typical and uncommon prey (e.g., a cricket). The amount of silk used, the number of bites, and overall time required to subdue the prey were all higher for the uncommon prey. Specialist spiders are rare, which highlights the importance of the underlying mechanisms of the intricate interaction between predator and prey. *Euryopis umbilicata* may have evolved specific hunting strategies that allow spiders to access food resources with little or no competition at great abundance, thereby reducing the risk from targeting ants.

Student oral presentation

Spider communities in rapeseed plantations versus semi-natural grassland

Szabó Ágota Réka[1]; Gallé Róbert [2]; Urák István[1]; Hartel Tibor[3]

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Small-parcel agriculture is increasingly replaced by extended monoculture in Romania. Intensive agricultural management changes the habitat structure and microclimatic condition. Additionally, insecticide application has a significant effect on the invertebrate fauna, mostly because these chemicals are not pest-selective. In our study, we compared the spider assemblage structure of semi-natural grasslands and rapeseed plantations. We selected 16 sampling points in Cluj-County. Eight sampling points were selected in the semi-natural grassland and 8 sampling points in the nearest rapeseed field. We used pitfall traps for sampling the ground-dwelling spiders: one sampling site was comprised of 5 pitfall traps, which were placed so that we moved from an edge to the inside of the habitat. Trapping was repeated three times (from 3th May to 23th May, form 13th June to 5th July, form 20th August to 9th September) in 2017. We collected 2654 adult spider individuals of 122 species. Species richness and adult abundance was higher in the grassland than in the rapeseed field. A subset of grassland spider assemblages was found on the rapeseed field, so a part of the surrounding species could colonise this habitat. Our results suggest that small-parcel cultivated fields could provide a higher quality habitat for invertebrate communities, both in semi-natural grasslands and agricultural plantations.

Student oral presentation

Route assessment in jumping spiders

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Salticids are characterised from other spider families by their highly acute vision, which mediates many behaviours, including prey capture and navigation. When going to a specific goal (prey, nest, a potential mate, etc.), salticids rely on visual cues and spatial memory to orient in three-dimensional space. Commonly living in complex environments, salticids are likely to encounter a wide variety of routes that could lead to a goal, and, as selection favours individuals that can more quickly and accurately make assessments, they may be able to assess alternative route distances to select the most efficient route. We tested whether two or three salticid species can discriminate and assess between different available routes by their length (to obtain prey), riskiness and difficulty (to escape a stressful scenario). Neither *Trite planiceps* nor *Marpissa marina* chose the routes leading to prey. However, *T. planiceps* tended to choose the short routes more often than the long routes, whereas *M. marina* chose routes randomly. We also found that, in order to escape from a stressful scenario, *Portia fimbriata* was more likely to choose the easiest escape routes than *T. planiceps*. These interspecific differences in spatial ability seem to correspond with the complexity of the environment inhabited by each species.

Symposium oral presentation

Exceptions that test rules: avant-garde females and demanding males in two sand-dwelling spiders from challenging environments

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Allocosa senex and *Allocosa marindia* are two sand-burrowing spiders that inhabit the coasts of Brazil, Argentina and Uruguay. The two wolf spiders show reversal in expected sexual dimorphism and reproductive tactics in spiders: males are larger than females and they are the sedentary sex, while females are wanderers who look for potential mating partners and initiate courtship. Both males and females are choosy when taking mating decisions: males based on female reproductive status and body condition, and females on male burrow length. Male burrows are donated to females after mating and females will lay their egg sacs there, leaving when it is time for spiderling dispersal. Both *Allocosa*are the first two cases of reversal in traditional sex roles reported in spiders so they offer the unique opportunity to study the factors driving the origin and evolution of non-traditional behaviours. One possible cause driving high male reproductive investment and female competition are the harsh and unpredictable sandy coasts in which both wolf spiders inhabit. In this talk I will expose some recent studies on *A. senex* and new data available from Allocosinae species inhabiting other landscapes in South America. Projects in progress will trace the evolutionary history of sex role reversal in the subfamily Allocosinae integrating behavioural, ecological, genetic and taxonomic data.

Symposium oral presentation

Parasteatoda tepidariorum **is a model spider that permits genome-based study of developmental biology**

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Parasteatoda tepidariorum (syn. *Achaearanea tepidariorum*) is one of the spider species whose genome sequence is already published. Availability of the genome sequence together with many techniques, such as RNA interference (RNAi), multi-colour in situ hybridization, and cell labelling and tracking, makes it possible to search for genes involved in phenomena of interest and examine their function without relying on knowledge from other animals. In our presentation, we will introduce several embryonic phenomena in *P. tepidariorum*that we are interested in. These include body axes specification dependent on intercellular signalling, self-regulatory capabilities of embryonic fields, and a diversity of segmentation modes in a field. One of our projects focuses on Hedgehog (Hh) signalling that regulates the formation of global anterior-posterior polarity in the early cell-based embryo, where the role of Hh corresponds to that of Bicoid in the *Drosophila* syncytial embryo. We combined parental RNAi and RNA sequencing to perform a genome-wide screen for Hedgehog signalling targets and identified about 50 genes that were expressed in a specific pattern in the early embryo under the control of Hh signalling. One of the genes, encodinga transcription factor, exhibited a wave-like expression, contributing to thoracis segmentation. The initial wave was followed by repeated generation of gene expression waves associated with opisthosoma segmentation. Knockdown of this gene blocked all segmentation processes, including head segmentation. This genome-based work identifies a key segmentation gene in *P. tepidariorum*, which has never been predictable from the *Drosophila* knowledge.

Symposium oral presentation

Kids that tell science: fearless and positive children after hands-on educational experience

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“Kids that tell science” is a novel ongoing Uruguayan educational proposal aiming to facilitate current scientific information of limited access to schools. We focus on enhancing children scientific knowledge, who transmit it to other children by the creation of educational short-films. In 2016, we worked in the fear toward animals as an important issue to foster knowledge and attitudes in nature conservation. Spiders are a challenging group, because they are generally feared and disliked while in fact the majority of species are harmless and importantly, they play a unique positive role in natural ecosystems. We examined how Uruguayan children knowledge, perceptions and potential attitudes toward spiders change by performing self-report questionnaires before and after two different extracurricular educational experiences. A short experience including two groups: Spider-single lesson group, children receiving 1-hour information and brief interaction with spiders and Control-single lesson group, children receiving 1-hour information in other topics. A long experience: Spider-multiple lesson group receiving 40 hours information and several interactions with spiders. Comparing the first and second evaluation from the questionnaires, we found that children knowledge improved only in the Spider-single lesson and Spider-multiple lesson groups. In the three groups, less proportion of students reported being afraid of spiders on second evaluation compared to the first one. Further, more children reported positive attitudes toward spiders, being higher in Spider-multiple lesson group. Our findings highlight the importance of hands-on and extended activities to demystify false concepts about animals and foster nature conservation.

Oral presentation

Sequencing 1,000 spiders to elucidate the design mechanisms of spider silk proteins

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Spider silks are proteinsthat exhibit extraordinary mechanical properties including high tensile strengths, extensibilities, and exceptional toughness, with potential applications in industry as renewable materials. Spiders produce multiple types of silk, each composed of specific proteins called spidroins and exhibiting a diverse range of mechanical properties, most of which are known to be monophyletic. Therefore, if we can obtain a multitude of spidroin sequences along with the mechanical properties of corresponding silks from diverse samples among the order Araneae, we can potentially identify quantitative linkages between sequence motifs and physical properties. To this end, we have sequenced 1,000 spiders using de novo transcriptome sequencing and assembly strategy. Spider silk genes, however, are extremely long (>10kbp) and highly repetitive sequences which are impossible to sequence in full length using short

reads. We combine multiple sequencing technologies, including PacBio and Oxford Nanopore long reads with Illumina short reads to conquer this challenge. In this talk, we would like to discuss our findings regarding the link between spidroin sequences and their mechanical properties.

Student oral presentation

Lycosa – species delimitation in the midst of diversity

Igor Armiach Steinpress[1,2]; Ariel Chipman[1,2]; Efrat Gavish-Regev[2]

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The genus *Lycosa* (Latreille, 1804) (Lycosidae, Araneae) currently has more than 200 species, distributedworld-wide. However, it has been suggested that the genus is polyphyletic and that many included species belong to different genera. The current species that are classified as *Lycosa* exhibit great variation in somatic and genital characters. Such variation of characters, often incongruent, may even be found in a single locality. Therefore, *Lycosa* represents an interesting but difficult case-study for species delimitation. We studied the somatic, genital and burrow construction characters of *Lycosa* populations from over 20 localities in Israel (both Mediterranean and arid regions). We hypothesise that burrow decoration and carapace proportions correlate with male genital characters and female vulva, but not epigynum, shape. In order to test this hypothesis, we used digital morphometry (Elliptical Fourier Analysis) to compare and evaluate the conflicting phenotypic characters present in the *Lycosa* found in Israel. The results of the analysis, partially confirming our hypothesis, are used for delimiting the three local species (two new to science), and identifying diagnostic characters relevant for the genus.

Symposium oral presentation

Go West! Colonisation and diversification of *Dysdera* ground dweller spiders in the Macaronesian Archipelagoes

Miquel A. Arnedo[1]; Adrià Bellvert[1]; Luís Crespo[1,2]; Jesús Lozano-Fernandez[1]; Alba Enguídanos[1]; Nuria Macías-Hernández[2]

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Lineage diversification on oceanic islands provide an experimental framework for investigating the mechanisms of speciation and identify the drivers of phenotypic and ecological change. Fundamental to this endeavour would be to infer the phylogenetic relationship of island taxa and their closest relatives. Unfortunately, phylogenies of islands radiations are frequently either incomplete or the outgroups are poorly sampled, compromising our ability to infer the colonisation pathways and reconstruct ancestral traits. The ground dwelling spider genus *Dysdera* includes more than 250 species of active nocturnal hunters. Species in this genus are unique among spiders in showing different dietary preferences, ranging from generalist to obligate woodlouse feeders, which seem to have evolved independently several times. Although *Dysdera* is mostly circumscribed to the Mediterranean

basin, it has managed to colonise most of the north-eastern Atlantic Macaronesian archipelagos. Macaronesia includes four different archipelagos of volcanic origin arranged in a latitudinal gradient, namely Azores, Madeira, Canary Islands and Cape Verde, which encompass different climatic regions, with distances to the closest mainland ranging from 100 to 1,600 km. Here, we present the results of a molecular phylogenetic analysis of the most thorough sample of island endemic and continental species of *Dysdera* conducted to date. We further estimate divergence times using multiple calibration points and reconstruct biogeographic history. Our results indicate that *Dysdera* colonised the different archipelagos independently at different times, and in some cases more than once. At least three colonisation events resulted in high local diversification processes. Although, as largely expected, the westernmost Mediterranean region acted as a colonisation source, we also identified several cases of long-distance dispersal between archipelagos.

Student oral presentation

Goblins underground: Termitophilous oonopids of the Afrotropical Region

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Spiders are the most evolutionarily successful terrestrial predators. The combination of complex biomaterials and striking morphological and behavioural adaptations have enabled them to exploit new trophic niches. Despite the extraordinary prey specificity observed in spiders, specialisation on termites remains relatively rare. Records of termite predation exist for only 8 of the 118 spider families. These species have been observed actively hunting termites and opportunistically raiding damaged nests. The only accounts of spiders as obligate predators of termites occur in the family Oonopidae. The spider family Oonopidae, commonly known as goblin spiders, includes 115 genera and over 1800 species. Goblin spiders have a worldwide distribution and can be found in a diversity of environments, including subterranean habitats such as termite nests. These species are eyeless, depigmented, and have special adaptations that enable them to live undetected among termites. Eight termitophilous species have been described from three genera that are restricted to the Afrotropical Region. In this study, a new species of termitophilous goblin spider from Cameroon was examined using a combination of morphological and molecular data. X-ray computed microtomography was used to examine the morphology, and molecular analyses were performed to detect prey DNA and place the focal species in a larger phylogenetic framework.

Oral presentation

Evolutionary patterns among hymenopteran predators and parasitoids of spiders

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Spiders are a major food resource for the developing larvae of Hymenoptera. Available biological data indicate that most groups exploit the egg or juvenile stages of spiders; only the Pompilidae, polysphictine ichneumonids and, to some degree, Crabrionidae have successfully used adult spiders as prey. Among other groups only the Scelionidae have radiated as a species-rich lineage parasitizing spider eggs. Recent, more robust phylogenies for various hymenopteran groups, and additional biological and host data in recent years, has made it possible to track the evolutionary transitions of hymenopterans that exploit spiders as food. In this respect, this presentation will examine several groups and discuss their biology and possible limitations in switching to spider parasitisation.

Oral presentation

The draft genome of Darwin's bark spider (*Caerostris darwini*) reveals an expanded capture spiral genetic toolkit

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Stronger than steel, tougher than Kevlar™, yet lighter than either of these man-made materials, synthetic spider silks have the potential to transform medicine and industry. However, the complete repertoire of genes responsible for the main components of spider silks, "spidroin" proteins, is not known, and our understanding of the structure of these genes is limited. To improve our understanding, we sequenced and assembled the complete genome of Darwin's bark spider (*Caerostris darwini*). We then performed RNA-sequencing of multiple tissues to annotate the genome and catalog all of *C. darwini*'s spidroins. First described only nine years ago, this amazing spider from the riverine forests of eastern Madagascar constructs the world's largest orb webs (~2.8 m^2) and the world's longest bridgelines (>25 m) that span rivers using the world's toughest spider silks (520 MJ/m^3). Our draft assembly includes 1.45 Gb of non-repetitive genome (100x coverage, 45,784 scaffolds, scaffold N50: 490 kb, contig N50: 95 kb). We identified 30 spidroin genes, including five that are novel. We observed a greater number of flagelliform spidroin genes (6) than reported for any other spider species, thereby adding broader diversity to this class of spidroins, used by spiders in silks to construct the orb web's "stretchy" capture spiral. Comparative analysis of *C. darwni*'s spidroins with those belonging to the distantly related golden orb-weaver spider (*Nephila clavipes*) suggests that the expanded set of *C. darwini* flagelliform spidroin genes likely arose following the diversification of orb weaver species, whereas aggregate spidroins that constitute the "sticky" coating of the capture

spiral likely diversified before species divergence – an intriguing pattern given the ancient age and putative functional relationship of flagelliform and aggregate spidroins following the origin of the viscous orb web, perhaps some 200 million years ago. Analysis of repetitive coding sequences of *C. darwini* spidroins revealed novel motifs in MaSp, MiSp, and TuSp classes. Meanwhile, we observed multiple spidroin genes located on individual scaffolds, supporting tandem duplication as a mechanism responsible spidroin gene diversification. In addition, full characterization of spidroin expression in distinct silk gland types indicates that *C. darwini* glands can express multiple spidroin types (similar to *N. clavipes*), and that flagelliform spidroins exhibit the highest level of expression of any spidroin "class". The collection of these resources will help improve our understanding of how silk genes and their structure confer the amazing biomechanical properties of silks, contributing to future efforts to mimic the extraordinary properties of *C. darwini*'s silks in man-made materials.

Student oral presentation

Diversity of springtails and spiders in three biomes in central South Africa

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South Africa is one of the 17 megadiverse countries of the world, partly due to the three biodiversity hotspots situated within its borders. Even in such a diverse country there are many organisms that are severely understudied, especially in the interior regions of South Africa, resulting in an underrepresentation of many invertebrate groups and a restraint on our knowledge of their ecological roles in the Nama Karoo, Savanna and Grassland biomes. This study focused on two invertebrate groups (Collembola: springtails and Araneae: spiders) within the Free State and Northern Cape Provinces, focusing on assemblages over a longitudinal rainfall gradient along 28°S latitude. We expected a progressive decline in species richness and abundance from the moist alpine grasslands in the east to the arid Nama Karoo in the west. Field collecting was conducted between September 2017 and October 2018, using various active sampling methods (beating shrubs, grasses and bushes, and hand collecting) to ensure broad coverage of species assemblages. A total of 3137 spiders representing 293 morphospecies and 40 families were collected during the study. There were no consistent patterns in species richness or abundance across the transect, with fluctuations between sites. Seasonality also showed contrasting patterns across the transect, peaking in summer in the two moister grassland sites and fluctuating elsewhere. As material from other sampling methods (pitfalls and litter sifting) still needs to be processed, we will refrain from making broad conclusions at this time.

Oral presentation

Long term monitoring of spiders in coastal dune and salt marsh habitats along the river Yzer estuary (Nieuwpoort, Belgium), final approach

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A long term monitoring of spiders and ground beetles has been carried since 1990 in coastal dune and salt marsh habitats of the river Yzer estuary (Nieuwpoort) along the Belgian coast. Pitfall trap sampling has been performed without interruption for 24 years between spring 1990 and spring 2014 in various habitats from seaside marram dunes, dune top, inland marram dunes, inland moss dunes, dune grasslands and salt marsh.

The 24 year cycle can be divided in two main periods; before and after the river Yzer estuary nature restoration project, which started in 1999 and ended in 2001 with the aim of restoring an intertidal area with several different ecological gradients. Between 1990 and 1999, the studied area could be divided in three parts; the dune area (coastal marram dune, inland moss dunes), a naval military base (buildings, harbor, roads and slipway) and a salt marsh area. The military base was removed between 1999 and 2001 and the area was restored with dunes (former naval headquarters), dune grassland (former soldiers quarters) and salt marshes (former harbor and slipway). A multidisciplinary monitoring of the newly created habitats was immediately started after the end of the restoration works. Colonization of the new habitats were followed. This resulted in 160 year cycles spread over 41 locations scattered over the whole estuary area.

The spider diversity of the whole area is very high and counts 246 species. A DCA is given for the whole of the 160 cycles. A yearly high species turnover can be observed for each habitat type. Many highly specialized and stenotypic spiders occur in the dunes and salt marshes of this high diversity hot-spot. Not all locations have been continuously monitored during the 24 years. Only the coastal marram dune (locations A, B and C) and the inland moss dune (location E) were sampled from the start of the study. These were not affected by the restoration works.

Oral presentation

Desiccation tolerance and humidity preferences of two species of riparian-zone wolf spiders from Arizona, USA

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The choice of habitat depends on a variety of biotic and abiotic factors. Some animals have wide tolerances for these factors and can occupy a variety of habitats; others have much narrower tolerances and are restricted in their habitat. In the Chiricahua Mountains of southeastern Arizona, USA, two wolf spider species (*Pardosa valens* and *Rabidosa santrita*) are restricted to the cobble zone near small streams. To understand this habitat choice, we examined desiccation tolerance and humidity preferences in these two species, as well as in

similar-sized wolf spiders that live on drier forested slopes near the streams. Desiccation tolerance was measured in a drying oven set at 40°C, while humidity preferences were determined using a four-choice chamber. In desiccation trials, males of both species survived for shorter times, and lost mass at a faster rate, than females (or juveniles in *R. santrita*). Male survival times were similar for both species, but female *Rabidosa* (12-20 h) survived longer than did female *Pardosa* (6-12 h). Wolf spiders (primarily *Schizocosa mccooki*) from drier areas all survived at least 21 h, with mass loss rates significantly lower than the two riparian-zone species. In the humidity preference trials, both *Pardosa* and *Rabidosa* preferentially selected high humidity chambers (those with >50% RH), with males generally preferring slightly higher humidity than females. These results suggest that both species may be restricted to the riparian zone due to a low tolerance for dry conditions in the surrounding habitat, perhaps due to high rates of respiratory or cuticular water loss.

Student oral presentation

Systematics and biogeography of Triaenonychidae (Opiliones: Laniatores) across Zealandia

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There are four families of Opiliones with largely concordant temperate Gondwanan distributions: Acropsopilionidae (Dyspnoi), Neopilionidae (Eupnoi), Pettalidae (Cyphophthalmi), and Triaenonychidae (Laniatores). While all four families have representatives in New Zealand, only one family, Triaenonychidae, is found on the other main landmass of the continent Zealandia – New Caledonia. Recent molecular phylogenetic analyses of Triaenonychidae suggest the fauna from New Zealand constitutes a non-monophyletic assemblage, and that the New Caledonian triaenonychids are derived from the New Zealand genus *Triregia* in particular. In this talk, we explore the origin and diversification of key clades within the Triaenonychidae of Zealandia, compare their biogeographic patterns to other co-distributed families of harvestmen in New Zealand and New Caledonia, and discuss our results in the context of the turbulent geologic history of Zealandia, including its multiple marine transgressions.

Oral presentation

Role of visual cues and aggression in jumping spider responses to ants and ant mimics

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Most jumping spiders are thought to avoid ants, yet little is known if they discriminate between them or their mimics. In this study we examined the response of jumping spiders from the genus *Plexippus (P. paykulli, P. petersi)* towards two different ant species (*Oecophylla smaragdina,* the weaver ants and *Camponotus sericeus* the golden-back carpenter ants) and their corresponding salticid mimics. Our study used a behavioural assay that excluded tactile and chemical cues, and prioritised visual cues. We recorded and analysed behaviours such as

‘look’, ‘approach’, 'attack', and ‘avoidance’ by *Plexippus* towards ants or mimics that were placed behind a transparent barrier. Our results show that reactions to the two species of ant differ depending on ant colour, movement and aggressive behaviour. *Plexippus* individuals gave significantly more ‘long looks’ to golden-back ants compared to weaver ants. There were no significant differences in the other behaviours, or significant differences between the two mimics in any behaviour. When the transparent barrier between the ants and *Plexippus* was then removed, weaver ants were more aggressive than golden-back ants. However, there did not seem to be significant differences in aggression between mimics, both of which exhibited aggressive behaviours such as raising the front limbs and abdomen and charging at or chasing the jumping spider. Furthermore, while both species of mimic were seen as prey by *Plexippus* in many cases inside the barrier, no mimics were attacked when the barrier was removed. This highlights the previously unexplored role of aggression as a predator-deterrent in ant-mimicking spiders.

Oral presentation

Do scorpions have different peg sensilla on pectine in different types of habitats and habits they occupy and lead?

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The scorpions occupy different habitats and habits of life style they lead such as Buthids normally inhabit under any cover they get to hide (omniphilous) and some Buthids lead arboreal life, the Euscorpiids, Chaerilids and Chiromachetes rock dwelling life (lithophilous), Scorpionids are exceptionally burrow making (psammophilous or pelophilous) leading their life in and around self-made burrows either in open velds (barren lands) or in support of medium to large boulders. These observations pertain to Indian Scorpio – fauna and by the author. The adaptability in these four types of different habitats and habits of scorpions, do really lead them to modify in their sensory systems such as “peg sensilla on pectines?” The Scanning Electron Microphotography (SEM) reveal such variations studied for species, under discussion *Hottentotta hendersoni*, *Compsobuthus rugosulus* (Buthidae), *Neoscorpiops deccanensis* (Euscorpiidae), *Chiromechetes sahyandrensis* (Liochilidae) and *Heterometrus xanthopus, H. pelekomanus*, and *H. swammerdami* (Scorpionidae).

Student oral presentation

Does trophic specialisation prevent ecological release?

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Ecological release is defined as the expansion of range, habitat and/or resource usage by an organism following colonisation of a new region. This phenomenon is ubiquitous in oceanic islands, where colonising species whose ancestors evolved in highly competitive environments, experiment relaxed selection as a result of lower species richness. Ecological specialisation, on the other hand, has been frequently considered an evolutionary dead end, since it would prevent reversal to a more generalist state even under relaxed competition. The genus *Dysdera* has colonised and undergone major diversification in the Canary Islands. Endemic species show contrasting levels of trophic specialisation, where some species are generalists while others specialize in feeding on isopods. The generalist species *D. silvatica* and the woodlouse feeders *D. calderensis* and *D. gomerensis* coexist with 7 additional *Dysdera* species in La Gomera. The three species, however, have also colonised younger islands, where they coexist with fewer congeners. The contrasting levels of competition and diet preferences provide a natural experiment where to test the predictionsof ecological release and the effect of ecological specialisation on these predictions. We hypothesize that species in the younger islands will show higher variability in somatic traits as a response to lower competition levels. We further predict that this pattern will be more evident in the generalist species, whereas trophic specialists will exhibit a lower potential for niche expansion. To test these hypotheses, we conducted a geometric morphometric analysis of a large sample of specimens of the target species. In the presentation we will discuss the results and their implications for our understanding of island evolution.

Symposium student presentation

Take a chance on me: second mating opportunities in a South American wolf spider

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Allocosa senex shows reversal in sex roles and size dimorphism, meaning that females search for partners and start courtship, being the smallest sex. Males should construct burrows, wait for females and be chosen by their partners, while females remain in males' burrows after mating and leave it for spiderling dispersal. Nevertheless, females inside males' burrows may be visited by other males. Males of *A. senex* can survive two reproductive seasons, what could determine variations in their mating tactics regarding the timing in their reproductive period. We aimed to: 1-describe males' sperm production during the reproductive and non-reproductive season; 2-evaluate male ability to find mated females inside other males' burrows; 3-test female receptiveness to remating. We dissected testes at the beginning, between periods and at endings of the reproductive period. Preliminary results show that males would exhibit smaller testes compared to wolf spiders of similar size and currently we are analysing sperm production through light microscopy. For the sexual trials, we exposed mated females located inside the donated males' burrows to second males. Males can detect and court mated females (46.7%), while 20% of females accepted remating, revealing that sexual dynamics in this species is much richer than it was expected.

Student oral presentation

Revision, molecular phylogeny and biology of the spider genus *Micaria* Westring, 1851 (Araneae: Gnaphosidae) in the Afrotropical Region

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The genus *Micaria* Westring, 1851 includes small diurnal gnaphosids about 2–5 mm in length. They are recognised by their elongate ant-like bodies, cylindrical abdomen, and unciferous and brachiate hairs on the legs, abdomen, chelicerae and carapace. Furthermore, the piriform spigots on their anterior lateral spinnerets are retracted and barely visible. There are 108 species of *Micaria* described to date, of which the majority have Nearctic and Palearctic distributions. A few species are recorded from Australia and South Africa. Three species, *M. beaufortia* (Tucker, 1923), *M. chrysis* (Simon, 1910) and *M. tersissima* (Simon, 1910) were described from South Africa, but no other species have been described from the Afrotropical Region. Males and females of recently collected and voucher specimens have been sorted into morphospecies. Thus far, a total of 859 individuals of *Micaria* were examined, of which 745 were adults. A total of 17 species were recorded, of which 14 may be new species for the Afrotropical Region. Two species, *Micaria* sp. 1 (411 individuals) and *Micaria beaufortia* (207 individuals), were the most abundant and widely distributed throughout the Afrotropical region. New species have been recorded from Ethiopia, Senegal, Mauritania, South Africa, Namibia, and Madagascar. Further analyses of the phylogeny, biology and behaviour will be investigated. Providing DNA barcode information on the *Micaria* of the Afrotropical Region may prove crucial to resolving the phylogenetic status and relationships of *Micaria*.

Symposium presentation

Venom evolution and its role in local adaptation, phenotypic plasticity, and diversification in *Tetragnatha* spiders

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Key innovations facilitate lineage diversification by opening previously inaccessible niches. Venoms served as key innovations that promoted adaptive divergences in many taxa, including snakes, anguimorph lizards, and cone snails. Additionally, venoms and "stinging" are known to function in sexual communication in vespid wasps, scorpions, and platypuses. This potential dual role of venoms provides many axes upon which local adaptation and reinforcement of reproductive boundaries may develop, sometimes leading to adaptive radiation. Members of the genus *Tetragnatha* Latreille, 1804 generally possess diverse and sexually dimorphic venoms. Among the dimorphic components, males possess high molecular weight proteins not found in females that appear to function in sexual communication. Additionally, the genus contains generalist species with broad ecological niches and others that have adaptively radiated to fill many specialised roles. The generalist mainland North American species *T. versicolor* ranges from Pacific to Atlantic coasts and Central America to Canada. Two ecologically divergent *T. versicolor* populations were investigated for niched divergence and concomitant signatures of molecular evolution, differential expression, and divergences in

alternative splicing of venoms. Additionally, venom gene families were reconstructed for species representing both major clades of a Hawaiian adaptive radiation. The resulting gene families were subjected to phylogenetic tests for pervasive selection and novel phylogenetic comparative methods (PCM) based differential expression analyses. Due to the paucity of existing knowledge of unique *Tetragnatha* venoms, a newly derived deep-learning approach to detect venoms (TOXIFY) was employed. The results highlight the various ways venom evolution contributes to local adaptation, phenotypic plasticity, and adaptive radiation.

Symposium student presentation

A molecular perspective of the biodiversity of Australian tarantulas (Theraphosidae)

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There has been no thorough taxonomic revision of Australian tarantulas, and all but one described species was named more than a century ago; consequently, their current biodiversity in Australia is not well characterised.As a first step in revealing their species richness, we use multi-locus DNA sequence data (*16S,COI*, *18S*, *28S* and *EF1gamma*) in a phylogenetic framework to determine the number of unique lineages that may represent distinct species.We find at least 19 undescribed putative species, distributed among four major clades. Each clade is endemic to one of four separate geographical regions: the Australian arid zone, the eastern coastal tropics, the Kimberley and Top End, and the Australian Monsoonal Tropics.There are likely to be additional species, as many of our samples were represented by singletons, and we found 123 undescribed species. More samples are needed for a full revision of the Australian tarantulas, including from Asia given that at least one South-East Asian species is nested among the Australian species.

Symposium oral presentation

Maintenance of sex via geographic heterogeneity and facultative parthenogenesis in a Japanese harvestman

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Sexual conflict may be uniquely manifested in facultatively parthenogenetic systems, producing characteristic female-biased geographic patterns. However, the relationship between mating success, fecundity, and the factors that maintain males in these populations, remains unclear. The facultative parthenogens *Leiobunum manubriatum* and *L. globosum* are Japanese harvestman species with morphological and population variation well-suited for studies of mating system maintenance of reproductive polymorphisms. In particular, males of these species have sexual traits that may affect coercive ability, and populations vary in the relative frequency of males. If coercive males are present at high frequency in a population of facultative parthenogens, will those parthenogens actually mate? How will their offspring production compare to conspecifics in low frequency male populations? We addressed these questions by collecting females and egg clutches of both harvestmen species from populations that varied in male frequency. In *L. manubriatum*, females from populations with few males

were not more fecund than females from populations with higher male relative frequency, despite the potential release of the former from sexual conflict. Both genotyping-by-sequencing (GBS) and a SNP array panel revealed that offspring of *L. manubriatum* from these high male populations were primarily produced via asexual reproduction. This is surprising because sex ratios in these southern populations approach equality, increasing the probability for females to encounter mates and produce offspring sexually. These data will provide inference on broader evolutionary questions regarding the maintenance of sex.

Oral presentation

Selection for male weapons boosts female fecundity in bulb mites

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Male dimorphism is usually linked to different tactics for securing matings, and its evolution should be facilitated if different morphs are genetically uncoupled and free to evolve towards their phenotypic optima. However, there is to date no direct evidence for male morphs responding independently to selection. We investigated correlated evolution between male morphs of the bulb mite *Rhizoglyphus echinopus*. Large males ('fighters') of this species have thick and sharp legs used to kill rival males, whereas small males ('scramblers') have unmodified legs, and look for unguarded females. Fighter legs in *R. echinopus* are expressed conditionally in larger males and low population densities, and a conventional interpretation of polyphenisms suggests that only fighters express certain genes for thicker legs, allowing morphs to respond to selection independently. Using fighters, we imposed morph-specific artificial selection on relative leg width in six paired replicate lines, three selected for thicker legs (up lines) and three selected for thinner legs (down lines). After nine generations, we observed correlated evolution in the width of the legs of scrambler males, as well as females. Moreover, females in the up lines evolved higher fecundity, revealing a mechanism that boosts the evolution of male weapons and extreme sex differences. Support for good condition genes driving this result comes from the evolution of sex and morph ratio, as well as their correlation with sire weapon size. This link between male weaponry and female fecundity might allow extreme male weapons and ornaments to evolve despite correlated evolution in females.

Oral presentation

Caribbean *Cyrtognatha, Tetragnatha* and *Trichonephila*: Biogeographic patterns of spiders with different dispersal abilities

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Dispersal ability is an organismal attribute that shapes biodiversity and affects species distributions. Island systems are excellent arenas to study dispersal. Here, we investigate the

biogeography of the Caribbean *Cyrtognatha*, *Tetragnatha* (both Tetragnathidae) and *Trichonephila* (Nephilidae), three orbweaving spider genera that contain species of different dispersal abilities. Our results suggest that *Cyrtognatha* colonised the Caribbean by recent overwater dispersal (mid-Miocene), and that it contains exclusively single island endemic species of putatively poor dispersal abilities. In contrast, *Tetragnatha* independently colonised the Caribbean on multiple occasions, and the genus comprises some excellent dispersers, as well as species that may have secondarily lost dispersal propensity. *Tetragnatha* thus features a complex combination of attributes of a 'dynamic disperser'. Finally, the Caribbean biogeography of *Trichonephila clavipes*, a textbook over-water disperser, is consistent with a single species spanning the Caribbean and North America. We interpret these three different biogeographic patterns to partially support the intermediate dispersal model of biogeography (IDM), which predicts the highest species diversity in the genus that contains species with intermediate dispersal ability.

Student oral presentation

From Gondwana to GAARlandia: Evolutionary history and biogeography of ogre-faced spiders (*Deinopis*)

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We explore the evolutionary history of the ogre-faced spiders (*Deinopis*) from their Early Cretaceous origins to present day. Specifically, we investigate how vicariance and dispersal in have fundamentally influenced distribution patterns of this lineage. Within the Caribbean, we test the role of GAARlandia, a hypothesised land bridge that connected South America to the Greater Antilles during the Eocene–Oligocene transition (~35-33 Ma), in the biogeography of *Deinopis.*Combining standard Sanger sequence data with an Anchored Hybrid Enrichment (AHE) phylogenomic dataset, we use Bayesian inference to estimate the phylogenetic relationships of *Deinopis*. 'BioGeoBEARS' is used to test the GAARlandia hypothesis, and to pinpoint major dispersal events in the biogeographic history of *Deinopis*.The phylogeny supports the nesting of a Caribbean clade within a continental grade. Model comparisons indicate GAARlandia as the best fitting model. Ancient and recent overwater dispersal events are also indicated within this lineage. There is also an ancient 113 Ma split into Old and New World clades. Additionally, our results support the GAARlandia land bridge hypothesis and the phylogenetic relationships within and among Caribbean islands mirroring nuances of Caribbean geologic history. The spider family Deinopidae is an ancient lineage with origins dating back to Gondwana. While overwater dispersal has clearly played a role in the biogeography of the genus, as implied by the colonisation of the volcanic and sedimentary Lesser Antilles and in a 'reverse' colonisation of North America, the *Deinopis* phylogeny bears a strong signature of ancient geological events.

Symposium presentation

Genetic basis for jumping spider aggression

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Aggression, an evolutionarily conserved personality trait, has been documented in diverse animal taxa. Most genetic studies on aggression are limited to laboratory model organisms, thus the molecular underpinnings of aggression in non-model animal remain unexplored. Here we use wild-caught spider-eating jumping spiders (*Portia labiata*) as a study system. Using transcriptomic approach with RT-PCR and genetic association analysis, we found that aggression is a multi-gene trait regulated by diverse biological pathways involved in pathogen infection, metabolism, and nervous systems. Spider aggression varies with virus species and loads, suggesting a relationship between animal personality and pathogen infection. In addition, peroxidase, an oxidative stress related gene, is upregulated in aggressive spiders, probably explaining the commonly observed link between metabolism and personality. Moreover, we identified nervous system genes associated with aggression. Furthermore, using genetic association analysis with the consistently differentially expressed gene, we discovered that genetic variants in peroxidase gene are associated with both sexes. Genetic variants in a transcription related gene, actin-related protein 8, and immune system related gene, BTB/POZ domain containing protein 17, are only associated with male aggression, while genetic variants in myotubularin-related protein 14 (related to serine/threonine and tyrosine phosphatase activity) and nervous system related gene, serine protease 30, are only associated with female aggression. We identified the heritable components regulating aggressive behaviour that selection may act on, and these genetic components are sex-specificin *Portia labiata*. Collectively, our results shed new insights into diverse biological processes in aggression regulation in non-model wild invertebrates.

Oral presentation

There's more than one way to build a leaf retreat: Convergent solutions in orb- and pseudo-orb web spiders

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Orb webs are a remarkable type of foraging web, and arguably the most efficient trap configuration to capture flying insects. Although the number of independent origins of the orb web is still contested for spiders formally grouped in the ‘Orbiculariae,’ recent phylogenomic analysis indicates there is little doubt that the pseudo-orb webs of *Fecenia* (Psechridae) represent either a completely novel instance of independent convergence, or a very distant atavistic resurrection. These remarkable spiders also share a trait common to a small subset of orb weavers: the use of a leaf retreat suspended in the hub — an adaptation that is undoubtedly convergent. Here, we examine this convergence from a behavioural perspective by studying the web construction process in *Fecenia protensa* and *Acusilas coccineus* (Araneidae). In particular, we compare the spiders’ strategies of building their leaf retreats in a variety of

circumstances. Preliminary results show that *Fecenia protensa* is more flexible with the retreat materials, is able to locate the retreat more quickly, and is more likely to retrieve the retreat in a topologically complex environment. We also noticed that the spiders use different strategies to hoist their retreat off the ground, and suggest that the different solutions to this task stem from differences in the spiders' anatomical or morphological constraints and differences in preexisting behavioural repertoires.

Oral presentation

Prolonged milk provisioning in a jumping spider

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Lactation is a mammalian attribute, and the few known nonmammal examples have distinctly different modalities. We document here milk provisioning in a jumping spider, which compares functionally and behaviourally to lactation in mammals. The spiderlings ingest nutritious milk droplets secreted from the mother's epigastric furrow until the subadult stage. Milk is indispensable for offspring survival in the early stages and complements their foraging in later stages. Maternal care, as for some long-lived vertebrates, continues after the offspring reach maturity. Furthermore, a female-biased adult sex ratio is acquired only when the mother is present. These findings demonstrate that mammal-like milk provisioning and parental care for sexually mature offspring have also evolved in invertebrates, encouraging a re-evaluation of their occurrence across the animal kingdom, especially in invertebrates.

Student oral presentation

Predation rates on North American *Leiobunum* harvestmen (Sclerosomatidae: Opiliones).

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Opiliones—commonly known as harvestmen or daddy long-legs—display a variety of defence mechanisms, with the most common being the secretion of noxious chemicals from scent glands to deter predators. Up until now, harvestmen were not known to use vision. In prior work, we compared whether males and females differed in the likelihood of secreting defensive chemicals, as well as fleeing from a visual disturbance, in a laboratory setting. We found sex-specific differences in both assays, and found evidence that vision may play a role in threat avoidance. Here, we test the effectiveness of these two defence mechanisms in the field. We assessed field predation rates for tethered *Leiobunum ventricossum* (Sclerosomatidae) each under one of the following treatments: clogging the chemical gland that secretes the chemical defence, painting the eyes to impair vision, or sham controls. We also conducted focal observations through video surveillance to determine likely predators, which is currently unknown for this group of harvestmen. We found that individuals with clogged glands were predated at significantly higher rates than blinded and control individuals, suggesting that

vision may be only useful under certain light conditions; these results were similar for both males and females. We found that ants were the primary predators of harvestmen. Overall, our results show a clear role for chemical secretions as a defence mechanism and suggest that ants may be a major predator of North American harvestmen.

Oral presentation

Spiders did not repeatedly gain, but repeatedly lost, foraging webs

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Much genomic-scale, especially transcriptomic, data on spider phylogeny has accumulated in the last few years. These data have recently been used to investigate the diverse architectures and the origin of spider webs, concluding that the ancestral spider spun no foraging web, that spider webs evolved *de novo* 10-14 times, and that the orb web evolved at least three times. In fact, these findings principally result from inappropriate phylogenetic methodology, specifically coding the *absence* of webs as logically equivalent, and homologous to, tenother observable (i.e. not absent) web architectures. “Absence” of webs is simply inapplicable data. To be analysed properly by character optimization algorithms, it must be coded as “?” or “-” because these codes, and these alone, are handled differently by such algorithms. Additional problems include critical misspellings of taxon names from one analysis to the next (dropping even one taxon affects taxon sampling and results), and mistakes in spider natural history. In sum, methodological error: 1) causes character optimization algorithms to produce illogical results, and 2) does not distinguish absence from secondary loss. Proper methodology and corrected data instead imply that foraging webs are primitive for spiders and that webs have been lost ~5-7 times, not gained 10-14 times. The orb web, specifically, may be homologous (originated only once) although lost 2-6 times.

Symposium presentation

Deep evolutionary history of spider venom phospholipase D toxins

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Sphingomyelinase D/phospholipase D (SMase D/PLD) toxins, expressed in venoms of sicariid spiders, evolved from the glycerophosphoryl diester phosphodiesterase (GDPD) family, which includes ubiquitous housekeeping enzymes. Compared to GDPDs, GDPD-like SMase D/PLDs share a signature C-terminal motif and $\beta\alpha1$ loop, and catalyse cyclization chemistry of phospholipids rather than hydrolysis of glycerol phosphates. GDPD-like SMase D/PLDs have also been found in pathogenic actinobacteria and fungi, inspiring consideration of the relative contributions of lateral gene transfer and convergent recruitment in their evolutionary history. We present an updated survey of the GDPD-like SMase D/PLD family and report a wider species distribution including strong conservation in chelicerates, myriapods and ctenophores. The chelicerate phylogeny suggests at least three convergent recruitment events for use in the

venom of arachnids, including ticks, scorpions and sicariid spiders. Chelicerate and myriapod sequences form a putative clade that, intriguingly, has a sister group in the anthozoans within Cnidaria. The ctenophore homologs belong to a larger clade of sequences sparsely distributed among a wide variety of aquatic organisms. A rooted phylogenetic tree of shows that the major GDPD-like SMase D/PLD clades derived from a basal paraphyletic group, most of which are proteobacterial sequences and some of which are on mobile genetic elements. The GDPD-like SMaseD/PLD enzymes probably derive from a single ancient bacterial ancestor and radiated into diverse organismal lineages in part through lateral gene transfer. These proteins, though best known as sicariid spider venom toxins, have an ancient origin and may carry out a variety of biological functions in diverse organisms.

Student oral presentation

Testing the hypothesised antipredator defence function of stridulation in the spiny orb-weaver, *Micrathena gracilis*

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The diversity of antipredator defences across organisms demonstrates predation’s impact on evolution. The spiny orb-weaver *Micrathena gracilis* is the only one of 105 described *Micrathena* species known to stridulate when grasped, and only its sister species has similar stridulatory organ morphology. Therefore, stridulation is likely a derived trait, and has potentially been under selection from predation. While stridulation in *M. gracilis* was first hypothesised to be an antipredator defence nearly 50 years ago, this has not been tested. We quantified the behavioural and acoustic properties of stridulation, and directly tested stridulation’s effect on survival in laboratory and field studies with adult female *M. gracilis*. Approximately 64% of *M. gracilis* stridulated when grasped, and those that did varied in their latency to and rate of stridulation. These measures are significantly, negatively correlated; individuals with lower latencies to stridulation stridulated at higher rates. Stridulatory behaviourwas not predicted by mass, body length, or condition. Stridulatory pulses produce broadband frequency spectra, consistent with acoustic antipredator defences in other taxa. In staged laboratory interactions with captive blue jays, we found no differences in survival between stridulation-ablated and sham-treated *M. gracilis*. Notably, some blue jays stopped attacking *M. gracilis* after repeated exposure. Pilot trials suggest that stridulation may repel jumping spider predators. In a mark-recapture field study comparing survival of stridulation-ablated and sham-treated individuals, we found no differences in survival or re-sighting rates between groups. We discuss these findings in the context of prey lines of defence, multiple predator types, and predator learning.

Symposium presentation

A spider-eating predator's capacity to decide when to take a detour

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Exceptionally complex predatory strategies are characteristic of *Portia*, a genus of jumping spiders (Salticidae) that specialise in preying on other spiders. We have been interested in the capacity these small predators express for making plans, including plans that require choosing detour paths that take them to otherwise inaccessible prey. Previous research has demonstrated *Portia*'s remarkable proficiency at choosing between two indirect routes (i.e., detours) when only one leads to the prey. Less is known about *Portia*'s proficiency at making strategic decisions regarding whether to adopt a more or a less direct path to prey. However, when freedom of movement was restricted by water and when prey was only visible at the beginning of a trial, we found evidence that *Portiaafricana* decides ahead of time whether to take a more direct path to the prey when available and, when not available, to take a less direct path.

Oral presentation

Camel spider (Solifugae: Eremobatidae) research past and future

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Over the past decade the DMNS arachnology lab's research has been focused on the evolutionary history, taxonomy, morphology, and behaviour of solifuges, commonly called camel spiders (Arachnida, Solifugae). An overview of this research including the results of a multi-locus molecular phylogeny of the North American solifuge family Eremobatidae, an overview of functional morphological studies of the pedipalps, and an update of future research plans will be given. Our multi-locus phylogenetic analysis supported the monophyly of the family Eremobatidae, but indicated that the subfamily Therobatinae was artificial. Our functional morphological analyses of the pedipalp revealed the possible function of specialized setae found on the surface of the pedipalps. Our labs at DMNS and ECSU will use next generation sequencing to re-analyse the phylogeny of the family with the goal of sequencing all species currently found in the Eremobatidae and explore the functional significance and the diagnostic potential for characters associated with the pedipalps and chelicerae. Our future research will also provide the first phylogeographic analysis of clades in North American Deserts with the goal of using camel spiders as a model system to explore the evolution of desert fauna.

Symposium presentation

Arachnology at the Denver Museum of Nature & Science: Foundations of biodiversity studies using volunteers and paraprofessionals

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The Arachnology collection and program at the Denver Museum of Nature & Science (DMNS) was established in 1998 when Paula Cushing was hired as the Curator of Entomology. Her title quickly morphed into the Curator of Insects and Spiders and then into the Curator of Invertebrate Zoology. In 1999, she initiated the Colorado Spider Survey (CSS). The DMNS arachnology collection began with two significant donations: a large collection from Bea Vogel, first president of the American Arachnological Society; and a transfer of arachnids from the Colorado State University arthropod collection. Specimens donated from other colleagues, from Cushing through her own fieldwork, and through CSS participants have grown the collection from near-zero vials in 1999 to over 60,000 vials (over 40,000 of which are identified and databased) 20 years later. The DMNS arachnology data has been online-accessible since its inception. Cushing established an efficient system for specimen processing, curation, and identification by training and using the skills, dedication, and enthusiasm of paraprofessionals recruited through the CSS. Today's presentation will provide an overview of how this collection was established, and how it has grown into one of the major collections housed at the DMNS largely through the support of teams of paraprofessionals.

Student oral presentation

Spiders in Agroecosystems: community structure and potential for biological pest control in Nebraska maize

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As generalist predators, spiders are capable of fulfilling a wide variety of ecological niches, allowing them to intercept and prey upon an array of insect species. This variety of niches could be particularly advantageous within agricultural ecosystems. This study sought to reveal the composition and abundance of spider communities within maize fields in western Nebraska, USA, and to determine the potential for spider predation upon key pests of maize. Spiders were collected from eight maize fields (four high-input; four low-input) from May to August 2017, and four maize fields (two high-input; two low-input) from May to August 2018. Additionally, the populations of two important pests of maize, western corn rootworm (*Diabrotica virgifera virgifera*) and western bean cutworm (*Striacosta albicosta*), were sampled to determine prey availability. During the 2017 collection period, a total of 656 spiders were collected represented by the following families: Lycosidae (53%); Linyphiidae (30%); Gnaphosidae (4%); Thomisidae (4%). In 2018, a total of 239 spiders were collected, representing a complex of families similar to those collected in 2017: Lycosidae (61%), Linyphiidae (34%), Araneidae, Gnaphosidae, and Salticidae (5% combined). Pest population sampling did reveal presence of both western corn rootworm and western bean cutworm in the sampled fields. The second half of this project will evaluate the gut contents of the collected spiders in order to determine

whether predation of key pests of maize is occurring. These results will help to reveal the role of spiders within agroecosystems, and can be used to improve conservation biological control programs in the future.

Oral presentation

Functional failures: flubbed intromissions act as cryptic sperm removal behaviours

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Sexual selection has resulted in an impressive diversity of genitalia and behaviour. One behavioural puzzle that remains to be solved is the occurrence of failed intromissions. Unsuccessful intromissions have been reported in diverse taxa from mammals to arthropods and are widespread across spider taxa. Researchers have hypothesized that failed intromissions result from male error or difficulties in aligning genitalia. Here we demonstrate for the first time that so-called “failed” intromissions function to remove rival sperm from females using ornamental genitalic structures. Ornamental (e.g. non-sperm transferring) genitalic structures such as spines are surprisingly common on male genitalia. Hypotheses such as cryptic female choice seek to explain their evolution and impact on paternity. Yet their function is only known for a handful of species. Here, we report for the first time that male orbweavers use corkscrew-shaped genital ornaments to remove rival sperm. The widespread occurrence of failed intromissions and ornamental genitalic structures in other taxa suggests that their functions should be re-evaluated in light of the possibility for cryptic sperm removal strategies.

Oral presentation

First record of the dwarf spider genus *Alioranus* Simon, 1926 from India with the description of a new species (Araneae, Linyphiidae, Erigoninae)

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The dwarf spider genus *Alioranus* Simon, 1926 is recorded from India for the first time. The genus is poorly known, with only six species so far described. The genus is reported from Asia, the Mediterranean region and Russia. A new species of this genus, *A. durgavati* **sp. n.,** is described here with a detailed taxonomic description of both the sexes and natural history notes. The distribution of the new species is mapped.

Student oral presentation

Spider silk: What's in those genes?

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Most genes of higher eukaryotes contain introns, intervening portions of DNA that are spliced out during gene transcription. Since their discovery it has been argued that they are simply 'junk' DNA, artefacts of an inefficient evolutionary process that has been unable to remove them. However, a wealth of evidence now exists to suggest that introns are essential for many parts of the gene transcription process. Characterising introns can inform our understanding of the forces governing the evolution of the proteins within which they are situated. However, the diversity and evolutionary history of introns in large and complicated gene families, such as the spider silks, is often poorly understood. In this study we investigate the distribution across spider taxa of all hitherto reported silk introns, and examine phylogenetic relationships using DNA sequence data. We find that two distinct gene intron-exon architectures are apparent: single or multiple intron. These may influence the type and quality of silk that a spider can produce through the regulation of transcription. Characterisation of a greater range of silk genes from divergent spider species will allow us to test the likelihood of evolutionary scenarios, such as the repeated loss or gain of introns, or rates of recombination amongst silk types. Furthermore, an improved understanding of the evolution of silks at a molecular level may lead to insights that are useful for the production of synthetic silks in the laboratory using eukaryotic organisms.

Oral presentation

Comparative nest construction in orthognate spiders

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Nest building is common in the world of spiders, both within the Orthognatha and the Labidognatha. In Orthognatha, however, nest building is virtually universal. The archetypical or stereotypical nest of orthognate spiders consists of a rather simple tube-shaped burrow, dug out in the soil and capped by a hinged cover at the soil surface. This type of spider nest is generally known as a "trapdoor burrow". Trapdoor burrows are built by all liphistiomorph spider species and by a wide range of mygalomorph species, taxonomically placed in a number of different families, that are commonly referred to as trapdoor spiders. Many variations in the basic trapdoor burrow design, as well as qualitatively different burrow types, have evolved within the Orthognatha. The comparative study of these variations and burrow types in relation to differences in the functional morphology and behaviour patterns seen in the spiders constructing them is expected to provide an improved understanding of early spider evolution.

Oral presentation

Phylogenomics of the Gondwanan Triaenonychidae (Opiliones, Laniatores), with discussion on UCE sequence capture from old museum specimens

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The laniatorean family Triaenonychidae, which currently includes ~480 species in ~110 genera, has a mostly Gondwanan distribution with taxa found in the temperate forests of southern South America, South Africa, Madagascar, Australia, New Zealand, and New Caledonia, with a single genus found in eastern North America. A thorough assessment of the relationships within Triaenonychidae has never been conducted using phylogenomic data, and current higher-level relationships are largely based on somatic characters of questionable utility. Here, we use sequence capture of ultraconserved elements to reconstruct the phylogenetic relationships of Triaenonychidae using 100s of loci. Our current taxon sample includes ~80% of known generic-level diversity, and representatives of several undescribed genera. Phylogenomic analyses reveal some interesting biogeographic patterns, show para- and polyphyletic origins in all major Gondwanan components, and do not support current subfamilial groupings based on morphology. Despite being relatively well-studied in certain parts of their distribution, the triaenonychids remain poorly studied in other regions like mainland Australia. This phylogeny provides the basis for future research including comparative biogeography of Gondwanan taxa, phylogenetic framework for biogeographical and phylogeographical studies of the highly diverse triaenonychids endemic to New Zealand, context for comparative studies of morphological evolution, and a backbone for regional taxonomic revisions. In addition, ongoing efforts to successfully incorporate standard ethanol-preserved (70-80%) museum specimens into UCE sequence capture phylogenomics using specimens dating back to the 1800s will also be discussed.

Oral presentation

Understanding pholcid relationships and diversification: recent advances and future directions

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With more than 1600 described species, Pholcidae is among the most species-rich spider families. In the last few decades, intensive research on pholcid diversity and evolution has resulted in several large-scale phylogenetic studies, and numerous monographic revisions and species descriptions. Here we present the results of our recent phylogenetic study on Pholcidae, which is based on six genetic markers and includes 600 species that represent all major lineages and 86% of all described genera. Based on these phylogenetic results, we review the higher-level relationships within the family and propose several changes in taxonomy. We also use this large phylogenetic framework to study macroevolutionary patterns in pholcids. We find strong evidence for multiple shifts in microhabitat preferences with multiple convergent

occurrences of above ground (e.g. leaf-dwelling) species. We show that such changes in microhabitat preference are not only linked to changes in morphology and behaviour, but also served as one of the major drivers of pholcid diversification, particularly in above-ground living taxa.

Student oral presentation

For all audiences: the impact of incorporating immature stages into biodiversity assessment of mega-diverse groups

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Early detection methods for monitoring ecosystem changes are essential to identify and tackle unanticipated threats. Arthropods have the potential to indicate biodiversity changes at finer spatial and shorter temporal scales than vertebrates. The use of rapid biodiversity assessment protocols can ameliorate the daunting task of sampling highly abundant groups. However, the poor taxonomic knowledge of many arthropods limits their use as bioindicators, especially in groups, such as spiders, for which traditional taxonomy is based on specific life stages (generally adults). Spiders are amongst the most abundant and ubiquitous predators in terrestrial ecosystems, and play a key role in trophic networks and ecosystem functioning. To date, spider inventories have been solely based on adult specimens, which may bias biodiversity estimates, especially in single surveys conducted in highly seasonal places. Here, we assess the impact of identifying and recording immature individuals on estimates of species-richness and replacement of spider communities associated with oak forests. We used a metabarcoding approach by sequencing a 313bp COI fragment to assess species richness of pools of immature spiders collected from 16 1-ha plots. We compared alpha diversity values and taxonomic and functional beta diversities with and without immatures, and we identified the variables associated with differences in the number of species represented by only immature specimens. Our results reveal that an important component of local diversity is missing if only adult specimens are analysed. The inclusion of immatures improves our ability to estimate biodiversity shifts in time and space.

Oral presentation

Long-term benefits of extended maternal care in a jumping spider

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Extended parental care, known as continued caring for nutritionally independent offspring, usually could increase offspring's fitness as it enables them to fully develop the skills of hunting, predator defence, and mate choosing. However, these have been studied overwhelmingly in long-lived social vertebrates. Here, we suggest that similar benefits of extended maternal care could also appear in a jumping spider (Salticidae), which provides

maternal care for sexually matured offspring despite the spiderlings acquiring foraging ability from around three weeks after hatching. We hypothesise that the maternal care in this species could enhance the adult offspring's fitness by improving their skills mentioned above. Specifically, we predict that the extended maternal care (caring for 20 days old to adult offspring), could enhance the offspring's: 1) hunting efficiency for small size prey items (fruit flies), 2) hunting success for large size prey items (crickets), 3) possibility of predator (*Portia* spp.) avoidance, 4) success in access to female (for male offspring), and 5) maternal care skills (for female offspring). These results suggest that extended parental care has also evolved in invertebrates, and it probably increases the offspring's fitness through affecting their later life-stage skills.

Student oral presentation

Individual and sex-specific differences in behaviour of the nursery web spider (*Pisaura mirabilis*)

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Most studies investigating personality in invertebrates focus only on a few behavioural traits in a single ecological context and situation, and disregard possible differences in behaviour between sexes. To fill in these knowledge gaps, we examined personality in nursery web spider (*Pisaura mirabilis*) in the foraging and anti-predator contexts. The main aim of the study was to identify repeatable traits and describe how they are interrelated and compare behaviour between sexes. We recorded several traits in subadults of *P. mirabilis* (25 females and 24 males) related to anti-predator behaviour (tonic immobility, exploration latency, and response to touching by a small brush) and foraging behaviour (attack rate, attack from a distance, and wasteful killing).Our results suggest that, although we observed behaviour in foraging and anti-predator contexts, repeatable traits created only a single continuum from bold and more aggressive to shy and less aggressive individuals. Specifically, individuals which did not display tonic immobility also responded more aggressively to touching by a brush, and attacked prey more frequently and from a larger distance. Interestingly, the most repeatable trait was the tonic immobility, which was significantly repeatable in both sexes. In other traits, we identified differences in repeatability between sexes, depending on the ecological context. While response to the brush was repeatable only in males, attack rate was repeatable only in females. We argue that aggressiveness is favoured in females in the foraging context and boldness in males during mating which leads to higher repeatability of these traits.

Symposium oral presentation

Good fences make good neighbours: Resolving evolutionary history and species delimitation of western Mediterranean ctenizid trap-door spiders

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The trapdoor spider genus *Cteniza* currently includes four species circumscribed to the North-Central Mediterranean basin, specifically the Maritime Alps, Calabria and the Tyrrhenian islands. Recent studies suggest that *Cteniza* together with the related yet divergent Aegean genus *Cyrtocarenum*, most likely represent the only true representatives of the family Ctenizidae. Despite of the evolutionary relevance and biogeographic significance of the genus, both the distribution and relationships among the recognised *Cteniza* species remain contentious. Trapdoor spider taxonomy has been traditionally hampered by a conservative morphology, with few yet highly polymorphic variable traits. Molecular based approaches have gained popularity to establish species boundaries in groups of conflicting taxonomy. However, trap-door spiders usually show highly structured populations, which challenge the basic tenets of quantitative delimitation methods. Here, we use a target multi-locus approach along with relaxed clock modelsto unravel the history and delimit *Cteniza* species. Additionally, we generate RADseq data to investigate fine-scale population genetic structure. Our study uncovers higher species diversity that previously assumed and confirms deep mitochondrial structuring of trap-door spiders. Furthermore, we suggest that *Cteniza* diversification was driven by the highly dynamic geology of the Western Mediterranean Basin and that the continent was secondarily colonised from the islands. Some biogeographic relationships recovered are at odds with the geology and geographical settings, which may hint at either long-distance dispersal events or high extinction rates during the evolution of the genus.

Symposium presentation

It's complicated: Patterns of Caribbean biogeography in arthropods

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We examine biogeographical patterns of arthropods in the Caribbean biodiversity hotspot using both previously published data as well as new data testing explicit hypotheses with probabilistic inference. Whereas the findings from vertebrate groups have been synthesised, terrestrial arthropods have not been subjected to such examination for >30 years. Since then, many new data collection techniques and analytical methods have been devised that help provide a deeper understanding into the patterns of establishment and diversification on Caribbean islands, instead of arguments that focus solely on dispersal v. vicariance. Here, we examine origins of taxa, major geographic breaks, patterns of diversity, and times and number of dispersal events, including dispersal across the Isthmus of Panama/Central American Seaway on the mainland. Our results indicate that while there isn't an overarching pattern for these extremely diverse

taxa, there are commonalities among arthropods and between these taxa and vertebrates. For example, there is no evidence of taxa entering the Caribbean before the appearance of the Greater Antilles. GAARlandia may have played a role in aiding dispersal from South America to the Greater Antilles for some taxa, but is not always invoked. Most dispersal events occur from the mainland to the islands and then from island to island, although there is also evidence of islands as sources of diversity for the mainland. The Central American Seaway was not an efficient barrier for most arthropod taxa examined, and founder event dispersal appears to be important among island taxa.

Oral presentation

Fauna and zoogeography of scorpions in Greece

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A remarkable diversity of the scorpion fauna and its distribution in Greece is discussed. The current list of Greek scorpions includes 32 confirmed species belonging to three families (one of Buthidae, seven of Iuridae, and 24 of Euscorpiidae), as well as a number of unassigned euscorpiid taxa. Uncovered only in the last decade, mainly through the use of DNA markers, the cryptic scorpion fauna of Greece is the most diverse in Europe and rivals that of many other countries.

Student oral presentation

Identification of the sex pheromone of the female false black widow spider, *Steatoda grossa* (Theridiidae, Araneae)

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Female web-building spiders such as the false black widow, *Steatoda grossa*, deposit sex pheromone on their webs that attract mates and elicit their courtship behaviour. During courtship, males cut and bundle pheromone-bearing web strands and wrap them by adding their own silk. A recent study demonstrated that methanol extract of virgin female *S. grossa* webs contains pheromone that attracts males and elicits web-wrapping behaviour. Using gas chromatography-mass spectrometry (GC-MS), we analysed silk methanol extracts of subadult females and males as well as adult virgin and mated females. We found seven compounds that were unique to virgin females, but none elicited courtship behaviour by males. We then fractionated methanol web extract of virgin females by high-performance liquid chromatography (HPLC) and bio-assayed each HPLC fraction for pheromonal activity. We analysed those fractions that induced web-wrapping behaviour in males by HPLC-MS, and isolated compounds for nuclear magnetic resonance (NMR) spectroscopy. Based on combined information of HPLC mass spectra and NMR spectroscopy spectra, we identified and synthesised three candidate pheromone components. The synthetic blend of these three components was as effective as methanol web extract in inducing courtship behaviour by males. This is the twelfth identified sex pheromone in a spider.

Oral presentation

The effect of metabolic rate on performance in the salt marsh wolf spider *Pardosa littoralis*

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Metabolic rate (MR) is the sum of all biochemical processes within organisms. The relationship between MR, individual performance (i.e. fitness), and higher-level ecosystem processes is a focus in ecological research and subject to considerable debate (e.g. Metabolic Theory of Ecology vs. Dynamic Budget Energy Model). Many spiders are key predators in ecosystems, and are thus important for investigating the effects of MR variation on both individual-level fitness consequences and ecosystem-level processes. As part of a broader research program investigating threatened salt marsh systems on Long Island, NY, USA, we explore the scaling relationship of routine MR with body size in *Pardosa littoralis (Lycosidae)*. Additionally, we test whether MR is an important predictor of performance, estimated as top burst speed, cruising speed, and maximum distance run. We use individuals from three distinct populations to evaluate spatial variation in MR and its relationship to performance traits. MR, as well as all performance traits, exhibit significant repeatability in our study. We find that MR scales isometrically with body size, and that mass-specific MR exhibits substantial variation. MR predicts performance during short, energetically expensive activity bouts, and is thus an important part of the phenotype to consider when estimating "whole organism performance". Neither MR nor its effect on performance traits covary with population origin.

Student oral presentation

Tarantula phylogenomics: A first phylogeny of major theraphosid spider lineages inferred from transcriptome data sheds light on the evolution of urticating setae

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The mygalomorph spiders of the family Theraphosidae, also known as tarantulas, are among the most recognisable spiders on earth due to their large size, cosmopolitan distribution, and

diverse array of synapomorphies. Their use of urticating setae is a particularly famous adaptation that has evolved exclusively in particular New World theraphosids, and has attracted a reasonable amount of scientific and media attention. It is hence both surprising and unfortunate that the evolution of Theraphosidae remains poorly understood. The field still largely relies on morphological data, which has previously been shown to be biased by high degrees of homoplasy. Comprehensive molecular studies on theraphosid phylogenetics are a relatively recent innovation, although the potential to derive meaningful inferences has previously been limited by poorly supported deeper core relationships. Here, the first robust phylogenetic hypothesis of theraphosid evolution inferred from transcriptome data is presented. A core otholog approach was used to generate a phylogeny from 2460 orthologous genes across 26 theraphosid genera, representing every recognised subfamily except Selenogyrinae. Theraphosidae, and most subfamilies, were recovered as monophyletic. Support for the paraphyly of Ischnocolinae is provided. Most deeper core relationships between these subfamilies are confidently inferred for the first time, with 100% bootstrap support recovered for all but two nodes across all analyses. We use our phylogeny in tandem with published morphological data to provide a phylogenomically informed overview of urticating setae evolution, and provide three separate hypotheses for the evolution of urticating setae types among New World Theraphosidae.

Oral presentation

The future of spider diversity on a mountain: habitat complexity and not elevation could explain their response to climate change

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Understanding the impacts of climate on spider diversity requires long term records that are systematically collected and should also be located at points where changes are inherently more detectable. Altitudinal transects span boundaries of biomes and is particularly suited to identify the effects of climate change. Here we report on a 5-year sequence of epigeal spider diversity along an altitudinal transect that spans three biomes. The analysis includes 390 assemblages stratified across space (elevation, aspect) and time (hot/dry and wet/dry seasons). Spider diversity is driven by habitat complexity, increasing with percentage bare ground and decreasing in tree dominated sites with complex vertical structure. Neither elevation nor temperature explained significant amounts of variation. Dynamic vegetation models based on IPCC climate change trajectories point to a general trend of increasing tree cover along the transect. These structural changes in vegetation could have a larger impact on spiders than climate change itself.

Oral presentation

Island biogeography: to be (indigenous), or not to be, that is the question

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Discriminating between indigenous or non-indigenous species is vital for interpreting biogeographical patterns on islands. Islands are subject to ongoing immigration and extinction processes, of which human introductions of tramp species have been shown to play a significant role in changing the local fauna and flora and thereby masking natural biogeographic patterns. Invasive species are of particular conservation concern, if an island fauna contains a high proportion of endemic species. Quarantine obligations for a resource project on a Western Australian island reserve provide the opportunity to explore biogeographic processes on a near-shore island. Major challenges include the identification of non-native species against a diverse native, but largely undescribed fauna; more than 3,500 species of terrestrial invertebrates have been collected on the island, ca. 500 of which represent arachnids (incl. mites). This presentation explores the challenges in identifying non-native species against a diverse, and apparently dynamic indigenous island fauna. Traditional taxonomic approaches include morphological identification, but we are currently applying more contemporary methods including Next Generation Sequencing (NGS)/meta barcoding approaches, but also Artificial Intelligence (AI)/Deep Learning of a photographic library of native species.

Student oral presentation

Testing for an anti-adhesive surface coating in *Uloborus plumipes* and the web-invader *Pholcus phalangioides* (Araneae: Uloboridae, Pholcidae)

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In this contribution we address the following question:do the cribellate orb-weaver *Uloborus plumipes* and the web invader *Pholcus phalangioides* protect themselves from cribellar capture threads by an anti-adhesive surface coating? We defined four experimental groups of spider legs, i.e. untreated legs, legs washed with two different organic solvents (C_6H_{14} and CS_2), and legs washed with purified water. We measured indirectly the force needed to detach the spider legs from a piece of *U. plumipes* capture thread of defined length. The results show no significant effect of treatment and very low adhesion in *U. plumipes* legs, pointing to a hitherto unknown anti-adhesive mechanism. The treatment with organic solvents led to significantly higher adhesion in legs of *P. phalangioides*. The meaning of this result is discussed with respect to the web-invading behaviour of this species.

Student oral presentation

How do whip spiders make their whips? Applying differential gene expression approaches to identifying genetic mechanisms

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Some arachnid orders have specialised sensory legs, which represent a remarkable functional convergence with the insect antenna. Yet little is known about the selector genes involved in patterning arachnid legs generally, let alone the sensory legs of individual orders. Here, we studied embryogenesis of the whip spider *Phrynus marginemaculatus* (Amblypygi), as an exemplar of an order where the first leg pair (L1) is modified into elongate, antenniform appendages. We generated leg-specific transcriptomic sequence data of L1 (antenniform) versus L2-L4 (non-antenniform) appendages dissected from embryos. Reads were mapped onto the first embryonic transcriptome of an amblypygid and differential gene expression analysis was conducted using DESeq2, with the aim of circumscribing candidate genes involved in leg antennification (i.e., genes differentially expressed in L1, in comparison to L2-L4). Our results with deutembryos validate the appendage sequencing approach to study non-model arachnids, by first showing that each leg has expression profiles according to known segment-specific genes. Moreover, we uncovered gene candidates for leg antennification, which can now be tested with expression (in situ hybridization) and functional (RNAi) assays in arachnid model systems. Understanding the development of this complex character is predicated on integrating transcriptomic data with detailed description of antenniform leg morphogenesis, including histological approaches and fluorescent confocal microscopy.

Oral presentation

Why are spiders so fast? A small biochemical history

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Spiders are characterised by being hunting animals. This implies that they must develop great speed to be able to catch their prey, and even jump on it; this characteristic is well-developed in spiders that do not generate webs, as in the case of *Polybetes pythagoricus* (Sparassidae). At present, no records are found concerning how spiders get energy to move so fast. Aerobic routes seem to be insufficient, but the most consistent hypothesis is that they obtain the energy through the enzyme arginine kinase (*Pp*AK). In this work, we studied *Pp*AK in spiders for the first time (using *P. pythagoricus*). The cDNA of *Pp*AK was cloned, which is comprised of 1068 nucleotides that encode a 384-amino-acid protein with a calculated mass of 43 kDa. The sequence displays extensive similarity to other invertebrate arginine kinases (spider, tick, horseshoe crab and crustaceans). The apparent Michaelis-Menten kinetic constant (Km) and maximum velocity (Vmax) were 1.703 mM and 27.77 μmol.min^{-1}.mg protein^{-1}, respectively. The crystal structure, shown with both ligand-free and arginine binary complexes, was found in the open conformation, with loops comprised from residues (310-320) fully disordered and not covering the active site as in the ternary complex reported for other guanidine kinases.

Finally, these results contribute to the knowledge of mechanism and function of spider arginine kinases, in addition to reporting DNA and protein data.

Student oral presentation

Does endosymbiont infection alter the behaviour of *Philodromus* spiders?

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All organisms are infected with a range of symbionts spanning the spectrum of beneficial mutualists to detrimental parasites and it has long been known that microorganisms can alter the behaviour of their insect hosts. Perhaps the most well-known example is that of the endosymbiotic bacteria *Wolbachia,* whose effects on mating behaviour are now well documented, and are estimated to infect around two-thirds of insects as well as other arthropod taxa including spiders. The relationship between microorganisms and arachnids - in general - is poorly understood, especially when put in the context of how/if endosymbionts are able to manipulate the behaviour of the host. In this study we investigated the behaviour of *Philodromus* spiders collected from apple orchards. We investigated the variation and repeatability of behaviours, assessed whether this had an impact on their feeding preferences, and then attempted to resolve any differences between infected and non-infected individuals.

Symposium presentation

Evolution of spiders on oceanic islands: The venture of few and gain of many

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Adaptive radiation can be considered the linchpin that unites ecology with evolution and is central to understanding evolutionary processes overall. However, the best examples of adaptive radiation are often in uniquely isolated insular environments, begging the question of the generality and predictability of the process. In this talk I will examine the predictability of the phenomenon across different oceanic archipelagos, as well as between lineages within the Hawaiian archipelago. I will focus on the Pacific Ocean, which 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: theSociety, Marquesas, and Australs. Each of these archipelagos is a hotspot, with islands arranged chronologically from the south east. 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 radiation of *Tetragnatha* in Hawaii is quite exceptional. So, I will then focus on the Hawaiian Islands to compare patterns of adaptive radiation and diversification among different spider lineages.

Oral presentation

The Opiliones of New Zealand: A revisionary synthesis for testing biogeographic hypotheses

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New Zealand offers an ideal setting in which to combine the study of biogeography and systematics. The archipelago has been shaped by processes of insularity since it broke up from Gondwana ca. 80 Ma, followed by drastic marine transgressions during the Oligocene, massive mountain building during the Southern Alps orogeny, and climate change during the Last Glacial Maximum, all of which have left a signature on its biota. In this project we aim to study these processes while tackling the taxonomy of a unique group of arachnids, the order Opiliones (harvestmen or daddy long-legs), represented in New Zealand by 223 named species (and subspecies) in five native families, one of which is endemic. The New Zealand Opiliones are all endemic, with the exception of two synanthropic species, and their closest relatives are in other Gondwanan landmasses. During this project we aim to tackle this entire fauna and study evolutionary processes at different time-scales. For this, we aim to combine classic taxonomic methods with cutting-edge molecular approaches to understand the diversity and evolutionary history of this under-studied group. Example phylogenies and clades will be discussed.

Oral presentation

The role of personality variation in the mating context

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Consistent individual differences in behaviour have been reported for numerous taxa, including spiders. While several studies suggest that individual variation in behaviour relates to fitness, few studies have examined the link between personality differences and sexual selection, such asthe role of personalities in mate choice, male-male competition, and reproductive success. We observed the behaviour of the Mediterranean black widow, *Latrodectus tredecimguttatus*, to assess the existence of individual differences in two biologically meaningful behaviours: aggression towards the same-sex conspecific, and voracity towards prey in males and females, respectively. We specifically tested for voracity towards prey in females to test the "aggressive spill-over hypothesis" suggesting that more voracious females are more likely sexually cannibalistic. While males exhibited consistent differences in aggression towards rivals, female voracity appeared plastic. Hence, we cannot consider voracity a personality trait, or support the aggressive spill-over hypothesis. We further tested the link between male aggression levels and behaviours during staged mating trials. Male aggression was correlated with performance during courting, and affected their reproductive success: more aggressive males were more active during courtship, had shorter latencies to copulate, and copulated more often and for longer duration than less aggressive males. Sexual cannibalism enabled females to control

frequency and duration of copulation. Our findings suggest that evolution of personality variation may be closely intertwined with sexual selection, and spiders which often exhibit peculiar sexual biology present excellent model systems to investigate the role of personality variation for reproductive success, a major fitness component.

Student oral presentation

Systematics and niche partitioning of a unique clade of tree-dwelling scorpion (Buthidae: *Centruroides*)

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Species of the scorpion genus *Centruroides* Marx, 1890 (Scorpiones: Buthidae) are good candidates to study niche partitioning due to their habitat plasticity, wide geographic distribution, and the presence of cryptic species. Within *Centruroides*, one previously identified subgroup, the Yucatan/Chortis (‘*thorelli*’) clade, is of particular interest both taxonomically and ecologically. The systematics of the clade have proven problematic due to their rarity in museum collections, unique morphology, and tree-dwelling habitat. Concurrently, species of the *‘thorelli’* clade reside in sympatry with species from another *Centruroides* clade along the Isthmus of Tehuantepec in Eastern Mexico, presenting a rare opportunity to study niche partitioning within a single genus. My project aims to: 1) delimit the number of species within the *thorelli* clade, and 2) determine the factors of microhabitat differentiation in sympatric *Centruroides* species inhabiting the Isthmus.I am conducting a phylogenetic analysis of the *‘thorelli’* clade using genetic sequencing and morphological data from field-collected and museum specimens. I am also employing ecological niche modelling techniques, using data from museum and field-collected specimens to determine the ecological niche differentiation. These findings will be important to uncovering the vast cryptic diversity within *Centruroides*, and making a case for niche partitioning within a relatively unexplored scorpion clade.

Oral presentation

Defining orb-weaving behaviour at a high spatiotemporal resolution

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Orb-weaving is a remarkable behaviour that spans the hour timescale, and involves coordinating many sub-behaviours to successfully construct the web. In essence, the structure of the web is an emergent property of underlying behavioural structure. The general orb-weaving paradigm of first building a proto-web, then radii, auxillary spiral, then sticky spiral, has been well-known for decades. However, what is less well-understood are the multiple sub-behaviours nested within these phases of web-building, and how they are coordinated to produce the web. Here, I will describe a highly automated experimental paradigm to monitor orb-weaving behaviour, and computationally define and quantify the numerous sub-behaviours

the spider performs during orb construction based on their limb movements. This will serve as a foundation for future physical, pharmacological, and genetic perturbation to understand how this behaviour is coordinated by neurons and neuromodulatory pathways in the brain.

Oral presentation

Spider webs as a source of environmental DNA

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Sampling of environmental DNA (eDNA) coupled with state-of-the-art molecular detection approaches can potentially overcome many limitations of traditional biodiversity monitoring. Several tissues from live organisms represent potential sources of eDNA, e.g. urine and other excretions, faeces, integument, seeds and spores, but eDNA from dead organisms can also be available in form of whole cells or extracellular genetic fragments. Also, eDNA can be amplified either using specific primers within a single-species approach, or using generic primers in a multiple-species approach (i.e. DNA metabarcoding). Spider webs as aerial traps/filters represent an interesting new eDNA source. Only two studies to date have investigated spider web eDNA using a single-species approach, and they have successfully obtained both spider and prey DNA directly from webs. However, these studies were conducted in controlled laboratory conditions, and thus DNA degrading factors, such as heat, humidity, and light, have likely been reduced compared to field conditions. No study to date tested spider webs as eDNA sources in a metabarcoding context. We address these topics by first, reporting how we investigate the detection efficiency of prey genetic material on two different web types in nature, the orb and sheet webs. In controlled laboratory conditions, we test how DNA degrading factors, specifically light, heat and humidity affect the detection efficiency of eDNA from webs. Second, we present preliminary results of a metabarcoding approach aimed at assessing the use of eDNA from spider webs to conduct biodiversity surveys of arthropods, plants and fungi.

Oral presentation

Spider assemblages in South African grasslands and the factors that shape them: a review of two decades of recent work

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South Africa is one of the 17 megadiverse countries of the world, with its rich fauna and flora shaped by considerable topographical variation and the occurrence of nine floral biomes within its borders. Since 1997, the South African National Survey of Arachnida (SANSA) has aimed to co-ordinate and enhance arachnid research to improve knowledge of the country's arachnid diversity. An intensive collecting and taxonomic effort, coupled with inputs into ecological research, have helped understand the factors shaping assemblages. Approximately 800 described species from 58 families have been recorded from South African grasslands to date (of ~2300 species recorded from South Africa), although the large number of undescribed species grossly underrepresents the true diversity. Prior to the launch of SANSA, only a single ecological study had been published on South African grassland assemblages. Here we provide a short synopsis of the subsequent ecological studies, which focused on grass-, foliage-, ground-, and litter-dwelling assemblages; spiders in abandoned termitaria; the influence of fires on grassland assemblages; assemblages in different vegetation communities; and edge effects on a small scale between leaf litter and the surrounding grassland matrix. Assemblages differ in habitat strata and also geographically, with Araneidae and Thomisidae often the most abundant and species-rich families on grasses and woody vegetation, while Gnaphosidae are prominent components of ground-dwelling assemblages in open grasslands, abandoned termitaria and leaf litter. As South African grasslands are poorly protected and heavily impacted by agriculture, mining and urbanisation, more effort is needed to effectively conserve their unique and rich biodiversity.

Oral presentation

Biomechanics of sexually selected weapons in New Zealand harvestmen

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Sexual selection acting both within and between the sexes has resulted in the evolution of remarkably diverse and exaggerated traits. While some secondary sexual traits are adapted for courtship, others are used in conflict and selected for their mechanical performance. Here we present data on the mechanical performance of the absurdly exaggerated chelicerae of duelling harvestmen (*Pantopsalis cheliferoides*). This species is remarkable in that males exhibit weapon trimorphism, with two exaggerated morphs and a third reduced morph. Males with different exaggerated morphs employ different behavioural strategies during fights. We demonstrate how behavioural strategies used during sexual conflict correlate with mechanical performance, and have likely shaped the evolution of their extreme weaponry.

Oral presentation

A molecular phylogeny of the feaelloid pseudoscorpions (Feaellidae and Pseudogarypidae) reveals ancient Pangean diversification

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The Feaelloidea represent one of the most intriguing pseudoscorpion clades. They possess several unique morphological traits that have confounded their systematic placement; they have been variously treated as members of the Monosphyronida, the Neobisiinea, sister to Chthonioidea, or sister to Iocheirata. Available molecular data provides best support for the latter hypothesis. Feaelloids currently possess allopatric distributions, with Feaellidae found in Africa, Madagascar, Seychelles, the Indian subcontinent, SE Asia, NW Australia and Brazil, and Pseudogarypidae in North America and Tasmania (Australia). Both families have been

found in mid-Cretaceous amber deposits (Feaellidae in Burmese amber and Pseudogarypidae in Rhenish Massif amber), and have also been found in Eocene Baltic amber, suggesting co-existence during the Tertiary. Feaelloids appear to have poor powers of dispersal and are absent from oceanic islands. The presence of both families in mid-Cretaceous amber deposits explains their widespread modern distribution, with post-Pangaean vicariance the most reasonable explanation of the Holocene fauna. Multi-locus sequence data from 59 specimens exhibit deep separation between each family, and significant divergence within the Feaellidae. The subfamilies Cybellinae and Feaellinae are reciprocally monophyletic, and the Australian feaellids are sister to all other sampled feaellines. Deep genetic divergence among the species from Africa and Sri Lanka demonstrate a hitherto unreported diversity in this fauna. Finally, the most widespread feaelloid, *Pseudogarypus bicornis,* from western USA, is found to have little genetic substructuring across its range, suggesting relatively recent range expansions.

Student oral presentation

Phylogeny and biogeography of the spider genus *Spinoctenus* (Aranae, Ctenidae) with comments on the systematics of Ctenidae

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Spinoctenus comprises 11 ground-dwelling spiders of medium to large size, distributed in the tropical Andes and Chocó regions of South and Central America. We address for the first time the placement, monophyly, and relationships of all species of *Spinoctenus* using molecular and total evidence phylogenetic analyses for a broad sample of Cteninae genera from the Neotropics and Africa. We analysed morphology and three nuclear (ITS2, H3 and 28S) and one mitochondrial (COI) markers under maximum likelihood, Bayesian and parsimony approaches. The data strongly support the monophyly of *Spinoctenus*, with *Ctenus* and *Phoneutria* as its closest relatives. Three unambiguous synapomorphies support the monophyly of *Spinoctenus* (embolus with folded process, tegulum with median process, and RTA curved internally). Our phylogenetic analyses suggest that *Ctenus nigrolineatus*, from the lowlands of the Chocó biogeographic region should be transferred to *Spinoctenus*. A biogeographic analysis of event-based models implies the origin of *Spinoctenus* in the Western and Central Andean Cordilleras of Colombia. Dispersal from this latter area to the Chocó biogeographic region followed by vicariance resulted in four species of *Spinoctenus* (*S. chocoensis*, *S. escalerete, S. pericos* and *S.* sp. nov.). We describe the first species of *Spinoctenus* from Central America and discuss Ctenidae systematics.

Symposium presentation

Eight-Legged Encounters: arachnids, volunteers, and art help to bridge the gap between informal and formal science learning

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In an effort to better bridge formal and informal learning contexts, we developed an educational model that employs the charismatic nature of arachnids to engage the public of all ages in science learning; learning that aligns with national standards related to disciplinary core ideas regarding Biodiversity and Evolution. We created, implemented, and evaluated a family-focused, interactive science event - *Eight-Legged Encounters (ELE*) - which encompassed more than twenty modular activities. Volunteers facilitated participant involvement for each activity and original artwork scattered throughout the event was intended to attract visitors. Initial *ELE* goals were to increase interest in arachnids and science more generally among *ELE* participants. In this study, we tested the efficacy of *ELE* in terms of (i) activity-specific visitation rates and self-reported interest levels, (ii) the self-reported efficacy of our use of volunteers and original artwork on visitor engagement, and (iii) self-reported increases in interest in both spiders and science more generally. We collected survey data across five *ELE* events at four museum and zoo sites throughout the Midwestern USA. We found that all activities were successful at attracting visitors and capturing their interest. Both volunteers and artwork were reported to be effective at engaging visitors, though likely in different ways. Additionally, most participants reported increased interest in learning about arachnids and science. In summary, *ELE* appears effective at engaging the public and piquing interest. Future work is now required to assess learning outcomes directly, as well as the ability for participants to transfer knowledge gain across learning environments.

Student oral presentation

Ancient processes versus environmental change in shaping diversity of spider communities across Gunung Galang and Gunung Torompupu, Sulawesi

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Sulawesi, a composite island located in Indonesia, provides an ideal system to study the interaction of historical legacies and the environment in shaping patterns of biodiversity. It is comprised of at least four formerly isolated paleo-island regions, each with extensive mountain ranges consisting of elevation and human disturbance gradients. I have been exploring the interplay between past diversification associated with ancient historical legacies versus current environmental factors and recent responses to human disturbance in shaping spider communities, using measures of both species and functional diversity (web architecture). Webs provide quantifiable structures which allow comparison of the ecological function of communities located at varying elevations and across gradients of disturbance. Specimens were collected using a variety of standardised techniques across elevational gradients at 400m intervals. I present results from Gunung Galang and Gunung Torompupu, Central Sulawesi. Taxa from high elevation sites, because they are more isolated, are expected to bear the

signature of ancient relationships, with diversity related to the paleo-island structure of Sulawesi. In contrast, taxa found at low elevation sites, because they have experienced long periods of habitat connectivity since the merging of the island fragments, will instead show patterns of diversity defined largely by current ecological dynamics.

Oral presentation

Phylogenomics resolves the phylogenetic relationships of the main lineages of spiders (Araneae)

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We have addressed the phylogenetic relationships of spiders (Araneae), with emphasis on the araneomorph and the ecribellate orb-weaving groups. We used a phylotranscriptomic approach based on ca. 800 loci from an extensive taxonomic sample that includes more than 250 species, with representatives of about 85% of the families of Araneomorphae and all the families of Araneoidea. Based on a resolved backbone of spider interrelationships, we have inferred the evolution of webs in spiders. As in previous phylogenetic analyses of transcriptomic data, the monophyly of cribellate and ecribellate orb-weavers (“Orbiculariae”) remains unsupported. Webs are primitive for spiders, as documented in our prior phylotranscriptomic comparative analyses (Fernández et al. 2018), and have been lost independently multiple times in Araneae.

Oral presentation

A new myrmecophilic spider from the Chihuahuan Desert of West Texas

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In the fall of 1999, a graduate student, Greg Broussard, found an unusual spider while conducting a pitfall survey of spiders on the Dalquest Desert Research Station (DDRS), owned by Midwestern State University, in the Big Bend area of Texas. The family could not be determined, so specimens were sent to taxonomic authorities for family placement, which has yet to be determined. In 2011 personnel from the University of New Mexico found this spider on the surface of an ant mound (*Pogonomyrmex rugosus*) 9.7 km S of Cuatro Ciénegas, Coahuila, Mexico.The DDRS is 335 km (208 mi) from the Mexico site.Concentrated pitfall collecting near harvester ant nests on the DDRS revealed the spider is associated with three different species of ants: *P. rugosus*, *Novomessor albisetosis*, and *N. cockerelli.*In 2017 three male spiders were collected from a nest of *N.cockerelli* at Indio Mountains Research Station in Hudspeth Co. TX, which is 180 km (112 m) NNE of the DDRS. To date, 145 spiders have been collected. This includes 61 males, 36 females, and 48 immatures. Details of the symbiotic relationship with the three ant species are unknown. The eye morphology suggests that it belongs to a group of Dionycha, having orthogonally oriented tapeta in the posterior median eyes. Morphological characteristics and DNA analysis indicate the species will be placed in a new family, yet to be determined.

Symposium presentation

Spiders in the desert: the role of climate refugia in maintaining lineage diversity of mygalomorph spiders in the Australia arid zone

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In Australia, climate and continental drift have given rise to a complex biota comprised of mesic specialists, arid adapted radiations, and taxa that have arrived on the continent from Asia. The relatively recent formation of the Australian arid zone, starting ca. 15 Ma, and the presence of many lineages in the arid zone with tropical and mesic origins raises questions about adaptation to the Australian arid zone, and subsequent diversification within. Here we explore the phylogenetic diversity and biogeographic history of the widespread Australian trapdoor spider genera *Conothele* (Halonoproctidae) and *Aname* (Nemesiidae). *Conothele* has a tropical and arid distribution in Australia and is found through SE Asia. *Aname* is an Australian endemic, belonging to the Gondwanan family Nemesiidae, suggesting an older history on the continent. In particular, we focus on the Pilbara bioregion, an area of topographic complexity in the arid zone, adjacent to the Indian Ocean. Using three mtDNA and five nuDNA markers, we detected high phylogenetic diversity within both genera, including many undescribed lineages. Molecular clock analyses revealed that both genera diversified concurrently with the formation of the arid zone, and that *Conothele* likely colonised Australia from Asia. Ancestral state reconstructions revealed complex biogeographic histories, with multiple unrelated clades within the Pilbara. The Pilbara has been proposed as a climate refuge for many vertebrate species. These results suggest that the Pilbara likely played a similar role for mygalomorphs during climatic fluctuations in the Plio-Pleistocene.

Symposium presentation

The cognitive lives of poly-specialist spiders

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Salticid behaviour can be complex in ways that defy easy description and often the innate predatory specialization by these spiders is distinctively cognitive in character. Salticid examples of pronounced poly-specialization illustrate the importance of a two-step procedure of first determining the ways in which salticids are specialised (i.e., express expertise) with respect to specific types of prey or circumstances and then, as a distinct second step, determining whether particular examples of specialization are accompanied by identifiable trade-offs (i.e., these salticids illustrate why trade-offs should not be simply assumed). The most extreme examples of poly-specialization come from the spartaeine genus *Portia*. A single *Portia* individual can deploy dozens of different prey-specific prey-capture methods for different types of prey and, in a single day, switch seamlessly from one method to another

(switching between being a specialist at using a self-made prey-capture web, a specialist at preying on other salticids completely away from webs, a specialist at invading the webs of other spiders and then using specialisedsignalling as a means of controlling prey behaviour, and more). Salticids also illustrate why careful attention needs to be given to distinctions related to animal cognition. Although the term “cognition” is often used nowadays simply for “information processing”, salticid behaviour pulls us toward an older tradition of more closely aligning use of the term “cognition” with the everyday expression “thinking”. More specifically, salticids are especially relevant for understanding the extent to which predators with small nervous systems rely on representation.

Symposium oral presentation

Gaze direction in jumping spiders

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Jumping spiders use their moveable principal eyes in order to track and scan objects. A spider-specific eye-tracker allows us to accurately track gaze direction in order to test hypotheses about visual perception and attention. In earlier work, we used the eye-tracker to show that the principal eyes are directed to moving objects by the anterior lateral eyes (ALEs). Here we explore how the spider attends to distracting objects that appear in the field of the ALEs while the principal eyes are scanning a different stimulus. We will also briefly discuss the role of cross-modal influences on eye movement.

Symposium oral presentation

Chelicerate type ovaries in spiders, solifuges, pseudoscorpions and scorpions – similar but not identical

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The ovaries of chelicerates distinguish among arthropods. The key difference concerns a changeable position of female germ cells during gonad development. Initially, oogonia and early previtellogenic oocytes occupy the internal part of the ovary. In previtellogenesis, the first stage of oocyte growth, accumulation in the oocyte cytoplasm increasing in number organelles and macromolecules (RNA and proteins) takes place. During the progress of previtellogenic growth the oocytes enlarge and bulge from the ovarian wall to the surface of the ovary where they continue previtellogenesis, undergo vitellogenesis (the second stage of oocyte growth, when deposition of reserve materials in the oocyte cytoplasm occurs), and maturation. Thus, the ovaries gain a distinguishing grape-like appearance. Growing oocytes maintain connection with the ovarian wall by oocyte stalks made by groups of ovarian epithelial cells. The ‘canonical’ chelicerate ovary is characteristic of e.g. spiders. Although in almost all chelicerates (excluding some mites) the basic structure of the ovary is alike, the ovaries of some chelicerates show significant structural and functional modifications. The differences mainly concern the structure of previtellogenic and vitellogenic oocytes, structure

and function of the stalk cells, cells covering growing oocytes, and the ovarian wall cells. We compare structural and functional variabilities of the female gonads in representatives of four arachnid taxa: spiders, solifuges, pseudoscorpions, and scorpions. The relations between the structural and functional modifications in the female gonads and the biology of arachnids are discussed.

Oral presentation

The adhesion of cribellate capture threads

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To survive, web-building spiders rely on their capture threads to restrain prey. Many species cover their threads with viscoelastic glue droplets for this task. Cribellate spiders, in contrast, use a wool of nanofibres as adhesive. Previous studies hypothesised that prey is restrained by van der Waals' forces and entrapment in the nanofibres. The large discrepancy when comparing the adhesive force on artificial surfaces versus prey implied that the real mechanism was still elusive. We therefore re-examined the adhesive mechanism of capture threads of several distantly related cribellate spider species, including possible interactions of cribellate nanofibres with cuticular surface features of prey insects. Characterising the adhesion area, we observed that epicuticular waxes of insect prey infiltrate the wool of nanofibres, probably induced by capillary forces. The composite thus formed led to an adhesion between prey and thread eight times stronger than that between thread and wax-free surfaces. Thus, cribellate spiders employ the originally protective coating of their insect prey as a fatal component of their adhesive, and the insect facilitates its own capture. We suggest an evolutionary arms race with prey changing the properties of their cuticular waxes to escape the cribellate capture threads that eventually favoured spider threads with viscous glue.

Symposium presentation

Nuptial gift chemistry reveals convergent evolution correlated with antagonism in mating systems of leiobunine harvestmen

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Nuptial gifts are material donations given from male to female before or during copulation, and are subject to sexual selection in a wide variety of taxa. The harvestman genus *Leiobunum* has emerged as a model system for understanding the evolution of reproductive morphology and behaviour, as transitions between solicitous and antagonistic modes of courtship have occurred multiple times within the lineage and are correlated with convergence in genital morphology. We analysed the free amino acid content of nuptial gift secretions from five species of *Leiobunum* using gas chromatography-mass spectrometry. Multivariate analysis of the free amino acid profiles revealed that, rather than clustering based on phylogenetic relationships,

nuptial gift chemical composition was better predicted by genital morphology and behaviour, suggesting that convergent evolution has acted on the chemical composition of the nuptial gift. Specifically, species with solicitous courtship produce gifts consisting of a 19% larger proportion of essential amino acids as compared to those with more antagonistic courtship interactions. This work represents the first comparative study of nuptial gift chemistry within a phylogenetic framework in any animal group and as such contributes to our understanding of the evolution of reproductive diversity and the participant role of nuptial gift chemistry in mating system transitions.

Student oral presentation

The shape of weaver: using geometric morphometrics to explore shape disparity in Araneidae (Arachnida: Araneae)

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Some of the most remarkable size variation in terrestrial animals can be found in the ecribellate orb-weaving spiders (Araneoidea), with numerous examples of females being many times longer and/or more massive than conspecific males. While sexual size dimorphism is a relatively well-studied aspect of spider biology, disparity – or the differences in shape – requires more attention. We use geometric morphometric techniques to examine shape differences in the carapace in members of the family Araneidae. The carapace is very conserved and correlates well with body size, but is not studied for quantifying araneoid body shape differences. We measured 106 specimens of 68 species, with 29 of those having both female and male representatives. We found that females and males occupy overlapping but distinct volumes of morphospace. Males typically have a more piriform shape with a relatively wider *pars thoracica* and thinner *pars cephalica* than conspecific females. We found no evidence of a correlation between size and shape dimorphism. Furthermore, both female and male carapace shape data show an overdispersed phylogenetic signal, but only females show a significant pattern. We discuss these results as they relate to the differing lifestyles of female and male orb-weavers.

Symposium presentation

The easy way to make any student into a scientist: The power of mobile devices

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Much of what students learn in science is invisible, which means scientific concepts are often difficult to explain. Additionally, when we ask students to run scientific studies, we often ask students to follow a recipe which often leads to failure since students have no experience. But what if we could create a way for students to experience what it's like to be a scientist? And what if we could help them practice scientific inquiry in a fun and engaging way that helps them learn through mistakes rather than through memorisation? I've simplified teaching scientific inquiry and concepts by creating a library of mobile applications that engage students

and encourage them to interact. As they interact, the applications collect data about the topic students are learning about and visualise these data anonymously at the front of class. After playing for 10-15 minutes, students and teachers can then spend time discussing the data together. This allows teachers to focus on teaching scientific inquiry, hypothesis testing, and experimental design, rather than focusing on the most boring part of science: the methodology.

Symposium presentation

Is it worth it? Let me work it: The role of physiology in sexual selection

Michael Kasumovic

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Whether it's male size, brighter colouration, or the vibrations males produce, we commonly attribute male fitness to the expression of one or a suite of easily measurable traits. But what if it's actually more complicated and the traits really responsible for fitness are the ones we're not measuring? What affect does this have on our understanding of the evolution of various traits and our understanding of mating systems? In this talk, I'll discuss the role of physiology in sexual selection and how we need to understand phenotypes from a more holistic perspective. I'll provide some examples of studies that demonstrate when and why understanding physiology is important and how exploring resting and active metabolic rates can help us understand female choice from a different perspective.

Student oral presentation

The evolution of ant mimicry in spiders

Michael Kelly[1]; Donald J. McLean[1]; Shahan Derkarabetian[2]; Jonas O. Wolff[1]; Gonzalo Giribet[2]; Marie E. Herberstein[1]

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The convergent evolution of traits is best exemplified in the phenomenon of mimicry. However, the tempo and pace of this process is not well-understood. While many mimics are strikingly accurate, others bear only a slight resemblance to their model. One hypothesis, the *perfecting* hypothesis, proposes that inaccurate mimics are in a transitory phase toward better mimicry. Here we used myrmecomorphic (ant-mimicking) spiders that vary in their level of mimic accuracy to investigate this concept. Using a relatively novel method of gene subsampling, known as ultraconserved elements (UCEs), this study reconstructed a phylogenetic tree depicting the relationships of myrmecomorphic species within the spider subfamily Myrmarachninae (Salticidae). Following this, the overall mimicry accuracy and associated morphological traits were evaluated using a scoring method, and were mapped onto the phylogenies. This allowed us to observe the pattern in mimic accuracy and trait evolution. Results indicated that mimic accuracy and traits, such as the constriction of the body, evolves in a step-wise fashion in ant-mimicking jumping spiders. This supported the prediction of the *perfecting* hypothesis that accuracy, and the traits that contribute to accuracy, are under directional selection and that inaccurate mimics are in the process of developing more accurate mimicry.

Oral presentation

Mechanical properties of spider silk enriched with carbon nanomaterials

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Major ampullate (MA) silk of spiders is of particular interest to science due to its combination of amino acids that form a natural polymer which rivals even the toughest man-made materials. In an effort to improve these natural fibres, researchers have begun to try infusing metals and carbon nanomaterials that have the potential to improve mechanical properties and other aspects such as the conductivity of spider silk. In this study, we fed solutions containing carbon nanomaterials to an orb-weaving spider, *Nephila pilipes*, with the objective of incorporating them into the matrix of MA silk. *Nephila pilipes* is a large orb-weaving spider common throughout Southeast Asia and are known to have some of the toughest silk among web-spinning spiders. Adult femaleswere collected from around central Taiwan, housed in the lab to become acclimated and then fed solutions containing either graphene sheets or nanotubes with a pipette. Single strands of major ampullate silk were collected by manually silking each spider for pre- and post-treatment analyses of treatment and control groups. Mechanical properties (e.g., ultimate strength, extensibility, toughness, Young's modulus) were measured using a nanobionix tensile tester, while structural properties of the silk were compared using Raman Spectra analyses. We found there to be no clear changes in the mechanical or structural properties of silk collected from spiders in treatment groups. Therefore, contrary to previously published findings, our results lead us to conclude that the incorporation of synthetic materials into the complex matrix of spider silk is unlikely to be successful.

Symposium presentation

The dual prey-inactivation strategy of the spider *Cupiennius salei*: dozens of possibilities to subdue a victim, more than just neurotoxins

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Over the last few decades, spider venom research has been characterised by the identification and characterization of selected venomous compounds to understand paralytic and toxic effects, mainly on arthropods and vertebrates. Researchers made vigorous efforts to identify neurotoxins and their target ion channels as a central step toward the development of possible drugs for human diseases or as a new generation of insecticides. This neurotoxin tunnel vision, however, disregards the exciting complexity of spider venoms and the interactions of their compounds during the envenomation process. Therefore, we analysed the venom gland transcriptome and proteome of the model spider *Cupiennius salei* with a holistic view. The identification of α-amylase as the main protein in a spider venom was a central moment that enabled us to solve the mystery of the occurrence of many peptides and proteins in venoms. Their contribution to the overall venomous effect is now unravelled and forms an important part of the dual prey-inactivation strategy that we are happy to present here. Both parts of this dual strategy, the metabolic (or unspecific) and the neurotoxic (or specific), closely interact together and disturb a prey's homeostasis through several enzymes, and block ion channels with highly selective neurotoxins. Moreover, many synergistic interactions between low molecular compounds, neurotoxins, cytolytic peptides, and enzymes functionally connect major venom components. This dual prey-inactivation strategy is very effective, and reduces the risk of losing prey by escape or the long-term development of resistance against the venom. Furthermore, the recruitment of body proteins and peptides after gene duplication into the venom and weaponizing them is an often-mentioned hypothesis. The discovery of an agatoxin-like peptide in the haemocytes of this spider, and the identification of corresponding peptides in the venom, as well as the identification of a venom gland-specific defensin, besides a tissue-specific defensin, support this hypothesis.

Student oral presentation

Big data, small spiders: analyses of ultraconserved elements give new perspectives on spider phylogeny and evolution of miniature orb-weavers

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Phylogenomic methods, such as transcriptomics and target-capture, are helping us to resolve deep polytomies and recalcitrant groups in the spider tree of life. While transcriptomic approaches may generate thousands of loci, the target-capture method using the recently developed arachnid probe-set can target a maximum of about 1,000 loci. Here, we demonstrate the utility of a specialised target-capture probe set for spiders, containing 2,021 ultraconserved elements (UCEs). We designed these probes using spider genomes (*Loxosceles, Parasteatoda, Stegodyphus*) and ensured that the newly-designed spider-specific probe-set included UCEs from the Arachnida probe set. The new spider-specific bait set was tested on 48 representative taxa across Araneae. We then added sequences from published literature, matched a total of 85 contigs to the spider-specific probes, and compared the performance with the Arachnida probe set. While the arachnid probe set could capture 54-700 UCE loci, the spider specific probe set captures 120-1,700 UCE loci from the same taxon sample. Furthermore, our results corroborate most nodes resolved by recent transcriptomic analyses, including the RTA Clade placement relative to the “UDOH grade”, monophyly of Palpimanoidea, and nephiline nesting within Araneidae, among others. We also address the contentious family relationships of the miniature orb-weaving spiders –the “symphytognathoids” – with a focus on the monophyly of Anapidae. We also demonstrate that ultra-conserved elements can be sequenced from old museum ethanol specimens. While such specimens are not suitable for RNA extraction, they are a valuable source of genetic data to resolve the spider tree of life through the use of UCEs.

Oral presentation

Golden orbweavers ignore biological rules: Phylogenomic and comparative analyses unravel a complex evolution of sexual size dimorphism

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Instances of sexual size dimorphism (SSD) provide the context for rigorous tests of biological rules of size evolution, such as Cope's Rule (phyletic size increase), Rensch's Rule (allometric patterns of male and female size), as well as male and female body size optima. In certain spider groups, such as the golden orbweavers (Nephilidae), extreme female-biased SSD (eSSD, female:male body length ≥ 2) is the norm. Nephilid genera construct webs of exaggerated proportions, which can be aerial, arboricolous, or intermediate (hybrid). First, we established the backbone phylogeny of Nephilidae using 367 Anchored Hybrid Enrichment (AHE) markers, then combined these data with classical markers for a reference species-level phylogeny. Second, we used the phylogeny to test Cope and Rensch's Rules, sex specific size optima, and the coevolution of web size, type, and features with female and male body size and their ratio, SSD. Male, but not female, size increases significantly over time, and refutes Cope's Rule. Allometric analyses reject the converse, Rensch's Rule. Male and female body sizes are uncorrelated. Female size evolution is random, but males evolve towards an optimum size (3.2-4.9 mm). Overall, female body size correlates positively with absolute web size. However, intermediate sized femalesbuild the largest webs (of the hybrid type), giant female *Nephila* and *Trichonephila* build smaller webs (of the aerial type), and the smallest females build the smallest webs (of the arboricolous type). Nephilid female gigantism is a phylogenetically-ancient phenotype (over 100 Ma), as is eSSD, though their magnitudes vary by lineage.

Symposium student presentation

Spider venom enzymes and the function of a specific protease from the venom of the spider *Cupiennius salei*

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Spider venom not only contains a large variety of neurotoxic peptides and smaller molecular mass compounds, but also a considerable amount of proteins. Some of these proteins are involved in the envenomation process of a prey, among them, amylases, hyaluronidases, and phospholipases. Other proteins play a central role in the toxin production machinery. A recently discovered serine protease from the venom of *Cupiennius salei* is responsible for cleaving

propeptides from immature neurotoxin precursors. The same protease is also involved in the heterodimerisation process of heterodimeric neurotoxins. These heterodimeric neurotoxins account for up to 50 % of all neurotoxin-like structures in the venom of *C. salei* but show significantly lower toxicity than the main monomeric toxins. In this respect it seems questionable how the spider benefits from the heterodimerisation of toxins. We show that the benefit bases on synergistic actions of heterodimeric and monomeric toxins that result in toxicity increases of up to 100-fold.

Student oral presentation

It helps to be red: A comparative study of male coloration, sexual size dimorphism, and male size in salticids

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The function and evolution of animal colour patterns is considerably diverse across taxa. Jumping spiders (family Salticidae) are an interesting group to study the evolution of coloration due to the diversity of striking colour patterns in adult males that encompass two common themes across species: red and black-and-white stripes. These colours are found on various male body regions, and often are notable on body surfaces displayed to females during courtship. We hypothesize that red and black-and-white striped coloration evolved to help courting males avoid cannibalism from females. This hypothesis predicts that these colour patterns should be most prominent in species with high sexual size dimorphism (SSD); high SSD (females larger than males) likely places males at higher risk of sexual cannibalism. In species with high SSD, males may also be particularly small, so we also considered the alternative idea that these differences in colour are driven only by male size. We used field guides to record male colour (presence/absence of red and/or striped body coloration, and whether this colour is displayed during courtship), SSD, and male size. With phylogenetic control (n=24 species), we found that species with red body coloration or red courtship coloration had higher SSD than species without, and we found no relationship with male body size. We found no relationships between striped coloration and SSD or male size. This study provides evidence for the idea that red coloration (but not striped coloration) in males may have evolved to reduce female aggression and sexual cannibalism.

Student oral presentation

Molecular phylogeny of lynx spiders (Oxyopidae) and taxonomic revision of *Oxyopes* in Taiwan

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Lynx spiders (Oxyopidae) contains nine genera and more than 450 species worldwide. They can be found in various habitats including the grassland, forest canopy, and farmland. The habitus and morphology of their abdominal and cephalothorax cuticular scales are distinctive among genera. *Oxyopes* is the largest genus of the lynx spider family, and is considered as a

potential candidate for pest management and biological control. Although numerous *Oxyopes* species have been described in Southeast Asia, the fauna is less well-known in Taiwan, and the higher-level phylogenetic relationship is still unclear. This study aims to investigate the generic relationships of the Oxyopidae and the *Oxyopes* fauna in Taiwan, based on morphology and DNA barcoding. Seven *Oxyopes* species are now recognised in Taiwan, including two new species (*O. hasta* and *O. taiwanensis*) and three newly recorded species (*O. fujianicus*, *O. shushilae* and *O. striagatus*). Sympatrically distributed species (*O. sertatus* and *O. hasta*) show similar colour patterns (abdomen black-brown with an ivory, longitudinal central band, and lateral region with three ivory, slant stripes connecting with central band), but they can be differentiated by characteristic silk signals and mating displays: *O. hasta* drums with two palps in consistent frequencies, while *O. sertatus* drums with one palp and waves the other palp simultaneously. The molecular phylogeny of the six genera (*Hamadruas*, *Hamataliwa*, *Oxyopes*, *Peucetia*, *Tapinillus* and *Tapponia*) was reconstructed using mitochondrial (CO1) and nuclear (18S rRNA) sequences. Our phylogeny supports the monophyly of the presently recognised six genera, and is largely consistentwith past studies using scale shapes. Additional taxon samplings of genera (*Hostus*, *Pseudohostus* and *Schaenicoscelis*) and species from Madagascar, Australia, and South Americaare needed to fully resolve the phylogeny of lynx spiders.

Symposium presentation

Behavioral and morphological precursors predict the evolution of exclusive parental care in harvestmen

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The evolution of maternal and paternal care in arthropods is hypothesised to depend on a set of behavioural and morphological precursors. For maternal care to evolve, females should have (i) an ovipositor that allows them to hide their eggs in protected places, (ii) a single reproductive event in a given breeding season (i.e., functional semelparity), and (iii) contusing defences to protect the offspring from predators. For the evolution of exclusive paternal care, in turn, (i) females should have more than one reproductive event in a given breeding season (i.e., iteroparity), (ii) eggs should be laid on exposed substrates where males may have access to them, (iii) males should have contusing defences to protect the offspring from predators, and (iv) defend an oviposition site where females lay their eggs. We gathered information for each morphological and behavioural precursor for more than 200 harvestman species belonging to the four living suborders. In the dataset we have species showing no care, maternal care or paternal care. We built phylogenetic binomial GLMs for each sex and compared the models using AIC. We found that the best models to explain the evolution of both maternal and paternal care include all morphological and behavioural precursors. Our findings suggest that morphological and behavioural precursors may be more important than we have previously thought for the evolution of parental care in arthropods.

Symposium presentation

A phylogenetic perspective on salticid spider behaviour

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When Robert R. Jackson began his work on jumping spider behaviour, their phylogeny was little resolved, hampering evolutionary interpretations of behavioural diversity. Since then, we have achieved a strong phylogenetic backbone and approximate placements of most genera. I take a retrospective look, placing past comparative behavioural work by Jackson and colleagues into a phylogenetic perspective. My purpose is twofold, to map the sequence of evolutionary changes, and to understand in what clades behavioural work is most needed. Not having done the analyses at the time of this writing, I don't know what characters will be most worth discussing. Among Jackson's comparative studies are works on predation, vision, and olfaction. Given the diversity of salticid behaviour, Jackson's approach of broad comparative studies stands to yield many insights.

Student oral presentation

Phylogeny of the crevice-weaver spiders (Araneae: Filistatidae)

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Filistatids are an ancient family of cribellate spiders, represent one of the first lineages of Araneomorphae, and present a complicated mixture of primitive and apomorphic characters. This makes them a key taxon to elucidate the evolutionary tree of spiders. Its moderate diversity (~ 160 species in 19 genera) is distributed mainly in arid and semi-arid subtropical zones of all continents, except Antarctica. To unveil the phylogenetic relationships among its genera, we assembled a matrix of ~275 morphological characters coded for 75 species of filistatids, and Sanger-sequenced four molecular markers for a similar number of species. The analysis of the data (morphological, molecular, and combined) supports the monophyly of Filistatidae and its two subfamilies, Prithinae and Filistatinae. Several groups of genera are recovered: *Filistata* and *Zaitunia*; *Sahastata* and *Kukulcania*; all Prithinae except *Filistatinella*; *Antilloides* and *Filistatoides*; a large Old-World group including *Pritha, Tricalamus, Afrofilistata, Labahitha, Yardiella, Wandella,* and putative new genera; and a South American group formed by *Lihuelistata*, *Pikelinia*, and *Misionella*. The exact positions of the enigmatic *Pholcoides* and *Microfilistata* remain unresolved, although they probably are early-branching genera. A new classification for the family based on the phylogenetic results is proposed, including new generic combinations and diagnoses.

Symposium presentation

Multi-scale effects of habitat heterogeneity on spider communities of oceanic islands

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Researchers have long considered islands as natural laboratories to test ecological and biogeographic hypotheses about speciation, adaptation and colonisation. Although there is an increasing understanding of the effects of island age, size and isolation on the diversity and structure of communities, we largely ignore the role of the variability in environmental and habitat conditions at different spatial scales. We will present our study, where we used the Macaronesian archipelagos to assess the effects of habitat complexity and stability on the diversity and composition of spider communities. Using data obtained from 60 sampling plots located on eight islands of four archipelagos with varying climatic and habitat conditions, we tested two hypotheses related to the consequences of the buffering or stabilising effect of forest on microclimatic conditions: 1) community turnover (beta diversity) is more important in dry areas than in forest areas; and 2) this pattern should be true at both regional and local scales.We found that, at three out of the four analysed spatial scales, the contribution of beta diversity to gamma diversity was smaller in forest areas than in dry areas. Furthermore, the species turnover (and its replacement component) was generally greater in dry areas than in forested areas at the local level, while it was greater than expected at the local (within plots) and regional (between plots) scales. Our results show that it is necessary to consider the different spatial scales at which habitat heterogeneity – and associated microclimatic factors – act on the assembly and structure of communities.

Student symposium presentation

The longest-lived spider: mygalomorphs dig deep, and persevere

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We report the longest-lived spider documented to date. A 43-year-old, female *Gaius villosus* Rainbow, 1914 (Mygalomorphae: Idiopidae) has recently died during a long-term population study. This study was initiated by Barbara York Main at North Bungulla Reserve near Tammin, south-western Australia, in 1974. Annual monitoring of this species of burrowing, sedentary mygalomorph spider yielded not only record-breaking discovery, but also invaluable information for high-priority conservation taxa within a global biodiversity hotspot. We suggest that the life-cycles of short-range endemics provide lessons for humanity and sustainable living in old stable landscapes.

Oral presentation

Daily activity patterns match the most effective light environments for courtship in *Schizocosa* wolf spiders

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Effective communication requires the transmission of signals from signallers to receivers through the signalling environment. Therefore, the signalling environment is expected to play an important role in signal evolution; some signals may evolve to function across multiple signalling environments, while others may evolve to function under specific environmental conditions. Courtship displays within the wolf spider genus *Schizocosa* vary widely in the use and types of signal elements, even between closely related species. Males of all *Schizocosa* species produce species-specific substrate borne vibrations, while some species also incorporate movements of the body and legs as visual signals in their courtship displays. Among these species, male secondary sexual characteristics often include ornamentation of the first pair of legs, including varying degrees of pigmentation or the addition of brushes. To assess the potential influence of the light environment on the evolution of courtship displays in *Schizocosa*, we (1) examined daily activity patterns and (2) ran mating trials under different light levels (bright, dim, and dark) for three species of *Schizocosa* that vary in their visual ornamentation and their use of dynamic visual movements during courtship. We found that the species that were more active during the day were more likely to copulate under increased light levels, while the species that were active throughout the light-dark cycle were more likely to copulate across all light conditions. These results suggest that the displays of each species have evolved for effective communication in the light environments in which courtship takes place.

Student oral presentation

Mimicry in motion: can good behaviour compensate for poor morphological mimicry?

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Some spiders mimic ants, thereby deceiving their predators and avoiding being attacked. We expect the deception to be most effective when the spiders resemble their models closely, yet the existence of many poor mimics appears to contradict this expectation. Mimicry is often comprised of multiple components (or mimetic traits), however the interactions between these components are not well-understood. According to the "increased deception" hypothesis, multi-component mimicry may provide one explanation for the persistence of imperfect mimicry. The hypothesis—as applied to mimicry—argues that one strong mimetic trait will relax selection for mimetic accuracy on another trait. We tested the increased deception hypothesis using ant mimicking spiders from several different families. We compared accuracy of morphological mimicry with that of behavioural mimicry. Our results to date suggest that, contrary to the prediction of the hypothesis, there is no relationship between morphological and behavioural mimetic accuracy. Rather, we argue that accuracy in different components of mimicry may be driven by selection from different sets of predators. Hence, in this case, multi-component mimicry does not help explain persistent imperfect mimicry.

Symposium presentation

The innervation of the male copulatory organ of spiders (Araneae) – a comparative analysis

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In spiders, the male copulatory organ is developed as a modified part of their pedipalps, the so-called palpal organ. For decades, it was thought that this copulatory organ lacks nervous tissue, which led to the assumption that it was insensitive. It was not until 2015, that nervous tissue was found in the palpal organ of the enigmatic Tasmanian cave spider *Hickmaniatroglodytes*, resulting in a paradigm shift regarding the role of male copulatory organs during copulation [1]. This new finding was supported in 2017, when neurons and a sensory organ were found in the male copulatory organ of *Philodromuscespitum* [2]. Since these studies only focused on distantly related spider species, the need for a comparative study, addressing the evolution of the innervation of the palpal organ across the spider tree of life became obvious. Here, we analysed the male palpal organs of key spider taxa covering all infraorders using histology, electron and X-ray microscopy. Our data show that the palpal organ is innervated across all spider groups and thus part of the ground pattern of spiders. Furthermore, we found a peculiar sensory organ in nearly all investigated taxa close to the base of the embolus. The function of this sensory organ is still unknown, but our preliminary ultrastructural data suggest it to be proprioreceptive which needs to be addressed in future studies.

[1] Lipke et al. (2015), *Biol Lett* 11:20150465.

[2] Sentenska et al. (2017), *Sci Rep* 7:12209

Oral presentation

Biocontrol efficiency of spiders across the globe: a meta-analysis

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The role of generalist predators, such as spiders, in biocontrol remains controversial as they can either suppress or enhance pest populations. The biocontrol function of spiders seems, therefore, to be context-dependent. Here we performed a meta-analysis of the published data on the effects of spiders on pest densities and crop performance. We investigated (i) the overall effect of spiders on pest density and crop performance, and (ii) whether the biocontrol efficiency of spiders depends on the crop type (vine, cabbage, wheat, and rice), climate or geography. We found that spiders, in general, supressed pests significantly. The pest suppression efficiency of spiders was enhanced not only by increased spider density, but also by increased spider taxonomic diversity. The effects of spiders cascade down, improving the crops' performances. In addition, the effects of spiders escalate, rather than attenuate, down through the food-chains. We also found that the biocontrol efficiency of spiders differed among crops. The highest efficiencies were in rice and vine. In addition, the biocontrol efficiency of spiders decreases with higher latitudes and increases with mean annual temperature. Our results provide evidence that generalist spiders are effective biocontrol agents, especially in crops with higher structural heterogeneity and under warmer climates. Our study also provides support for the hypothesis that the predation pressure in terrestrial ecosystems intensifies towards the tropics.

Oral presentation

A multi-taxon cyberdiversity inventory of a small Caribbean island

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In October 2015, a team of researchers and students conducted a rapid inventory of Sint Eustatius, a 21 km^2 island in the Lesser Antilles. The sampling protocol targeted vascular and non-vascular plants, lichen, vertebrates, gastropods, butterflies, and selected megadiverse arthropods (spiders, ants, beetles, and true bugs) across a gradient of habitats and anthropogenic impacts. For megadiverse groups, not all species were determined using formal scientific names. Nevertheless, all were assigned persistent identifiers linked to digital image libraries and DNA sequences, as prescribed by the cyberdiversity approach. We contrast the cyberdiversity approach with a recent broad-spectrum taxonomic inventory of the Caribbean island of Montserrat. The Montserrat inventory targeted plants, vertebrates, and arthropods, with emphasis on beetles. Montserrat exemplifies the asymmetries that make the challenge of building knowledge about megadiverse groups different from inventories of groups such as plants and vertebrates, a problem referred to as the taxonomic impediment. Of the 718 beetle species sampled, only a few can be confidently associated with a valid scientific name due to

deficiencies in the literature and limited comparative work across Caribbean islands. Unfortunately, the situation following the Montserrat inventory is only marginally better. A partial list of beetle names was produced and specimens were vouchered in an accessible research collection. But determining which beetle species present on Montserrat might be shared with samples from other islands remains a daunting challenge. By using the cyberdiversity approach, we make it much more likely that independent researchers will be able to reconcile their collections with ours.

Student oral presentation

Phylogenomics of Neotropical Nemesiidae (Araneae, Mygalomorphae)

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Like other mygalomorph spiders, nemesiids appear to be quite conservative in morphology and thus tend to have far fewer characters for phylogenetic or cladistic analysis than their araneomorph counterparts. Nevertheless, the current classification system and embedded subfamily delimitation relies largely on morphological evidence. Past gene-targeted molecular analyses that employ Sanger Sequencing approaches appear to suggest that the family may be para- or polyphyletic. Next-generation sequencing technologies have very recently significantly enhanced access to genomic scale data, allowing the spider systematics community to rapidly generate large amounts of sequence data at a substantially lower cost. The aim of this study is to test the hypothesis that neotropical Nemesiidae form a monophyletic group using next-generation high-throughput sequencing methods, specifically anchored hybrid enrichment. Although our results indicate that substantial revision of nemesiid classification will be required, this newly-derived phylogeny provides a robust framework for investigating the group's rich biogeographic history and unique morphology and behaviour.

Oral presentation

Seven years of spider community succession in a *Sphagnum* farm

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The cultivation of peat moss (*Sphagnum*) is a promising sustainable perspective in the production of horticultural growing media. In 2011, one of the first *Sphagnum* farms in Europe was established near Rastede in northwestern Germany. We continuously monitored succession of spider communities from time of construction of the *Sphagnum* farm until 2018. Within the first two years, a rapid change from a community dominated by pioneer species to a diverse assemblage of peatland generalists was observed. Abundance and species density reached the plateau in the third year. However, the proportion of disturbance-intolerant peat bog specialists increased steadily. Every year, new species with special affinities to mires and fens reached the *Sphagnum* farm, indicating ongoing colonisation dynamics. High proportions of rare and red-listed species demonstrate the conservation value of such artificial peatlands, though the diversity is still far from that of natural peat bogs.

Oral presentation

Female genital mutilation and the rejection of second males in *Cyclosa ginnaga*

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Throughout the animal kingdom, males sometimes harm females during copulation. In spiders, such as *Cyclosa argenteoalba* and *Larinia jeskovi*, female genitalia are damaged during mating, i.e., scapes are mutilated. Mutilation rate is high, and mutilated females cannot mate. Thus, female genital mutilation realises monogamy in these species. The purpose of this study was to examine whether female genital mutilation and monogamy occurs in *Cyclosa ginnaga*, a close relative of *C. argenteoalba.* I collected virgin females of *C. ginnaga* and paired with males. After successful mating, I inspected the presence of scapes. Mated females were paired with second males on a different day. The second males courted females, and I observed whether the second mating occurred. Among the 36 virgin females observed, scapes were mutilated in 15 cases (= 42%), which was significantly lower than the mutilation rate of *C. argenteoalba* (90%). Unexpectedly, all mated females attacked the second males (n = 26), and 21 males stopped courting and left females' webs. The remaining five males continued courting, and females subsequently accepted them (acceptance rate did not differ between mutilated and unmutilated females). Three unmutilated females successfully mated with a male, but two mutilated females failed. Thus, female genital mutilation accounted for only 8% (= 2/26) of the unsuccessful second mating. Females with damaged genitalia were found in many other species from wide groups of spiders, and mutilations supposedly occur at the mating by males. However, its role to limit the number of female matings may not be always important.

Symposium presentation

Spare a thought for boredom

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The inability to maintain signal detection performance with time on task, or vigilance decrement, is widely studied in people. Despite suggestions that limitations in sustained attention may be a fundamental characteristic of animal cognition, there has been limited research on the vigilance decrement in other animals. Using *Triteplaniceps*, a jumping spider (Salticidae) that actively hunts its prey based on vision, we investigated vigilance decrement to repetitive visual stimuli in a series of experiments. We first established that the vigilance decrement occurs in salticids and shows similar patterns to those of humans. We also found that dishabituating salticids did not change declining responses, suggesting that the vigilance decrement is due to more than simply peripheral sensory habituation. We then ran a series of experiments exploring the effects of biological relevance and signal salience, as well as using a central nervous system (CNS) stimulant (caffeine) to explore the cognitive underpinning of vigilance decrement in salticids. All our experiments suggest that a significant portion of the vigilance decrement in salticids is due to CNS processing. However, in contrast to the underload theory, which predicts steeper decrements in 'boring' tasks that provide too little

cognitive load (understimulation), our results align with the resource depletion theory, in which a faster decrement is expected in tasks that are overstimulating, or more cognitively demanding.

Student symposium presentation

Testing the placement of Pseudoscorpions through rare genomic changes

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Understanding evolutionary relationships among the orders of Arachnida has proven challenging despite the availability of vast amounts of genetic data. The placement of pseudoscorpions remains especially uncertain due to a phylogenetic artefact, long branch attraction, which leads to statistically inconsistent relationships among the arachnid orders, even with datasets spanning thousands of genes. Alternative classes of phylogenetic data are a potential solution for reconstructing relationships where sequence data have not achieved topological stability. One such alternative data class is the occurrence of rare genomic events. To determine the relationship between Pseudoscorpiones and the rest of Arachnida, we investigated the signature of shared duplicated genes as phylogenetic characters as indicative of membership within Arachnopulmonata, which are inferred to have undergone an ancient whole genome duplication. We sequenced the first developmental transcriptome of the pseudoscorpion *Conicochernes crassus* to investigate the incidence of duplicated genes shared by the arachnopulmonates. Our transcriptomic data show that pseudoscorpions retain many duplicated genes across a variety of disparate gene families. Analysis of gene trees recovered topologies consistent with a single shared genome duplication with Arachnopulmonata, suggesting pseudoscorpions are closely related to this group of orders.

Oral presentation

Ground spiders of family Gnaphosidae on Zealandia: current distribution and relationship with adjunct lands

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Zealandia is considered a drowned continent. Its largest extant fragments are New Zealand (NZ), New Caledonia (NC), the Loyalty Islands, Lord Howe Island, and the Norfolk Islands. Zealandia has a complicated geological history, including submersion and glacial periods, both of which had a major influence on its ground spiders (Gnaphosidae). Currently, Gnaphosidae are represented in Zealandia by 11 genera and 30 species: NZ with 24 species and NC with 6 species. As a rule, introduced genera are represented by only one species. These species are widely distributed over all New Zealand, Australia and South-East Asia (*Intruda signata, Hemicloea rogenhoferi, Odontodrassus javanus*). At the same time, endemic species are strongly restricted in terms of distribution, and can be divided into four groups. The first group includes the species *Notiodrassus distinctus, N. fiordensis, Matua valida* and *M. festiva,* which occur only on very restricted parts of the South Island of NZ (Forster 1979). The second group includes species that are endemic to both the North and South Islands of NZ: *Nauhea tapa* and *Scotophaeus pretiosus.* The third group includes the genus *Hypodrassodes,* which is the only

genus endemic to all of Zealandia, and is represented by seven species in NZ and three species in NC. The fourth group, with genera *Anzacia* and *Zelanda*, contain species endemic to either NZ or Australia, and lack common species across both continents.

Oral presentation

A new species of spider from Mexico in the genus *Frontinella* F. O. Pickard-Cambridge (Araneae: Linyphiidae)

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A new species in the genus *Frontinella* F. O. Pickard-Cambridge 1902 is described based on the embolic division and other characteristics of the male, and on the epigynum and other characteristics of the female. This new species resembles *Linyphia trifalcata* (F. O. Pickard-Cambridge 1902), which is probably misplaced and should also be in the genus *Frontinella*. The current specimen is from secondary tropical forest near Hidalgo, Chapulhuacán, Mexico.

Oral presentation

Enlightening the dark: A phylogenetic framework for Dinaric cave-dwelling dysderid spiders

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Caves are one of the last uncharted territories on Earth. The Dinaric karst in the Balkan peninsula is home to many of them, but despite of darkness and harsh conditions, life thrives there. Spiders of the family Dysderidae are among their most abundant and conspicuous inhabitants. Yet, we know very little about their biology, ecology, and evolutionary history. As a first step towards improving our knowledge on cave dysderids, we here present an explicit phylogenetic hypothesis of the group based on an extensive biotic survey of the region. Seven Dysderidae genera with 21 species are known in the Dinaric caves: *Stalagtia* and *Folkia* in the Harpacteinae subfamily, and *Rhode*, *Stalita*, *Mesostalita*, *Parastalita* and *Stalitella* in the Rhodinae. Almost all species show high level of cave adaptation and are narrow endemics. We used a target multi-locus approach based on 4 concatenated genes to infer a phylogeny, delimit species boundaries and estimate divergence time combining fossil and biogeographic node calibrations. We uncovered major overlooked diversity at both species and genera levels. Quantitative species delimitation methods confirmed the existence of many new species, and revealed high levels of cryptic diversity within Harpacteinae. All cave lineages showed a common pattern of long stem branches, which may hint at high levels of extinction during the history of these groups. We hypothesise that Miocene climatic changes may have played a crucial role in shaping the extant diversity of these cave-dwelling spiders. Finally, we reconstructed the biogeographic scenario for the diversification of the Dinaric dysderid fauna.

Oral presentation

Coevolution of stridulation and hard cuticle resulted in the defensive acoustic mimicry

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Vision-based defensive traits are not ideal for low-light conditions, so prey may instead resort to the use of other modalities, such as acoustic signals. Nocturnal spiders have adapted to defend themselves against nocturnal predators in a variety of ways. Here we tested a hypothesis that *Palpimanus gibbulus* spiders that are nocturnal hunters use stridulation to defend themselves from a range of nocturnal predators, such as other spiders and reptiles. We suspected that the sound they produce is imitation of a distress stridulation produced by sympatrically occurring mutillid wasps. We compared sound characteristics of *Palpimanus* with five species of co-occurring mutillid wasps and found is the sounds to be similar in most characteristics. Thus, palatable *Palpimanus* spiders seem to imitate acoustically unpalatable mutillids. We staged predator feeding experiments in which we offered predators, *Eusparassusdufouri* spiders and geckos, mutillid wasps, sham-operated *Palpimanus*, silenced *Palpimanus,* and a non-stridulating spider. Both predators captured non-stridulating spiders, but geckos captured and then released mutillid wasps. Silenced *Palpimanus* were attacked by *Eusparrasus* spiders more frequently than sham-operated, while geckos regularly captured *Palpimanus*, but attempts to swallow silenced individuals were more frequent than sham-operated individuals which were more likely dropped before any attempt to swallow. Our findings provide initial support for the first example of inter-ordinal defensive acoustic mimicry.

Oral presentation

Back to the future: between Barychelidae and Theraphosidae the ex-Paratropidid *Melloina* Brignoli 1985 (Araneae, Mygalomorphae)

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The Theraphosoidina originally included Paratropididae, Barychelidae and the speciose Theraphosidae. In the first cladistic studies of Mygalomorphae, Paratropididae was considered as sister group of Theraphosidae. *Melloina* originally described as *Melloa* in Theraphosidae was transferred to Paratropididae in those early cladistic studies of the infraorder. This genus was interpreted as presenting plesiomorphic states of the Paratropididae and constitute a key genus to resolve some mygalomorph relationships. Recent molecular information used in phylogenies suggested that Paratropidids are not closely related to Theraphosidae nor Barychelidae, but *Melloina* was not represented in taxon samples. Additionally, Barychelidae has been suggested as the sister group of Theraphosidae. Furthermore, some unpublished data suggest that part or all Barychelids could be Theraphosids. Our recent study including *Melloina* in a previous molecular/morphological matrix of Mygalomorph families recover *Melloina* as the sister group of Theraphosidae, remaining Barychelidae as the sister group of the clade *Melloina* + Theraphosidae. In our opinion *Melloina* is a Theraphosidae genus which lost

scopulae but retain claw tufts. There are very few examples of this character combination, the fourth legs in the Theraphosinae *Agnostopelma*, and all legsin other undescribed Theraphosinae species from a cave in Colombia. The loss of the scopula is probably related with troglobian habits.

Oral presentation

Relative efficiency of pitfall trapping vs. hand-collecting to sample ground-dwelling spiders along a structural gradient of neotropical habitats

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Assessing spider diversity and composition still remains a methodological challenge, especially in tropical habitats where huge numbers of species co-exist at small spatial scales. Although pitfall trapping is one of the most widely-used sampling techniques to collect ground-dwelling spiders, it suffers from several biases, and its accuracy probably varies together with habitat complexity. In this study, we compared the efficiency of two sampling techniques, one passive (pitfall trapping) and one active (nocturnal hand collecting, further called NHC), to capture ground-dwelling spider taxonomical and functional diversity along a structural gradient of habitats in French Guiana (South America). We found no difference between the two methods in determining the ground-dwelling spider taxonomic diversity. However, nocturnal hand-collecting was more efficient than pitfall traps to sample soil-dwelling spider functional diversity (based on hunting guilds of spiders), especially when vegetation is high, such as in forest and forest edge habitats. Given that pitfall traps require more effort than NHC, we suggest an optimised protocol using only NHC to collect soil-dwelling spiders in tropical habitats. However, for a standardised protocol in line with biodiversity inventories across the globe, we recommend both pitfall trapping and nocturnal hand collecting to assess tropical spider biodiversity.

Student oral presentation

Mechanical integration of wet axial fibres enhances adhesion in cribellate silk of *Hickmania troglodytes*

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Prey retention is a critical aspect of foraging for web-building spiders that is achieved in some species through the use of the cribellate silk composite: puffs of adhesive nanofibrils surrounding a core axial fibre. It its native state, the stiff axial fibre of cribellate silk has been thought to be relatively uninvolved in adhesion, aside from simply suspending the nanofibrils. We hypothesised, however, that by increasing the compliance of the axial fibre through

exposure to water, adhesive forces could be transferred from the fibrils to the axial fibre, improving the overall effect of adhesion. To test our hypothesis, we examined silk from the Tasmanian cave spider, *H. troglodytes*: a web-building spider that lives in caves with nearly complete water saturation. We found that axial compliance and adhesive extension, i.e. the displacement of a silk thread while still in contact with a substrate, of silks tested at at high humidity (>90% RH) were both significantly correlated and greater than silks tested at lower humidity (~45% RH). We also compared the maximum adhesive force generated by a cribellate thread to its equivalent tensile force value and found that axial threads of silks exposed to high humidity achieved higher strain than those at low humidity. As a result, adhesion increased in silks exposed to high humidity. Our findings suggest that some adhesive forces are transferred from cribellar fibril to axial fibre, causing deformation as energy is absorbed by the fibre, which highlights a previously unknown function of the axial fibre.

Student symposium presentation

The physiology of alternative reproductive tactics in New Zealand harvestmen

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Across animal taxa, sexual selection drives males to brandish exaggerated structures, weapons, used in male-male competition to secure access to mates. Weapon size is constrained by the ability to acquire resources and expected to act as an honest signal of quality, conveying information about an individual's fighting aptitude to opponents. As such, males of a single species can exhibit extreme variation in weapon size and less commonly, weapon shape. To explain the evolution and maintenance of weapon polymorphism, studies have focused on exploring the morphological and behavioural costs and compensatory traits that allow males to bear the most extreme weapons, yet few have used a physiological approach. We predicted that weapon polymorphism and its associated behavioural variation (e.g. alternative reproductive tactics) may be reflected by interindividual physiological variation. For example, minor males scrambling for mates may possess greater *aerobic* poise. Alternatively, we might expect pronounced *anaerobic* poise in major males engaging in short bursts of contest to defend resources or territories. Males of the New Zealand harvestmen (Arachnida, Opiliones) *Forsteropsalis pureora*, bear exaggerated chelicerae which exhibit extreme variation in both weapon size and shape. Using this uniquely polymorphic species, we tested for physiological differences between morphs with multiple measures including whole animal resting and active respirometry, high resolution respirometry to examine mitochondrial function, and enzyme assays. Our comprehensive approach begins to reveal physiological variation rarely considered in the pursuit to understand the evolution of diverse exaggerated structures.

Student symposium presentation

Phylogeny of wolf spiders from the island of Hawai'i inferred from multilocus genetic data

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The Hawaiian archipelago is one of the world's finest natural laboratories for the study of evolution and patterns of speciation. Yet the evolution and phylogeography of much of its biota remain poorly understood. We investigated the species radiation of the wolf spiders (Lycosidae) on the island of Hawaii, which is especially unknown. The 6 species historically described from the island of Hawaii share the particularity of having colonised the most extreme habitats found there: lava fields, alpine stone deserts and lava caves. We sampled specimens across the three main volcanoes of the Big Island at various elevations, including caves, to generate phylogenetic hypotheses for Lycosidae species and populations. We generated an entirely new data set for the Lycosidae using mitochondrial and nuclear genes, multiplex PCR and next generation Illumina amplicon sequencing. Phylogenies of these spiders were reconstructed by maximum likelihood and Bayesian methods. Results from this study constitute the first step of a reconstruction of the phylogenetic relationship between Hawaiian and Pacific Lycosidae, and represent an important insight in the understanding of the still deficient evolutionary history of the Lycosidae.

Oral presentation

Colour as deterrence: An empirical test of the anti-predator function of wing interference colours

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Some flies of the family Tephritidae perform a wing display against their jumping spider predators and this display deters attacks ~80% of the time. The effectiveness of the display has been attributed to the mimetic effect of bands on the wings which resemble jumping spider legs. However, the complete display comprises visual features such as pigment colour, wing interference colouration (hereafter, WIC) and wing shine of the hyaline parts of the wings, and their effect will be influenced by the angle of wing inclination, lighting conditions and most importantly, the sensory capabilities of the predator. We studied the effect of WICs and shine on the likelihood of preventing a predator attack in the context of predator deterrence signalling using the tephritid fly *Anastrepha ludens* as the prey and the jumping spider *Phidippus audax* as the predator. Using full spectrum digital photography and by visual modelling of the acuity and colour perception of the spider, we evaluated the efficacy of WICs in deterring attacks under different light conditions. Spiders were less likely to attack flies with prominent WIC than control flies. We suggest that the distraction caused by multiple information sources, along with intermittent wing and head movement results in a hesitation on the part of the spider, which ultimately allows for the fly to escape.

Oral presentation

Neotropical Sparassidae: who are they? Where are they? Where do they fit in?

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Members of the family Sparassidae are commonly known as huntsman spiders because of their hunting habits and speed. The family is monophyletic, supported by the presence of a dorsal, flexible trilobate membrane at the distal end of the leg metatarsus, and claw tufts composed of setae with indented tips. Currently it comprises 1225 species distributed in 88 genera. Of these, 216 species in 30 genera occur in the Neotropical region (including Mexico). For the past 15 years, the neotropical fauna has been intensely studied, resulting in the revision of 10 genera and the description of seven new ones. A total of 89 species were newly described, representing more than 40% of the currently known fauna. Currently, Sparassidae is divided into 10 subfamilies: Chrosioderminae, Clastinae, Deleninae, Eusparassinae, Heteropodinae, Palystinae, Polybetinae, Sparassinae, Sparianthinae and Staianeinae. Nevertheless, the monophyly of these subfamilies is questionable, and many genera remain *incertae sedis*. A cladistic analysis, based on morphological characters and including representatives of 20 Neotropical genera, shows that thirteen of these genera arise within the subfamilies Sparianthinae (6), Sparassinae (1), Polybetinae (2) and Heteropodinae (4). Five genera arise, together with *Olios* Walckenaer, *Cebrennus* Simon and *Chrosioderma* Simon, in a clade sister to Clastinae + Deleninae. Another genus is placed within a clade, together with Neotropical *Olios* species, sister to Eusparassinae and Heteropodinae. Additionally, five unplaced species arise as two separate new genera within Sparianthinae.

Student oral presentation

Asymmetric genitalia in spiders: an overview of this rare phenomenon with emphasis on *Teutamus politus* Thorell 1890 (Araneae; Liocranidae)

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Evolution of genital asymmetry has been observed far and wide in the animal tree of life. In arthropods, occurrences vary greatly from one group to the next; there seems to be no common explanation in all the independent origins. General hypotheses include packing of internal organs, mating position, sexual selection, and antagonistic coevolution. In spiders, genital asymmetry seems to be especially rare. Few examples have been studied in detail, but isolated reports are scattered in taxonomic literature. Here we conducted a broad review of taxonomic descriptions and genitalia illustration. We found several species in eight families with evidence of genital asymmetry; most cases were found only in females. Male palp asymmetries were only known in Oonopidae, Pholcidae and Theridiidae. Here we document thoroughly the case of the liocranid *Teutamus politus* Thorell 1890, collecting live specimens in the field to test hypotheses on both morphology and mating behaviour. A sample of 188 specimens (60 females and 35 males) was obtained. Male-female interactions were observed in 25 couples under standardised conditions. We show that spider asymmetries, although rare, are more common than previously thought, and taxonomic literature is useful but not entirely reliable for studying them. We hypothesise that relative complexity of the male bulb may be related to appearance

of internal female asymmetry, while external asymmetries may exemplify female choice or antagonistic coevolution. Finally, we consider *T. politus* to be the first known case of directional asymmetry, and the first report of developmentally asymmetric male genitals in entelegyne spiders.

Symposium presentation

Conservation systematics of Australia’s spiny trapdoor spiders (Idiopidae): revealing a continental fauna before it’s too late

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The arbanitine spiny trapdoor spiders (Idiopidae) are an iconic and highly diverse component of the Australasian ground-dwelling spider fauna, renowned for their longevity, cryptic fossorial life history, biogeography and conservation significance. The Australian fauna is remarkably diverse and highly endemic, with southern-temperate ‘on-the-continent’ biogeographic origins, and at least four lineages that have independently radiated in the arid zone since the Eocene. Using integrative molecular methods and comprehensive monography, we have now started to understand the phylogeny, biogeography and species-level taxonomy of these spiders across mainland Australia. These insights have revealed a complex fauna of unexpectedly high diversity, especially in the transitional and arid zones of Western Australia, where topography, substrate heterogeneity and rainfall appear to be important drivers of speciation. The biodiversity hotspot of south-western Australia is especially diverse, although severe population declines in some species are evidence of an increasingly threatened fauna. Indeed, we outline how a lengthy research program incorporating molecular phylogenetic research, complementary taxonomic revisions and detailed natural history studies has helped to shine a light on the Idiopidae of Australia, and how a ‘conservation systematics’ approach is beginning to reveal the urgency of the conservation challenges facing this group in the 21st Century.

Oral presentation

Interspecific contests cannot explain species replacement in cellar spiders (Pholcidae).

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Spiders that live in high densities and build semi-permanent webs may compete for web sites or the webs themselves. When similar species co-exist, direct contests may determine their success. In recent years, *Pholcus manueli* has largely displaced *Pholcus phalangioides* in SW Ohio. We evaluated the impact of ownership, body size, and hunger level on interspecific contests in the laboratory. When adult females fought over webs or web sites, the smaller *P. manueli* never won, but there were a significant number of encounters that ended as apparent ties with little engagement. In contests among juveniles, the size difference, often a proxy for resource-holding potential, determined the outcome. In addition, well-fed *P. manueli* were more likely to take over *P. phalangioides* webs, whilst hungry *P. manueli* were more likely to disengage from the contest, resulting in a tie. Thus, we can conclude that large, well-fed *P. manueli* could take over a habitat patch occupied by juvenile *P. phalangioides*; however, this does not seem sufficient to explain their success replacing *P. phalangioides* in most suitable habitat patches in our region. The lack of engagement observed in these staged contests might suggest that the replacement occurred by a subtler pathway. We posit that *P. manueli* individuals, immersed in a population of *P. phalangioides,* could remain on the side-lines but still be able to reproduce and/or seize smaller advantages over time that ultimately enabled them to exclude *P. phalangioides* through exploitative competition, and/or by preventing juveniles from occupying profitable web sites.

Symposium presentation

Resurrected ancestral activity of sicariid toxins informs evolution of specificity and consequences for prey immobilisation

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Venom toxins typically evolve from housekeeping genes that serve non-venom functions. The key dermonecrotic venom toxins in sicariid spiders (*SicTox*) are no exception. These toxins are phospholipase Ds with widespread homologs in chelicerates; however, homologs are only present in venom and salivary secretions of a few arachnid taxa, suggesting independent recruitment for venom function. Following recruitment to venom in sicariid spiders, the gene family lineage has evolved functional specificities with respect to which phospholipid head group they prefer. Some paralogs specifically act on choline headgroups, others ethanolamine headgroups, and others non-specifically act on both. Using phylogenetic ancestral sequence reconstruction, we successfully cloned and expressed a protein representing the inferred most recent common ancestor of venom-expressed *SicTox* homologs in sicariid spiders. Tests of activity indicate these ancestral toxins act on both headgroups, similar to the extant non-specific variants. Thus, it is likely that the directionality of evolution was from non-specific to specific. We are now able to refine estimates of when and how within this gene family lineage the evolution of phospholipid headgroup specificity occurred. Bioassays indicate these toxins are all insecticidal, independently of specificity. We are assessing differences in potency and specific effects of these functional variants on different insect prey types.

Symposium presentation

Using phylogenomics and 3D protein modelling to study the evolution of scorpion venom

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Scorpions, an iconic lineage of arthropods, have evolved venoms diverse in toxins with a plethora of biological targets, but characterizing the evolution of this molecular diversity has been limited by the lack of a comprehensive phylogenetic hypothesis of scorpion relationships. Here, we generated the most comprehensive scorpion phylogenomic tree to date, providing an evolutionary framework to pinpoint the origins of several components, including calcins, a type of inhibitor cystine knot (ICK) peptides that bind to ryanodine receptors in skeletal and cardiac muscle in mammals, and sodium channel toxins. We surveyed scorpion genomes and transcriptomes to compile a comprehensive sampling of these peptides across the breath of scorpion diversity, used molecular 3D modelling coupled with geometric morphometrics to characterise evolutionary changes in the shape of these peptides, and applied phylogenetic comparative methods to describe the selective pressure and evolutionary trends in these molecules. We show that the use of a stable phylogenetic framework, and the 3D structures of toxins, can be used to characterise the largest clades within Scorpiones, which have proven difficult to define using anatomical characters alone.

Symposium presentation

The evolutionary origin of scorpion pectines

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The versatility of the articulated appendages of arthropods has contributed to their evolutionary success, granting them unforetold access to ecological niche space. While the genetic mechanisms controlling the patterning of appendages are well understood for insect models like *Drosophilamelanogaster*, the patterning of appendages unique to arachnids (e.g., book lungs, chelicerae, and opisthosomal appendages) largely remains a mystery. Within Arachnida, scorpions are among the first lineages to appear in the fossil record and are distinguished from other arachnid groups by a unique pair of wing-like organs called pectines, whose homology to the walking leg is unclear. We searched the genome of *Centruroides sculpturatus*for homologs of appendage-patterning genes common to arthropods, such as *dachshund* (*dac*), *homothorax* (*hth*), *extradenticle* (*exd*), *Distal-less* (*Dll*), and *wingless* (*wg*). To elucidate the nature of the scorpion pectine and build upon understanding of its positional and genetic homologies to other appendages, we surveyed the expression of these genes in developing scorpion embryos. Separately, we assayed embryos of *C. sculpturatus* and the horseshoe crab *Limulus polyphemus* using immunohistochemistry to assess the homology of book gills and pectice. Here, we homologise the inner ramus of the pectine with walking legs, whereas our data suggest that the blade of the pectine represents an exopod derivative. These data provide support for the pectine as a derivative of the external horseshoe crab book gill and therefore as a waypoint in the evolution of the internalised arachnid book lung.

Oral presentation

Wolbachia infections in *Nephila senegalensis*

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Spiders are known to harbour a large diversity of intracellular bacteria, so-called endosymbionts such as *Wolbachia*, but very little is known about their effects on spider hosts. *Wolbachia* are maternally inherited and require cytoplasm for their vertical transmission, which means that landing in a male may constitute a dead end. It is therefore adaptive for the bacteria to increase the production of infected females relative to males. Recently, we found female-biased sex ratios in several clutches of *Nephila senegalensis*, as well as an infection with *Wolbachia*. However, there was no straightforward correlation between sex ratio bias and *Wolbachia* infection, but female-biased sex ratios were most likely to appear in egg sacs from infected but small females. Our current data suggest that the sex ratio distortion is due to male-biased post-hatching mortality, but the evidence is ambiguous. *Nephila* are known for a mating system that relies on a male-biased OSR, so that a shortage of males should have interesting effects. Only around half of the field-collected females were infected, and inheritance of *Wolbachia* was imperfect, allowing for a comparison between infected and uninfected offspring. Egg sacs of infected mothers were heavier and contained not only more, but also larger, eggs than those of uninfected females. Furthermore, infected daughters grew to a larger adult size and had a higher fecundity than uninfected ones. These patterns may suggest a mutualistic relationship between *N. senegalensis* and *Wolbachia*.

Student symposium presentation

Spider silk and sex: from mating threads to veils and gift-wrap

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All spiders produce silk, and even in non-web building spiders, silk is intimately tied to courtship and mating. Silk produced by females provides a transmission channel for male vibratory courtship signals, while webs and draglines provide a substrate for female sex pheromones. Observations of male spiders producing silk during sexual interactions are also common across phylogenetically widespread taxa. However, the function of male-produced silk in mating has received very little study. Exploring the function of male silk use during mating will provide a deeper understanding of the complex mating systems of spiders and allow tests of hypotheses about the evolution of male and female traits under sexual selection and/or conflict. In this review, we outline functional hypotheses that may explain three main categories of silk deposition males exhibit during courtship and mating: (1) silk deposition on females' webs or other silk structures (e.g., mating threads), (2) silk deposition on females ('bridal veils') and (3) silk associated with nuptial gifts. We summarise the current knowledge of silk use by male spiders within these categories, the types of mechanisms that may lead to functional effects, and discuss areas where future work can be targeted.

Student symposium presentation

Twitter as a tool for arachnological outreach: reflections on a year of @RecluseOrNot

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Engaging with the public is easier than ever thanks to social media. Twitter is a popular online social networking service that allows real-time sharing of information with people from all over the world. We will discuss the advantages and disadvantages of using Twitter for science communication and outreach, using an education and data-collection campaign called Recluse or Not as an example. Recluse spiders (genus *Loxosceles*) are widely feared and poorly understood, particularly in North America. In a 2005 study, Rick Vetter reported that members of the public believe the range of brown recluse spiders (*Loxosceles reclusa*) to cover vast areas of North America, including areas far outside their known distribution, and that almost any common spider species may be mistaken for a brown recluse. We started the Twitter account @RecluseOrNot in September 2016 with the goals of (1) providing accurate identification of spiders in photographs submitted by people who suspect they have found a brown recluse; (2) communicating scientifically accurate information about the range of recluse spiders in North America and the risk of envenomation; and (3) collecting data about the current distribution of recluse spiders and the spider taxa commonly mistaken for them. After one year we have received more than 500 submissions, mostly from North America, of which 19% were recluse spiders. Feedback and engagement have been overwhelmingly positive and our webpage (www.spiderbytes.org/recluse-or-not) receives an average of 120 visitors per day.

Student symposium presentation

Ticklish females: a sensory structure specialized to sense male stimuli in *Leucauge mariana* (Araneae, Tetragnathidae).

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Males often stimulate pre-existing female sense organs that originally evolved under natural selection, and a male's paternity success can depend on female responses to these stimuli. Most studies of male courtship signals have involved visual, auditory or chemical stimuli, but tactile stimulation of the female almost inevitably occurs. Tactile stimuli are often amenable to study, because the relevant female receptors tend to be localized on certain parts of the body, and some have little apparent function in other contexts; in such cases it is feasible to experimentally modify the female's receptors, and thus modify the male simuili that she perceives, without producing other major effects on the female. This study concerns a sexually dimorphic sensory structure in the spider *Leucauge mariana* (Tetragnathidae) (12 elongate setae on the sternum) that are apparently specialized in females to sense rhythmic movements of the male's cheliceral fangs during copulation. Removal of the setae caused a sharp reduction

in the frequency of copulatory plug formation, which in this species depends on female contributions. This evidence reinforces the model of Cryptic Female Choice as similar conclusions can been drawn from increases in female sensitivity to male stimuli during the mating season in several other animals.

Oral presentation

Immature mating and male mate choice in the cannibalistic brown widow spider *Latrodectus geometricus*

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Males of many spider species cohabit with immature females. Mating, however, has been considered to occur only after female maturation, which is connected to a suite of changes in morphology, physiology, and behaviour. Nevertheless, in the brown widow spider *Latrodectus geometricus*, mating with immature females is common and results in successful production of offspring. Adult females generally cannibalise males, and thereby limit them to a single copulation. From the male perspective, immature mating is beneficial, because males are not cannibalised and can achieve more than one mating. We conducted choice experiments to elucidate whether males are able to distinguish immature from adult females, and whether they prefer to mate with immature, non-cannibalistic females. In contrast to our expectations, males preferred adult females. One possible explanation is that there may be costs arising from immature mating. These costs can vary from loss of sperm in the moulting process to disadvantages in sperm storage due to unfavourable storage conditions. Therefore, we compared the morphology of the copulatory organs of immature and adult females by means of micro-computed tomography and histology. We discuss our results in the light of male mate choice, and the potential costs and benefits of immature mating.

Student symposium presentation

The genetic architecture of spider spinnerets: a new spin on an old question

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The phylum Arthropoda is a formidable system for understanding the developmental genetics of novel structures, with an abundance of structural innovations across the diversity of this group. Candidate gene approaches, grounded in established insect models like the fruit fly *Drosophila melanogaster*, have helped answer questions about some novelties, such as insect wings. This approach, however, is not suitable for study of evolutionary novelties that are restricted to distantly related lineages and is thus inadequate for addressing a major question in spider evolutionary developmental biology: what is the genetic architecture of spinnerets? Here we offer an alternative to the insect-based candidate gene approach toward a more comprehensive understanding of spinneret genetic architecture. We used appendage-specific transcriptomes of nascent spinnerets in the tarantula *Aphonopelma hentzi* and applied

differential gene expression (DGE) analyses to derive a list of candidate genes specific to spinneret primordia. Here we share preliminary data for genes identified as highly differentially expressed in the developing spinnerets compared to primordial legs. More broadly, our novel application of transcriptomic data and DGE analyses opens the door to identifying genes putatively important in the specification of other appendages types found exclusively in lineages distantly related to insects.

Oral presentation

Phylogenomic disruption of basal Grassatores relationships: A Levantine relict precipitates further deconstruction of Phalangodidae (Arachnida: Opiliones: Laniatores)

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After tumultuous revisions to the family-level systematics of Laniatores, the armoured harvestman family Phalangodidae presently bears a disjunct distribution. One of the curious lineages assigned to Phalangodidae is the monotypic Israeli genus *Haasus*, the only Laniatores species that occurs in Israel, and whose presence in the Levant has been inferred to result from biogeographic connectivity with Eurasia. Recent surveys of Israeli caves have also yielded a new troglobitic morphospecies of *Haasus*. Here, we describe this new species as *Haasus naasane* sp. nov. To test the biogeographic affinity of *Haasus*, we sequenced DNA from both species and RNA from *Haasus naasane* sp. nov. to assess their phylogenetic placement. Our results show that the new species is clearly closely related to *Haasus judaeus*, but *Haasus* itself is unambiguously nested within the largely Afrotropical family Pyramidopidae. In addition, the Japanese "phalangodid" *Proscotolemon sauteri* was recovered as nested within the southeast Asian family Petrobunidae. Phylogenomic placement of *Haasus naasane* sp. nov. in a 1,550-locus matrix indicates that Pyramidopidae has an unstable position in the tree of Laniatores. Exploration of phylogenetic signal reveals considerable topological conflict at the base of Grassatores, suggesting that the basal phylogeny of Laniatores may not yet be stable to addition of taxa. We transfer *Haasus* to Pyramidopidae (**new familial assignment**). Additionally, we transfer *Proscotolemon* to the family Petrobunidae (**new familial assignment**). Future studies on basal Laniatores phylogeny should emphasise the investigation of small-bodied and obscure groups that superficially resemble Phalangodidae.

Student symposium presentation

Whole-collection COI barcoding of New Zealand neopilionids (Opiliones: Neopilionidae)

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The diverse order of Opiliones has provided New Zealand with two biogeographic models in two of its four extant suborders: Pettalidae (Cyphophthalmi) and Triaenonychidae (Laniatores). The Neopilionidae (Eupnoi) with more than 60 species worldwide is emerging as a third biogeographic model. New Zealand members of this southern temperate family have already been the subject of several taxonomic revisions. We have used CO1 barcoding for about 400 neopilionid specimens in the Museum of Comparative Zoology at Harvard University, and about 200 specimens from the University of Auckland to compile the most broadly-sampled phylogeny of New Zealand neopilionids, complemented with almost 100 specimens from South America and Australia The resulting phylogeny and distribution maps serve as a backbone for future study and collection efforts by the team, and provide the most broadly sampled phylogeny of New Zealand neopilionids. Of the over 500 terminals from New Zealand, approximately 87% are newly-sequenced. Additionally, previously unpublished data with almost 100 terminals of South American genera has been included in the analysis.

Oral presentation

Taxonomic validation of the genus *Nemesiellus* Pocock, 1900(Araneae: Idiopidae) with a description of a new species from Odisha, India

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In India, the subfamily Genysinae is represented by a single valid genus, *Scalidognathus*Karsch, 1892. *Scalidognathus* is endemic to South Asia, known only by six species, three species each from India and Sri Lanka. Further, the Indian *Scalidognathus* spp. are described only based on the female. However, the genus *Nemesiellus* Pocock, 1900 was described from Yercaud in Shervaroy Hills, Tamil Nadu based on a single female specimen. This genus was later synonymised with *Scalidognathus* Karsch, 1892 due to lack of distinct morphological characters. Amongst idiopids, female specimens show little interspecies morphological variation. Therefore, in absence of male specimens, the taxonomic position of this genus remained unresolved. With fresh morphological and molecular data, here we validate the genus *Nemesiellus*, and remove it from the synonym of *Scalidognathus*. We also describe a new species of *Nemesiellus* from Odisha, India, and provide additional characters for diagnosis for the genus.

Oral presentation

Advances on Amblypygi research: past, present and future directions

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Amblypygids (whip spiders) show unique morphology, exclusive behaviour and quirky anatomy. Despite several advances in amblypygid research, details of their natural history and morphological/molecular characteristics remain unknown. In this talk, I will summarise and put into context past and recent progress, as well as future perspectives, on the study of whip spiders. New molecular dating shows, for example, that amblypygids branched off from their sister group (Uropygi) around 400 mya. Despite their age, modern amblypygids are still morphologically similar to fossils from ~300 mya, and are well adapted to their environment (tropical forests and caves). Amblypygids seem to have enough genomic flexibility to allow them survive large environmental shifts, as evidenced by their persistence to major extinction events. The marked sexual dimorphism (with pedipalp and antenniform legs longer in males than in females) has been shown to be widespread in the order, and more prominent in species closer to the equator. The large and widespread familly Charinidae was found to have a different genus composition (*Weygoldtia*+*Charinus*+*Sarax*) and had its peak of diversification during mid-Cretaceous. Amblypygids have also been shown to be good models for phylogeography and biogeography, being used in studies in the Atlantic Forest, Caribbean and New Caledonia. Finally, the exoskeleton of whip spiders was found to secrete a hydrophobic layer of colloidal material that self-assembles into microstructures, making amblypygids unwettable, which may help them to avoid bacterial and fungal infection. Future research should focus on details of amblypygid dispersal ability, ultrastructure, anatomy, gene expression, and systematics.

Student presentation

A total evidence phylogenetic analysis of sheet web spiders (Araneae, Linyphiidae) with comments on the effects of missing data

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Linyphiids are the largest family-level lineage of the ecribellate orb-weavers (Araneoidea). In recent years a number of cladistic studies have begun to unravel its phylogenetic structure, but the phylogeny of the family remains poorly understood. We have addressed this problem by combining morphological (more than 250 characters) and nucleotide sequence data from five markers, from both the mitochondrial and nuclear genomes, for a taxonomic sample of 295 species with representatives of the main lineages of Linyphiidae and its close relatives. Based on the phylogenetic analyses of the combined data we propose a new phylogenetic hypothesis for the main lineages of Linyphiidae. We also discuss the effects of missing data on our phylogenetic analyses.

Student presentation

Complex integration of visual information: The secondary eye pathway of the jumping spider brain

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Jumping spiders are known for a large repertoire of complex behaviours. They possess extraordinary cognitive abilities including planning, learning, and reversal learning. Their eyes, which display the highest-known spatial acuity among all terrestrial invertebrates, aid in generating such behaviours. Jumping spidershave one pair of large primary eyes and three pairs of smaller secondary eyes, which all serve a different task. We explored structure, arrangement, and connectivity of visual neuropils within the brain of the jumping spider *Marpissa muscosa* by means of paraffin-histology, microCT analysis, immunohistochemistry, and backfills. We found that every eye supplies its own first order visual neuropil, and the second order visual neuropils of the lateral eyes are fused. Furthermore, *M. muscosa* possesses an additional visual neuropil not found in other spiders. This neuropil receives input from the first order neuropils of all secondary eyes, and is connected to the mushroom body. Our results show that the visual system in the brain of *M. muscosa* differs in number, arrangement, and connectivity of neuropils from that of other spiders. We suggest that the unique visual capabilities of jumping spiders demand a complex visual system within the brain that enables a fast integration of incoming information from the different eyes.

Oral presentation

Towards spider glue: long-read scaffolding for extreme length and repetitious silk family genes AgSp1 and AgSp2 with insights into functional adaptation

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The aggregate gland glycoprotein glue coating the prey-capture threads of orb web and cobweb weaving spiders is comprised of spidroins (spider fibroins) encoded by at least two members of the silk gene family. The glue functions to retain prey that make contact with the web, but differs from solid silk fibres as it is a viscoelastic, amorphic, wet adhesive that is responsive to environmental conditions. Most spidroins are extremely large, highly repetitive genes that are impossible to sequence using only short-read technology. We discovered for the first time the complete genomic Aggregate Spidroin 1 (AgSp1) and Aggregate Spidroin 2 (AgSp2) glue genes of *Argiope trifasciata* using error-prone long reads to scaffold for high accuracy short reads. The massive coding sequences are 42,270 bp (AgSp1) and 20,526 bp (AgSp2) in length, the largest silk genes currently described. The majority of the predicted amino acid sequence of AgSp1 consists of two similar but distinct motifs that are repeated ~40 times each, while AgSp2 contains ~48 repetitions of an AgSp1-similar motif. Comparisons of AgSp1 repetitive motifs from orb web and cobweb spiders show regions of strict conservation followed by striking diversification. Glues from these two spider families have evolved contrasting material properties in adhesion, extensibility, and elasticity, which we link to mechanisms established for related silk genes in the same family. Full-length aggregate spidroin sequences from diverse

species with differing material characteristics will provide insights for designing tunable bio-inspired adhesives for a variety of unique purposes.

Symposium presentation

Highly diversified population structure of *Lycosa ishikariana* inhabiting sandy beach habitat

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The burrowing wolf spider *Lycosa ishikariana* lives only on sandy beaches. It is designated as VU (vulnerable) in the Red List of Japan, because the total shoreline length of Japanese sandy beaches is declining drastically in Japan. In case of local extinction by habitat loss, does the restoration of sandy beaches alone make it possible to re-establish spider populations by natural immigration? The ability of spider populations to re-establish themselves depends heavily on their dispersal ability. In this study, we analysed the population structure of *L. ishikariana* in order to infer their dispersal ability, using mitochondrial CO1 sequencing data and microsatellite data. As a result, highly diversified population structure was detected, and it was concluded that *Lycosa ishikariana* are poor dispersers. Consequently, in case of local extinction, the restoration of sandy beaches alone is not sufficient to re-establish *L. ishikariana* populations by immigration from distant habitat.

Symposium presentation

Blood-related prey-odour primes females to attend to red in both foraging and mate choice contexts in a mosquito-specialist jumping spider

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In some animals, males have evolved colourful display traits that are effective because they exploit females' pre-existing biases for those same colours in other contexts, such as foraging. Such sensory traps might be more likely to evolve in cases where ecologically-relevant odours (that are present in both contexts) prime females to pay attention to these colours. *Evarcha culicivora* is a mosquito-specialist jumping spider with a strong preference for red, blood-filled mosquitoes. Blood odour acquired from consuming mosquitoes increases mating success in males and females. Males display red faces to females during courtship, suggestive of a sensory trap. Here, we show that females preferentially selected red-dyed mosquitoes from a group of grey-dyed mosquitoes, and that they found these red mosquitoes faster when blood-related odour was present. Similarly, in the context of mate choice, females showed increased receptivity towards red-faced male models (compared to models with their red coloration concealed); this effect was also more pronounced in the presence of blood-related odour. These data suggest that similar odours (derived from vertebrate blood) prime females to seek out red coloration in both foraging and mate choice. We discuss these findings broadly in the context of sensory trap evolution.

Student presentation

From liquid dope to solid fibres: Studying factors influencing assembly within native spider silk glands

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Spider silk fibroins are stored within internally situated glands that are connected to spinnerets through which extrusion occurs to the outside. The way in which the liquid dope is converted to solid fibres involves polymerisation of the protein subunits in response to changes in the chemical environments and is largely irreversible. The precise mechanisms underpinning this transition from liquid dope to solid proteins with such a diverse range of physical properties are not fully understood. In our study we have developed a novel ex-vivo system for studying silk production in more detail. We have developed a method whereby silk glands dissected from orb weaving species can be maintained in cell culture conditions for extended periods whilst continuously producing silk dope at a steady and predictable rate. By studying the effects of temperature, media, polarised light and viscoelasticity we have confirmed that dope continues to be expelled from the distal end of the gland for up to 32 days and that the gland's 'behaviour', in terms of the rate of dope production, is influenced by external stimuli such as nutrient availability sudden temperature shock and excess waste products. This system allows for the first real-time studies into the cellular and tissue mechanics of how silk is produced. Coupling this with high resolution microscopy techniques will allow us to study the way that silk proteins assemble within the glands in much more detail.

Symposium presentation

Size matters: Possible cases of character displacement in Japanese harvestmen for preventing reproductive interferance

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Two closely related species sympatrically found often differentiate their body size one another by a factor of ca. 1.3 that evokes Hutchinson's rule. On the other hand, two similar-sized congeneric species rarely overlap their ranges. These are the rules generally observed in Japanese harvestmen. Reproductive interference may be liable to occur in harvestmen, because of their non-elaborated mating behaviour and presence of nuptial gift that may elicit female's less discrimination to mates. Thus, it is probable that substantial difference in body size is crucial for building sympatry for two closely related species of harvestmen lacking effective pre-mating barrier for reproductive isolation. I will review some possible cases of character displacement found in Japanese harvestmen: 1) *Leiobunum montanum* and *L. hiraiwai*: These two species occurring widely in beech forests in western Japan show a checkerboard pattern of distribution (Diamond 1975), i.e., they do not coexist in a local area. A single exception to the rule is found on the northern slope of Mt. Hyonosen, Tottori, where *L. montanum* with extremely elongated body coexists with L. hiraiwai. 2) *Gagrellula ferruginea* and *G. testacea*: Distributional ranges of the two species meet at western part of Hiroshima Prefecture, making a narrow zone of sympatry, though a few introgressions of genes are also indicated. *Gagrellula testacea* becomes smaller in Kyushu where larger *G. grandis* occurs and attains smallest body in Shikoku where it becomes sympatric with *G. ferruginea*. Other examples include 3) *Nelima genufusca* and *N. nigricoxa* 4) *Pseudobiantes japonicus* and *Epedanellus tuberculatus* (Laniatores: Epedanidae).

Student presentation

Macroevolutionary rate estimations in a nephilid phylogeny

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Extant taxa exhibit considerable variation in species richness across phylogenetic groups. Species richness of a clade is determined through the speciation and extinction rates over a clade's evolutionary time. However, the factors that drive the disparities in species richness among taxa remain elusive. Several types of traits have been proposed to affect diversification: for example, body size, indicators of sexual selection such as sexual dimorphism, ecological specialisations, and the origin of novelties, sometimes referred to as 'key innovations'. Extreme sexual size dimorphism (SSD) and its correlated phenotypes could be examples of such traits. In theory, if they pose an increased risk of extinction, extreme phenotypes should be confined to relatively derived and species-poor clades. The spider family Nephilidae exhibits a wide range of phenotypic 'extremeness' in body size and correlated traits, making it an ideal model for addressing such evolutionary questions. We report on using Bayesian analysis of macroevolutionary mixtures (BAMM) with a new, well-supported nephilid phylogeny, in order to estimate speciation and extinction rates as they relate to SSD evolution. We use this analysis to explore whether an increased degree of SSD accelerates or inhibits diversification, and in addition test specific biogeographical predictions that attempt to link the evolution of extreme phenotypes with latitude and species range sizes.

Oral presentation

Latitudinal differences in life history traits of a rapidly range-expanding spider

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Global climate change can result in poleward range expansions. A well-established model species for studying rapid range expansion is the orb-weaving spider *Argiope bruennichi,* which spread from the Mediterranean region into continental climates and up to Baltic countries in less than 100 years. Consequently, individuals have to cope with very different climates and environments. We collected mated females from the northern range limit (three populations from Estonia) and from within its original range (three populations from southern France). After oviposition, the spiderlings overwintered in egg sacs that were allocated to a common garden experiment, mimicking the winter conditions from both regions of origin. We investigated the effect of origin on morphology and reproductive investment of females. Aiming to illuminate the effects of winter treatment and origin, we explored hatching success, survival probability, and body weight of the spiderlings. Overall, we found significant effects of origin on all traits inspected in females. In particular, females from the northern range are smaller but show similar reproductive investment to females from the original range, indicating adaptations to local environmental factors. Effects of both origin and winter treatment on the traits of spiderlings suggest an interplay between genetic adaptation and phenotypic plasticity. In conclusion, our results highlight latitudinal variation in life history traits in a range-expanding spider.

Oral presentation

No major progress in web decoration research – Why is that?

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It has been 130 years since Henry McCook described the extra silk structures he observed in webs of North American orb web spiders as ‘web decorations’. After that, many arachnologists have tried to substantiate this rather neutral term with evidence for a function that explains the selective advantage of the decorating behaviour. Many orb web spider species construct them in various shapes and with varying frequencies. Many hypotheses have been proposed and tested. Evidence has been found for silk decorations serving as warning signals, predator avoidance devices, and prey attractants. However, in retrospect, most progress has been done in the 1990s and early 2000s, and recently it became much quieter around web decoration research. In a brief review, I will explore whether this is due to a hesitation to engage in increasingly elaborate experiments, due to a shortage of ideas how to proceed, or whether arachnologists believe that all important answers have already been found. In disagreement with the latter two possibilities, I will point towards still existing knowledge gaps, and suggest improvements for future approaches and how the methodologies could be adjusted to eventually solve a century-long question in arachnology.

Student presentation

Influence of the spinneret’s morphology onto the complex fibre processing in cribellate spiders

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Web-building spiders rely on their capture threads to retain prey. The threads of many species are therefore equipped with viscoelastic glue droplets. In contrast, cribellate spiders build a complex multi-fibre system endued with a wool of nanofibres. The processing of these cribellate capture threads is nearly unstudied, presumably due to the small scale of involved micro- and nanofibers, and an incomparable complexity of fibre processing. The general structure and the spinning process of cribellate capture threads have been partially ascertained e.g. in uloborids. At least three different types of fibre are interweaved: nanofibers, axial fibres, and paracribellate fibres. Each type of fibre originates from a specific type of spigot on the spinnerets. The spatio-temporal adjustment of spinneret movement influences the combination of fibres. However, when screening the spinneret morphology across the phylogenetic tree of

spiders, this alterable aspect has to be considered for an investigation. We created abstracted models of the spinneret's morphology in different cribellate spiders to get a visual impression of distinct spigot arrangements. By characterising the quantity and distribution pattern of the spigots, we aim to understand how morphological differences of the spinnerets influence the final thread structure. Despite species-specific characteristics, the relative position of spigots involved in the cribellate spinning process show definite similarities within all investigated species. Additionally, an exposed and distinct presence of the paracribellate spigots reveal the importance of this type of spigot for the cribellate spinning process. Here, we focus on three species (*Kukulcania hibernalis*, *Uloborus plumipes*, *Brigittea civica*) as representatives to get to a universal model of necessary morphological conditions for the production of complex cribellate threads.

Symposium presentation

Constraints on courtship signalling in web-building spiders

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Courtship signals can convey information about species identity, mate quality and receptivity. However, for some taxa courtship signals are also used to reduce mate aggression. Many male web-building spiders must enter the female's predatory trap, the web, in order to commence courtship. This generates strong selection on male courtship behaviour to not induce predatory behaviour in females. We used laser vibrometry, vibratory playback techniques, high speed video recordings and experimental manipulations to elucidate the mechanisms that male web-building spiders use to reduce female aggression during courtship interactions. We identified courtship vibrations ('shudders') that are generated very early in courtship interactions that reduce female aggression, even when real prey is present in the web. Male courtship shudders show extremely high short-term repeatability. We hypothesise that this high repeatability helps females gather information about male quality while also allowing males to maintain a vibratory signature that is distinct from the vibrations generated by prey struggling in the web. In addition to generating vibrations, courting males often tap or stroke females with their legs. We show that physically tapping spiders reduces aggressive responses in spiders. Repeatable vibratory signals and tapping are common features in male courtship behaviours and indicate conserved constraints on courtship signalling in web-building spiders.

Oral presentation

Our past and current knowledge on the sensory biology of harvestmen (Opiliones)

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Sensory ecology deals with the relevant stimuli to animals in distinct contexts. Understanding cues and signals used by a species is a requisite for researchers in most areas of animal behaviour, including sexual and anti-predatory behaviour, foraging, navigation, and habitat selection. I will provide a brief historical review of the literature and then focus on the latest findings on the sensory biology of Opiliones, from both behavioural and morphological perspectives. The first studies that date back from the nineteenth century were followed by other morphological studies mainly describing slit sensilla, setae, and eye morphology in the twentieth century. Behaviourally, some authors provided important data in papers that dealt indirectly with sensory features. In this century there was a boom of studies in this area, both in morphology and behaviour. Harvestmen were mostly considered to rely on contact chemoreception, but I will show published and unpublished results with evidence that they may also use olfaction and vision in a variety of contexts. These results combined should greatly change our view of how harvestmen understand the environment, and should influence our approach to behavioural studies in the present and future.

Student symposium presentation

Enigmatic architects of eastern Australia: integrating morphology, molecules and burrow architecture to resolve the systematics of the golden trapdoor spiders (Idiopidae: Arbanitinae: Euoplini)

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Mygalomorph spiders can be difficult to study in the absence of fundamental life history information. Their cryptic nature hinders sampling, linking sexually dimorphic males and females can be challenging, and their morphology is relatively homogeneous and homoplastic. Recently discovered differences in burrow architecture and morphology indicated that these challenges had impeded our understanding of the Australian trapdoor spider tribe Euoplini. To investigate the evolutionary significance of these discoveries, and overcome the challenges associated with poorly understood mygalomorph groups, we combined morphological, molecular and behavioural data in both iterative and integrative (i.e. total-evidence) analytical frameworks. These analyses revealed three lineages in the Euoplini, two of which had not previously been documented from mainland Australia. One lineage contains species which construct plug-door burrows typically associated with the tribe, but also contains a clade of species which construct remarkable palisade burrows with species-specific structural differences. A second lineage, previously only known from Tasmania but revealed to be widespread throughout mainland eastern Australia, contains species which construct cryptic, wafer-door burrows. This lineage was found to occur sympatrically and syntopically with the plug-door/palisade lineage. The third lineage contains a single divergent species from Victoria. All lineages were found to be diagnosable based on both male and female morphology. Our

results led to a new classification of the tribe; two new genera were erected, *Cryptoforis* (wafer-door lineage) and *Narellea* (monotypic lineage), in addition to *Euoplos* (plug-door/palisade lineage); but also revealed broader insights into the evolution of morphology, behaviour, and microhabitat preferences in mygalomorph spiders.

Student presentation

Static allometry and evolutionary allometry of enlarged chelicerae in the Myrmarachnines

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This meta-analysis addresses the static allometry and evolutionary allometry of weapon size among the ant-mimicking jumping spiders (Salticidae: Myrmarachne) in relation to other measures of morphometry. We first evaluate static allometry of the morphometrics in various species and investigate the compensation and trade-off between traits. We then mapped values derived from morphometrics to the *Myrmarachne* phylogeny to look at variations across the phylogeny, which provides insight to evolutionary allometry of the trait for the genus. We seek to establish the mode of selection that resulted in the evolution of enlarged chelicerae within the genus.

Student presentation

Remote sensing derived habitat indices can predict spider species richness in urbanisation gradient

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Dynamic Habitat Indices (DHIs) have been suggested as good indices of habitat features, but have seldom been used in studies of small arthropod distribution. We aimed to test the effectiveness of Normalised Difference Vegetation Index (NDVI) derived DHIs on explaining both spider assemblage composition and species richness at different spatial scales. We recorded spider species and abundance by pitfalls in 1,145 sampling sites along an urbanisation gradient in central Taiwan. NDVI was obtained from Landsat 8 images. The relationship between DHIs and spider assemblage composition and species richness were examined by generalised linear mixed models at four spatial scales: 1, 6, 25, and 100 ha grids. Results show that at spatial scale of 6 ha grids provides DHIs the highest variance in assemblage composition. We also found positive exponential relationship between DHIs and species richness at all spatial scales. However, the pseudo R^2 of the predictive models increased with grid size, but became saturated at grid sizes larger than 6 ha (pseudo R^2 0.66 at 100 ha scale). Minimum DHI, which represents the annual minimum productivity, was the most significant factor; its significance level increased with grid size. We recommend 6 ha grid size is an appropriate spatial scale when using remote sensing derived indices to explain or predict spider species diversity and assemblage composition. Our findings also indicate that DHIs, especially minimum DHI, can be good predictors of spider species richness. Maintaining higher

productivity in non-growing season is an important conservation strategy to ground-dwelling spiders in urbanised environment.

Oral presentation

Comparative morphology of ground spider trichobothria (Araneae, Gnaphosidae)

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Trichobothria are cuticular mechanoreceptors on the superior surface of the pedipalps, and on the tarsus, metatarsus, tibia, and patella of walking legs in ground spiders. Trichobothria are sensitive to a very weak air movement, and play an important role in spider life. The substantial body of data on trichobothria demonstrates the importance of their morphology and distribution in arachnid taxonomy. The ground plan of trichobothrium organisation is similar among spiders, and constitutes the bowl-shaped socket in the cuticle with a single long, hollow inside filament at the centre. In gnaphosids, the socket is surrounded by distal and proximal plates that may have distal and proximal margins. Plates may have ridged folds. The first fold on the proximal plate that borders a socket forms a hood. Presence, number, and shape of ridges on the proximal plate are different among ground spiders. Our study shows that this diversity in sculpture of distal and proximal plates clusters in morphological groups. The shape of cuticular ridges is also characteristic for gnaphosid subfamilies, genera and, in some degree, species. The results of the study suggest usefulness of trichobothrium morphology for ground spider classification on these taxonomic levels.

Student presentation

Function of colour pattern in intra-specific interactions: a case study with jumping spiders

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Animal colouration usually plays a key role in sexual selection via mate choice and intra-sexual competition. While the effect of the chromatic and achromatic properties of colours on intra-specific interaction has been widely explored, how colour patterns may affect such interactions remains largely unexplored, especially in invertebrates. Here, we addressed this question using an ornate jumping spider *Siler semiglaucus* (Salticidae), in which multiple colour patches - irregular red patch and oval/irregular blue patches - on the dorsal abdomen are displayed in intra-specific interactions. With the purpose of testing the potential function of male colour patches, we first examined the intersexual differences between dorsal abdomen colour patterns in *S. semiglaucus*. We found that, proportionally, the total coloured area of the male was significantly smaller than the female; specifically, males had a relatively larger red patch and smaller blue patch compared to females. We then investigated whether intraspecific interactions, for both female mate choice and male-male competition, are affected by male colour patterns. Our preliminary results suggest that the relative size of a male's red patch is an important factor in intraspecific interactions: 1) females were more likely to visit the males

with a larger red patch, and 2) males with a larger red patch were more likely to win the intrasexual contest. Our study highlights the importance of colour pattern in intra-specific interactions in invertebrates, and encourages an assessment for the function of colour patterns in other ornate invertebrates.

POSTERS AT A GLANCE

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2	Yu *et al.*	Predator avoidance: bird dropping masquerading in a crab spider
3	Yin Yip & Tso	* Can I borrow a “light”? Does fireflybioluminescence act as a visual lure on *Psechrus clavis* webs?
4	McGinley *et al.*	Hunger influences behaviour but not outcome in male-male contests of *Servaea incana* jumping spiders
5	Rao *et al.*	Reeling in the prey: Fishing behaviour in an orb web spider
6	Shigemiya	Female genital mutilation in *Cyclosa confusa*
7	Fischer *et al.*	* Spider women talk – Females of the cob-web spider *Steatoda grossa* adjust their web architecture and web pheromone titer in response to mate competition
8	Segura-Hernández *et al.*	* This smells... familiar? Learning of chemical cues in two sympatric species of amblypygid
9	Robledo-Ospina & Rao	* Colour fidelity in prey selection by an araneophagic wasp
10	Deutsch	* Deception & Manipulation: Argyrodinae spiders as a parasite and host
11	Gonnet-Cendán *et al.*	Testing the occurrence of sexual size dimorphism in Allocosinae species from Uruguayan grasslands
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14	Xu *et al.*	Formation of rivers and mountains drive diversification of primitively segmented spiders in continental East Asia
15	Vink *et al.*	New Zealand Pirates: Evolutionary origins and diversity of Zealandia’s mimetid spider revealed through morphology and molecular data
16	Steele *et al.*	* Chronoecology of the cave dwelling orb-weaver spider, *Meta ovalis*
17	Audisio & Mikheyev	* Evolution of the venom system in spiders
18	Chamberland & Stafstrom	* Untangling the evolutionary and biogeographic history of Old-World net-casting spiders (Family: Deinopidae)
19	Montes de Oca *et al.*	* Thermal preferences in seven species of Theraphosidae (Mygalomorphae): ecological implications
20	Albín *et al.*	Standard metabolic rates in a Neotropical burrowing wolf spider with sex role reversal
21	Malumbres-Olarte *et al.*	CEBRA – Optimised and standardized sampling protocols for citizen science

22	Řezáč *et al.*	Neonicotinoid insecticides suppress the ability of spiders to re-colonise disturbed agroecosystems
23	Laino *et al.*	Is it worth having an adequate energetic state so as to detoxify a pesticide?
24	Dippenaar-Schoeman *et al.*	Red List of South African spiders: an end-product of the South African National Survey of Arachnida
25	Engelbrecht *et al.*	The Baboon Spider Atlas: mapping tarantula diversity in southern Africa with citizen science
26	Ridel *et al.*	Complementary of trait- vs diversity-based metrics in spider and carabid assemblages
27	Urfer *et al.*	Morphology, CO1, and ITS2 provide different specimen clusters in a widespread crab spider
28	Setton *et al.*	* Embryogenesis in a Colorado population of *Aphonopelma hentzi*, (Girard, 1852) (Araneae, Mygalomorphae, Theraphosidae), an emerging system for the study of spider development
29	Jones & Cushing	* Morphology of Male Abdominal Ctenidia in North American Camel Spiders
30	Gainett *et al.*	From eggs to longlegs: Embryonic development and staging of the harvestman *Phalangium opilio*
31	Steinhoff *et al.*	* Lifestyle matters: Brain morphology in cursorial and stationary hunting spiders
32	Laudier	Silver, Gold and Copper Staining: Histochemical Applications for Arachnid Neural Tissue
33	Tsurusaki *et al.*	Chromosomal hybrid zone showing heterzygote superiority in *Gagrellula ferruginea* (Opiliones)
34	Setton & Sharma	Differential gene expression approaches elucidate systemic effects of Wnt signalling inhibition during segmentation in the spider *Parasteatoda tepidariorum*
35	Santibáñez-López *et al.*	Neglected no longer: Phylotranscriptomics and molecular modelling reveals venom homologs in Pseudoscorpiones and Palpigradi
36	MacDougall *et al.*	* Species delimitation of New Zealand Neopilionidae (Opiliones) based on COI sequence data
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38	Silva de Miranda & Wood	Phylogeography of the Atlantic Forest amblypygids
39	Fet *et al.*	Revision of the *Mesobuthus caucasicus* complex from Central Asia (Scorpiones: Buthidae)
40	Privet *et al.*	* New insights into the systematics of the "*Arctosa villica* group", including observations on the halophilic species *A. fulvolineata*
41	Ono *et al.*	The spider fauna of Myanmar (Arachnida, Araneae), a prologue

42	Mitchell *et al.*	Under the trapdoor: Unravelling the phylogenetic relationships and phylogeography of cork-lid trapdoor spiders, Stasimopus Simon, 1892 (Araneae, Mygalomorphae, Ctenizidae) in the Karoo
43	Richardson *et al.*	A key to the genera of Australian jumping spiders (Araneae: Salticidae)
44	Ríos-Tamayo & Lyle	First systematic revision of the subfamily Anaminae (Mygalomorphae: Nemesiidae) in South Africa
45	Machado *et al.*	* Taxonomic revision of the Australian crab spider genus *Stephanopis* O. Pickard-Cambridge, 1869 (Araneae: Thomisidae)
46	Machado *et al.*	* Shaking the tree of the bark crab spiders: Phylogeny of the Neotropical *Stephanopis* species reveals a new genus and revalidates *Paratobias* (Araneae: Thomisidae)
47	García *et al.*	* Investigating the poly-paraphyly of North American camel spiders (Solifugae: Eremobatidae: Therobatinae) and their unique moveable palpal spines
48	Gavish-Regev *et al.*	Below or above-ground? Where are the closest relatives of troglobite *Tegenaria* species?
49	Baker *et al.*	* A densely-sampled Sanger-based phylogeny of the temperate Gondwanan family Triaenonychidae (Opiliones: Laniatores), inferred from three markers

POSTERS

Poster 20

Standard metabolic rates in a Neotropical burrowing wolf spider with sex role reversal

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Allocosa senex inhabits sandy coasts from Argentina, Brazil and Uruguay. The habitat of this species includes beaches of fine and coarse-sand. The species shows a reversal in typical sex roles and sexual size dimorphism expected in spiders. Copulations occur inside male burrows and females prefer to copulate with males that construct deep burrows. We tested whether *A. senex* shows sexual dimorphism in standard metabolic rate (SMR) and total evaporative water loss (TEWL) and explored SMR differencesin individuals from beaches with coarse or fine substrate. We collected 10 individuals of each sex at each location and estimated SMR and TEWL using an open-flow respirometry system. To test sexual differences in SMR and TEWL, we fitted mixed models with beach as random effect and sex and body mass and their interaction as predictor variables. Differences in SMR between sand beaches were evaluated fitting generalised linear models (GLM). We found that adults of *A. senex* do not differ in mass-specific SMR, while males show higher TEWL values than females ($p=0.0197$). Additionally, we did not find an effect of sand type over SMR. Thus, *A. senex* does not exhibit sexual dimorphism in metabolism as other spiders that could be related to the sex-role reversal occurring in this species.

Poster 1

Deceptive worthless nuptial gifts: the role of resource availability, sexual selection and individual differences

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Males of the Neotropical spider *Paratrechalea ornata* can use two reproductive tactics: offering nutritive (fresh prey) or worthless (prey leftovers) nuptial gifts. The proportion of worthless gifts varies between 50-90% depending on the population, and field data suggested an important effect of the environment on these tactics. We studied a population with 50% worthless gifts and examined the relative occurrence of both types of gifts in relation to pre/post- copulatory sexual selection (OSR/sperm competition) and resource availability (number of prey) in the field. We found that worthless gifts were mainly negatively correlated with prey availability. Second, by controlling prey availability we tested how mate competition and individual differences affect male tactic choice under laboratory conditions. Males were repeatedly exposed to five different females every four days, in two groups: presence and absence of competition (N = 18 each). We gave males opportunity to produce either nutritive or worthless gifts by offering a prey (*Musca domestica*) and exuviae (larvae of *Tenebrio molitor*) in the terrarium, respectively. The gift type produced in each encounter was recorded, and the repetitiveness of the behaviour was estimated to be 0.045 (p = 0.18), indicating absence of individual differences in the male tactic choice. In contrast, we verified males are highly plastic adjusting their tactic according to competition, as males reduced the production of worthless gifts by 11.6% in the presence of a rival males. This is evidence that environmental predictability may modify how sexual selection shapes the use of deceptive worthless gifts.

Poster 17 (student)

Evolution of the venom system in spiders

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The success of spiders is largely attributed to the evolution of complex biologically active venoms that have enabled them to become ecological specialists. Research on spider venoms has focused almost exclusively on toxic components secreted by medically important species without exploring the venom system as a whole. Recent phylogenomic analyses confirm deep molecular divergence between the Opistothelae (Mygalomorphae and Araneomorphae) and Mesothelae (Liphistiomorphae). The Opistothelae account for most of the observed spider diversity, while the Mesothelae are represented by only one extant family with eight genera restricted to Southeast and East Asia. Although venom glands were discovered in the Southeast Asian genera, venom composition in this ancient lineage has never been explored. This study aims to examine the morphology of venom glands across liphistiomorph, mygalomorph, and araneomorph spiders using X-ray computed microtomography and refine venom extraction methods to collect venomic data for liphistiomorph spiders in the Ryukyu Archipelago (Araneae, Mesothelae, Liphistiidae, *Heptathela* and *Ryuthela*). This combined methodological approach will provide key insight into the relationship between morphological and biochemical complexity in the venom system. While characterization of the venom system in the Mesothelae is fundamental in determining the patterns and processes of venom evolution in spiders, preliminary results reveal the absence of venom glands in species endemic to the Ryukyus. This represents a major shift in the understanding of the evolution of the venom system in spiders.

Poster 13

Movement patterns and home range size of two species of riparian-zone wolf spiders from Arizona, USA

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While many spiders live relatively sedentary lives (either in webs or in burrows), the group of wandering spiders are typically much more active. Most wolf spiders fall into the latter group, but information about their movement (daily distances moved, home range sizes) is poorly known. In this study we used a mark-recapture method over three years (2015-2017) to examine these traits in two species of wolf spider (*Pardosa valens* and *Rabidosa santrita*) found in the cobble zone along small streams in the Chiricahua Mountains of southeastern Arizona, USA. Spiders were initially captured along a 100 m transect, and this transect was then visually searched 1-2 times per day over the following 7-10 days for marked spiders. As is typical, males were more active than females and had larger home ranges in both species. Surprisingly, the smaller species (*P. valens*) typically had larger home range estimates than the larger species (*R. santrita*). For both species, we found that movement was relatively restricted, with relatively small home ranges in both sexes. This may in part reflect their limited abilities to disperse far from streams due to susceptibility to water loss.

Poster 49 (student)

A densely-sampled Sanger-based phylogeny of the temperate Gondwanan family Triaenonychidae (Opiliones: Laniatores), inferred from three markers

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The armoured harvestman family Triaenonychidae (Opiliones: Laniatores) has a predominantly temperate Gondwanan distribution, with representatives in southern South America, South Africa, Madagascar, Australia, New Zealand, New Caledonia, and one genus in eastern North America. Despite being one of the most diverse families of harvestmen with *ca*. 477 described species and subspecies, they have received little systematic attention until recently, and no phylogeny focusing on this family, molecular or morphological, has been published. Herein, we present a molecular phylogeny of Triaenonychidae inferred from three markers (18S rRNA, 28S rRNA, and COI), representing all the geographic areas from which they are known, and including over 300 terminals spanning ~60% of described genera. We demonstrate that nearly all the landmasses from which triaenonychids are found contain non-monophyletic assemblages, and while most recognised genera are monophyletic, some, including the diverse trans-oceanic genus *Nuncia*, as well as the New Zealand genera *Karamea* and *Triregia*, are poly- or paraphyletic and require taxonomic revision. Our phylogeny also rejects the monophyly of all four currently accepted subfamilies (Triaenonychinae, Triaenobuninae, Adaeinae, and Sorensenellinae), and calls into question the familial rank of the New Zealand-endemic Synthetonychiidae. Despite limited nodal support along the backbone of the phylogeny, we recover an apparent division between taxa from Eastern Gondwana (Australia, New Zealand, New Caledonia) and Western Gondwana (South America, Africa).

Poster 12

The architecture, dynamics, and silk investment in social spider webs

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Animal architecture is diverse in form and structure, and extraordinarily intricate, often facilitated by collective behaviour of hundreds of individuals. Webs built by social spiders are one such example of animal architecture. We discuss the architecture, dynamics and silk investment in a tropical social spider *Stegodyphus sarasinorum* whose webs are built within a few days but maintained for several months. One of the benefits of sociality in spiders is to conserve silk. We test this hypothesis by allowing spiders in different group sizes (1, 5, 10 and 25 spiders per group) to build webs in a pre-defined space over 10 days and tracking web evolution through image analysis. Specifically, we ask a) if spiders in larger group size produce more silk, and b) if per capita silk investment reduces with increase in group size. Our results indicate that spiders in larger group invest more silk compared to spiders in smaller groups. However, spiders do not save silk by living in larger colonies. Additionally, we discuss the spatio-temporal evolution of web of *S. sarasinorum*. From an architectural point of view, unlike man-made structures, these webs achieve moderate stability and functionality even when they are not fully complete.

Poster 18 (student)

Untangling the evolutionary and biogeographic history of Old World net-casting spiders (Family: Deinopidae)

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We aim to untangle the evolutionary and biogeographic history of the net-casting spider (Deinopidae) using a combination of molecular and morphological data. Historically, morphology has indicated two genera of Deinopidae, *Deinopis* (the ogre-faced spiders) and *Menneus* (the humpback spiders). Both genera share the unique net-casting hunting strategy; however, they have drastically divergent morphology. Most notable are the giant posterior medial eyes (PME) of *Deinopis*. This pair of light sensitive eyes enables *Deinopis* to hunt at night in low-light conditions, while *Menneus* are postulated to hunt at dusk. Unexpectedly, we found in our previous molecular phylogenetic study *Menneus* nested within *Deinopis*. Thus, we hypothesised that the size of the uniquely large posterior median eyes (characteristic of *Deinopis*) has been secondarily reduced in *Menneus*. To uncover the evolutionary shifts within this lineage, we will test whether *Menneus* dispersed over water to Australia from Africa or *Menneus* morphology (large PME) evolved independently on both continents. Here, I present preliminary data and proposed methodology for addressing these exciting questions and unexpected phylogenetic relationships.

Poster 10 (student)

Deception & manipulation: Argyrodine spiders as a parasite and host

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Symbiosis describes the ‘living together’ of separate organisms; often with a host forming the environment that symbionts must master in order to survive and reproduce, carrying its own unique risks and benefits. Where one organism steals resources from another a parasitic relationship can form, with the kleptoparasite saving time and energy but risking the consequences of detection. Within spiders many forms of kleptoparasitism emerge, as webs prove a valuable resource to be exploited. One such example is that of *Argyrodes*, small spiders within the sub-family Argyrodinae. These tricksters often live in groups on the web borders of numerous spiders across the globe, scavenging prey and feeding with the host, even eating host eggs and young. Southern Spain plays host to *Argyrodes argyrodes* on the webs of *Cyrtophora citricola*, a colonial orb weaver made especially attractive by large and long-lasting web structures. This study aims to quantify the relationships between parasite and host, exploring the impact of *Argyrodes* presence as well as the strategies they use to maximise their success. The *Argyrodes* themselves are also host to many other organisms, including endosymbiotic bacteria. These bacteria have been found to impact sex ratios, reproductive success, dispersal and protection from natural enemies in a wide range of arthropods but their impacts on spiders are currently unclear. Spiders within in this study were screened for such bacteria with the aim of exploring their impact as well as adaptations to maximise their propagation within a such an unusual host.

Poster 24

Red List of South African spiders: an end-product of the South African National Survey of Arachnida

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The South African National Survey of Arachnida (SANSA) was launched in 1997 to improve knowledge of the arachnid diversity of the country through collaboration and co-ordination of arachnological research. During the last two decades considerable effort has been made to collect, identify, database and create products on the biodiversity of the country’s arachnids, including the First Atlas of the Spiders of South Africa (Arachnida: Araneae). This book included detailed information on the localities, biome records, conservation status etc. of 2003 species known from South Africa in 2010. Since then, considerable effort has gone into identifying and describing species in preparation for the Red Listing of South African spiders, which will also include the species from Lesotho and Swaziland. This process is nearing finality, with an assessment being made for each of the approximately 2300 species in 70 families now known from the country. Assessment information includes the common name, taxonomic status (sexes known, recently redescribed, illustrated or not etc.), national status and

rationale for this classification, distribution globally and in South Africa, habitat, threats, assessment comments, and a list of georeferenced localities from the three countries (Country, Province, Locality, Sublocality, decimal degree co-ordinates). A large proportion of the species (~60 %) are endemic to South Africa, Lesotho and Swaziland; a sizeable proportion are more widespread African endemics (~38 %), and a small portion are cosmopolitan species (~3 %). The Red List should be completed and submitted for layout in March 2019, and will be available to users as an e-book.

Poster 25

The Baboon Spider Atlas: mapping tarantula diversity in southern Africa with citizen science

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Basic species distribution data are critical for conservation purposes like Red Listing and spatial conservation planning. Baboon spiders (Araneae: Theraphosidae) are large, long-lived mygalomorph spiders with limited tolerance for environmental disturbance. They are protected by law in several southern African countries, but are in demand by collectors for the international pet trade. The taxonomic diversity and conservation requirements of these spiders are poorly understood, despite their size and charisma. The goal of the Baboon Spider Atlas is to document the diversity and to map the distributions of all southern African baboon spider species using citizen science. The project is integrating photographic records submitted by the public to an online database with museum specimen data, and field work is targeted at under-sampled areas to collect new records as well as topotypic material. The project has already assembled the largest single dataset for baboon spider distributions, which is publicly available online at http://vmus.adu.org.za. The diversity of these animals has been found to be vastly underestimated in the region, highlighting the need for ongoing research. In particular, foundational taxonomic studies are required to describe the high proportion of new species being discovered.

Poster 39

Revision of the *Mesobuthus caucasicus* complex from Central Asia (Scorpiones: Buthidae)

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A widespread *Mesobuthus caucasicus* complex, which includes some of the most common scorpions found from the Caucasus to China, is revised for the first time based on new, extensive collections from Central Asia, using both morphological and DNA marker data. *Mesobuthus caucasicus* (Nordmann, 1840) is restricted to the Caucasus Mountains. Four taxa are elevated to species rank. Six new species are described from Afghanistan, Iran, Kazakhstan, Tajikistan, Turkmenistan, and Uzbekistan. A DNA phylogeny based on COI and 16S rRNA markers is presented including nine Central Asian species. A deep phylogenetic diversity across Central Asia is revealed. Historical biogeographic scenarios for this scorpion group are discussed, including fragmentation in mountain valleys and expansion across sand deserts in Central Asia.

Poster 7 (student)

Spider women talk – Females of the cob-web spider *Steatoda grossa* adjust their web architecture and web pheromone titre in response to mate competition

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Females of cob-web spiders such as the false black widow *Steatoda grossa* can alter the architecture of their webs in relation to external cues to upturn prey-capture, safety, or mating opportunities. Here, we tested the hypothesis that female *S. grossa* respond to mate competition in that they change the architecture of their web and the amount of pheromone they deposit on it in response to the number density of webs in the microhabitat. In each of seven replicates of experiment 1, three females (low-number density) were allowed to build their webs in the same room for two days. Following a 12-day intermission, the same three females were then be allowed to build a new web for two days together with 27 other females (high-number density) present in the same room. The design of experiment 2 was similar except that females first build their webs in the high-number density setting and then in the low-number density setting. The females' web architecture in low- and high-number density settings were measured and all webs were extracted individually to quantify the amount of pheromone present. Our data support the hypothesis that females change their web architecture and the amount of pheromone they deposit on it in response to the number density of webs in the microhabitat.

Poster 30

From eggs to longlegs: Embryonic development and staging of the harvestman *Phalangium opilio*

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Opiliones, also known as "harvestmen" or "daddy longlegs", is an arachnid order with an ancient fossil record and considerable extant diversity, both in terms of number of species and overall morphology of the body and appendages. Studying morphological evolution of this group under the lens of comparative development is emerging as a promising approach, after decades of hiatus in harvestmen embryological study. The prolific and synanthropic species *P. opilio* is easily accessible in many parts of the world, as well as in a laboratory setting. Resources for this species include a developmental transcriptome and protocols for RNA interference, but the embryogenesis of this species has not been well characterised. We present a staging system of *P. opilio* embryogenesis using different morphological landmarks to delimit

key events during the development of this harvestman. Using confocal microscopy and *in situ* hybridisation, we tracked the development of a single synchronous clutch of eggs from egg laying through adulthood and described key events in neurogenesis, myogenesis and metamerisation of the body. This staging system provides a valuable reference for *P. opilio* that we anticipate will be useful to the arthropod evo-devo community, and will revitalise research in the comparative development of arachnids.

Poster 47 (student)

Investigating the poly-paraphyly of North American camel spiders (Solifugae: Eremobatidae: Therobatinae) and their unique moveable palpal spines

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The North American solifuge family Eremobatidae Kraepelin 1899, is one of the most diverse families of camel spiders, comprised of two subfamilies (Therobatinae and Eremobatinae) and 179 species. A recent molecular phylogenetic analysis of Eremobatidae unveiled the dire need for further study since many groups, including the subfamily Therobatinae, were rendered as polyphyletic and paraphyletic. The goal of this comparative study is to provide morphological characteristics that could demarcate Therobatinae and Eremobatinae by comparing moveable pedipalp spines, a unique structure yet to be documented in any other arachnid. Preliminary scanning electron microscopy (SEM) data suggests that while moveable spines are present in all eremobatid genera, the bases of the spines display variable phenotypes. Obvious external differences in ridge shape between eremobatid genera could suggest that spine performance is variable among the eremobatids. Further investigation using histological techniques to examine the muscle microstructure involved in the movement of these spines could provide crucial characters that will help test the monophyly of Therobatinae. Ultimately, information acquired from this study will be integrated with a phylogenomic framework to thoroughly investigate the monophyly of the subfamily Therobatinae and the interrelationships of the Therobatinae genera.

Poster 48

Below or above-ground? Where are the closest relatives of troglobite *Tegenaria* species?

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Caves are excellent systems to study evolution and speciation due to their isolation and unique conditions. Limitation of light may act as a filter and promote speciation. The Mediterranean genus *Tegenaria* Latreille, 1804 (Agelenidae) includes 105 species with many cave-dwellers. While European *Tegenaria* were recently revised, many Levantine and southwest Asian species remain poorly understood, particularly troglobites. Here we report several undescribed morphospecies of *Tegenaria* from Israeli caves with troglobitic characters (reduced eyes and depigmented). To address how troglobitic *Tegenaria* morphospecies are related to each other and to epigean species, we undertook a combined morphological and phylogenomic approach to resolving this species complex. Our work tests the hypothesis of single vs. multiple origins of the trolobitic morphology in the Israeli morphospecies using detailed descriptions and a RAD-Seq approach as complementary datasets. Here we show that at least two morphologically distinct troglobitic morphospecies occur in the caves, as well as two distinct non-troglobitic epigean morphospecies. We present the suggested relationships of the troglobite and non-troglobite species, and discuss the implications for understanding the main drivers of cave adaptation in habitats masked from the effects of the Quaternary glacial cycles.

Poster 11

Testing the occurrence of sexual size dimorphism in Allocosinae species from Uruguayan grasslands

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Knowledge about the systematics of the subfamily Allocosinae (Lycosidae) in South America is scarce. However, several studies in taxonomy, behaviour and ecology have been performed on two members of this subfamily, *Allocosa senex* and *A. marindia*. Both species inhabit the coasts of southern South America and show reversal in traditional sex roles and sexual size dimorphism expected in spiders. The occurrence of these non-traditional traits may be related to their strict dependence with the harsh coastal habitat. Our aim was to investigate the occurrence of sexual size dimorphismin *Allocosa* sp. from Uruguayan grasslands. We performed nocturnal samplings in two localities in Montevideo, Uruguay, and classified the individuals as morphospecies. We sequenced the mitochondrial gene *CO1* of adults of each morph and recorded body measurements of the most abundant morph (*Allocosa* sp.). We measured carapace and abdomen width of 20 adult individuals of each sex and calculated body condition through the index abdominal width/carapace width. We found three morphs of Allocosinae based in morphological characteristics, but we did not find genetic differentiation among them. We did not find significant differences in body size between males and females ($p=0.61$), but females showed higher body condition compared to males ($p=0.00003$). According to these results *Allocosa* sp. does not show the reversal in sexual size dimorphism described for the coastal species. In future studies we will increase sample size, test other molecular markers and perform mixiological sexual trials to test reproductive isolation among the three Allocosinae morphs.

Poster 29 (student)

Morphology of male abdominal ctenidia in North American camel spiders

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Solifuges, commonly referred to as camel spiders, are an enigmatic group of desert-adapted, cursorial arachnids. Notoriously hard to rear in captivity, many aspects of camel spider biology remain unknown. Ctenidia, swollen setae on the ventral side of the fourth abdominal segment, are taxonomically diagnostic yet functionally obscure. Ctenidia are sexually dimorphic characteristics, being prominent on males and highly reduced in females, yet play no obvious role in courtship or mating. They can vary in shape, size, and number across species of solifuges. The present study utilises scanning electron micrographs (SEM) and traditional light microscopy to survey the morphology of these structures. A preliminary survey of ctenidia indicates that they are structurally different from the neighbouring setae yet has thus far failed to elucidate their function. An examination of the ctenidia "stalk" as well as the basal socket at the articulation with the abdomen may further explain why these characters are so variable within Solifugae and may provide evidence for their function, and provide further taxonomically diagnostic information.

Poster 23

Is it worth having an adequate energetic state to detoxify a pesticide?

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The use of pesticides for pest control impacts on ecosystems, affecting directly or indirectly non-target organisms such as spiders. How they respond in the face of xenobiotics depends, among other factors, on their energetic state, which is a reflection of their metabolic state. In the present work we assess the energetic state of *Polybetes pythagoricus* in different metabolic situations (females before and after vitellogenesis, juvenile, and adult males), and how cypermethrin affects mortality, the enzyme activity of the antioxidant system, and lipid peroxidation. As a result, it was observed that the calories provided by both glycogen and lipids in females before and after vitellogenesis were 38.1 and 22.4 cal/gr respectively. In the case of malesand juveniles, the values were of 33.4 cal/gr and 56.1 cal/gr respectively. The triacylglyceride/free fatty acid relation determined that juveniles have higher lipid dynamics. The LD50 for females before and after vitellogenesis were 969 and 1108 ngr/gr, and was 1060 ngr/gr and 103 ngr/gr for males and juveniles respectively. In exposed adult spiders, we observed an increase of 0.8 to 5.5 times in superoxide-dismutase activity compared to control. The catalase activity of males saw no significant increase while an increase in females was observed. Lipid peroxidation showed an increase in adults of 0.5 times. Although juveniles had a high caloric content, no increase was observed in superoxide-dismutase activity and catalase, coinciding with the high increment observed in the lipid peroxidation (14 times) produced by the reactive oxygen species.

Poster 32

Silver, gold and copper staining: Histochemical applications for arachnid neural tissue

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Fluorophore staining, coupled with various reflected light imaging technologies, has become a popular way of examining invertebrate neural tissue structures. However, classical metal based histochemical staining remains a powerful, high-resolution option and provides a level of morphological fidelity and permanence not offered with fluorescence methods. This poster will explore a variety of metal histochemical staining techniques useful for arachnid neural tissue morphology and spatial localization of neuronal proteins.

Poster 36 (student)

Species delimitation of New Zealand Neopilionidae (Opiliones) based on COI sequence data

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The harvestmen of the family Neopilionidae are distributed across temperate Gondwana, in Chile, Argentina, southern Brazil, South Africa, Australia and New Zealand. In New Zealand neoplionids are represented by 27 described species in seven genera. We have assembled an extensive dataset of cytochrome *c* oxidase subunit I (COI) sequence data of New Zealand neopilionids to assess species limits in the group. We present the results of a species delimitation analysis using multi-rate Poison tree processes (mPTP) under maximum likelihood. The resulting molecular species delimitation will then be contrasted with our current understanding of species based on anatomical and biogeographic data.

Poster 45 (student)

Taxonomic revision of the Australian crab spider genus *Stephanopis* O. Pickard-Cambridge, 1869 (Araneae: Thomisidae)

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The subfamily Stephanopinae has been the focus of many revisional works during the last decade, however, most of its component genera are still little known and poorly diagnosed, which in part justifies the lack of resolution and constant recovering of its relationships as polyphyletic. In spite of these recent efforts to better describe the morphology and understand the phylogenetic relationships in this subfamily, its type genus remains in need of a taxonomic

review. Here we present a revision of the Australian species of *Stephanopis*, where the type species *S. altifrons* is redescribed and *S. aspera*, *S. depressa*, *S. monticola*, *S. elongata* and *S. scabra* are considered its junior synonyms. The males of *S. altifrons*, *S. nigra* and *S. armata* are described for the first time and neotypes for *S. ornata* and *S. vilosa* are proposed (both species are redescribed based on males and females); *S. minuta* is considered senior synonym of *S. barbipes*; six new species are described and new distribution records are provided. We also briefly discuss the relationship of the genus with *Sidymella* species from the Australian region.

Poster 46 (student)

Shaking the tree of the bark crab spiders: Phylogeny of the Neotropical *Stephanopis* species reveals a new genus and revalidates *Paratobias* (Araneae: Thomisidae)

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The present study is aimed at the cladistic analysis and taxonomic review of the Neotropical species of *Stephanopis* and also provides discussions on its relationships with other close related genera. Our results were based on parsimony analyses of a matrix with 42 terminal taxa scored for 97 morphological characters that suggested *Stephanopis* as polyphyletic, with its component species emerging in four different clades. Based on the strong branch support and strong morphological evidence we propose that five species previously assigned as "Neotropical *Stephanopis*" (*S. macrostyla*, *S. parahybana*, *S. pentacantha*, *S. reniformis* and *S. quinquetuberculata*) and four new species to be described form a new genus. New distribution records are provided and the male of *S. parahybana* is presented for the first time. We discuss the historical taxonomic background of some genera related to *Stephanopis.* We propose the revalidation of the genus *Paratobias* and describe a new species. We transfer *Stephanopis furcillata* to *Sidymella*, propose *Stephanopis borgmeyeri* as *nomen dubium*, transfer the female of *S. stelloides* to *Epicadus*, and consider this species as senior synonym of *S. trilobata* and *E. caudatus*.

Poster 21

CEBRA – Optimised and standardised sampling protocols for citizen science

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Despite the many potential uses of citizen science activities (e.g. BioBlitzes) in conservation and ecology, most are usually limited by the lack of: 1) comparability of samples due to variability in the sampling effort (number of participants, sampling time, etc.); 2) quantitative data (relative species abundance); and 3) information on the efficiency of the sampling. Here we will present our project, which is addressing these three limitations by developing widely applicable, standardised and optimised sampling protocols termed CEBRA (Citizen-led Educational Biodiversity Rapid Assessment). Based on the COBRA protocols (Conservation Oriented Biodiversity Rapid Assessment), the CEBRA protocols will increase the value of the generated data and facilitate their analyses thereby encouraging more scientists – many of which are reluctant to participate – to contribute to the collection and identification of the samples. The use of CEBRA will enrich civic-scientific activities, not only by overcoming their current limitations, but also by contributing to the *scientific literacy* of citizens. Furthermore, by increasing comparability of data from different locations and years and the participation of increasingly expanding network of participating organisations, CEBRA will turn citizen science events into tools for monitoring biodiversity and not only for measuring it. Attendees of the ICA congress will have the opportunity to learn about the CEBRA project and consider their involvement in it during the BioBlitz/EcoBlitz that we will hold in the area of Lincoln at the weekend after the congress.

Poster 4

Hunger influences behaviour but not outcome in male-male contests of *Servaea incana* jumping spiders

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Animal contests can entail sophisticated decision-making to balance investment, risk, and returns, drawing on information both from fixed properties of each rival and from variable properties of rivals and contexts. Body size is the most often studied fixed property of individuals, and is often a strong predictor of contest outcome. Here we examine the effects of size together with a variable property, hunger, on outcome and behaviour during male-male contests of *Servaea incana* jumping spiders. Hunger may impair fighting ability through energetic constraints, but hungry spiders may also be more inclined to fight because rivals are

also prospective meals. We investigated the contest behaviour of spiders that had either been fed within the previous two days or deprived of food for seven days. Contests were staged between spiders that were (1) matched for both size and hunger state, (2) matched for size but not matched for hunger state, and (3) not matched for either size or hunger. Size was a strong predictor of contest outcome but hunger was not. However, both size and hunger influenced behaviour of spiders in contests, including tendency to engage in interactions and duration of contests. Contests between male jumping spiders are usually characterised as highly ritualised processes, but the tendency to study only well-fed spiders and to reduce variation from other factors in laboratory studies may have led to underestimation of variation in context dynamics and complexity of factors contributing to decisions.

Poster 42

Under the trapdoor: Unravelling the phylogenetic relationships and phylogeography of cork-lid trapdoor spiders, *Stasimopus* Simon, 1892 (Araneae, Mygalomorphae, Ctenizidae) in the Karoo

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The Karoo BioGaps collaborative project was established to assemble baseline biodiversity data on various taxa in the Karoo region of South Africa, in order to support decision making regarding land-use change. This is vital in light of the land transformation occurring in the Karoo for farming, mining, the square kilometre array (SKA) and shale gas exploration. Spiders (order Araneae) are one of the focal taxa for the project. Trapdoor spiders are long-lived and sensitive to habitat destruction making them a valuable conservation tool. The aim of this study is to perform an assessment of the phylogeographic relationships oork-lid trapdoor spiders (Ctenizidae: *Stasimopus* Simon, 1892) in the Karoo BioGaps study area. A total of 118 individuals were collected from 60 surveyed sites in 2017 and 2018 for the analysis. Phylogeographic insights were drawn from the 16S, CO1 and EF1g nucleotide sequences and suggest substantial undescribed diversity. The pattern of an east-west divide observed in other arachnids is newly recorded for these spiders. There were between 9 and 12 species found in the sampled region. According to current literature only between 5 and 7 are known for the region, indicating either new locality data for already described species or novel undescribed species. Most of the potential species found are short-range endemics which makes them vulnerable to change. The conservation status of *Stasimopus* should be reconsidered as well as their inclusion in environmental impact assessments.

Poster 19 (student)

Thermal preferences in seven species of Theraphosidae (Mygalomorphae): ecological implications

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Tarantulas are sedentary, spending the major portion of their lives inside their burrows. However, adult males will ultimately start an errant life searching for females to copulate with. As spiders are ectotherms, this errant life makes them sensitive to climatic conditions. We hypothesised a correlation between several parameters and preferred body temperature (Tpref) within the environmental temperature during the mating season. We collected a total of 84 individuals of *Grammostola quirogai, G. anthracina, Plesiopelma longisternale, Hommoeoma uruguayense, Eupalaestrus weijenberghi, E. campestratus and Acanthoscurria suina.* Weestimated Tpref in a thermal gradient (from 10 to 50ºC), holding individuals for 2 hours before measuring body temperature. We analyzed how Tpref varies between sexes, body mass (mb) and time of day. Subsequently we tested mixed models including sex, mb and time as predictor variables, using AIC for model selection. We also analysed the correlated evolution between Tpref, mb and environmental temperature (i.e. mean, minimal and maximal temperature) using phylogenetically independent contrasts (PIC). The best fit for Tpref in for most of species did not include time, sex or mb as predictor variables. However, the best fit *in A. suina* included time. Moreover, we found a positive correlation of PICs between Tpref and Tmin (r=0.748).

Poster 41

The spider fauna of Myanmar (Arachnida, Araneae), a prologue

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Since the first report of the spiders from Myanmar made by Thomas Workman with the article titled "Description of two new species of spiders" published in the *Annals and Magazine of Natural History*, fifth series, Vol. 2, pp. 451-453, 1878, in which several species of Pholcidae and Theridiidae were recorded from Rangoon (Yangon), hundreds of spider species have been recorded from this country, including those described in the major works published by Tamerlan Thorell (1887, 1895, 1897 and 1898). However, little research on spiders was done in the 20th century because of changing and unstable national circumstances. Since the start of the 21st century, we conducted spider expeditions in Myanmar under the joint research project between the National Museum of Nature and Science, Japan, and the Forest Research Institute in the Forest Department of the Ministry of Natural Resources and Environmental Conservation, Myanmar, particularly in Tanintharyi Region (January, 2017), in the Myeik Archipelago (May-June, 2017), in Chin State (November-December, 2017) and in Bago, Kayin, Kaya and Shan States (August, 2018). Although accurate identification of the specimens collected is still proceeding, some notes on taxonomy and zoogeography obtained so far are

reported. A list of known species of spiders from Myanmar is made as a useful step to the elucidation of the spider fauna of this country.

Poster 26

Complementary of trait- vs diversity-based metrics in spider and carabid assemblages

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Many metrics have been developed to monitor species assemblages of arthropods in applied conservation projects. Recent works highlighted the importance of trait-based indices, e.g. based on phylogeny, relative rarity, ecological specialisation and or functional diversity, as they bring complementary information compared to 'traditional', taxonomy-based only, metrics (e.g. Devictor *et al*. 2010). These different metrics have been critically assessed independently, but are rarely combined in the examination of applied conservation problems, especially for highly diversified taxa such as ground-dwelling predatory arthropods. In this study, by using both a bibliographical survey and case studies (Pétillon et al. 2007; Leroy et al. 2014), we assessed how complementary assemblage-based metrics are depending on (i) the trait on which they are based, (ii) the habitat where they are computed (according to management and disturbances regimes) and (iii) the taxa studied (spiders vs. Coleoptera Carabidae).

Poster 40 (student)

New insights into the systematics of the "*Arctosa villica* group", including observations on the halophilic species *A. fulvolineata*

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Arctosa is a large genus of Lycosidae, currently comprising around 170 described species worldwide (World Spider Catalog 2018). If some species are well known, others are taxonomically unclear even in Europe (see Breitling et al. 2016). Among them, *Arctosa villica* (Lucas, 1846) and its several closely related species were taxonomically confused for a long time (e.g. Murphy and Toggiorgy 1979). Both a detailed examination of collections from the National Museum of Paris and a first molecular-based phylogeny were performed here. A special attention was paid to a Southern halophilic species, *Arctosa fulvolineata*, also described by Lucas (1846) from Algeria, but only found in coastal habitats although with several unclear records (e.g. Bosmans & Van Keer 2012).

Poster 5

Reeling in the prey: Fishing behaviour in an orb web spider

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When an insect is intercepted by a spider web, most spiders quickly locate the prey, and run towards it. Once they make contact with the prey, they immobilise the prey and relocate it to the centre of the web or the retreat for consumption. However, in rare circumstances, the spider can also pull the prey towards itself, either while running to the prey, or from a stationary position, a behaviour termed as 'reeling'. Reeling is paradoxical since it can lead to web deformation or damage, thereby jeopardising future foraging success. Reeling may lead to increased retention time for heavier prey or for information acquisition with respect to the prey's identity, especially when these prey can cause damage to either the web or the spider itself. We explored the function of reeling behaviour in a neotropical orb web spider *Verrucosa arenata*. We show that spiders performed reeling behaviour irrespective whether they were approaching heavy or light prey, but they changed their trajectories of approach. Spiders approached heavier prey more slowly than light prey and they showed significantly higher frequencies of changes in velocities. We discuss these findings in the context of prey capture strategies and prey recognition.

Poster 22

Neonicotinoid insecticides suppress the ability of spiders to re-colonise disturbed agroecosystems

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Agroecosystems are characterised by regular disturbances that cause extinction or migration of much of their fauna. Therefore, these ecosystems must be repeatedly recolonised from surrounding refuges. In spiders, such recolonization is potentiated by their ability to rappel and balloon. These are complex behaviours that we hypothesised to be affected by neurotoxins, namely, neonicotinoids. We tested this hypothesis using two model species of common farmland spiders, *Oedothorax apicatus* (Linyphiidae) and *Phylloneta impressa* (Theridiidae). The spiders were subjected to two modes of contact exposure to formulations of neonicotinoids that are widely used in agriculture, namely, Actara 25 WG, Biscaya 240 OD, Mospilan 20 SP and Confidor 200 OD, at concentrations that are recommended for application in agriculture. We then recorded the effects on ballooning and rappelling behaviours at 1 h and 24 h following the treatment with neonicotinoids. We found that contact exposure to neonicotinoids suppressed the ability of spiders to produce the major ampullate fibre and anchor it to the substratum by piriform fibrils. Contact exposure to neonicotinoids also suppressed the ballooning behaviour that is manifested by climbing to elevated places, adopting a tiptoe position and producing silk gossamer in the wind. We found that all four tested neonicotinoids, including those with previously claimed negligible effects on spiders, severely inhibited both

ballooning and rappelling behaviours of spiders when applied at concentrations recommended by the manufacturers for use in agriculture. Impaired ability of affected common farmland spiders to quickly recolonise disturbed agroecosystems after their regular disturbances may explain their decline in multiple farmland ecosystems, in which neonicotinoids are applied.

Poster 43

A key to the genera of Australian jumping spiders (Araneae: Salticidae)

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Jumping spiders are a diverse component of the Australian fauna, with over 90 genera and 400 species described and probably more than 120 genera and 1000 species present. The family is found in all terrestrial and arboreal habitats throughout Australia and its territories, except the sub-Antarctic islands. The fauna is highly endemic, especially in central and western parts of the continent. This LUCID-based key is intended to meet the needs of naturalists, biologists and taxonomists who wish to identify Australian jumping spiders. The character set has high redundancy (98 characters, 294 character states) allowing users to begin with whatever observable characters are available to them when using photographs, a high-powered hand lens or a microscope. An information sheet attached to each genus provides a list of known species and information on evolutionary relationships, distribution, habits, a simplified diagnosis, and some key references. A series of diagrams and photographs (of living specimens and of aspects of the morphology, including palps and epigynes) are provided for each genus.

Poster 44

First systematic revision of the subfamily Anaminae (Mygalomorphae: Nemesiidae) in South Africa

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The mygalomorph spiders of South Africa are poorly documented. Past studies have been restricted to the large-bodied tarantulas (Theraphosidae), while the other mygalomorph families have been neglected. The Nemesiidae of South America comprises 86 species in 15 genera, and 110 species in 15 genera are known from Australia. By comparison, the South African fauna is currently represented by only 51 species in five genera belonging to two subfamilies: Anaminae, with three genera (*Entypesa* Simon, 1902; *Hermacha* Simon, 1889, *Lepthercus* Purcell, 1902) and Bemmerinae, with two genera (*Pionothele* Purcell, 1902 and *Spiroctenus* Simon, 1889). *Hermacha* and *Spiroctenus* are the most speciose genera, with 16 and 30 species respectively. The other genera are represented by only a few species in the region (*Entypesa,* with one species, while *Lepthercus* and *Pionothele* each have two species). No taxonomic revisionary work has been done on these genera since they were first described. Our study is the first to treat the South African Nemesiidae as a whole. In the light of current knowledge, around 836 members of the subfamily Anaminae were reviewed and analysed. This

extensive work has increased our knowledge of the African nemesiids, with the discovery of three new species of *Entypesa*, four of *Lepthercus* and two of *Hermacha*, as well as new genus. Our revision contributes relevant characters that will aid differentiation of the genera of this subfamily, and will lead to an improved understanding of the relationships between these cryptic organisms.

Poster 9 (student)

Colour fidelity in prey selection by an araneophagic wasp

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Spider predators, such as birds, lizards, other spiders and wasps, are generally visually oriented. Among them, the mud dauber wasps are thought to hunt spiders primarily using their vision, with chemical information playing an important role in the early stages in the detection-attack sequence. Wasps locate their prey in the sequence's final stage using visual searching. In order to evaluate the prey colour selection and fidelity in the wasp *Trypoxylon mexicanum*, we carried out a survey in an urban area in Xalapa (Mexico). We collected the spiders parasitised in the nests and quantified their body colouration by means of multi-spectral digital images. We then used visual modelling to simulate how they are likely to be perceived according to the visual system of the wasp. We found that orb-web spiders were the dominant prey guild. The body colour properties (brightness, saturation, and hue) were similar in the spiders captured during the nest construction process. Our results suggest that the wasps maintain colour fidelity across time irrespective of spider species. We discuss these findings in the context of predator prey interactions and visual ecology.

Poster 35

Neglected no longer: Phylotranscriptomics and molecular modeling reveals venom homologs in Pseudoscorpiones and Palpigradi

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Venom represents a key evolutionary innovation that has repeatedly evolved in metazoans. Transcriptomic and genomic analyses have illuminated the diversity of venom components in four arachnid orders which harbour venomous species (pseudoscorpions, scorpions, spiders and ticks). However, their phylogenetic relationships remain uncertain. In this study, we surveyed recently generated transcriptomes (including the first palpigrade transcriptome) for several venom peptide components known from spiders, scorpions and ticks. We generated gene trees to test their orthology and 3D models generated using known peptide structures of venom components in spiders. In addition, the phylogenetic placement of Palpigradi was assessed using a dense phylogenomic matrix. Taken together with the phylogenomic placement of these orders in the chelicerate tree of life, our results suggest that venoms may have evolved deeper in the phylogeny of arachnids than previously inferred.

Poster 37

Benzoquinones in eupnoan scent glands (Opiliones): homology vs. homoplasy in an exocrine system

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Benzoquinones are widespread constituents of arthropod defensive secretions, having independently evolved multiple times such as in beetles, dermapterans, millipedes, but also in opilionids. Particularly in the latter group, benzoquinones are characteristic of the secretions of the Laniatores but were not known from the secretions of other harvestmen suborders. Recently, however, 1,4-benzoquinone was detected in the secretions of Eupnoi of several taxa belonging to Phalangiidae (*Rilaena*, *Megabunus*, *Platybunus*), Sclerosomatidae (*Gyas*) and *Amilenus* (taxa *incertae sedis*). While there are strong arguments for the rise of eupnoan benzoquinones independently of those of laniatoreans, an evolutionary explanation for the scattered occurrence of benzoquinones across eupnoans is still missing. Using a selection of eupnoan taxa, we performed genetic analyses based on nuclear and mitochondrial genes. We show by ancestral character state reconstruction that *i)* the mosaic-like distribution of benzoquinones across Eupnoi is an artifact of misplacement of several taxa in traditional systems, and *ii)* all benzoquinone-producing taxa are found exclusively in the Phalangiidae, most likely indicating a single evolutionary origin of these compounds in eupnoan harvestmen.

Poster 8 (student)

This smells... familiar? Learning of chemical cues in two sympatric species of amblypygid

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Amblypygids possess one of the largest mushroom bodies (a higher order central nervous system processing centre) known among arthropods. In insects, mushroom bodies are involved in olfactory processing, as well as in learning abilities. In amblypygids, we hypothesise that these processing centres are similarly involved in processing olfactory stimuli as well as in facilitating navigation. Field evidence suggests that amblypygids rely on olfactory cues to solve the navigational challenge of returning to a home refuge in their complex and ever-changing neotropical forest understory habitat. In the present study, we directly test the ability of amblypygids to learn chemical odours associated with refuges. Using a design in which we repeatedly paired an open refuge with the presence or absence of a distinct chemical stimulus, we ran amblypygids through a series of training trials and ultimately a test trial. Using slight

modifications of this experimental design, we tested two sympatric species - *Paraphrynus laevifrons* and *Phrynus pseudoparvulus*. Our analyses, which are currently underway, will explore changes in the time it took amblypygids to enter refuges over the training trials, as well as potential differences in the time amblypygids spent associated with the appropriate stimulus in the test trial. We will compare and contrast our results with respect to each species' learning ability and will discuss any species-specific responses to different chemical stimuli.

Poster 34

Differential gene expression approaches elucidate systemic effects of Wnt signaling inhibition during segmentation in the spider *Parasteatoda tepidariorum*

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Segmentation is a key characteristic of the phylum Arthropoda that is linked to the evolutionary success of this lineage. The formation of segments, both along the antero-posterior axis of the body and along the proximo-distal appendage axis, requires the activity of the Wnt family of secreted proteins, as inferred from functional data in insect model organisms, but comparable data are limited in Chelicerata. Here we examined the inhibition of canonical Wnt signalling in the cobweb spider *Parasteatoda tepidariorum* using parental RNA interference (pRNAi) against the Wnt-1 co-receptor *arrow* (*arr*; vertebrate homolog: *LRP5* and *LRP6*), which is known to be a key member of the canonical Wnt-signalling pathway in holometabolous insects and vertebrates. Toward a more refined characterization of the ensuing phenotype, we sequenced the transcriptomes of embryos displaying loss-of-function phenotypes and mapped reads to the recently sequenced genome of *P. tepidariorum*. Here we show that knockdown of *Ptep-arr* resulted in systemic reduction almost all Wnt expression, as well as disrupting various segmentation genes (e.g., *Notch* and *Delta*), hindgut markers, and posterior Hox genes. Intriguingly, however, differential gene expression analysis and *in situ* hybridisation revealed that Ptep-*arr* loss-of-function phenotypes undergo overexpression of the canonical Wnt gene *Wnt8* and its target *caudal* (*cad*), resulting in presumptively ectopic posterior fate. These data elucidate a complex role for canonical Wnt signalling in regulating the anterior segment addition zone via *Notch-Delta* signalling and modulation of the *cad*/*Wnt8* circuit. More broadly, this work underscores the diagnostic power of differential gene expression tools in categorizing catastrophic phenotypes.

Poster 28 (student)

Embryogenesis in a Colorado population of *Aphonopelma hentzi*, (Girard, 1852) (Araneae, Mygalomorphae, Theraphosidae), an emerging system for the study of spider development

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The mygalomorph spider *Aphonopelmahentzi* (Texas brown tarantula) is a geographically widespread andpotentiallyaccessible system for the study of comparative development in

spiders. However, remarkably little information is available regarding the timing of cocoon deposition and duration of embryogenesis in this species, a gap that can directly affect the success of field collecting efforts. Here we describe the habitat, collection methods for cocoons, and development of embryos of *A. hentzi* found in the Comanche National Grasslands of Colorado. To demonstrate the tractability of this system, we show the outcomes of our protocols for fixation, *in situ* hybridization, immunohistochemistry, and histology of lab-reared embryos. Finally, we place the development of mygalomorph spiders into a broader phylogenetic context by comparing development of the embryo's posterior region to other, non-spider arachnid lineages.

Poster 6

Female genital mutilation in *Cyclosa confusa*

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Cyclosa confusa weaves orb webs with debris decoration. As in *C. argenteoalba*, female genitalia were damaged through copulation (i.e., scapes were mutilated), but the rate and the function of female genital mutilation are unclear in *C. confusa*. The mating behaviour in *C. confusa* typically proceeded as follows: males vibrated silk, females spread their anterior legs in front of males, males tapped female legs and hugged females to copulate, females turned towards web centre, and males moved away from females. Virgin females lost their scapes in 49 % of mating. The females without scapes were also courted by males that tried copulation, but seemed to fail. The number of genital contacts in a mating pair varied from one to seven, but scapes were lost in pairs of one and two contacts. The females with scapes after copulation tended to sustain them in following copulations. Comparing the durations of each behaviour revealed that longer tapping by male was correlated with scape mutilation, but body size of each sex was not related with durations of each stage or to mutilation.

Poster 38

Phylogeography of the Atlantic Forest amblypygids

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The Brazilian Atlantic Forest (AF) is one of the world's 25 recognised biodiversity hotspots, with one of the greatest diversities in the world and one of the highest threatened environments on the planet. Only 70% of the original vegetation cover survives, but traces of the origin of the biodiversity are still present in the remaining forests. The best way to uncover the diversification history of the AF is through understanding the phylogeography of its plant and animal species, i.e. study the spatial arrangements of genetic lineages. With this in mind, we used ultraconserved elements (UCEs) to calculate a range of population genetic summary statistics from single nucleotide polymorphisms (SNPs) in the genome of whip spiders of the genus *Charinus*. For that, we collected fresh material from more than 20 points in the AF, from the northernmost to the central region of the forest, sequenced hundreds of UCEs, and analysed the population genetics of the species sampled. With this fine-scale approach to forest diversity, we are seeking understand past effects of tectonic events and climatic changes on the forest's *Charinus* fauna, and predict the effects of future climate changes in this hyper-diverse forest. This is one of the first phylogeographies of the AF using an invertebrate as a model. This research is an important step towards understanding South American biodiversity and preliminary results will be presented and discussed.

Poster 16 (student)

Chronoecology of the cave dwelling orb-weaver spider, *Meta ovalis*

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Circadian clocks are endogenous time-keeping mechanisms that are ubiquitous among animals. They enable coordination of many essential biological and metabolic processes in relation to the 24-hour light cycle on earth. However, there are many habitats on earth that are not subject to this light cycle. This study aims to look at the circadian rhythmicity of a subterranean spider, *Meta ovalis*, as well as gathering general natural history information on this under-studied spider. We are integrating circadian and foraging theory to evaluate species as circadian specialists and generalists based on how narrowly or widely their activity is spread over the 24 h cycle. We suggest that *M. Ovalis* benefits from a generalist strategy, showing small bursts of focused activity widely dispersed across the 24 h cycle, allowing it to capture prey opportunistically whenever it is available.

Poster 31 (student)

Lifestyle matters: Brain morphology in cursorial and stationary hunting spiders

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The structure of brain areas that process sensory information reflects the specific lifestyle of an animal. Spiders (Araneae) include stationary species that build webs and cursorial species that do not build webs for prey capture. This diversity in lifestyles is associated with major differences in sensory equipment. We investigated the brain morphology of four spider species, using microCT analysis and immunohistology: Two cursorial hunters *Marpissa muscosa* (Salticidae) and *Pardosa amentata* (Lycosidae) that strongly rely on visual cues, and two stationary, web building hunters *Argiope bruennichi* (Araneidae) and *Parasteatoda tepidariorum* (Theridiidae) that detect prey by vibrational cues. We predicted that the differences in primary sensory input between the different species are mirrored by differences in those brain areas that process the incoming information. We show that the brains of the investigated species differ in number, arrangement and structure of neuropils. These differences are especially pronounced in the secondary eye pathway of the brain, and pertain to first order, second order and higher order brain centres. Our results demonstrate that spider brain morphology is highly diverse, and that depending on the sensory specializations of the respective species, profound differences in brain morphology exist.

Poster 33

Chromosomal hybrid zone showing heterzygote superiority in *Gagrellula ferruginea* (Opiliones)

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Gagrellula ferruginea (Loman, 1902) (Opiliones: Sclerosomatidae) is a polytypic species that comprises more than 10 geographic races with extremely different coloration in Japan. This species also shows enormous geographic variation in chromosome number with a range from 2n= 10 to 24, forming a hybrid zone, in general, at each boundary where two neighboring populations with different chromosome numbers meet. Chromosome number of the Daisen race, which is one of the geographic races of the species occurring in the Chugoku District of Honshu, changes from 2n= 12 to 14 o across the Hino River near Mt. Daisen (Tottori Prefecture) moving from west to east. Recently, we found a chromosomal hybrid zone (2n=12/13/14) ca. 3 km wide, at the left bank of the river. We performed a Hardy-Weinberg equilibrium test for a population in the hybrid zone and found that frequency of the hetrozygotes with 2n = 13 was significantly higher than the expected ratio, and contrary to this, frequencies of both homozygotes (2n=12, 14) were lower than those expected. Heterozygote superiority like this is extremely unusual in chromosomal hybrid zones, where deficiency of the heterozygote karyotype is the norm probably due to chromosomal non-disjunction which is inevitably expected at meiotic divisions in heterozygotes. Karyotypic analysis and geographic pattern of distribution of the karyotypes suggest that the chromosome number changed from 2n = 14 to 12, and the 2n=12 karyotype resulted from tandem fusion of two pairs of small non-sister chromosomes of the 2n=14 karyotype.

Poster 27

Morphology, CO1, and ITS2 provide different specimen clusters in a widespread crab spider

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Recent CO1 barcoding of 75 specimens of the widespread crab spider *Synema globosum* (Fabricius, 1775) from 10 populations from all over Europe resulted in three well-separated CO1 clades (Lasut, unpubl.). Here, we investigated genital morphology and a nuclear marker of *S. globosum*. ITS2 and the morphology of the copulatory organs of both sexes also provide defined clusters of individuals. However, the different datasets show no or only weak congruence. We conclude that *S. globosum* is a genetically and morphologically variable species and suggest caution before delimiting taxa, especially “cryptic species”, based on a single dataset.

Poster 15

New Zealand pirates: Evolutionary origins and diversity of Zealandia's mimetid spider revealed through morphology and molecular data

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The evolutionary origins and phylogenetic affinities of Zealandia's (New Zealand & New Caledonia) biota are the subject of ongoing debate. Many studies have suggested that most of Zealandia's fauna results from recolonisation events since a major drowning episode that occurred in the Oligocene, but few data are presently available to evaluate both mode and direction of such dispersal events. Here, we investigated the evolutionary origins of Zealandia's fauna of pirate spiders through a combination of molecular phylogenetic analyses (3 genes: COI, H3 and 28S), spinneret morphology, and taxonomy. We find that New Zealand's fauna of pirate spiders is polyphyletic and represents three independent colonisation events of a single genus (*Australomimetus*) from mainland Australia whilst the fauna of New Caledonia comprises a single species, which is unrelated to the New Zealand fauna. There is evidence for *in-situ* speciation in one of the New Zealand clades, and of the 8 species found here, only two are shared with Australia. We further discuss an "out-of-Australia" biogeographical model for *Australomimetus* by which this genus evolved in Australia and dispersed northwards into Southeast Asia and further east to several Pacific islands. We document the fauna of Zealandia at the species level through taxonomy and detailed morphological investigations of the spinneret structures. We further document biogeographical patterns of this genus in Australia, such as major divergences in the fauna between eastern and western Australia, and investigate possible causes.

Poster 14

Formation of rivers and mountains drive diversification of primitively segmented spiders in continental East Asia

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Complex topography in continental East Asia mirrors geological events such as formation of rivers and mountains, but to what extent these events drive diversification remains underexplored. Using the primitively segmented spider genera *Sinothela* and *Ganthela*, we address this question by employing a three-way test of six vicariant hypotheses derived from river and mountain formation: 1) phylogenetically, we evaluate the sister group relationships of lineages on either side of each barrier; 2) chronologically, we estimate the timing of splits in a time calibrated phylogenetic framework; 3) biogeographically, we infer whether each of these splits shows a reduction in ancestral areas. Three-way tests fully support five barrier

formation events: 1) the Oligocene-Miocene origin of *Sinothela* + *Ganthela* coincides with the 23–36.5 Ma range of the Yangtze River formation; 2) the *Sinothela* split into lineages on each side of the Qinling-Dabie mountains overlaps with the estimated uplift; 3) the origin of lineages on each side of Taihang Mts fits its hypothesised uplift; 4) the origin of lineages on each side of mid-lower Yellow River supports the timing of its formation; 5) lineages on each side of the Yellow River eastern Ordos bend coincide with its origin. However, the Taishan Mts uplift as barrier formation is only partially supported. Our results suggest vicariant origins of *Sinothela* and provide evidence for continental wide vicariant events that have shaped these spiders' evolutionary history in continental East Asia. Primitively segmented spiders thus provide an excellent model for exploring how geological events shape biodiversity.

Poster 3 (student)

Can I borrow a "light"? Does firefly bioluminescence act as a visual lure on *Psechrus clavis* webs?

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Some predators living in low-light conditions, such as larva of glowworms and fireflies, use bioluminescent cues, a type of visual cue, to lure prey. Web-spinning spiders have been known to use web decorations (e.g., stabilimentum, dead insects) to attract prey into their webs. Observations have shown that some web-spinning spiders prefer to build webs near luminous organisms (e.g. glowworms and fungi), as well as retaining firefly prey to lure other individuals. This suggests that spiders may use bioluminescent organisms to lure prey into their webs. The two main objectives of this study were: (1) to determine if *Psechrus clavis* are able to sense luminescent cues of fireflies and if the spider then retains the prey in their webs in a way that they continue producing bioluminescent cues; (2) determine if the presence of bioluminescent cues from fireflies retained in the web result in an increase in prey capture rates. It was found that firefly prey retained in the webs of *P. clavis* produced bioluminescent cues for up to more than one hour after being captured and there was an increase in the predation rate in webs with retained prey. The majority of prey captured were male fireflies of the species *Diaphenes lampyroides* and therefore the use of luminescent cues by *P. clavis* may be species specific. This study provides evidence for a novel use of bioluminescent cues as web-decorations in order to increase predation rates, which represents a new form of visual lure-based cues by web-spinning spiders.

Poster 2

Predator avoidance: bird dropping masquerading in a crab spider

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Prior theoretical and empirical studies have primarily focused on the function of adaptive coloration such as crypsis, aposematism and mimicry, but masquerade remains largely unexplored. Bird dropping masquerade is well known in many animals, including spiders. *Phrynarachne* is a genus of sit-and-wait crab spiders whose shape, size and colour bear striking resemblance to bird droppings, and is often cited as a textbook example of bird dropping masquerade. However, this notion has yet tested empirically. Here we provided the first evidence that bird-dropping crab spiders benefit from masquerade. We used domestic chicks (*Gallus gallus domesticus*) as predators, and bird-dropping (*Phrynarachne ceylonica*) and ordinary, non-bird dropping (*Ebrechtella tricuspidata*) crab spiders as prey. By manipulating predators' prior experience of bird droppings and testing them with *P. ceylonica* and *E. tricuspidata.* We showed that chicks' prior experience had no significant effects on their latency to make the first peck and number of pecks. However, chicks routinely preyed on ordinary crab spiders, but avoided *P. ceylonica* when spiders were presented alone or together with bird droppings. We therefore concluded that *P. ceylonica* functions to avoid predation by being misidentified as bird droppings by their predators, and predators have an innate aversion to attacking bird droppings.

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