

THE 4TH CONFERENCE OF ASIAN SOCIETY OF ARACHNOLOGY
&
THE 15TH MEETING OF ARACHNOLOGICAL SOCIETY OF CHINA

www.spidersofchina.com/www.asianarachnology.com

PROGRAM & ABSTRACTS

Chongqing China 中国・重庆
October 9-13，2017

SOUTHWEST UNIVERSITY

中国动物学会蛛形学专业委员会
ARACHNOLOGICAL SOCIETY OF CHINA

蛛形学报
ACTA ARACHNOLOGICA SINICA

重庆动物学会
Chongqing Zoological Society

CONTENTS

INVITATION

Welcome to the ASA Conference 2017 & ASC Meeting 2017

It is our great honour and pleasure to invite you to the Fourth Conference of Asian Society of Arachnology (ASA) (www.spidersofchina.com/hy/index.asp, or www.asianarachnology.com/conference2017/) and the Fifteenth Meeting of Arachnological Society of China (ASC). The ASA, found in 2012, is the regional scientific society of Arachnology of Asia and provides the primary forum for arachnologists by hosting annual conferences. The fourth conference of ASA is the first ASA meeting held in China, is also the first international meeting of Arachnology in China. The ASC, found in 1986, is a society for Chinese arachnologists to accelerate the development of Chinese Arachnology.

Arachnology is a traditional, but very active field that seeks to understand the diversity, systematics, evolutionary biology, behaviour, ecology, biogeography, physiology, developmental biology, molecular biology, conservation biology, etc. of spiders and other arachnids. In this conference, three symposia will be included: 1) Phylogeny, Genomics and Evolution; 2) Diversity and Systematics; 3) Behavior and Ecology.

Widely acknowledged as the largest industrial and economic center in southwestern China, **Chongqing** is a popular travel destination for its hilly slopes, rivers, night views and spicy foods. In 1997, it was set as the 4th municipality directly under the China central government. Now Chongqing is the youngest, but the largest city in terms of area (about 82.4 thousand km^2) and population (more than 33.7 million). Three famous “business cards” of Chongqing are thought as “delicious foods”, “splendid scenery” and “beautiful girls”.

This conference will be hosted by the **Southwest University** (SWU, www.swu.edu.cn). SWU was founded in July 2005, by the merger of two old Universities with more than 110 years’ history. Now SWU is a comprehensive and national key university sponsored by the Ministry of Education of China, with garden-like campus, about 3000 teachers and 50,000 full-time students.

We believe that the joint meeting of ASA and ASC 2017 will provide a platform to communicate new findings and technologies and the future development of Arachnology.

张志升	刘杰
Zhi-Sheng Zhang	Jie Liu
Professor of Zoology	Secretary of ASC
School of Life Sciences,	Professor of Zoology
Southwest University	College of Life Sciences, Hubei University

On behalf of the Organizing Committee

ORGANISERS AND COMMITTEES

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Yuri M. Marusik, Institute for Biological Problems of the North, Russia

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Jing-Xia Zhao, Southwest University, Chongqing, China

Jing-Yi Chen, Southwest University, Chongqing, China

Jia-Chun Jiang, Southwest University, Chongqing, China

CONFERENCE INFORMATION

1. Conference Venue

Guiyuan Hotel of Southwest University
Address: Near Gate 5 of SWU, No. 2, Tiansheng Road, Beibei District, Chongqing, 400715, China.
Tel:+86-023-68293000

2. Registration on spot

Time: 9:00 ~ 19:00, October 9, 2017

Upon registration, you will receive your conference materials and a name badge, which should be worn at ALL times during the conference functions.

All registered conference participants are entitled to:

- Attendance to all conference sessions
- Conference materials
- Welcome banquet [Chinese Restaurant of the 2nd Floor, Guiyuan Hotel;19:00-21:00,Oct. 9, 2017]
- Lunch [Chinese Restaurant of 2nd Floor, Guiyuan Hotel; 12:00-13:30, Oct. 10, 11, 13, 2017]
- Coffee break [Hall of 3rd Floor, Guiyuan Hotel]
- Opening Ceremony [Room 10 of the 3rd Floor, Guiyuan Hotel, 8:30-9:00, Oct. 10, 2017]
- Russia Party [Jingui Hall, Guiyuan Hotel, 20:30-23:00, Oct.11, 2017]
- Mid-Meeting Excursion [Jinyun Mountain Scenic Spot,Oct. 12, 2017]
- Closing Ceremony [Room 10 of the 3rd Floor, Guiyuan Hotel, 16:30-17:30, Oct. 13, 2017]
- Poster Session [Hall of the 3rd Floor, Guiyuan Hotel, October 9-13, 2017]

3. Secretariat

No special Secretariat Room is deposited, any request, call the reception desk of hotel (+86-23-68293000) or ours (Zhi-Sheng Zhang, +86-15823916558; Tian Lu, +86-13101379032).

4. Preview of talks

All talks will be happened in the Room 10 of the 3rd Floor. In the morning or noon before your turn, all speakers need to stop by the conference laptop and preview your presentation materials and hand in the file to the volunteers.

5. Poster Session

In conjunction with the conference, the poster session will be held at the Hall of the 3rd Floor (outdoor Auditorium). The poster session is open to all participants.

6. Coffee Break

Coffee will be served during breaks in the 3rd Floor of Guiyuan Hotel.

7. Liability

The conference organizer is not liable for personal accidents or loss/damage of private properties of registered participants during the congress. Participants are encouraged to make their own arrangement for personal insurance.

8. Disclaimer

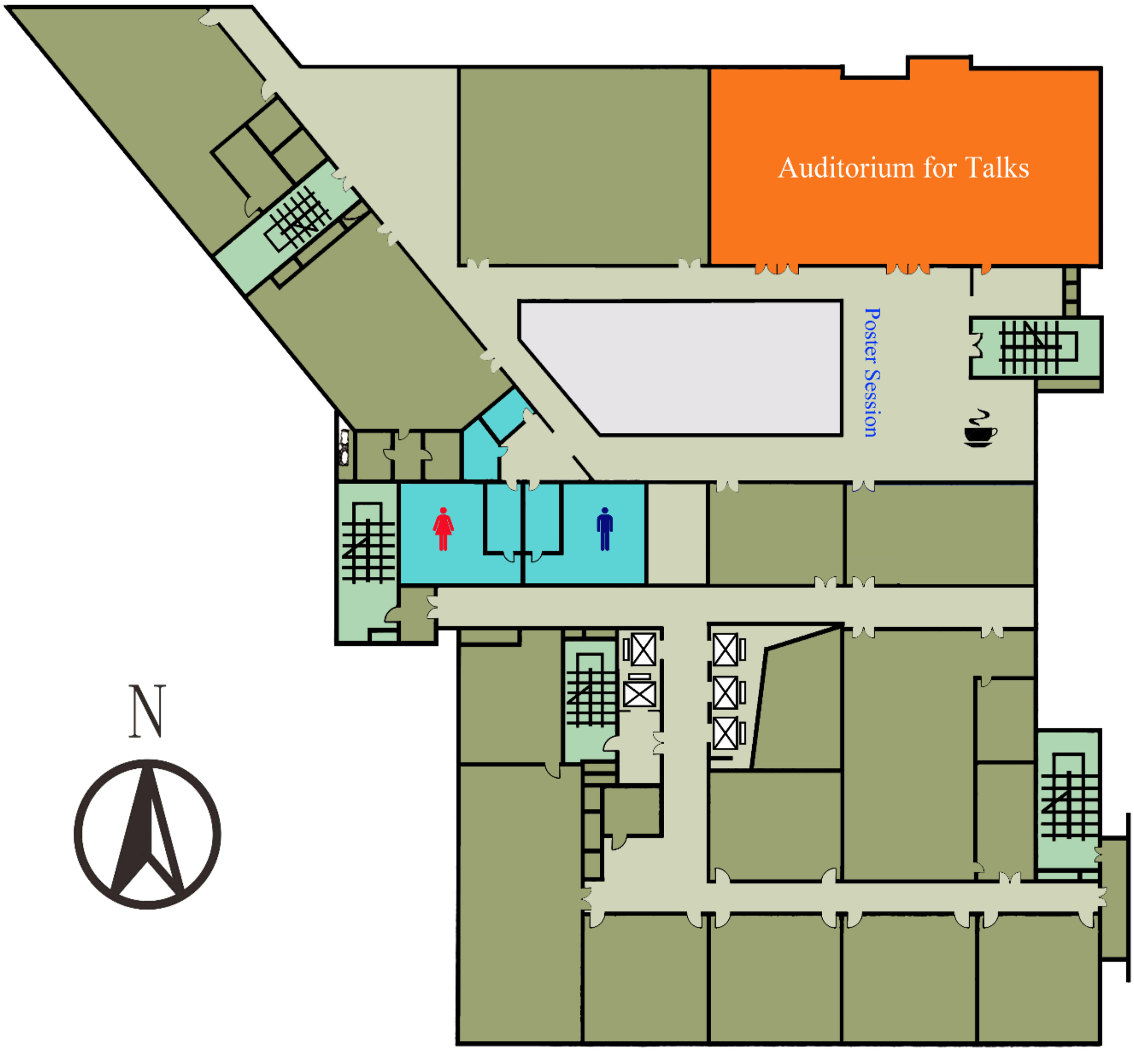
Whilst every attempt will be made to ensure that all aspects of the conference mentioned will be as scheduled, the conference organizer reserves the right to make changes should the need arises. The conference organizer is not responsible for any personal expenses incurred or any loss suffered by any attendee or his guest in connection with the conference.

9. Emergency

Police 110
Emergency Medical Services 120
Fire alarm telephone 119

VENUE LAYOUT

3F



🚻 Toilet ⌧ Elevator ☕ Coffee/ Tea Break ▦ Stairs

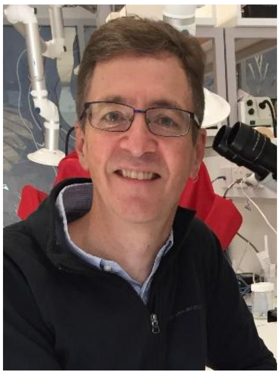
PROGRAM AT A GLANCE

	Oct. 9 Monday	Oct. 10 Tuesday	Oct. 11 Wednesday	Oct. 12 Thursday	Oct. 13 Friday
8:00-8:30	Registration	Registration		Mid-meeting Excursion	
8:30-9:00		Opening Ceremony	Plenary / Oral Talks		Plenary / Oral Talks
9:00-10:00		Plenary / Oral Talks			
10:30-11:00		Coffee Break	Coffee Break		Coffee Break
11:00-12:00		Oral Talks	Oral Talks		Oral Talks
12:00-14:00		Lunch Break	Lunch Break		Lunch Break
14:00-16:00		Plenary / Oral Talks	Plenary / Oral Talks		Oral Talks
16:00-16:30		Coffee Break	Coffee Break		Coffee Break
16:30-18:00		Oral Talks	Oral Talks		Closing Session
19:00- Or 20:00-	Welcome Banquet	ASC Council Meeting		Russia Party	

PLENARY LECTURES

Jonathan A. Coddington, Smithsonian Institution, USA

Jonathan A. Coddington is a Senior Scientist and the Interim Chair in the Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution. He is also the Director of the Global Genome Initiative. His research fields are phylogeny and comparative morphology of the spider family Theridiosomatidae and higher systematics of spiders in general, comparative ethology of theridiosomatids and orb weavers, implications of phylogenetic analysis for evolutionary theory, theory and design of biological inventories and preservation and understanding of genomes of life.



Mark S. Harvey, Western Australian Museum, Australia

Mark S. Harvey is a Senior Curator & Head at the Department of Terrestrial Zoology at the Western Australian Museum. His main research interests are the systematics and biogeography of Australasian arachnids, with major contributions to the study of pseudoscorpions, spiders and water mites, as well as some of the smaller orders, such as the Schizomida and Amblypygi. More than 570 new species, 75 new genera, 4 new subfamilies, 4 new families were described in his more than 250 papers and other publications. He wrote several catalogues of the smaller arachnid orders including Amblypygi, Uropygi, Schizomida, Palpigradi, Ricinulei and Solifugae.

Daiqin Li, National University of Singapore, Singapore

Daiqin Li is an Associate Professor in the Department of Biological Sciences at the National University of Singapore. He has a broad research interest in animal behaviours, including animal communication, sexual selection, predator-prey interactions, and the evolutionary significance of prey-specific prey-catching and prey-preference behaviour. He has published more than 118 peer reviewed papers in international journals.

Miquel A. Arnedo, University of Barcelona, Spain

Miquel A. Arnedo is an Associate Professor and director of the master program in Biodiversity at the University of Barcelona in Catalonia, Spain. His research focuses on inventorying biodiversity and unveiling the processes that shape temporal and spatial dynamics of life. He studies biological evolution in a phylogenetic framework, boosting traditional natural history approaches with modern molecular and omics tools to infer genealogical information, understand trait evolution and accelerate biological inventories. He has co-authored more than 60 papers in peer-reviewed journals.

Zhi-Qiang Zhang, University of Auckland, New Zealand

Zhi-Qiang Zhang is Curator (Acari) in New Zealand Arthropod Collection and Professor in the School of Biological Sciences at the University of Auckland, New Zealand. He has broad interest in systematics, ecology and evolution. He has published over 300 papers and also authored/edited more than 20 books, most of these on mites. His passion in the last twenty years has been the revival of taxonomy, mainly through his work in founding and editing of two of the largest journals in biology (Zootaxa and Phytotaxa).

SCIENTIFIC PROGRAM

DAY 1 TUESDAY, OCTOBER 10, 2017, Auditorium (3F)

08:30-09:10	**Opening Ceremony**hosted by **Joseph K.H. Koh and Shu-Qiang Li**
	Chang-Yong Zhou *Vice-president, Southwest University, Chongqing, China*
	Joseph K.H. Koh *President, Asian Society of Arachnology* *Honorary Research Affiliate, Lee Kong Chian Natural History Museum, National University of Singapore*
	Jian Chen *Chairman, Arachnological Society of China* *Professor, College of Life Sciences, Hubei University, China*
	De-Shou Wang *Dean, School of Life Sciences, Southwest University, China*

09:00-12:00	**Plenary and Oral talks: Evolution, Phylogeny and Biogeography** hosted by **Jian Chenand Miquel A. Arnedo**
09:00-09:50	**No. 1 (Plenary talk)** **Jonathan A. Coddington** (Smithsonian Institution, USA) *Sexual size dimorphism: evolution and perils of extreme phenotypes in spiders*
09:50-10:05	**No. 8: Xin Zhou** (China Agricultural University) *From alpha taxonomy to evolution of complex traits: insects as examples*
10:05-10:20	**No. 6: Ingi Agnarsson** (University of Vermont, USA) *Biogeography of two dispersal-limited Gondwanan spider lineages in the Caribbean (Deinopis, Deinopidae; Loxosceles, Sicaridae)*
10:20-11:00	Group photographingand Coffee / Tea Break
11:00-11:15	**No. 29: Stefan H. Foord** (University of Venda, South Africa) *Phylogenetic and functional perspectives on β-diversity: the case of spiders and ants along elevations*
11:15-11:30	**No. 9: Cheng-Min Shi** (Institute of Zoology & Beijing Institute of Genomics, Chinese Academy of Sciences, China) *The genetic legacy of climate change in temperate Asia: insights from scorpions*
11:30-11:45	**No. 20: Ren-Chung Cheng** (National Taiwan University, China) *Global phylogeny and biogeography of silver-faced spiders (Argiope, Araneidae)*
11:45-12:00	**No. 14: Zhe Zhao** (Institute of Zoology, Chinese Academy of Sciences, China) *The uplift of the Tibetan Plateau and the biodiversity pattern of Eurasian spiders*

14:00-18:30	**Plenary and Oral talks: Phylogeny, Evolution, Biogeography and Systematics** hosted by **Jonathan A. Coddington and Xian-Jin Peng**
14:00-14:40	**No. 4 (Plenary talk)** **Miquel A. Arnedo** (University of Barcelona, Spain) *Through the looking glass: How high throughput sequencing technologies are revolutionizing our understanding of arachnid diversity and evolution*
14:40-14:55	**No. 7: Matjaž Kuntner** (Slovenian Academy of Sciences and Arts, Slovenia) *Nephilid spider phylogenomics: complex evolution of sexual size dimorphism*
14:55-15:10	**No. 17: Yong-Chao Su** (National University of Singapore; Kaohsiung Medical Univ.) *Using ultra-conserved elements (UCEs) genomic approaches resolve the phylogeny of Argyrodinae (Araneae: Theridiidae) – a progress report*
15:10-15:25	**No. 57: Zong-Xu Li** (Kunming Institute of Zoology, Chinese Academy of Sciences) *Strengthening the Spider Tree of Life and Facilitate Phylogenetic Placement of Araneae*
15:25-15:40	**No. 11: Yuri M. Marusik** (Institute for Biological Problems of the North, Russia) *Amazing morphological characters recently found in Palpimanidae and Salticidae*
15:40-15:55	**No. 16: Zhi-Yong Di** (University of Science and Technology of China) *The discovery of homeotic scorpion*
15:55-16:30	Coffee / Tea Break and Poster Session
16:30-16:45	**No. 19: Danilo Harms** (University of Hamburg, -Zoological Museum, Germany) *The fossil history of pseudoscorpions (Arachnida: Pseudoscorpiones)*
16:45-17:00	**No. 51: Xin Xu** (Hunan Normal University, China) *Oligocene-Miocene mountain building and fluvial formation driving diversification of the primitively segmented spider genus Sinothela*
17:00-17:15	**No. 37: He Zhang** (Hubei University, China) *Phylogeny of Chinese Pseudopoda spiders (Araneae: Sparassidae) based on target-gene analyses*
17:15-17:30	**No. 41: Juan Wang** (Hunan Agricultural University, China) *Effects of Bt rice on growth and development of Pardosa pseudoannulata*
17:30-17:45	**No. 39: Fan Li**(Hubei University, China) *Multilocus sequence data reveal more than two species of Calommata Lucus, 1837, the purse-web spiders, in China (Araneae: Atypidae)*
17:45-18:00	**No. 52: Marjan Komnonov** (Blwd Kuzman Josifovski - Pitu, Republic of Macedonia) *An overview on the genus Pardosa* (Araneae: Lycosidae)

DAY 2 WEDNESDAY, OCTOBER 11, 2017, Auditorium (3F)

08:30-12:20	**Plenary and Oral talks: Diversity, Systematics and Ecology**

hosted by **Zhi-Qiang Zhang andIngi Agnarsson**

08:30-09:10	**No. 2 (Plenary talk)** **Mark S. Harvey** (Western Australian Museum) *What do we known about the smaller arachnid orders in Asia?*
09:10-09:25	**No. 13:Peter Jäger**(Senckenberg Research Institute, Germany) *Revision of the genus Ctenus in Asia (Araneae: Ctenidae)*
09:25-09:40	**No. 15: Stephanie F. Loria** (American Museum of Natural History, New York, USA) *Systematics and biogeography of the Asian forest scorpions, genus Heterometrus Ehrenberg, 1828*
09:40-09:55	**No. 10: Yuri M. Marusik** (Institute for Biological Problems of the North, Russia) *Palaearctic and Nearctic versus Holarctic: How do spider distribution corroborates with zoogeographic regions?*
09:55-10:10	**No. 18: Hirotsugu Ono** (National Museum of Nature and Science, Japan) *Primitively segmented spiders (Mesothelae, Liphistiidae) of Myanmar*
10:10-10:40	Coffee / Tea Break and Poster Session
10:40-10:55	**No. 54: Zhi-Sheng Zhang** (Southwest University, China) *Geographical distribution of spiders*
10:55-11:10	**No. 33: Xuan-Kong Jiang**(Institute of Hydrobiology, Chinese Academy of Sciences; Guizhou Institute of Biology, China) *Progress in taxonomy of millipede (Arthropoda, Diplopoda) in China*
11:10-11:25	**No. 31: Suphapipatana Yothee** (Kasetsart University, Thailand) *Diversity and Composition of Riparian Spider in Rayong Botanical Garden, Rayong Province, Thailand*
11:25-11:40	**No. 55: Tian Lu** (Southwest University, China) *Consistency of Lycosidae: A comparative analysis of male bulb*
11:40-11:55	**No. 44: Muhammad Irfan** (Hunan Normal University, China) *Two new genera of linyphiid spiders from Southern China (Araneae: Linyphiidae)*

14:00-18:25 **Plenary and Oral talks: Diversity, Systematics, Ecology and Application**

hosted by **Mark S. Harvey and Peter Jäger**

14:00-14:40 **No. 5 (Plenary talk)**
Zhi-Qiang Zhang (The University of Auckland;Landcare Research, New Zealand)
An inordinate fondness for mites

14:40-14:55 **No. 27: Li-Hong Tu** (Capital Normal University, China)
Connection between female internal reproductive ducts and epigynal tracts and its biological implications in entelegyne spiders

14:55-15:10 **No. 30: Mathew M. Joseph**(Sacred Heart College, India)
Diversity of spiders (Arachnida: Araneae) in the high-altitude shola ecosystems of the Western Ghats biodiversity hotspot in India

15:10-15:25 **No. 49: Guo Zheng** (Shenyang Normal University, China)
The Use of Spiders (Araneae) as Ecological Indicators

15:25-15:40 **No. 43: Zhong-Hua Liu** (Hunan Normal University, China)
Heteropoda venatoria as an insect hunter revealed by the biochemical and pharmacological studies of its venom

15:40-15:55 **No. 26: Peter Koomen** (Natuurmuseum Friesland, The Netherlands)
Towards a spider photo guide of Xishuangbanna, Yunnan, China: new photographic techniques

15:55-16:30 Coffee / Tea Break and Poster Session

16:30-16:45 **No. 53: Sunil Jose Kanniparambil** (Deva Matha College, India)
Endemic theraphosids in Western Ghats, India (Araneae: Theraphosidae)

16:45-17:00 **No. 22: Michelle Strickland**(University of Nottingham, UK)
Diversity of the Silks and Spinning Apparatus of the Water Spider Argyroneta aquatica

17:00-17:15 **No. 28:Rui Yin**(Helmholtz-Centre for Environmental Research(UFZ), Germany)
The effects of climate and land use change on soil mites-trophic structure, body size and biomass

17:15-17:30 **No. 42:Hui-Lin Yang**(Hunan Agricultural University, China)
Effects of cadmium on the safety of the wolf spider Pardosa pseudoannulata

17:30-17:45 **No. 48: Ting-Ting Zhang** (Sun Yat-Sen University, China)
Beta diversity of arboreal spider under different spatial and temporal scales reflects dissimilar mechanisms of community assembly in a temperate forest

17:45-18:00 **No. 56: Gui-Qiang Huang** (Southwest University, China)
A systematic review of the family Hahniidae (Arachnida, Araneae)

DAY 4 Friday, OCTOBER 13, 2017, Auditorium (3F)

08:30-12:20 **Plenary and Oral talks: Behaviour and Ecology**

hosted by **Matjaž Kuntner and Daiqin Li**

08:30-09:10	**No. 3 (Plenary talk)** **Daiqin Li** (National University of Singapore, Singapore) *Personality and decision-making in specialized spider-eating jumping spiders*
09:10-09:25	**No. 24: Shi-Chang Zhang** (Hubei University, China) *Post-maturity molting in web-building spiders*
09:25-09:40	**No. 21: Radek Michalko** (Masaryk University, Czech Republic) *The predictability in predatory activity of the spider Oxyopes lineatipes is interactively influenced by behavioral type, prey density, and neem application*
09:40-09:55	**No. 23: Rong Xiao** (Guizhou University, China) *Olfactory response to the herbivore-induced rice volatiles of the wolf spider Pardosa pseudoannulata(Araneae: Lycosidae)*
09:55-10:10	**No. 38: Ling-Bing Wu** (Hubei University, China) *Dispersal modality determines the relative partitioning of beta diversity in spider assemblages on subtropical land-bridge islands*
10:10-10:25	**No. 25: Zhan-Qi Chen** (Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences) *Extreme long-lasting maternal care in a jumping spider*
10:25-11:00	Coffee / Tea Break and Poster Session
11:00-11:15	**No. 47: Hua Zeng**(National University of Singapore) *Ornamental coloration associated intra-sexual contest in jumping spider Siler semiglaucus*
11:15-11:30	**No. 36:Long Yu**(Hubei University, China) *Bird-dropping masquerading visually and chemically by a crab spider*
11:30-11:45	**No. 40: Qi-Chen Su** (Hubei University, China) *Wolbachia impacts on developmental time, sex ratio and horizontal transmission in Hylyphantes graminicola (Araneae: Linyphiidae)*
11:45-12:00	**No. 45: Ji-He Liu**(Hunan Normal University, China) *Spider Resilience to Disturbance: A Comparative Study on Predatory Spider Communities in Natural and Extensively Managed Pomelo Orchards*

14:00-15:40 **Oral talks: Diversity, Systematics and Phylogenetics**

hosted by **Joseph K.H. Koh**

14:00-14:15
No. 12: Yuri M. Marusik (Institute for Biological Problems of the North, Russia)
Phylogenetic ties or morphological convergence in two araneoid genera occurring in South America and South-East Asia?

14:20-14:40
No. 50: Guang-Yu Liu (Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences)
Spider diversity and the education in a botanic garden

14:40-14:55
No. 34: Zhi-Zhong Gao (Hebei University, China)
Systematics of Infraorder Panctenata from China (Arachnida: Pseudoscorpiones)

14:55-15:10
No. 32:Nitiphong Kaewman(Takhliprachasan school, Thailand)
The application of Daddy longlegs (Pholcus phalangioides) as a proton exchange membrane in the production of electricity from the fuel cell

15:10-15:25
No. 35: Chi Jin (Hebei University, China)
Research progress of spider families Corinnidae, Phrurolithidae and Trachelidae in China (Araneae: Dionycha)

15:25-15:40
No. 46: Ke-Ke Liu (Hunan Normal University, China)
Research Progress of the spider diversity from Mt. Jinggang, Jiangxi, China

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16:30-17:30 **Closing Ceremony**

Hosted by **Peter Jäger**

Award Ceremony for excellent talks of students

Summary of Organizing Committee

ASA Summary

Concluding remarks

ABSTRACT: PLENARY PRESENTATIONS

No. 1

Sexual size dimorphism: evolution and perils of extreme phenotypes in spiders

Jonathan A. Coddington* &Matjaz Kuntner
Department of Entomology, National Museum of Natural History, Smithsonian Institution, Washington DC, United States.
*Email: coddington@si.edu

Abstract: Sexual size dimorphism (SSD) is one of the most striking animal traits. It is also widespread, with multiple evolutionary origins and losses. Male-biased SSD in vertebrates is often explained by sexual selection for larger males. Female-biased SSD, more typical of invertebrates, is a more complicated outcome of gendered evolutionary drivers whose strength and direction are diverse. Here we review the occurrences, the evolution, and the biology of SSD in spiders, a hyper-diverse order with the most extreme sexual size dimorphism among terrestrial animals (eSSD, female:male body length ≥ 2.0). A statistically random sample of spider body lengths implies an average SSD of 1.2. At least sixteen spider clades contain eSSD species and are worthy of further research. We review these cases, explore why the literature does not converge on an overall explanation for eSSD, then compare the evolutionary patterns in the best known eSSD cases (nephilids and argiopines). We recommend phylogenetic work that will strengthen comparisons and improve understanding of evolutionary causes and phenotypic effects of eSSD. Macroevolutionary patterns differ strikingly between nephilids and argiopines, suggesting diverse outcomes of natural and sexual selection in each case. An equilibrium model featuring clade- and context-specific drivers of gender size variation explains discrepancies. Finally, eSSD affects other traits such as sexual cannibalism, genital damage, emasculation, and monogyny with terminal investment. Experimental work should rigorously test the adaptive significance of these traits, and their co-occurrence with eSSD.

No. 2

What do we known about the smaller arachnid orders in Asia?

Mark S. Harvey

Western Australian Museum, Welshpool DC, AUSTRALIA

Abstract: The larger arachnid groups, spiders and mites, are hyper-diverse and represent some of the largest orders of living organisms. They constitute the vast majority of documented arachnid diversity and several species are used as model organisms to document various ecological and behavioural processes. The smaller arachnid orders, i.e. those with a total world diversity of less than 10,000 species, on the other hand, tend to garner less interest although scorpions have a dedicated following with enthusiastic researchers and amateur hobbyists. While not in a position to discuss orders such as Opiliones and Scorpiones, this presentation is designed to provide an update on our knowledge of the Asian smaller arachnid orders, and highlight recent and ongoing research into them. For example, recent research into the archaic pseudoscorpion family Feaellidae has revealed the first presence of modern representatives in south-east Asia, as well as the first Cretaceous species from 99 mya Burmese amber deposits. The presence of Mesozoic feaellids is consistent with their phylogenetic relationships (most likely sister to all Iocheirata) and their modern distribution which strongly indicates an ancient Pangean origin for the family. Other research into feaellids from other parts of the world such as north-western Australia and south-east Asia confirms them as short-range endemic species, each with small distributions. Other Asian pseudoscorpions recently studied at comprehensive, regional bases are the family Ideoroncidae, with a new genus and numerous new species, in which the diversity of this group has been expanded nearly three-fold. The discovery of Cretaceous fossil ideoroncids and hyids in Burmese amber that are barely distinguishable from modern species illustrates the great age and morphological stasis of some pseudoscorpions. On the other hand, a new species of Chthoniidae Burmese amber is quite different to modern species. Ongoing taxonomic research in the modern Asian pseudoscorpion fauna, particularly by researchers in China, is increasing the knowledge base of these poorly studied arachnids. The other smaller orders that are worthy of mention include the discovery of a diverse Cretaceous ricinuleid fauna from Burmese amber, even though the only Holocene species occur in tropical Africa and America, and new Cretaceous whip spiders (Amblypygi) and whip scorpions (Uropygi). Although these taxa represent significant advances in our knowledge of Mesozoic arachnids, the modern whip scorpion fauna of Asia is imperfectly known with an uncertain generic classification and phylogenetic inferences. Despite notable advances in some arachnid orders from the modern Asian fauna or from Cretaceous ambers, there is a dearth of information on other orders. The most glaring example is of the Schizomida, with a recent molecular phylogeny revealing numerous unnamed clades that most likely represent new genera. Comprehensive assessments of the numerous new species in museum collections and their relationships are now needed to allow a more thorough documentation of the Asian schizomid fauna.

No. 3

Personality and decision-making in specialized spider-eating jumping spiders

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Abstract: Individuals of the same sex, age or size within a given animal population consistently differ from one another in their behaviour referred to as personality. These between-individual differences in behaviour are consistent over time and/or across contexts or situations. Such differences within populations have often been traditionally considered as either the consequence of inaccurate measurements or as noise around an adaptive population mean. Nevertheless, in the past two decades personality has been documented in animals as diverse as limpets, fish, lizards, birds, rodents, sea anemone, squids, octopuses, insects and spiders, and with new taxa frequently added to the list, suggesting that personality may exist across the entire animal kingdom. However, studies of spider personality are still scarce. In this talk, we will try to address a several questions concerning research on spider personality using *Portia* spiders, a group of specialized spider-eating jumping spiders, as model systems: (1) inter-individual variations in behaviour; (2) Intra-individual variations (IIV; predictability) in behaviour; (3) a suite of correlated behaviours (i.e., behavioural syndrome); (4) the joint effects of both personality and predictability on species interactions; (5) How personality influences jumping spider decision-making? and (6) The future directions in studies of spider personality.

No. 4

Through the looking glass: How high throughput sequencing technologies are revolutionizing our understanding of arachnid diversity and evolution

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Abstract: Despite their diversity, key predatory role in ecosystems and impact on human societies, for instance in agriculture (pests and controls), health (venoms) and engineering (silk), arachnids have been rarely represented among the model system organisms used in biology. Consequently, evolutionary and genetic studies on these groups were traditionally hampered by the limited genomic and transcriptomic information available. The irruption in the late nineties of the former century of pyrosequencing and the subsequent development of additional, ever progressing sequencing technologies, have eased the cost-effective generation of a wealth of genomic and transcriptomic data for non-model organisms. The generalization of these sequencing technologies has brought about a paradigm shift in the way data are not only gathered, but also analyzed and stored, posing important computational challenges and opportunities. Massively parallel sequencing has provided fundamental insights into the structure and function of the arachnid genome, for instance by revealing the gene repertoire and their levels of gene expression in different tissues and under different environmental conditions, and by unveiling the existence of whole genome duplication events. In this talk, I will review and discuss some of the major contributions of the new sequencing technologies to our current understanding of the tree of life of arachnids and the genomic basis of the evolutionary novelties that drove their diversification.

No. 5

An inordinate fondness for mites

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Abstract: When J.B.S. Haldane wrote his famous quote in biology—"God has an inordinate fondness for beetles", he was referring to the incredible diversity of beetle species on Earth. In the Arachnida, only mites can rival beetles in that aspect. Mites and beetles have a lot in common—they are both the most successful group in their subphylum; they are both super abundant and extremely diverse; they both enjoy almost every possible animal way of living, and they both live almost anywhere. Indeed, mites exceed beetles in habitat diversity and are found in deep seas where beetles and other insects have failed to conquer. In this presentation, I will ask why there are so many species of mites. I will provide an introduction to the diversity of mites and a review of its phylogeny. Key innovations responsible for its evolutionary success will be discussed in light of the mite tree of life, with a special focus on the evolution of parasitism in two major groups of mites: Acariformes and Parasitiformes.

Key words: Diversity, evolution, speciation, parasitism, Acari

ABSTRACT: ORAL PRESENTATIONS

No. 6

Biogeography of two dispersal-limited Gondwanan spider lineages in the Caribbean (*Deinopis*, Deinopidae; *Loxosceles*, Sicaridae)

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Abstract: The importance of islands in revealing evolutionary processes was already highlighted by Darwin's work on the Galapagos and Wallace's work in the Malay Archipelago. Island biogeography has provided many elegant examples of the evolutionary mechanisms involved in generating biodiversity. These include geological processes such as plate tectonics and volcanism, and traits of organisms such as their size, generation time, and dispersal ability. The focus on dispersal has long revolved around its role as an alternative to vicariance in explaining distributions. Here I discuss the Caribbean biogeography of two ancient lineages that we expect are dispersal-limited, in other words that do not readily cross oceanic barriers. We predict that for those lineages vicariance will be the primary biogeographical force, and to the extent that their biogeography is vicariant, they should share very similar histories. On the other hand, to the degree that the biogeography of the two lineages differ, the role of dispersal and other factors that potentially are dispersal-independent will be revealed. We find that stochastic events, and the reliance of one of the lineages on caves, likely explain differences in the biogeography of the two lineages, while ancient vicariance readily explains shared patterns.

No. 7

Nephilid spider phylogenomics: complex evolution of sexual size dimorphism

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Abstract: Golden orb spiders, *Nephila* and relatives of the family Nephilidae, are biological models, notably for the evolution of sexual size dimorphism (SSD). SSD is defined as female to male size ratio. All values over 2.0 are extreme (eSSD) and rare in animals, but in nephilids, eSSD is the norm. We report on phylogenomic research intended to arrive at a robust and reliable species level phylogeny of Nephilidae to test hypotheses specific to body and web size evolution in a comparative framework. We combine anchored hybrid enrichment (AHE), a phylogenomic pipeline designed to resolve both deep and shallow phylogenetic hierarchies, with data from a prior six-gene phylogeny. Phylogenetic optimizations reveal complex patterns of size evolution in nephilids: female and male body lengths are inferred to increase on 26 and 24, and to decrease on 28 and 30 occasions, respectively. SSD (average 4.80; range 1.36-11.44) increases on 24 and decreases on 30 occasions, and is extreme in nearly all terminals and deeper phylogenetic nodes; the exceptions are three island species that independently evolve moderate SSD on Madagascar, Comoros, and Sri Lanka. An exaggerated SSD>5.0 is reconstructed at the nephilid root. Such eSSD is retained or further exaggerated in the tropical *Nephila, Nephilengys,* and *Nephilingis*. Combined, our results refute the validity of Cope's Rule (phyletic size increase) in golden orb spiders, but support the hypotheses of disentangled male and female size evolution, and of correlated female body and web size evolution. We conclude that SSD, a complex phenotypic outcome of independently and rapidly evolving body sizes of each gender, is more pronounced in the tropical clades and species, and less extreme on islands.

No. 8

From alpha taxonomy to evolution of complex traits: insects as examples

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Abstract: Diverse organismal groups, such as insects and arachnids, are ideal model systems for biodiversity research and evolutionary studies. While tremendous diversity of life is being described for these animals, model species (e.g., *Drosophila*, *C*. *elegans*) have provided opportunities to understand how lives function and evolve. Research domains, however, seem to have been largely compartmentalized and isolated. For instance, taxonomists are not regularly updated on new findings in gene functions and researchers focusing on molecular mechanisms of *Drosophila* don't necessarily think of insect phylogenies. Apart from academic culture and tradition, the lack of genomics resources for non-model organisms presents a major roadblock preventing the generalization of knowledge gained from just a few model organisms.

Recent rapid developments in genomics and the vast amount of –omics data have opened a new venue for the understanding of evolution of life, including phylogenetic relationships and how complex traits have evolved, including key characteristics responsible for the success of extant taxa. Therefore, we now have a chance to examine how generally/uniquely the genetic mechanisms found in model species can be concluded in most other insects. These new findings in turn will provide answers to some of the most intrinsic questions in biology, e.g., why insects are so successful? This presentation will introduce some of these new trends in evolutionary studies using insects as examples. I will report progresses of large projects, such as Barcode of Life and 1000 Insect Transcriptome Evolution, and how findings of these projects can be cross-referenced to improve our understanding of insect evolution.

No. 9

The genetic legacy of climate change in temperate Asia: insights from scorpions

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Abstract: Climate sets the baseline condition under which species can persist and form viable populations across space and time, and influences biota in a rich variety of ways. As climate change has unfolded in varying modes and extents across the globe through evolutionary time, it impacted animals and plants on multiple dimensions across spatiotemporal scales. Temperate Asia is such a place where the biota were profoundly influenced both by the global climatic oscillations and by localized geographical features. Although no continental ice sheets developed in temperate Asia during the Quaternary, the far-field effects of ice sheets have led to drastic environmental changes in step with the global glacial cycles, expressed as sea level fluctuations near coast and acidification of inland. The biological consequences of those environmental changes have been suggested by palao-environmental evidences, but not explicitly tested using modern molecular bio/phylogeographic approaches. We examined the role of climatic changes since the Mid Miocene onwards on genetic architecture of temperate Asian biota using *Mesobuthus* scorpions as model organisms. Our results indicated that the climate change impacted the bio/phylogeography and demography of scorpions in different mode and extent at different geographic locations through time. The final outcomes were molded by both short-term climate oscillations (related to glacial cycles) and long-term climatic shifts (acidification trend), which were spatially tuned by geographic settings.

Keywords:acidification, demography, ecological niche modeling, *Mesobuthus*, phylogeography

No. 10

Palaearctic and Nearctic versus Holarctic: How do spider distribution corroborates with zoogeographic regions?

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Abstract: There are several alternative opinions about zoogeographic subdivision of the Northern Hemisphere. Some zoogeographists recognize Holarctic with two main subdivisions: Palaearctic and Nearctic, while many experts consider Palaearctic and Nearctic as separate biogeographic realms. In my presentation distribution of spiders in the northern half of Eurasia, northern Africa and North America will be analyzed and compared with different zoogeographical schemes. Special emphasis will be given to spiders distributed in the temperate and arctic regions. Spiders of these regions are much better studied in both hemispheres than in southern regions.

Keywords: biogeography, zoogeographical realm, range

No. 11

Amazing morphological characters recently found in Palpimanidae and Salticidae

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Abstract: In the presentation we will speak about the features recently found in several genera of Palpimanidae and Salticidae, such as unique eye pattern in two new genera of Chediminae; mechanism locking epigastral furrow in *Chedima*; weakly sclerotized embolus in all genera; new mechanism of sperm transfer in *Diaphorocellus*, unusual mating plugs.

No. 12

Phylogenetic ties or morphological convergence in two araneoid genera occurring in South America and South-East Asia?

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Abstract: Two genera *Diphya* Nicolet, 1849 (Tetragnathidae) and *Tekellina* Levi, 1957 (Theridiidae) display unusual distribution pattern. Both are represented in the Neotropics (South America) and South-East Asia, but unknown in Australasia. *Diphya* is also known in Africa, and type species of *Tekellina* occurs in Florida. Study of copulatory organs in *Diphya* reveals that Asian and African species misplaced in the genus and species from that regions can be placed at least in three genera. Searching of collections allow us to found *Tekellina s.l.* species in India and Tasmania. Study of copulatory organs in genus led us to solid conclusion that genus is misplaced in Theridiidae.

No. 13

Revision of the genus *Ctenus* in Asia (Araneae: Ctenidae)

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Abstract: The genus *Ctenus* is revised in Asia by means of freshly collected specimens as well as of museum and private collection material. So far, 36 new species are recognized, 28 further species are redescribed, new records are given or the unknown sex is described for the first time. Few groups of seemingly closely related species are recognized. Most striking is the *cladarus*-group with 14 species distributed in Nepal, India, Bhutan, Sri Lanka and Myanmar: the RTA tip is breakable and was observed in one species to penetrate the cuticle of the female's epigyne. An apparently relatively recent speciation event in Taiwan shows a geographic separation between northwestern parts and southern parts of the island. All species are named in order to generally raise awareness for taxonomy and the biodiversity on our planet.

No. 14

The uplift of the Tibetan Plateau and the diversity pattern of Eurasian spiders

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Abstract: It was generally recognized that the warm and humid climate caused by the strong monsoons in the southeastern margin of Asia and the aridity in Central Asia since the Miocene period is the reason for the Eurasian biodiversity pattern formation. However, our newest research on coelotine spiders shows that the Tibetan uplift since the late Eocene has prevented the dispersal of some coelotine lineages and promoted their radiation, and caused extinction in some coelotine lineages, which should be the major driving force shaped the current diversity pattern of Eurasian spiders. Our another study shows that the Tibetan uplift resulted in the formation of the Truong Son Mountain Range, Mekong River, Beibu Gulf, Red River and Ma River driven the diversification of spiders in southeastern Asia. In addition to geological factors, rapid decline of global temperatures since Miocene promoted the southeastern Asia cave spiders diversification. As well as the destruction of biodiversity occurred in Europe during the glacial period have also lead to the formation of the current spider diversity pattern in Eurasia.

No. 15

Systematics and biogeography of the Asian forest scorpions genus *Heterometrus* Ehrenberg, 1828

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Abstract: Asian forest scorpions of the genus *Heterometrus* Ehrenberg, 1828 include some of the world's largest scorpions, e.g., *H. swammerdami* Simon, 1872, reaching almost 180 mm in length. As their vernacular name suggests, the 37 described species of *Heterometrus* are distributed throughout the tropical and subtropical forests of South and Southeast Asia, from Pakistan to Wallace's Line. All *Heterometrus* species are fossorial, rarely leaving their underground burrows and, consequently, their dispersal abilities are limited. We present the first phylogeny of *Heterometrus* and the first biogeographical analysis of Southeast Asian scorpions combining morphological and molecular data. The dataset comprised approximately 95 samples representing 28 ingroup species from across the distribution. Other genera of family Scorpionidae Latreille, 1802 from Africa and the Middle East were included as outgroups. The origins and diversification of *Heterometrus* were tested using divergence time estimation and ancestral range estimation. Results of this study have implications for the systematics of Asian forest scorpions and understanding the complex geological history of South and Southeast Asia.

Keywords: systematics, scorpions, biogeography, Southeast Asia

No. 16

The discovery of homeotic scorpion

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Abstract: The origin and evolution of arthropods receives much research attention, especially the structural changes that may have occurred in water-to-land transitions. Among the most ancient arthropods, scorpions are often considered as “living fossils” since known oldest fossils, quite similar to modern species, are from the mid-SilurianEramosa Formation (430 myr). Their evolutionary history of scorpions is controversial while evidences for their ancestral aquatic existence are uncertain same as their phylogenetic position and structure evolution. A homeotic scorpion, mutational young male *Scorpiops luridus* was found in Xizang, China. It reappears some “ancient” abdominal appendages that may belonging to scorpions' aquatic ancestors: “gonopods”, “hold legs” and “pleopods”, similar to those in malacostracans, while their homologous structures can be found in scorpion fossils, scorpion embryos and stem-group chelicerates. Basal piece and two sternites of homeotic scorpion developed remarkable notches same as the scenario in Branchioscorpionina and early embryonic development of scorpions. The presence of these “ancient” structures suggests the aquatic history of scorpion ancestors and the evolutionary history for genital operculums,pectines, basal piece, book lungs and sternites of all extant members. The “gonopods” and “hold legs” may be indicative of direct fertilization with an “abdomen-to-abdomen” mating embrace in aquatic scorpion ancestors in contrast to the indirect fertilization with “hand-to-hand” mating dance as in extant scorpions. That might imply the oldest internal fertilization among ancient animals. The relationship between book lung and “pleopod” provides evidence to new "Gill theory" that book lung originated from the “gills” of abdominal appendages’ telopods of their aquatic ancestors. The multi-structure and nonparallel of symmetrical structures’ homeosis is rarely reported, its hereditary basis was discussed here. The homeotic scorpion provides new indications for the origin and evolution of scorpions and other arthropods.

No. 17

Using ultra-conserved elements (UCEs) genomic approaches resolve the phylogeny of Argyrodinae (Araneae: Theridiidae) – a progress report

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Abstract: Spiders in the subfamily Argyrodinae (Araneae: Theridiidae) are known for their web invasion behaviors to the web of other spiders. These host-parasite associations include two forms: araneophagy and kleptoparasitism. Although the behaviors of argyrodine spiders have been the interest of behavioral ecologists for a long time, the lack of a robust phylogenetic treatment of this group has hindered the study of the evolution of these behavioral traits. Su and Smith (2014) reconstructed the first molecular phylogeny of the subfamily. However, Sanger data did not resolve the deep nodes of the Argyrodinae phylogeny. The results of the restriction enzyme associated DNA sequencing (RAD-seq) showed that RAD-seq approach is suitable for species group or genus level phylogenies. The number of homologous loci dramatically dropped when filtering the DNA fragments for constructing the phylogeny among genera. I have developed 1982 UCE loci for phylogenomics using six genomes including the species from Theridiidae and closely related families. The UCEs approach is promising for a fully resolved phylogeny for Argyrodinae.

Keywords: Phylogenomics, restriction site associated DNA sequencing, ultra-conserved elements, probe design, character evolution

No. 18

Primitively segmented spiders (Mesothelae, Liphistiidae) of Myanmar

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Abstract: The present knowledge about spiders of the genus *Liphistius* Schiödte, 1849 (Liphistiidae) of Myanmar is reported. Although 32 species of the genus are hitherto known from neighboring Thailand, only two recent species are recorded from Myanmar, that is, *Liphistius birmanicus* Thorell, 1897 from Carin Hill, Kayah State and *L. lordae* Platnick & Sedwick, 1984 from Taunggyi, Shan State. During an expedition to southern Myanmar made by the joint research project of the National Museum of Nature and Science, Japan, and the Forest Department of the Ministry of Natural Resources and Environmental Conservation, Myanmar in May, 2017, a third and presumably new species (two adult females and three juveniles) of *Liphistius* was found on Lampi Island and on Bo Cho Island, an adjacent small island to Lampi, of the Myeik Archipelago, Bokepying Township, Tanintharyi Region located at the base of Malay Peninsula. The Myeik archipelago geologically characterized mainly by limestone and granite comprises several hundred islands distributed along the coastline for 600 km in the Andaman Sea and their shoreline consists of sandy beaches, rocky headlands and mangrove swamps. This sea area has been isolated from modern civilization under the traditional lifestyle of the fishing tribe Moken, and the islands are covered with thick tropical growth, which preserves habitat of some endangered animals (Lampi Marine National Park Guidebook, 2016). Mainly in the structure of female genitalia, the Lampi species has little relation to the known two species from northern Myanmar but seems to belong to the *trang* group (Schwendinger, 1998) recorded from the area between Chumpon and Yala Provinces, southern Thailand, especially close to *L. bicoloripes* Ono, 1988 and *L. castaneus* Schwendinger, 1995.

No. 19

The fossil history of pseudoscorpions (Arachnida: Pseudoscorpiones)

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Abstract: Pseudoscorpions have attracted human attention since the time of Aristotele but their origins and evolutionary history are still largely unknown. Here, we summarise their fossil record but also suggest perspectives for future study and novel methods to interpret fossils. Pseudoscorpions are one of the oldest colonisers on land and probably diversified before other, more diverse groups, such as spiders. They represent an interesting case of evolutionary stasis and even Devonian fossils look rather modern whilst the 49 described fossil species from various amber sources essentially mirror modern faunas. There is a major gap in the fossil record of almost 250 Myr but it appears that some families had much wider past distributions then today and significant range shifts or extinction events must have occurred over time. Overall, 16 of the 26 Recent families of pseudoscorpions are known from fossils, suggesting that the diversification into major lineages occurred early in pseudoscorpion evolution. Novel techniques, such as synchrotron microscopy, provide exciting possibilities to study fine aspects of fossil morphology and may become essential tools in analysing fine aspects of morphology in a largely cryptic fauna.

No. 20

Global phylogeny and biogeography of silver-faced spiders (*Argiope,* Araneidae)

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Abstract: The global araneid subfamily Argiopinae includes three genera totaling 100 species, many of which are conspicuous and common. Renowned for pronounced sexual dimorphism, unusual mating behaviors, and web decorations, among other traits, argiopines are subjects of diverse evolutionary research. Nevertheless, their global biogeographic patterns have not been resolved. We present an updated time-calibrated phylogeny using three nuclear and three mitochondrial genes for 64 out of 100 argiopine species, and use it to reconstruct their biogeographical history. Our analyses support silver-faced spiders (*Argiope* sensu lato) monophyly if including species of *Gea* and *Neogea*, and excluding *A. ocula*. The ancestral area estimations reveal that the *Argiope* center of origin (Africa, the Palearctics, and Indo-Malaya) does not match its center of diversity (Australasia + Indo-Malaya). As predicted by the known biology and species diversity over all continents, silver-faced spiders show a mixed biogeographic imprint with a pervasive pattern of diversification within biogeographic regions, but also with some diversification events following long distance dispersal. The Intermediate Dispersal Model predicts that organisms with an intermediate (rather than very high or very low) dispersal propensity will diversify the most across barrier-filled landscapes. The here established mixed diversification pattern of silver-faced spiders, a roughly 38 million year old global clade of web building spiders, seems to fit this model, but for more conclusive tests, a comparison with additional global lineages will be necessary.

No. 21

The predictability in predatory activity of the spider *Oxyopes lineatipes* is interactively influenced by behavioral type, prey density, and neem application

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Abstract: The behavioral predictability, i.e. short-term intra-individual variability under relatively constant environmental conditions, has only recently started to gain attention. No experimental study, so far, has investigated how predictability changes along an environmental gradient depending on the behavioral types of the individuals (BTs, constant inter-individual differences in mean behavior). Here, we investigated the relationship between mean predatory activity and predictability in predatory activity along prey density gradient in the lynx spider *Oxyopes lineatipes*. We further examined how is this relationship influenced by exposure to two pesticides, neem and plant extract from *Embelia ribes*. We found that predictability decreased with increasing prey density in a BT-specific way. In the control and *Embelia* treatments, the individuals with low predatory activity were relatively less predictable than those with high activity from low to moderate prey densities but more predictable at high prey densities. This pattern has been altered by neem and the individuals with low predatory activity were less predictable than those with high activity along the whole gradient of prey density. We suggest that the BT-specific change in predictability along prey density might be caused by an interaction among the following three factors: 1) encounter rate between spiders and prey, 2) the difference in metabolic rate between the BTs, 3) the cognitive styles of BTs. Our results have important implication for further studies on behavioral predictability as they show that it can change along an environmental gradient in a BT-specific way and the relative predictability of the BTs candepend on the value of the environmental gradient.

No. 22

Diversity of the Silks and Spinning Apparatus of the Water Spider *Argyroneta aquatica*

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Abstract: Spider silk is a remarkable material: Highly elastic, stronger than steel and applied to wounds as an healing aid by the Ancient Greeks. Of circa. 46,000 species of spider, only *Argyroneta aquatica* have adapted to spin silk whilst submersed. The diving bell, a sheet of silk spun to hold a bubble of air underwater, acts as a physical gill, providing an adult spider with a constantly replenishing underwater air supply.

In this project, we investigate the diving bell and the spinning apparatus of the spider, using transcriptomics and environmental Scanning Electron Microscopy (eSEM).Here, we present the first eSEM images of hydrated *Argyroneta* silk, showing the range of fibres present including microthreads and ribbons of silk coated in a proteinaceous hydrogel. SEM images of the spinnerets show a typical spigot structure and arrangement, with an unusual coating of suspected hydrogel. Additionally, we identified a number of silk types which, until now, have not been identified outside of a group of highly specialised orb weaver spiders. Finally, we show how structural features are conserved genetically and phylogenetic relationships are maintained, suggesting that the silk of the diving bell spider is not so far removed from that of "normal" spiders.

These results mean that spider silk may be even more versatile than previously imagined–and exploitable. Coupled with new technologies and advances in synthetic silk research, this biomaterial has a diverse range of potential applications.

Keywords: Silk, *Argyroneta aquatica*, spinnerets, silk phylogeny

No. 23

Olfactory response to the herbivore-induced rice volatiles of the wolf spider *Pardosa pseudoannulata* (Araneae: Lycosidae)

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Abstract: The wolf spider *Pardosa pseudoannulata*is the dominant invertebrate predator in paddy ecosystems and an important biological control agent of rice pests which induce rice plants to releases some specific volatile compounds. These herbivore-induced rice volatiles play an important role in plant-herbivores-predators three trophic levels. Although spiders are sensitive to odors, such as in mate tracing and detecting of prey and predators, majority of the attentions have been paid to direct chemical signals that from their mates, prey and predators, far few studies paid attentions to the herbivore-induced olfactory signals to spiders. Therefore, we comparatively investigated this olfactory response of *P. pseudoannulata* to 10 herbivore-induced rice volatiles using Y-tube olfactometer and animal behavior observation and analysis system. Our results showed that 4 herbivore-induced volatiles (Methyl salicylate, cis-3-Hexen-1-ol, 2-Heptanone and Linalool) were significantly induced the olfactory behavioral of the male *P. pseudoannulata*, but the female *P. pseudoannulata* were not response. There was no significant difference in the time of the male spiders making a choice among the four herbivore-induced rice volatiles. These results indicate that the male *P. pseudoannulata* can sensitive to herbivore-induced volatiles and use these chemical signal substances.

No. 24

Post-maturity molting in web-building spiders and its mechanism

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Abstract: In arthropods, the exoskeleton grows in discrete steps through molting as body mass and size change continuously, and molting normally stops once sexual maturity is achieved. Interestingly, there are several animal species that continue to molt after sexual maturity, which is called post-maturity molting (PMM). In spiders, this phenomenon has predominantly been known in phylogenetically more ancestral and sexually monomorphic spiders such as liphistiids and mygalomorphs, and it has rarely been reported in web-building spiders. Here we show that females in the giant wood spider *Nephila pilipes* (Fabricius 1793) become giants through post-maturity molting, a phenomenon resulting in female carapaces on average 4.27 times longer than males' (ranging from 3 to 6.4 times), and female mass averaging 125 times the male's (ranging from 28 to 502 times). Though the mechanism of molting has been studied intensively, the mechanism of PMM remains unknown. We investigated factors that potentially induce PMM in the *N. pilipes*, which has the greatest degree of sexual dimorphism among terrestrial animals. We manipulated the mating history and the nutrient consumption of the females to examine whether they can affect PMM. The results showed that female spiders under low nutrition were more likely to molt as adults, and mating had no significant influence to the occurrence rate of PMM. Moreover, spiders that experienced PMM lived longer than those without and their body sizes were significantly increased. Therefore, we concluded that it is the nutritional condition rather than the mating history that has affected PMM.

No. 25

Extreme long-lasting maternal care in a jumping spider

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Abstract: Long-lasting parental care (parents providing care for their young from birth to sex maturity) is vital for the learning and survival of offspring. Yet this extreme parental care is only known from long-lived social vertebrates and has never been observed in any solitary invertebrate species. We provide the first evidence of this extreme long-lasting maternal care in a jumping spider *Myrmarachne magnus* (Aranea: Salticidae) through a combination of field and laboratory investigations. First, the number, body length, and sex of siblings (if adults) of each nest were recorded from breeding nests in the field. Second, the number and body size of offspring, form and duration of food provision, growth and nest departure of offspring, and sex ratio and body size of sexually matured offspring were investigated under laboratory conditions. Third, a comparative study was conducted to investigate the adaptive value of this extreme maternal care through mother removal and observation of the nutritionally independent offspring. Results show that 1) *M. magnus* females provide maternal care until offspring sexual maturity in both field and laboratory conditions. 2) Food provision is conducted though "milk" feeding. 3) Offspring start hunting at around 25 days from hatching (around 3.5 mm in body length) but continue milk provisioning until 43 days (i.e. until the subadult stage). 4) Male offspring leave the nest after reaching maturity while females remain in the breeding nest after maturity for several more days. 5) 20 days after hatching, offspring could survive to the adult stage without maternal assistance, but with decreased growth rate and survival rate, increased hunting levels, and earlier nest departure compared to those spiderlings remaining with their mother. 6) Adult sex ratio of spiderlings is 7:1 (female/male) when maternally reared, yet the ratio in the absence of the mother (from the 20th day to the adult stage) was around 1:1. These results suggest that a short-lived, solitary invertebrate can exhibit complex, long-lasting maternal care; maternal food provisioning is necessary to maintain proper offspring development; and the nest sex ratio may be manipulated by the mother to acquire more adult females.

No. 26

Towards a spider photo guide of Xishuangbanna, Yunnan, China: new photographic techniques

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Abstract: Reliable field guides with nice, colourful photographs of spiders, with their correct names, are not widespread in South East Asia. Most of the scientific literature describes how spiders look like in collections, after at least several years of preservation with consequent loss of colours. This all makes it difficult to interest the general public or even life science students in tropical arachnology. We need more field guides (printed, on the internet, or both) to show what magnificent creatures live in tropical rain forests, which are constantly under threat.

In 2015 the first steps were taken to prepare a field guide with photographs of live spiders of Xishuangbanna prefecture, in the very south of China, close to Laos. These preparations were continued during three weeks before the 4th Conference of the Asian Society of Arachnology. More Xishuangbanna spiders were collected and photographed, using new techniques like automatic focus bracketing and stacking, and very high resolution photography with a moving sensor. These techniques will be explained and their usefulness for spider photography will be discussed. A few results of the last photo shoot will be shown.

Keywords: spiders, identification, photography, field guide, South China

No. 27

Connection between female internal reproductive ducts and epigynal tracts and its biological implications in entelegyne spiders

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Abstract: Terrestrial animals have generally evolved genitalia for sperm transfer from the male to the female in order to perform internal fertilization. Entelegyne spiders have complex and diverse genitalia, and fertilization process separating from copulation. Both features are related with internal fertilization; however, the structure of their female genitalia, the epigynum, that is responsible for directing the sperm to meet eggs, and the exact site where internal fertilization takes place, remain obscure. In the present study, based on a broad sampling of entelegyne epigyna, we combined information collected by using a stereomicroscope, scanning electronic microscope and serial histological sections to depict the connection between epigynal tracts and internal reproductive ducts. Our results indicate that the speculated direct connection between fertilization tracts and the uterus externus is not present in general. This scenario makes the widely accepted idea problematic: how entelegyne spiders perform internal fertilization? Furthermore, results of the present study support the hypothesis of the entelegyne epigyna origin from the tegument folds located above the epigastric furrow, rather than the uterus externus, and the monophyly of the entelegyne spiders.

No. 28

The effects of climate and land use change on soil mites– trophic structure, body size and biomass

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Abstract: Soil mites are individual-rich in agriculture and grassland ecosystem. The on-going changes of climate and land use, which induced by human activities, might cause a degradation of soil conditions and further lead to variations in trophic structure, body size and biomass of soil mites. In order to understand of the response of soil mites to climate change under different land use type. Our study was carried out at a huge global change experimental facility–GCEF in Bad Lauchstädt near Halle, Saxon-Anhalt, Germany. The results showed that (1) a warmer climate favored the small-bodied mites. (2) Predatory mites often had higher body size, biomass and longer generation cycles, which were less affected by climate change. (3) a decreased total body size of the mite community due to a higher proportion of detribivores. (4) more individuals of mites in grasslands than in croplands. Land use affected the trophic structure and abundance of soil mites significantly, rather than climate change, but the effect of climate change can be modified by land use.

No. 29

Phylogenetic and functional perspectives on β-diversity: the case of spiders and ants along elevations

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Abstract: Understanding broad-scale patterns in community composition has both theoretical and practical implications. Key to this understanding is identifying the drivers of beta diversity in both space and time. Much of this research has focused on taxonomic approaches, but recent advances provides for the inclusion of functional and phylogenetic approaches. Ants and spiders were caught along an elevational transect across a mountain in South Africa. β-diversity was decomposed into turnover and nested components. Functional and taxonomic β-diversity was similar, but functional β-diversity was driven by nestedness, while taxonomic β-diversity was the result of turnover. Phylogenetic β-diversity low with turnover and nestedness contributing equal amounts. Similar results were found for both ants and spiders. Although there are considerable turnover in species along the transect, trait diversity is filtered out with increased elevation on the mountain. While distance and elevation is important in explaining taxonomic β-diversity, functional β-diversity is driven by soil properties and habitat structure. This analytical framework could provide a basis for monitoring the impact of anthropogenic influences on spider and ant diversity.

No. 30

Diversity of spiders (Arachnida: Araneae) in the high-altitude shola ecosystems of the Western Ghats biodiversity hotspot in India

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Abstract: An exploratory survey and analysis of spider diversity was conducted in tropical montane cloud forests (TMCFs) of Western Ghats, one of the 36 global biodiversity hotspots. Western Ghats is a mountain range that runs parallel to the western coast of the Indian peninsula. It is a UNESCO World Heritage Site and is one of the eight "hottest hot-spots" of biological diversity in the world. .TMCFs of Western Ghats between 1,000 and 3,000 m are commonly known as cloud forests or shola habitats which are a natural mosaic of grasslands and forest patches. The study was conducted in the TMCFs of southern Western Ghats in the state of Kerala. A total of 165 species of spiders belonging to 26 Families and 101 genera have been sampled from this area for during a sample period of 30 months. Among these, 10 spp. have been identified to be new to science. Theridiidae were the most dominant family represented by 19 spp. Guild structure analysis revealed nine feeding guilds viz., orb-weavers, ground runners, stalkers, burrowers, ambushers, foliage runners, space web builders, sheet web builders and tangle web builders. Comparative study of species collected from upper montane cloud forests (UMCFs) and lower montane cloud forests (LMCFs) in Western Ghats revealed exceptionally high degrees of endemism, as well as marked intraspecific variation among some genera, especially with regard to *Plebs, Martensopoda* and *Hermippus.* The isolated geographical nature and unique environmental conditions of this ecosystem contributes to the extreme speciation in the area. High degree of endemism along with the occurrence of several new species makes cloud forests hottest in respect of species diversity.

Key words: Araneae, shola, spiders, tropical montane cloud forests (TMCFs), Western Ghats

No. 31

Diversity and Composition of Riparian Spider in Rayong Botanical Garden, Rayong Province, Thailand

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Abstract: The riparian zone is a transitional area between aquatic and terrestrial biomes. Spiders play an important role in this area as predators in the riparian food web. This research aims to study the diversity and distribution of riparian spiders in Rayong Botanical Garden, Rayong Province. The spiders were collected monthly using a pitfall trap and semi-quantitative sampling from October 2016 to March 2017. Seven collection stations were used. 215 mature specimens were obtained and a total of 46 species in ten genera were recorded. The most diverse family was Araneidae, with 15 species. In addition, the Lycosidae family was dominant in swamp forest sites, and the Zodariidae family was dominant in sites affected by human activity. The collected spiders were classified into guilds using their foraging behaviors. The most dominant guild was ground hunters (46.96%), followed by orb web builders (22.47%), other hunters (12.87%), specialists (11.86%), space web builders (2.52%), ambushers (2.02%) and sheet web builders(1.26%). Soil temperature, soil humidity, canopy cover and dissolved oxygen were important for species distribution, particularly canopy cover (Eigenvalue Axis1 = 0.681,Axis2= 0.566, P = 0.007). Canopy cover provides shade for animals beneath it. This shade may support ambushing or the building of webs, and leaf litter may represent afood source for spiders' prey.This research project will provide information that will aid in the future study of the swamp forest ecosystem in Thailand.

Keywords: Riparian, Spider, Diversity, Swamp forest, Guild composition, Thailand

No. 32

The application of Daddy longlegs (*Pholcus phalangioides*) as a proton exchange membrane in the production of electricity from the fuel cell.

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Abstract: The study about the application of Daddy longlegs (*Pholcus phalangioides*) as a proton exchange membrane in the production of electricity from the fuel cell of algae. The objectiveare 1. To study general characteristics of Daddy longlegs (*Pholcus phalangioides*). and 2. To compare studying between the application of Daddy longlegs (*Pholcus phalangioides*) web as proton exchange membrane for the production of single cell algae and the PEM (proton Exchange Membrane) as proton exchange membrane for the production of single cell algae by use *Chlorella* sp. and single cell algae from natural water sources (Mixed algae) are electron supply.Form the study of part 1 found Daddy longlegs (*Pholcus phalangioides*) arranged in Phylum Arthropoda, Class Arachnida , Order Araneae, Family Pholcidae has 8 legs , 8 eyes . They live in the corners of the ceilings of the rooms, tables, chairs or other materials store in the house. The average body size of the Cephalothorax wide 0.2 centimeters long 0.5 centimeters and the average body size of the Abdomen wide 0.3 centimeters long 1.5 centimetersand form the study part 2 found that the application of Daddy longlegs (*Pholcus phalangioides*) silk as a proton exchange membrane in the production of single-celled algae compared to using PEM (Proton Exchange Membrane) as proton exchange membrane in the production of single cell algae. There are 5 sets of five algal fuel cell experiments. The 5 experiments with 50 ml of waste water from my local. Series A (*Chlorella* sp. 50 ml. + waste water 50 ml.) has the average electricity 0.014 µA. B series [natural water sources (Mixed algae) 50 ml. + waste water 50 ml.] has the average electricity 0.07 µA. C series (Water filterfrom *Chlorella* sp. 50 ml. + waste water 50 ml.) has the average electricity 0.04 µA. D series [Water filters from natural sources (mixed algae) 50 ml. + waste water 50 ml.] has the average electricity 0.05 µA. E Series (Distilled water 50 ml. + waste water 50 ml.) has the average electricity 0.04 µA. Controller 3 sets include series A (Distilled water 100 ml.) has average electricity 0.00 µA. , series B [100 ml. water purifier from 100 ml. natural water source(mixed algae)] has an average electricity 0.19 µA and series C (Water filterfrom *Chlorella* sp. 100 ml.) has average electricity 0.00 µA. By using a single microbial fuel cell and using a graphite cathode as an anode chamber and cathode poles for 9 hours, the amount of electrical current used by the spider web of Daddy longlegs (*Pholcus phalangioides*) was proton exchange membrane. The amount of electricity is more than the amount of electricity using PEM as the proton exchange membrane. In the beginning, it can be concluded that the use of spider[Daddy longlegs (*Pholcus phalangioides*)] web as a proton exchange membrane can actually cause the exchange of protons. But not yet effective enough because there are many factors involved and can’t control it. So the studying will continue.

No. 33

Progress in taxonomy of millipede (Arthropoda, Diplopoda) in China

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Abstract: The Diplopoda (millipede) is the largest class of the subphylum Myriapoda, and the third largest class of terrestrial Arthropoda following Insecta and Arachnida, with about 16,000 described species of 16 orders and 140 families. The diplosegment condition is its key taxonomic feature in which two pairs of legs present in each of most body segments. Millipedes occur on all continents except Antarctica, and occupy almost all terrestrial habitats, with a preference for humid environment, such as forest floor and caves. Brandt (1833) decribed the first Chinese millipede species (*Spirobolus bungii*) from Beijing. So far, 354 species belonging to 11 orders and 33 families have been recorded in China. Here, we introduce briefly the state of millipede taxonomic study in China, determine its main taxonomic problems and impediments, and provide future taxonomic and systematic perspectives.

Keywords: millipedes,Diplopoda, taxonomy, China

No. 34

Systematics of Infraorder Panctenata from China (Arachnida: Pseudoscorpiones)

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Abstract: The Panctenata, an infraorder of the suborder Iocheirata (Arachnida: Pseudoscorpiones), is currently divided into four superfamilies: Garypoidea, Cheliferoidea, Sternophoroidea and Cheiridioidea, and it has been reported 1957 species in 319 genera, 13 families throughout the world. However, very limited specific researchers cover this group of pseudoscorpions of China, although it has a very high species diversity.

The present study deals with a comprehensive systematics research of Chinese Panctenata pseudoscorpions. Totally, 82 species of 41 genera, belonging to eight families, three superfamilies, are recorded, including one newly recorded family; one new genera; 14 newly recorded genera; 38 new species; four newly recorded species; one female supplement and two new combinations. The phylogeny of Panctenata is studied based on the molecular data of COI and 28S rRNA, result shows that the current four-superfamilies classification system should be reviewed to a new five-superfamilies classification system.The phylogeny of Cheliferoidea is also studied based on the molecular data of COI, 18S rRNA and 28S rRNA, result shows: 1) Withiidae is a well supported monophyletic group; 2) the taxonomic status of the subfamilies Miratemninae (Atemnidae) and Philomaoriinae (Cheliferidae) should be reviewed; 3) the monophyly of Chernetidae is well supported by the result based on COI and 28S rRNA, but not supported by that of 18S rRNA.

No. 35

Research Progress of spider families Corinnidae, Phrurolithidae and Trachelidae in China (Araneae: Dionycha)

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Abstract: Corinnidae is a large family, including four subfamilies Corinninae, Castianeirinae, Phrurolithinae and Trachelinae until Ramírez (2014) redefined the Corinnidae to a restricted sense, including only the subfamilies Corinninae and Castianeirinae, and elevated the Phrurolithinae and Trachelinae into family status as Phrurolithidae and Trachelidae separately.

Now these three families comprise a total of 1204 species in 97 genera throughout the world, but currently only 95 species in 11 genera are reported from China. It is clear that the number of species is unreasonable in China where biodiversity is very high. Our laboratory has been studying this group for many years and has found many species new to science, new records and new genus. For the family Corinnidae, we found three new record genera (*Pranburia* Deeleman-Reinhold, 1993, *Allomedmassa* Dankittipakul & Singtripop, 2014 and *Medmassa* Simon, 1887), two new genera and more than 30 new species; for Phrurolithidae, we found one new record genus (*Plynnon* Deeleman-Reinhold, 2001), one new genus and more than 50 new species; for Trachelidae, we found one new genus and more than 15 new species. It now appears that these three families should be estimated at least 190 species in 19 genera of China.

No. 36

Bird-dropping masquerading visually and chemically by a crab spider

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Abstract: A masquerading animal evolves to closely resemble inedible and generally inanimate objects such as bird droppings to avoid predation by being misidentified as inedible objects by its predators and/or gain access to prey by not correctly identified as innocuous objects by its prey. Almost all previous theoretical and empirical studies have exclusively focused on visual masquerade, in which the animal's body colour, size and shape mimic an inanimate object. Here we provide the first evidence of both visual and chemical masquerade in animals. The crab spiders of the genus *Phrynarachne* not only visually resemble a typical bird-dropping in colour, size and shape, they are also smelled like bird droppings, yet this notion remains untested. We hypothesized that the bird-dropping crab spiders resemble bird-dropping not only visually but also chemically to repel predators and also attract prey. We tested this hypothesis by performing behavioural assays using a specialized spider-eating jumping spider *Portia* sp. as predators and houseflies (*Musca domestica*) as prey. We provided the first empirical evidence that like bird droppings, either visual, volatile chemical cues emitted from *P. ceylonica*'s body and silk alone or both repelled significantly more *Portia* and attracted significantly more flies compared to the controls. Accordingly, we concluded that *P. ceylonica* forms a visual and chemical masquerade that resembles bird droppings, thus reducing predation risk and at the same time increasing foraging success.

Keywords: bird-dropping, visual masquerade, chemical masquerade, predator avoidance, prey attraction

No. 37

Phylogeny of Chinese Pseudopoda spiders (Araneae: Sparassidae) based on target-gene analyses

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Abstract: The taxonomic impediment is characterized by dwindling classical taxonomic expertise, more rapid taxonomic assessments are needed. Here we pair rapid DNA barcoding methods with swift assessment of morphology in an effort to gauge diversity, establish species limits, and rapidly disseminate taxonomic information prior to completion of formal taxonomic revisions. We focus on a poorly studied, but diverse spider genus, *Pseudopoda*, from East Asia. We augmented the standard barcoding locus (COI) with nuclear DNA sequence data (ITS2) and analyzed congruence among datasets and species delimitation methods for a total of 573 individuals representing 23 described species and many potentially new species. Our results suggest that a combination of CO1 + ITS2 fragments identify and diagnose species better than the mitochondrial barcodes alone, and that certain tree based methods yield considerably higher diversity estimates than the distance-based approaches and morphology. Combined, through an extensive field survey, we detect a twofold increase in species diversity, in the surveyed area, at 42–45, with most species representing short range endemics. Our study demonstrates the power of biodiversity assessments and swift dissemination of taxonomic data through rapid inventory, and through a combination of morphological and multi-locus DNA barcoding diagnoses of diverse arthropod lineages.

Pseudopoda is exclusively distributed in the southern, eastern and north-western parts of Southeast Asia. Most species show limited distribution ranges, but they may be locally abundant and co-occur frequently. Therefore *Pseudopoda* is a good model to analyse evolution and biogeography in the region. In order to solve the matter of morphologically diagnostic groups and geographical distributions of focal *Pseudopoda* spiders much better, we added more fresh specimen and more gene segments (16s, 28s, h3). We use a total of 361 individuals' molecular data including download from Genbank representing 44 described species and about 57 new species.

Keywords: taxonomy, barcoding, morphologically diagnostic groups, geographical distributions

No. 38

Dispersal modality determines the relative partitioning of beta diversity in spider assemblages on subtropical land-bridge islands

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Abstract: Beta diversity describes the extent of change in community composition in relation to complex gradients of environmental variation. However, the widely used broad-sense measures of compositional dissimilarity are not able, in their own right, to reveal the processes and underlying mechanisms that drive community assembly.Here, we identify geographical drivers determining the relative partitioning of species replacement and richness difference or nestedness-resultant components of beta diversity in spider groups with differing dispersal modalities. We sampled spider assemblages on 31 land-bridge islands for two years in the Thousand Island Lake, China. Each species was classified into a dispersal group based on ballooning propensity (frequent, occasional or non-ballooners). Two frameworks were used to separate beta diversity (β_{cc} or β_{jac}) of each group into either species replacement (β_{-3}) and richness difference (β_{rich}) components, or turnover (β_{jtu}) and nestedness-resultant (β_{jne}) components. Mantel and partial Mantel tests were performed to determine correlations between pairwise dissimilarities and difference in island area, difference in distance to mainland and inter-island distance for each group. Results showed that the multiple-island dissimilarity of spiders was primarily driven by turnover. Beta diversity (β_{cc} or β_{jac}) was positively associated with difference in island area in frequent ballooners, and negatively associated with difference in island area in occasional ballooners. Difference in island area had positive effects on β_{jne} for all groups, but negative effects on β_{-3} and β_{jtu} for occasional or non-ballooners. β_{rich} was positively associated with difference in island area in frequent and non-ballooners. We did not find any significant isolation effects for these three measures of dissimilarity. The dominant process of extinction resulted in a high contribution of turnover to the multiple-island dissimilarity of spiders. Specifically, frequent ballooners contributed less turnover to multiple-island dissimilarity than occasional and non-ballooners. The most likely explanation for this is that frequent ballooners were potentially able to colonize all islands, whereas occasional and non-ballooners were constrained by water barriers and were unable to occupy most islands. Contrasting dissimilarities among dispersal groups of spiders demonstrates the importance of beta diversity partitioning, and the mechanistic insight gained on trait-dependence in community assembly.

No. 39

Multilocus sequence data reveal more than two species of *Calommata* Lucus, 1837, the purse-web spiders, in China (Araneae: Atypidae)

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Abstract: The purse-web spider family Atypidae as an ancient branch of the Mygalomorphae represents three genera (*Atypus* Latreille, 1804, *Calommata* Lucus, 1837 and *Sphodros* Walckenaer, 1835) and 52 species over the world. *Calommata*, a unique atypid genus with four cauliflower-like spermathecae, contains 13 described species, of which, two *Calommata* species are known from China – *C.signata* Karsch, 1879 and *C.pichoni* Schenkel, 1963,but *Calommata pichoni* is questionable. While its phylogenetic hypotheses remain untested, here we tested its monophyly, explored its phylogeny, and performed species delimitation of *Calommata* spiders from China using multiple molecular markers (three mitochondrial (COI, 16S and 12S) and two nuclear (28S, H3) gene fragments). Our results supported the monophyly of *Calommata* and presumably revealed several cryptic species. Our analyses also revealed that what was previously considered one widely distributed species (*C. signata*) in East Asian (China, Korea and Japan) actually consists of more than one species, thus the species diversity in this genus and the other two genera may be unexpectedly much higher than previously thought.

Keywords: Atypidae, *Calommata*, Taxonomy, Phylogeny, Species Delimitation

No. 40

Wolbachia impacts on developmental time, sex ratio and horizontal transmission in *Hylyphantes graminicola* (Araneae：Linyphiidae)

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Abstract: The alpha-proteobacteria *Wolbachia* are widely distributed in arthropods and can affect the host's reproduction, growth and development. Although *Wolbachia* are considered to be clonally inherited via vertical transmission, a large number of studies have confirmed the existence of horizontal transmission of *Wolbachia* between different hosts. *Hylyphantes graminicola* is an important natural enemy of agricultural pests, and widely distributes in the field. In order to combine the effects of *Wolbachia* on the reproduction, growth of the host with the use of the spider for the biological control of the pest. Here, the dominant symbiotic bacteria were detected in *H. graminicola*, the effects of *Wolbachia* infection on its developmental time, sex ratio and the horizontal transmission of *Wolbachia* via mating were also studied. We found *Wolbachia* was the dominant symbiotic bacterium in *H. graminicola*, accounting for 50% of the total symbiotic bacteria group. *Wolbachia* could shorten the spider's developmental time and increase female-male ratio of offspring. In addition, *Wolbachia* can be transmitted through mating behavior in *H. graminicola,* but the infection rate is very low. In summary, the developmental time and sex-ratio of spider hosts may affect biological control programs, and our study provides direct evidence for the horizontal transmission of *Wolbachia*via mating behavior. This pathway of *Wolbachia* transmission may be relevant in nature as well as in the lab, and maybe have a variety of biological consequences.

No. 41

Effects of Bt rice on growth and development of *Pardosa pseudoannulata*

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Abstract: *Bacillum thuringiensis* (Bt) toxin produced in Cry1-expressing genetically modified rice (Bt rice) is highly effective to control lepidopteran pests, which reduces the needs for synthetic insecticides. Non-target organisms can be exposed to Bt toxins through direct feeding or trophic interactions in the field. The wolf spider *Pardosa pseudoannulata*, one of the dominant predators in South China, plays a crucial role in the rice agroecosystem. Therefore, it is an important content that evaluate the safety of Bt rice on the spider *P. pseudoannulata*.

The Bt rice has significant impact on developmental time of spider. For total developmental time, the Bt spiderlings spent more time to reach the mature stage when compared to the controls (control group: 67.2 ± 1.58 days, test group: 73.2 ± 1.022 days, $p < 0.05$). The intermoult period of each instar in Bt spiderlings was also longer than that of controls at each instar, except for the 2nd and 8th ($p < 0.05$). The comparative transcriptome analysis resulted in 136 DEGs between Bt containing spiderlings and controls. Functional analysis suggested that many DEGs were involved in metabolism of chitin, cuticle and protein, implying a potential effect on the formation of new cuticles of spider during molting, which may contributed to the delayed development of spiderlings.

The fecundity of adult female spider was not influenced response to Bt rice. The reproductive parameters (pre-oviposition period, post-oviposition stage, number of eggs, and egg hatching rate) of the Bt containing spiders were not different from the controls. Furthermore, the accumulated Cry1Ab did not influence several vitellin (Vt) parameters, including stored energy and amino acid composition, during one generation. We considered the possibility that the Cry toxins exert their influence on beneficial predators via more subtle effects detectable at the molecular level in terms of gene expression. This led us to transcriptome analysis to detect differentially expressed genes in the ovaries of spiders exposed to dietary Cry1Ab and their counterpart control spiders. Eight genes, associated with vitellogenesis, vitellogenin receptor activity, and vitellin membrane formation were not differentially expressed between ovaries from the treated and control spiders, confirmed by qPCR analysis. We infer that dietary Cry1Ab expressing rice does not influence fecundity, nor expression levels of Vt-associated genes in *P. pseudoannulata*.

We also carried out a tritrophic bioassay to assess the potential effect of Bt rice on the foraging behavior of the *P. pseudoannulata* and its underlying molecular mechanism. Results indicated the Bt-containing spiders expressed a higher foraging range when compared to controls. The high throughput de novo transcriptome sequencing was further carried out for central nervous system (CNS) of *P. pseudoannulata* with and without Bt protein intake. In all, the expression of 42 unigenes was significantly changed in Bt-treated spiders, compared to controls. Functional analysis of DEGs showed the expression levels of genes related to energy metabolism were changed in response to Cry1Ab, which may contribute

to a more active foraging behavior. In addition, some DEGs also have a function related to metal ion binding, implying a potential influence on metal ions-dependent reactions. This may be associated with Cry1Ab resistance mechanism in the spider.

In addition to, the venom were dissected from Bt and non-Bt spiders respectively for RNA sequencing. The gene expression analysis was indicated many DEGs were involved in immune and stress responses, including genes encoding heat shock protein, toll-like receptor, GST, NADH dehydrogenase.

No. 42

Effects of Cadmium on the safety of the Wolf Spider *Pardosa pseudoannulata*

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Abstract: Cadmium (Cd) can be transferred and accumulated in the spider, affecting their physiological and ecological traits and/or show toxicological effects, and posing a survival risk for them. *Pardosa pseudoannulata* is one of the most common wandering spiders in rice fields across the rice growing regions of China. To understand the exact molecular and cellular basis of spider when exposure to Cd, we conduct a transcriptomic analysis of cerebral ganglions and venom glands in *P. pseudoannulata* adults, and 5th instars spider *P.pseudoannulata*, in which the adults spiders were fed with Cd-accumulating fruit fly for30 days, and the instars spider were fed for 2, 5, and 8 days respectively.

From the transcriptomic analysis of cerebral ganglions and venom glands, 123,328, and 92778 assembled unigenes, 1,441 and 237 Cd stress-associated DEGs were obtained respectively. We found that DEGs from transcriptomic analysis of cerebral ganglions falling into the categories of oxidative phosphorylation-associated, calcium signaling-associated, cGMP-PKG signaling, nervous disease-associated and ribosomal-associated categories showed changes in expression. The immunity-related DEGs from transcriptomic analysis of venom glands involved in bacterial invasion of epithelial cells, leukocyte transendothelial migration, platelet activation, apoptosis, Rap1 signaling pathway showed changes in expression. We obtained 92778 unigenes, 302, 655, and 424 DEGs in TS-2, TS-5, and TS-8 respectively from the transcriptomic analysis of 5th instars spider. The GO enrichment analysis showed that the terms related to neural signal transduction, multiple tissular, organic maturation, and molt cycle regulation were heavily enriched in all spiders implying a potential effect on growth and development of spider during postembryonic development period.

Our results provide the comprehensive transcriptome dataset of cerebral ganglions and venom glands response to Cd, and some key Cd-responsive genes, which revealed the molecular events status in *P. pseudoannulata* by means of RNA-Seq.The results were valuable for throws light on the toxicity mechanism of Cd, and ecological protection of spiders under heavy metal pollution.

No. 43

Heteropoda venatoria as an insect hunter revealed by the biochemical and pharmacological studies of its venom

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Abstract: *Heteropoda venatoria* is a venomous spider species distributed worldwide and has a characteristic habit of feeding on insects. Its venom is the important tool for the spider capturing insect preys, so we want to know the component, biochemical and pharmacological properties of the venom from the spider. We first found the venom is a complex mixture mainly containing diverse peptides with molecular weights ranking 3000-5000 Da, as revealed by RP-HPLC, MALDI-TOF and cDNA library analyses. Second, intra-abdominal injection of the crude venom had severe toxic effects on cockroaches and caused death at higher concentrations, but low effects on mice. The LD_{50} was 28.18 μg/g of body weight in the cockroach. It was found that the venom had potent inhibitory effect on voltage-gated sodium channels (VGSCs) in *P americana* cockroach dorsal unpaired median (DUM) neurons with an IC_{50} values of 6.25±0.02 μg/mL. However, 100 μg/mL venom only partially blocked VGSC currents in rat dorsal root ganglion cells, a much lower inhibitory effect than that on DUM VGSCs. Third, we isolated an insecticidal peptide from the venom. Injection of the insecticidal peptide into cockroach induced death, LD_{50}=14 μg/g. It has no effect in mice when injected intraperitoneally at dose of 7 mg/kg.The peptide dramatically inhibited DUM VGSCs, IC_{50}=670 nM, and hardly inhibited on Kv and Cav currents at a high concentration of 10 μM . These data indicated high selectivity of the peptide to insect sodium channels and high safety for mammals. Taken together, our study provided insights into the spider *H venatoria* feeding on insects, and the insect-selective peptide identified might have potential for novel insecticide development.

No. 44

Two new genera of linyphiid spiders from Southern China (Araneae: Linyphiidae)

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Abstract: The recent collection from Chongqing, Hubei and Yunnan Provinces have revealed two new genera ***Badongnus* gen. nov.** (type species: *Badongnus inversus* sp. nov.(♂♀)) and***Tengchongnus* gen. nov.** (type species: *Tengchongnus triangularis* sp. nov. (♂♀). In this paper, the detailed morphological description, illustration of the new genera, new species and distribution are provided.

***Badongnus* gen. nov.**

Etymology. The generic name is derived from the type locality. Gender masculine.

Diagnosis. The new genus is diagnosed by its unique structure of embolic division, notably by its long, broad lamella characteristica, running parallel to the cymbium; embolus stout, rounded, highly sclerotized with a pointed end and the inverted loops of copulatory ducts in female's epigyne.

***Badongnus inversus* sp. nov.**

Etymology. The specific name is derived from the Latin adjective "*inversus*", meaning "inverted", referring to the inverted loops of copulatory ducts in female's epigyne.

Male Palp. Tibia with two retrolateral trichobothria and several dorsolateral short spine like hairs, provided with two apophysis, the retrolateral one small and the other one is large with a blunt end; paracymbium J-shaped and distal end provided with a long tooth; protegulum long, transparent, covering the distal suprategular apophysis in prolateral view; distal suprategular apophysis red, round, running parallel to embolus; lamella characteristica long, broad, running parallel to the cymbium; embolus stout, rounded, highly sclerotized with a pointed end.

Epigyne. Wider than long; ventral plate somewhat rectangular; dorsal plate prominent, slightly trapezoid; copulatory ducts long, proximal part with a broad loop, distal part forming four inverted loops before joining the spermathecae; spermathecae oval shaped.

***Tengchongnus* gen. nov.**

Etymology. The generic name is derived from the type locality. Gender masculine.

Diagnosis. The new genus is distinguished by, thorax region of male provided with a triangular projection. Terminal apophysis with two arms; 1) long, prominent, bottle shaped, protruding upward and above the cymbium. 2) short, distal part broad with blunt end. Median apophysis short with pointed end. Protegulum much longer and membranous. Embolus long, starting from the pro-lateral side of the embolic division, arch shaped distally curved. Dorsal plate of epigyne ventrally with a depression, divided by a septum, which connects it with the ventral plate.

***Tengchongnus triangularis* sp. nov.**

Etymology. The specific name is derived from the combination of two Latin adjective "*triangularis*", meaning "triangular", referring to the thorax region of male provided with a triangular projection.

Male Palp. Patella 0.68mm long, much longer than the length of tibia and cymbium, provided with short spine like hairs; Tibia with one dorsolateral trichobothria and several short spine like hairs; in ventral view tibia with one long reterolateral apophysis, protruding upward with a broad distal end, looks like cross-shaped; paracymbium hook-shaped; protegulum much long, membranous and distal part tapering, curved around the terminal apophysis; Terminal apophysis with two arms; 1) long, prominent, bottle shaped, protruding upward and above the cymbium. 2) short, distal part broad with blunt end. Median apophysis short with pointed end. Embolus highly sclerotized, long, arch shaped, distal part tapering, curved around the terminal apophysis.

Epigyne. Wider than long; ventral plate semi-spherical with long spine like hairs; dorsal plate of epigyne ventrally with a depression, divided by a septum, which connects it with the ventral plate; copulatory ducts looks like question mark shaped (?); spermathecae round, protruding in lateral direction.

Keywords: Erigoninae,Taxonomy, Chongqing, Hubei, Yunnan

No. 45

Spider Resilience to Disturbance: A Comparative Study on Predatory Spider Communities in Natural and Extensively Managed Pomelo Orchards

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Abstract: Spiders are the main natural predatory enemies in agroecosystems. The quantity stabilization or recovery capability of natural enemies is important in agricultural management. From 2015 to 2016, a spider survey was conducted in a non-managed pomelo orchard (NMPO) and a moderately managed pomelo orchard (MMPO). In total, 872 spider specimens, which belong to 15 families, 31 genera, and 43 species, were collected in the NMPO and 863 spider specimens, which belong to 11 families, 21 genera, and 24 species, were collected in the MMPO. In both the NMPO and MMPO, Salticidae was the family with the greatest species diversity, Theridiidae was the family with the greatest number of individuals, and *Theridion xianfengense* was the dominant species. Indices of species diversity, richness and evenness were greater in the NMPO, while spider dominance was greater in the MMPO. In the NMPO, the total number of spiders showed regular annual fluctuations, while in the MMPO, the spider quantity was significantly reduced in April and August, when insecticides and fungicides were applied. However, owing to the quantities of the dominant families, such as Theridiidae and Salticidae, that were recovered in the second half of the year, the total spider quantity curve in the MMPO showed a rise-after-suppression trend. Our study verified that spider species were significantly reduced in the MMPO, which is undergoing moderate disturbances, but the total number was relatively stable owing to the quantity recovery of spiders in Salticidae and Theridiidae. This benefits pest control in the moderately managed agroecosystems.

Keywords: Spider, Predatory enemy, Artificial disturbance, Resilience, Agroecosystem

No. 46

Research Progress of the spider diversity from Mt. Jinggang, Jiangxi, China

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Abstract: In recent four years, an extensive faunal survey of the Jinggangshan National Natural Reserve (Jiangxi Province, South China) focused on spiders were conducted.More than 500 species of 44 spider families were collected, using a variety of sampling techniques such as trees beating, leaf litter sieving, net- sweeping, hand collecting etc. Currently part of the work including some identified and unidentified species list by families is as follows: Anyphaenidae (2 genera, 4 species); Araneidae (13genera, 37 species, 3 new species, 20 uncertain); Clubionidae (6 genera, 13 species, 3 new species); Corinnidae (2 genera, 2 species, 1 new species); Ctenidae (1genus, 1 species, 1 uncertain); Eutichuridae (1 genera, 6 species, 1 new species); Gnaphosidae (5 genera, 11 species, 2 uncertain); Hahniidae (1 genera, 2 species); Hersiliidae (1 genera, 1 species); Hexathelidae (2 genera, 4 species); Liocranidae (2 genera, 2 species, 2 new species); Lycosidae (6 genera, 14 species, 6 uncertain); Mimetidae (1 genera, 4 species); Miturgidae (2 genera, 7 species, 1 new species); Oecobiidae (1 genera, 1 species); Oonopidae (5 genera, 10 species, 5 new species); Oxyopidae (2 genera, 9 species, 5 uncertain); Philodromidae (2 genera, 6 species); Pholcidae (4 genera, 8 species); Phrurolithidae (4 genera, 8 species, 7 new species); Pisauridae (2 genera, 5 species, 1 uncertain); Salticidae (40 genera, 108 species, 28 new species); Scytodidae (1 genera, 1species, 1 uncertain); Segestriidae (1 genera, 1 species); Sparassidae (4 genera, 15 species, 3 new species); Tetragnathidae (5 genera, 12 species, 1 new species, 2 uncertain); Theridiidae (27 genera, 67 species, 13 new species, 20 uncertain); Thomisidae (23 genera, 40 species, 21 new species); Trachelidae (1 genera, 1 species); Zodariidae (1 genera, 1 species).

Keywords: Spider; Taxonomy; Mountain Jinggang; Jiangxi Province; China

No. 47

Ornamental coloration associated intra-sexual contest in jumping spider *Siler semiglaucus*

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Abstract: Animals engaging in potential time and energy cost contests are expected to estimate either the resource-holding potential (RHP) of their own (‘self-assessment strategy’), or difference between their rivals and their own (‘mutual assessment strategy’). Body size are commonly used a proxy for RHP in animal contests. However, ornamental coloration is also used as a visual signal in intraspecific communications in many species. In the present study, we staged intra-sexual contests between size-matched *Siler semiglaucus*, an ornate species of Southeast Asia widely distributed jumping spider, for both sexes, to examine whether and how natural body coloration could be an appropriate proxy for RHP in intra-sexual contests, in terms of its effect on both contest outcomes and assessment strategies. Our results suggested that red color expressed on the dorsal abdomen was a reliable parameter to predict contest outcome in both sexes; however, no robust conclusion of assessment strategy was to drawn based on the available data. We first discussed the function of red color in animal communication, further moved onto the appropriate choice of RHP estimates and contest costs.

Keywords: intraspecific communication, intra-sexual contest, assessment strategy, body coloration, jumping spider, *Siler semiglaucus*

No. 48

Beta diversity of arboreal spider under different spatial and temporal scales reflects dissimilar mechanisms of community assembly in a temperate forest

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Abstract: Most of the canopy spider research were mainly explored how to measure and estimate the biodiversity of a community or compare the biodiversity of different habitats. However, studies focusing on detect the spatial and temporal variation of spider community composition is noticeably rare. Beta diversity, which represents the variation in species composition between habitats, allows the ecologists to explore the mechanisms and processes underlying the community assemblage. We used the spider data collected from 324 European beech trees (*Fagus sylvatica* L.) along 18 months (June, August, October of 2005 and 2007; from November 2005 to October 2006) and the trees were distributed in three isolated patches (old-growth patch: >150 years old; mature: 50–60 years old and young: 20–25 years old) in Würzburg University Forest (Germany). In order to detect how species composition change under different spatial and temporal scales, we used the variance-based method to estimate beta diversity at three scales: (i) spatial scale; (ii) temporal scale; (iii) spatial-temporal scale. After that, the beta diversity(s) were partitioned into local contribution to beta diversity (LCBDs) and species contribution to beta diversity (SCBDs). Then the relationship of LCBDs (SCBDs) and community metrics (species richness, species abundance, occupancy), environmental factors (mean temperature, precipitation) and species characteristics (relative ballooning ability) were explored by using Pearson correlation coefficients and beta regression model. Main results are as follows: 1) The BD_{Total} increased as the grain size decreased (i.e. Patch-Temporal community-Singer tree). 2) The beta diversity of high stratum (old-growth patch) were significantly higher than the other under spatial, temporal and spatial-temporal scales. 3) The LCBDs of high stratum contained all of the significantly time period and contributed more than the other temporally, represented the uniqueness of high stratum among the patches. 4) Species occupancy showed a very strong relationship with SCBDs under different scales among habitats, suggested that species occupied more stratum/trees or occurred more often contributed most to beta diversity. Our findings of exploring the contribution of habitats, time or species to overall beta diversity are of high importance to community ecology and spider conservation in European economic forest.

No. 49

The Use of Spiders (Araneae) as Ecological Indicators

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Abstract: Spiders are key predators in ecosystems thus have an important role in the biological control of pest species. Meanwhile, spider assemblages can serve as good indicators of biodiversity when comparing habitats because they are sensitive to a wide range of environmental factors and are suitable for evaluating the impact of habitat changes. We report on our investigation on spider assemblages in importance while fragile ecosystem in Yunnan Province and Inner Mongolia. We focus on the effects of land-use change on spiders from canopies, barks and forest floor in Xishuangbanna, Yunnan Province since 2006. Spiders were collected by using the methods of canopy fogging, trunk traps and direct searching, respectively. The results show that (1) spider composition differ among forests types, and also among canopy, trunk and forest floor in the same forest, (2) spider diversity differ significantly from rubber plantation to natural forests, rubber plantation has lower species richness and abundance in canopies and on floors, whereas has higher abundance on trunks when comparing with natural forests, (3) more complex habitats have a more diverse spider fauna, increase plant diversity and vegetation complexity will be helpful in spiders conservation. We also focus on the effects of sheep grazing, extra rainfall, grass mowing, and simulated N deposition on spiders on grassland in Inner Mongolia since 2016. Spiders were collected by using suction machine. Based on the collection data in 2016, the results show that (1) spider diversity increase significantly with extra rainfall, while decrease significantly with increasing livestock grazing and grass mowing, (2) different type of N or different level of N did not affect spider diversity significantly.

No. 50

Spider diversity and the education in a botanic garden

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Abstract: Spiders are most common animal, people may see in their daily life. It could be found in cities, towns, countryside and all kind of forests. Spiders may be the most easily approached creatures in outdoor education in China. However, spider are usually recognized as dangerous and poisonous animals, and people are extremely scared of it. Public's perception, emotion and attitude are negatively shaped by media and documentary, which expressed a wrong knowledge of spiders. In reality, spiders are cute and interesting, they also play an important role in ecosystem, but heavily threatened by deforestation. Spiders' weird appearance, superb color and amazing behavior are extremely attractive for public. In Xishuangbanna tropical botanic garden, more than 700 spider species were found, the garden afford a nice platform for spider education. We integrated the interesting scientific spider stories into our night hiking and other outdoor activities, we also trained an environmental educator team to lead the kids to enjoy spiders. Here, I will present the spider diversity in Xishuangbanna and share the experience about how we developed the education programs to help people overcome arachnophobia and finally fall in love with spiders in our botanic garden.

Keywords: spider diversity; Arachnophobia; education; Xishuangbanna

No. 51

Oligocene-Miocene mountain building and fluvial formation driving diversification of the primitively segmented spider genus *Sinothela*

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Abstract: Mountain building and fluvial formation are well-known biogeographical barriers that drive diversification and distribution by limiting dispersal and gene flow, thereby promoting divergence among fragmented populations especially in the organisms with low vagility. Here we used the primitively segmented spiders of the genus *Sinothela* (Araneae: Liphistiidae) with limited dispersal ability and disjunct geographical distributions, which are mainly confined to the north of the Yangtze River, the largest river in Asia, as a model system to: 1) investigate its origin and diversification; and 2) explore how mountain and river systems act as barriers in shaping its phylogeography. Phylogenetic analysis and integrated species delimitation based on the fragments of two mitochondrial genes (CO1, 16S rRNA) and three nuclear genes (28S rRNA, H3, ITS2) supported the monophyly of *Sinothela* and validated the ten species recognized by morphological characters. The dating analyses and biogeographical reconstruction revealed that *Sinothela* split from *Ganthela* that is restricted to the south of the Yangtze River when the Yangtze River started through-flow pre-Miocene (29.1-12.2 Ma). The formation of the Yellow River, Qinling-Dabieshan Mountains (Mts) and Taihangshan Mts also served as barriers for the species diversification and speciation of *Sinothela*. We conclude that Oligocene-Miocene orogeny and fluvial formation as biogeographical barriers may have facilitated the process of diversification and speciation in *Sinothela*. Our findings provide the first evidence linking the evolution of organisms to the pre-Miocene birth of the Yangtze River.

No. 52

An overview on the genus *Pardosa*

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Abstract: The present study is based on a critical review of the existing literature data. *Pardosa* is the largest genus in Lycosidae currently counting about 550 species. Its highest species diversity is in the Holarctic and Central and Southeast Asia. The genus is relatively well studied only in the Neartic and Europe. Most of its species occur in Eurasia (272), the Nearctic (100), and Africa (74). The genus has been split into about 33 species groups. *Pardosa nebulosa*-group is the largest species group with about 66 species. The second largest group is *P. monticola*-group with about 25 species, mainly with European and Caucasian distribution. In Europe *Pardosa* is represented by 116 species, of which 14 species containing no figures and are known by original description only. Mediterranean species of *Pardosa*, especially from North Africa and the Middle East are not well known at the moment.

Despite the diversity, worldwide distribution and ecological importance, the taxonomy of *Pardosa* still remains problematic. Judging from the somatic morphology and morphology of the copulatory organs, many of the species considered in the genus are misplaced and belong to other or undescribed genera. Some of them are known by their brief original descriptions and containing no figures. Some previous studies demonstrated that some species groups should gain a status of separate genera. The whole genus is of urgent need of thorough revision.

No. 53

Endemic theraphosids in Western Ghats, India (Araneae: Theraphosidae)

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Abstract: Very little is known about the endemic theraphosids in Western Ghats due to their secluded nature. Fifty-five species of theraphosids in 11 genera are so far known from India (WSC, 2017). Two new species *Annandaliella nigra* sp. nov. and*Neoheterophrictus chimminiensis* sp. nov are now recorded from Western Ghats in Kerala. Rediagnosis of *Annandaliella ernakulamensis* Jose & Sebastian 2008, *Annandaliella travancorica* Hirst, 1909, *Neoheterophrictus bhori* (Gravely, 1915) are also given. Photos and data on distribution, habits and morphometry of the recorded species are given.

Keywords: Taxonomy, Biodiversity, Mygalomorph spiders, Kerala.

No. 54

Geographical Distribution of Spiders

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Abstract: Spiders are popular animals from all continents of the world, except the Antarctic. Spider groups and diversity from different lands are more or less different, that means the distributional patterns of spiders in different continents or areas are different. Besides the internal factors of spiders (capacity for action, etc.), some external factors strongly effect this pattern, such as the continental drift history, climate change and several severe geologic historical events. That is, the status of geographical distribution of spiders is somewhat similar to the spiders' genomes, implying the trace of significant historical events during the evolution and dispersion of spiders. Here on the basis of the database of the world spiders' catalog, we summarized the distribution of all spider families of the world and found most spiders distributes in Gondwana-originated lands. Six patterns / types were divided for all spider groups: Cosmopolitan Type, Sub-cosmopolitan Type, Gondwana Type, Laurasia Type, Limited-area Type and Relic Type. Three transitional areas, Mediterranean region, Southeast Asia and Central America were proposed for spiders' dispersion. And activities of human beings globalizationally accelerate the spiders' distribution. Additionally, we tried to divide the distribution of Chinese spiders into fifteen geographical zones.

Keywords: Dispersion, Gondwana, Laurasia, distributional types, transitional area.

No. 55

Consistency of Lycosidae: A comparative analysis of male bulb

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Abstract: The wolf spider family Lycosidae is one of the most diverse spider group, with 124 genera and 2418 species presently. Species of Lycosidae have almost the same arrangement of eyes, while their genitalia seem different. In order to find the relationships of different species, genera and even subfamilies, 23 species from 11 genera of 8 subfamilies were used to compare their male palpal bulbs on three states (normal, expanded, disassembled). Some structural characters (shape, spatial arrangement and orientation of embolus, conductor, terminal apophysis, median/tegular apophysis, tegular depression, etc.) were carefully compared. The result shows a high consistency when expanded and disassembled. A basic model pattern of the bulbs is given and the suggested terms are discussed.

Keywords: Lycosidae, consistency, bulb, morphology, comparison

No. 56

A systematic review of the family Hahniidae (Arachnida, Araneae)

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Abstract：The comb-tailed spider family Hahniidae is a small group, with only 28 genera and 252 species presently, while species of this group have been recorded from all the continents except the Antarctic. Traditionally, the specific character of hahniids is their transversely arranged spinnerets. But now the phylogenetic status and monophyly of it is still unresolved. Here we give a review to the research history, diversity and distribution, make a discussion of their spinnerets topology, stridulatory organ and epigynal hoods.

Keywords: comb-tailed spider, systematics, discussion, new discovery, new records

No. 57

Strengthening the Spider Tree of Life Trough Phylogenetic Placement

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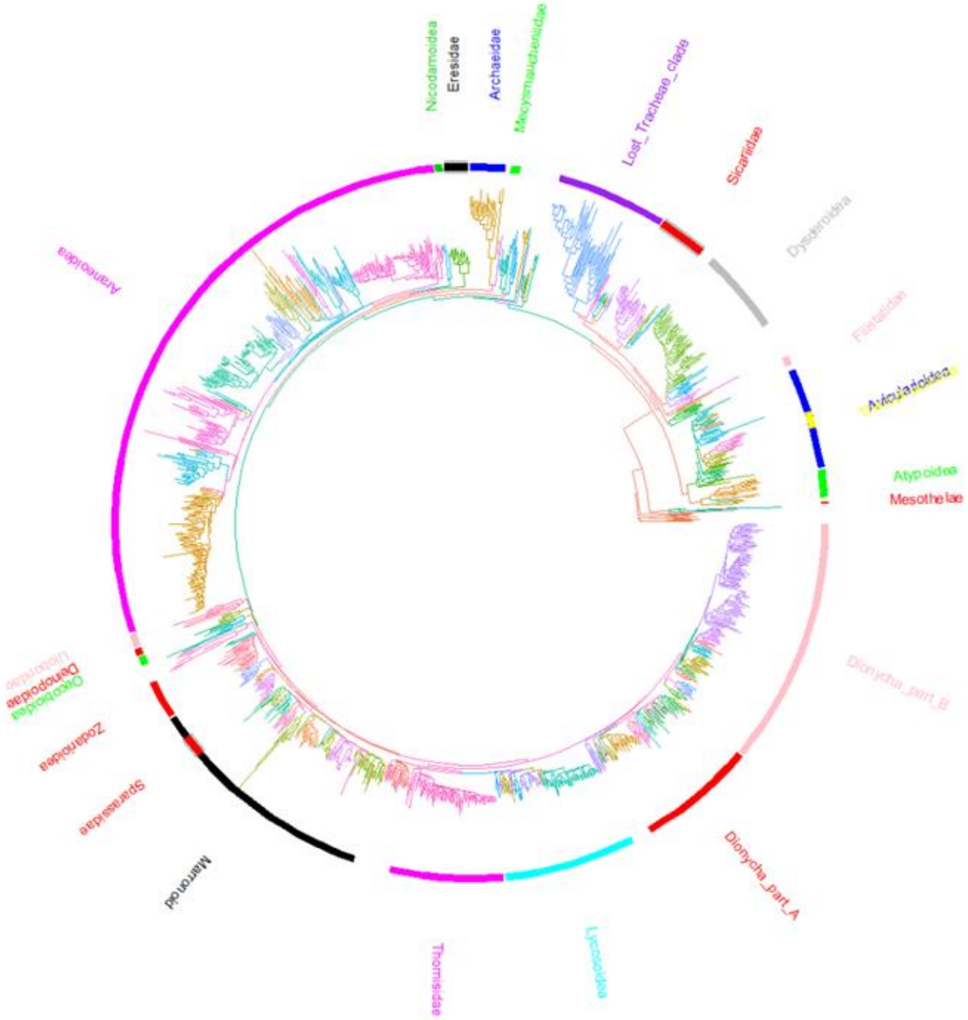
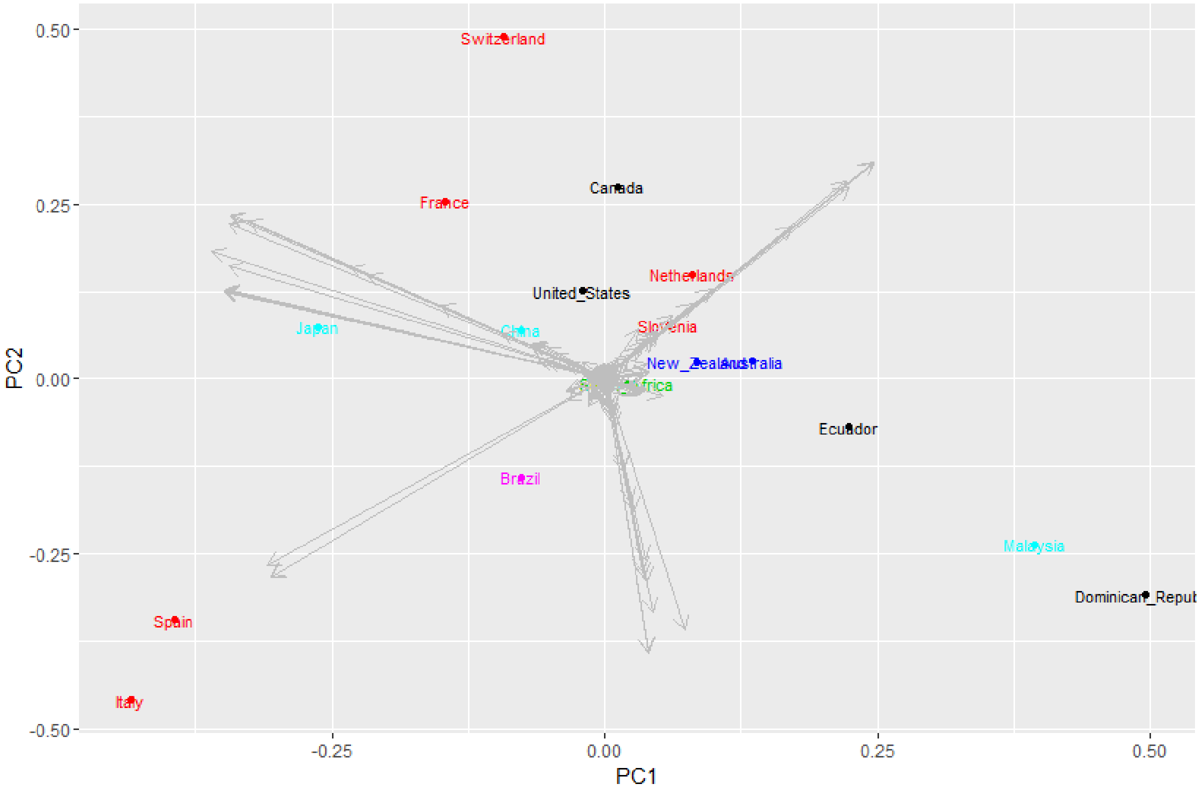
Abstract: The spider tree of life has changed relatively little in the last two decades. Although the phylogenetic backbone for the entire spider order Araneae was not reliably established until the flushing in of Next Generation Sequencing (NGS) data, the “usual suspect genes” such as COI and 28S are still considered useful makers in spider phylogeny constructions, especially at the interfamily level. Wheeler’s recent phylogeny of Araneae employed these “usual suspect genes”, including both mitochondrial (12S, 16S, COI) and nuclear (histone H3, 18S, 28S), for an unprecedented taxon sampling.Here we retrieved, from Genbank and Machida *et al.*’s (2017) Midori reference database, protein-coding genes from 1198 spider species (703 genera; 115 families except Synaphridae) to strengthen spider phylogenetic analyses. Our dataset include 15 mitochondrial genes and 3 nuclear genes and were analyzed using two supermatrices with curated (after removal of the hypervariable expansion segments) and non-curated alignments. Our results showed that: (i) since about 60% of our raw data came from Wheeler’s original dataset, most clades recovered the backbone topology of Wheeler’s original tree; (ii) our data were ambiguous as to the placements of Eresidae, Sparassidae and Thomisidae; (iii) Wadicosinae of Lycosoidae is robustly supported as a junior synonymy of Pardosinae.

Although the incomplete lineage sorting may damp a phylogenetic resolution, as revealed in Frédéric *et al.*’s (2017) study of tropical soils, even if almost all the tips are missing in the spider tree of life, a tree that comprises a broad systematic coverage allows phylogenetic placements to recover most of the novel diversity using Berger *et al.*’s (2011) Evolutionary Placement Algorithm (EPA). We used EPA to place sequence data from Coddington *et al.* (2016) (848 species from 49 families, 313 genera) on the two different reference trees (non-curated and curated ML trees) generated in this study. Our placement results with Coddington *et al.*’s sequence data suggest: (i) EPA is a reliable tool in identifying the higher spider taxa and outperforms the blast-hits method; (ii) even if some raw sequences have mistaken taxonomic annotations, EPA performs better than the blast-hits method; and (iii) EPA can become a quick and reliable tool for spider identification with applications in ecology.

In order to explore worldwide spider distribution patterns, we conducted EPA analysis on spider sequences (with strict binomial species names) stored in the public Barcode of Life Database (BOLD). We obtained, in BOLD, sequences of 1385 species from 57 families and 458 genera. Although DNA barcoding has been developed and used for more than ten years, spider COI sequences with strict binomial species

names are still scarce and restricted to limited genera, mostly outside of the world's biodiversity hotspots. EPA with the non-curated reference tree outperformed that with the curated reference tree. We observed differences in spatial relationships in the resultant PCA planes obtained with EPA using different reference trees. Since RAxML EPA takes base frequencies of the whole alignment (reference sequences plus query sequences) into account to make query placement more accurate, if the reference alignment is curated (i.e. with ambiguously aligned regions removed), it might cause errors in RAxML EPA. Interestingly, we found a potential 'out of Africa' distribution pattern in the world spider fauna from our PCA results. This hypothesis should be taken with doubt because of the missing number of characters in the reference alignment and the limited COI queries in our dataset. The hypothesis is proposed here to facilitate and encourage the barcoding of spiders, especially in Asia, where more sequences and more reliable analytical methods are needed.

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ABSTRACT: POSTER PRESENTATIONS

No. 58

Evaluation of spiders preying on insect pests in a tea plantation through comprehensive indices

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Abstract: Integrated pest management (IPM) dealing with pests should reduce toxic pesticide use and it has long been one of the highlights of agricultural research. Biological control using natural enemies control pest species, and it has gained recognition as an essential component of successful IPM. During the process, it is significant to identify the interactions between the pest and the potential control agent, and then screen the natural enemy species which can be effectively used to biological control. Predatory natural enemies play key functional roles in biological control. However, the screening and evaluation of the main predators of insect pests has seldom been reported in the field. Here, we employed comprehensive indices for evaluating the predation of the main pests by dominant spider species in Chinese tea plantations.

Through a year of intense fieldwork we found nine dominant spider species (*Evarcha albaria*, *Phintella bifurcilinea*, *Coleosoma octomaculatum*, *Meotipa pulcherrima*, *Araneus ejusmodi*, *Neoscona mellotteei*, *Xysticus ephippiatus*, *Clubiona deletrix* and *Oxyopes sertatus*) and two main pest species (*Ectropis obliqua* and *Empoasca vitis*) in tea canopy in study area. We established the relative dominance of the spider species and their temporal niche overlap with the pest species, and analyzed DNA from the nine spider species using targeted real-time quantitative polymerase chain reaction to identify the residual DNA of *E. obliqua* and*E. vitis*. The predation rates and predation numbers per predator were estimated by the positive rates of target fragments and the residual minimum number of *E. obliqua* and *E. vitis* in predators' guts, respectively. The results showed that only four spider species preyed on *E. obliqua*, and the order of potential of the spiders to control *E. obliqua* from greatest to smallest was *N. mellotteei*, *X. ephippiatus*, *E. albaria* and *C. octomaculatum* by the Z-score method. All tested spider species preyed on *E. vitis*, and the order of potential of the spiders to control *E. vitis* from greatest to smallest was *E. albaria*, *N. mellotteei*, *A. ejusmodi*, *P. bifurcilinea*, *C. deletrix*, *X. ephippiatus*, *M. pulcherrima*, *O. sertatus* and *C. octomaculatum* by the same method.

The orb-weaving spider *N. mellotteei* and wandering spider *E. albaria* have the maximum potential as a biological control agent of *E. obliqua* and *E. vitis* in an IPM strategy, respectively. In this study, Z-score integrated four indices (spider species dominance, temporal-niche overlap value between spiders and pests, the average positive rate and the average of residual minimum number of insect pests in individual spider guts) were firstly employed to evaluate predation of predatory natural enemies on insect pests. It is more comprehensive and reliable than any single index. An approach of screening and evaluating main predators of insect pests through comprehensive indices was preliminarily established.

Keywords: spiders; insect pests; predation; tea plantation; molecular gut analysis; real-time quantitative PCR; comprehensive indices

No. 59

Histological study on venom gland apparatus in *Odontobuthus doriae* (Scorpions:Buthidae), *Scorpio maurus townsendi* (Scorpiones:scorpionidea) and *Hemiscorpius lepturus* (Scorpions:Hemiscorpidea) from Iran

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Abstract: Histological investigations were carried out on the venom gland of *Hemiscorpius lepturus*, *Scorpio maurus townsendi*, *Odontobuthus doriae*. The results revealed that the walls of *H.lepturus* poison sacs were single folded whereas those of both *S. m. townsendi* and *O. doriae* were complex folded. The number of folds *O.doriae* was higher than *S. m. townsendi*. It is notable that in *O. doriae*, there were two groups of cells in the poison sac. The venom-producing cells were visible on one side and the mucosal cells on the other side. The mucus cells observed by Masson trichrome staining were darker at the base of the cell than the apex.

Keywords: *Odontobuthus doriae*, *Scorpio maurus townsendi*, *Hemiscorpius lepturus*, scorpion, telson, venom gland, histology

No. 60

Environmental Factors that Affect Bush Dwelling Spider Community Composition in Urban Area

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Abstract: Spiders are the main arthropod predator in terrestrial ecosystems. They are sensitive to disturbance and good indicators of environmental change and habitat quality. However, the effects of vegetation structure (foliage height diversity and plant species diversity) and landscape structure remain unclear. We established 18 transect lines in Fuyang Eco Park, the main campus and the dorm area of National Taiwan University in Taipei City. Samplings of sweep net and visual sighting were conducted monthly in each transect to calculate spider population density, species richness, Shannon diversity index, and functional group composition. We used Generalized Linear Model to analyze the influences of vegetation structure and landscape structure on the spider species diversity. We recorded 1303 spider individuals that belong to 106 species, 76 genera and 20 families. Vertical vegetation structure (foliage height diversity) and the building coverage ratio within 50 m buffer distance were the most important factors which showed significantly positive and negative correlations with spider species richness, respectively. Plant species richness, on the other hand, showed no significant effect. Our results agree with most of previous studies. To conserve bush dwelling spider species diversity, we suggest that vertical vegetation structure should be considered as high priority in constructing and managing suitable habitats in urban area.

Keywords: Urbanization, habitat preference, species richness, functional group

No. 61

Bioassay of components derived from venom of Iranian medically important scorpions to indicating the bradykinin potentiating peptides

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Abstract: Recently decades studies have shown the venom of each scorpion included about 50 proteins and peptides, usually a number of them have toxic effects on mammals and other organisms, particularly arthropods. Some of nontoxic peptides in the venom of scorpions have specific physiological properties such as reducing the blood pressure in the victims. The aim of the present study was determining biomolecules with bradykinin potentiating functions. The venom components of the medically important scorpions including species *Odontobuthus doriea*, *Hottentotta saulcyi* and *Mesobuthus eupeus* were isolated by HPLC and assessed biologically on isolated tissue by organ bath instrument. The obtained groups of fractions (Zones) were selected and assessed on both guinea pigs ileum and rat uterus simultaneously. The region fractions Z_1 and Z_2 derived from venom of *H. sulcyi*, Z_2 and Z_3 zones of *O. doriea* and Z_2 from the venom of *M. eupeus* scorpion have shown potentiating effects on bradykinin during the bioassay.

Keywords: Scorpion Venom, Bradykinin potentiating peptides, Organ bath

No. 62

Body size and personality affect reproduction in raft spiders (*Dolomedes fimbriatus*)

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Abstract: Individual reproductive success depends on behavioural and physical characteristics, but because these attributes are usually studied in isolation, their relative importance remains poorly understood. We studied how physical and behavioural traits affect reproduction in raft spiders, *Dolomedes fimbriatus*. To investigate if personalities (consistent between-individual differences in behaviour) affect sexual behaviour and mating success, we staged three types of personality tests. In males, two situations assessed locomotory activity and one tested for shyness, the latter was also assessed in females. To investigate if male body size affects sexual behaviour and mating success, we staged mating trials exposing a female to two differently sized males. We found consistent behavioural differences among individuals of both sexes in all tested situations. Male activity correlated across all test situations, as well as during mating trials. Our data show that raft spider male mating success relates to individual size and shyness. Male shyness was negatively correlated to aggressiveness towards a rival and copulation success. Male behaviours during mating trials varied according to female characteristics. Males encountering bolder and larger females were less active and less aggressive towards rivals. Compared with smaller rivals, larger males were less active, but had higher mating success. In conclusion, raft spider reproduction depends on the interplay of both male and female personality types, and sizes.

No. 63

Cross-sex genetic correlation does not extend to sexual size dimorphism in spiders

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Abstract: Males and females are often subjected to different selection pressures for homologous traits, resulting in sex-specific optima. Because organismal attributes usually share their genetic architectures, sex-specific selection may lead to intra-locus sexual conflict. Evolution of sexual dimorphism may resolve this conflict, depending on the degree of cross-sex genetic correlation(r_{MF}) and the strength of sex-specific selection. In theory, high r_{MF} implies a tight genetic base for a given trait and consequently sexual monomorphism, while low r_{MF} indicates a loose genetic base and sexual dimorphism. Here, we broadly test this hypothesis on three spider species with varying degrees of female-biased sexual size dimorphism, *Larinioides sclopetarius* (sexual dimorphism index, SDI = 0.86), *Nuctenea umbratica* (SDI = 0.60), and *Zygiella x-notata* (SDI = 0.48). We find moderate body mass heritability, but no obvious patterns in sex-specific heritability. Against the prediction, the degree of sexual size dimorphism is unrelated to the relative strength of same-sex versus opposite-sex heredity. Our results do not support the hypothesis that sexual size dimorphism is negatively associated with r_{MF}. We conclude that the theory behind this prediction is too simplistic, and that a sex-specific genetic architecture may not be necessary for the evolution of a sexually dimorphic trait.

No. 64

First Record of *Rhomphaea Labiata* (Zhu & Song, 1991) (Aranae: Theridiidae) from India

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Abstract: Theridiidaeis one of the largest family of spiders in the world with about 2472 species in 124 genera (World spider catalogue, 2016). These include 58 Indian species belonging to 19 genera (Sebastian & Peter, 2009). In spite of rich diversity, studies about Indian theridiids are highly neglected, probably due to their small size and lack of literature (Siliwal, 2009). Rhomphaea is an odd-looking genus of the spider family Theridiidae. About 33 species of genus *Rhomphaea* is reported from different parts of world, but only one species of Rhomphaea is reported from India so far. *R. labiata* (Zhu&Song, 1991) is first time reported from Kerala, India. Female of *R. labiata* was collected from Peechi-Vazhani wild life sanctuary, Kerala, India*)R. labiata*is earlier reported from China, Korea, Laos and Japan

Keywords: Theridiidae, *Rhomphaea*, taxonomy, first record, India

No. 65

Taxonomy of the Spider Family Araneidae from the Wuling Mountan Area of China

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Abstract: The present paper deals with the taxonomy of orb weaving spiders of the family Araneidae (Arachnida: Araneae) from the Wuling Mountan Area, 142 species belonging to 31 genera have been studied including 1 new genus: *Chorizopesoides* gen. nov.; 17 new species: *Argiopehupingensis* sp. nov., *Araneusbicornutus* sp. nov., *Araneusdigitatus* sp. nov., *Araneusmicroscapis* sp. nov., *Araneuspseudoshunhuangensis* sp. nov., *Araneusrhombus* sp. nov., *Araneusspinosus* sp. nov., *Araneustianfuenis* sp. nov., *Araneustrimaculatus* sp. nov., *Chorizopesconcavus* sp. nov., *Chorizopesoidesquadrituberculatus* sp. nov., *Cyrtarachneelliptica* sp. nov., *Eriovixialingulata* sp. nov., *Larinialongiscapa* sp. nov., *Lariniatriangula* sp. nov., *Neosconacylindrata* sp. nov., *Porcataraneusfoliosa* sp. nov.; 1 single male supplements species: *Chorizopeswulingensis* Yin, Wang et Xie, 1994.

No. 66

Taxonomy of the Spider Family Theridiidaea (Arachnida: Araneae) from the Wuling Mountan Area of China

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Abstract: The present paper deals with the taxonomy of spider family Theridiidae (Arachnida: Araneae) from the Wuling Mountan Area. Totally 132 species belonging to 36 genera have been studied, including 15 new species: *Chrysso atomata* sp. nov.; *Chrysso marsupiata* sp. nov.; *Chrysso rhyncha* sp. nov.; *Dipoena mirabile* sp. nov.; *Dipoena yinae* sp. nov.; *Episinus subnubilus* sp.nov.; *Meotipa caudigera* sp. nov.; *Molione hupingiensis* sp. nov.; *Parasteatoda aequipeiforma* sp. nov.; *Phoroncidia hupingiensis* sp. nov.; *Steatoda cucurbitina* sp. nov.; *Theridion hamatum* sp. nov.; *Theridion obtusum* sp. nov.; *Theridion shimenensis* sp. nov. and*Theridion trimaculatum* sp. nov.. 3 single male supplements: *Phoroncidia concave* Yin & Xu, 2012; *Phoroncidia crustula* Zhu, 1998 and *Theridion obscuratum* Zhu, 1998.

No. 67

Morphology and molecules reveal an unexpected heterogeneous population structure in the pantropical *Heteropoda venatoria* (Linnaeus 1767)

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Abstract: Populations of *Heteropoda venatoria* from Africa, South America, Australia and different regions of Southeast Asia were studied using landmark-based geometric morphometrics and partial sequence data from one nuclear (ITS2) and one mitochondrial (COI) locus. In total, 116 specimens were studied so far using morphometric methods, and sequence data were generated for 29 specimens. The shapes of epigyne and sternum were analysed using principal components analysis, canonical variate analysis and discriminant function analysis to test for differentiation between distinct populations. Molecular datasets were analyzed using TCS networks, and Bayesian and Maximum Likelihood methods to infer phylogenetic relationships. Both data sets reveal a close relationship of African and South American populations, which are separated from Asian and Australian populations. Further, both data sets indicate divergence of the northwestern and the southern populations of Taiwan. The northwestern population clusters with that from mainland China and is distinctly separated from all other Asian populations both by morphological and molecular traits.

No. 68

Geometric morphometrics as a tool for spider species delimitation, the *Micrommata* case (Araneae: Sparassidae)

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Abstract: *Micrommata* Latreille 1804, is the type genus of the family Sparassidae. The diversity of *Micrommata* spiders from Europe, Northern Africa, and Central Asia was studied in order to delimit potential new species. In total 102 specimens were used for this purpose. Besides traditional, visual way of examination, statistical methods were applied using landmark-based geometric morphometrics. Principal component analysis, canonical variate analysis, and regression analysis were applied to test differences between specimens. Five species, including two previously undescribed, were found among the specimens using both methods. According to our knowledge, morphometric geometrics have never been used for spider species delimitation. We suggest that this method serves as a good supplementation for the traditional way of describing new spider species.

No. 69

The Distribution of Canopy Spiders (Araneae) Along an Elevational Gradient of Changbai Mountain, China

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Abstract: Canopy spider assemblages were compared on the northern slope of Changbai Mountain, along an elevational gradient of 800 m, 1100 m, 1400 m and 1700 m. Spiders were sampled by fogging tree canopies in four replicate sites at each elevation once in the middle of August 2016. A total of 8848 spiders comprising 88 species were collected from 16 samples covering a total of 800 m^2 of projected area. The results show that the most abundant families of canopy spider are Thomisidae, Araneidae and Linyphiidae (69.2% of total individuals). The diversity of canopy spiders decrease along the elevational gradient from 800 m to 1700 m, whereas the highest abundance of canopy spiders are found from the samples collected at the elevation of 1100 m. A redundancy analysis (RDA) and the Monte Carlo permutation test (4,999 permutations) were performed using CANOCO to describe the influence of the environmental variables on assemblages of canopy spiders. The results of significance test show that elevation and tree height significantly explains species assemblages.

No. 70

Review on the wolf spider subfamily Evippinae from China (Araneae Lycosidae)

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Abstract: Eleven Chinese species of wolf spidersubfamily Evippinae are reviewed. A new genus, *Desertocosa***gen. nov.** is erected, on the type of *Pardosa hatanensis* Urita, Tang & Song, 1993 (both sexes), the other species, *Desertocosa apsheronica* (Marusik, Guseinov & Koponen, 2003) (both sexes), transferred from *Evippa*, and is firstly recorded from China. Five *Evippa* species are reported: *E. beschkentica* Andreeva, 1976 (both sexes), *E. onager* Simon, 1895 (female only), *E. sibirica* Marusik, 1995 (both sexes), *E. sjostedti* Schenkel, 1936 (both sexes) and *E. tianshanensis***sp. nov.** (both sexes). Four *Xerolycosa* species are reviewed in here: *Xerolycosa miniata* (C.L. Koch, 1834) (both sexes), *X. mongolica* (Schenkel, 1963) (both sexes), *X. nemoralis* (Westring, 1861) (both sexes) and *X. xinjiangensis***sp. nov.** (male only). *Desertocosa hatanensis* is senior synonym of *Pardosa jartica*Urita, Tang & Song, 1993.

Keywords: new genus, synonym, taxonomy, morphology, distribution

No. 71

Coelotinae Spiders from Mt. Jinyun of Chongqing, China (Araneae: Agelenidae)

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Abstract: Coelotinae spiders inhabit in the northern hemisphere, especially the North Temperate and Subtropical regions. Southern China, with a subtropical humid monsoon climate, is rich in coelotines, which are very various among different habitats. Closely related Coelotinae species are infrequently discovered in a same habitat. Most coelotines have narrow distribution, except a few widespread species such as *Iwogumoa plancyi* (Simon, 1880), *Pireneitega luctuosa* (L. Koch, 1878), etc. As the result of these phenomena, survey of coelotines in a certain area tend to discover some unique or endemic species.

Mt. Jinyun is located in Chongqing of China and covers 7600 hectares by the side of Jialing River at an altitude of 200 to 952 metres, with only four coelotines recorded by Wang et al. (2010), while a great deal of studies on other creatures of Mt. Jinyun have been well done.

Based on the collections from 2007 to 2016, fourteen Coelotinae species belonging to eight genera were found, including eight new species: *Coelotes arcus***sp. nov.** (male), *Coelotes jinyunensis***sp. nov.** (male, female), *Coelotes zhui***sp. nov.** (male), *Coelotes decussatus***sp. nov.** (male, female), *Draconarius sphaericus***sp. nov.** (male, female), *Draconarius xishuiensis* (Zhang, Zhu & Wang, 2017) (male, female), *Iwogumoa plancyi* (Simon, 1880) (male, female), *Lineacoelotes subnitidus***sp. nov.** (male, female), *Orumcekia gemata* (Wang, 1994) (male, female), *Pireneitega luctuosa* (L. Koch, 1878) (male, female), *Pireneitega xinping* (Zhang, Zhu &Song, 2002) (female), *Platocoelotesexiguprocessus* **sp. nov.**(male, female), *Tonsilla jinyun* **sp. nov.** (male, female) and *Tonsilla truculenta* (Wang & Yin, 1992) (male, female). All specimens were preserved in 75% alcohol and deposited in the spider collection of the School of Life Sciences, Southwest University (SWUC).

Keywords: Coelotinae, biodiversity, taxonomy, Mt. Jinyun, new species

No. 72

Scorpion Fauna of Phong Nha–Ke Bang region, Vietnam (Arachnida: Scorpiones)

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Abtract:A survey on scorpion has been prospected in the karst cave system in Vietnam, and several specimens of a new pseudochactid scorpion were collected in the Tien Son cave which belongs to the Phong Nha-Ke Bang cave system. These were described as a new genus and species, *Vietbocap canhi* Lourenço & Pham, 2010 which corresponds to a true troglobitic element. Another survey in the cave system of Phong Nha-Ke Bang have been carried out and again, another pseudochactid scorpion was collected in the Thien Duong cave which belongs to the Phong Nha-Ke Bang cave system. The new species also belongs to the genus *Vietbocap*, and again corresponds to a true troglobitic element. The fact that already three pseudochactid elements were originated from caves belonging to the same karst system found in Laos and Vietnam, suggest that this region of Southeast Asia may represent a refuge or an endemic centre for elements of this family. And the first time, *Liocheles australasiae* (Fabricius, 1775) also recorded in Phong Nha-Ke Bang region.The redescriptions and illustrationsof three species, *Vietbocap canhi* Lourenço & Pham, 2010; *Vietbocap thienduongensis*Lourenço and Pham, 2012 and *Liocheles australasiae* (Fabricius, 1775) from Phong Nha – Ke Bang national park are presented. Distribution data and current status of Phong Nha – Ke Bang scorpions are provided.

No. 73

Cloning and characterization of three isoforms of SOD genein the carmine spider mite, *Tetranychus cinnabarinus* (Boisduval) (Acari: Tetranychidae)

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Abstract: The carmine spider mite, *Tetranychus cinnabarinus* (Boisduval) (Acari: Tetranychidae), is a widely distributed agricultural pest of significantly economic importance in China. The rapidly developed resistance has become a great challenge to its chemical control.The respiration of the organism can produce reactive oxygen species and free radicals. However, the superoxide dismutase (SOD) can effectively prevent cells from being damaged by reactive oxygen species and free radicals, and then reduce the oxidative damage from the environment. In order to study the antioxidant function of SOD genes, cytoplasmic Cu-ZnSOD (*TcSOD1*, GenBank accession numbers KY348746), extracellular Cu-ZnSOD (*TcSOD2*, KY348747) and mitochondrial MnSOD (*TcSOD3*, KY348748) were cloned using rapid amplification of cDNA ends (RACE) technology, and further bioinformatics analyses and phylogenetic analysis were conducted in this study, which can provide a foundation for the further studies of these genes.

Three full-length cDNA sequences of *TcSOD1*, *TcSOD2* and *TcSOD3* gene were 827, 1034 and 1003 bp, contained the ORF of 459, 699 and 678 bp, encoding 152, 232 and 225 aa, respectively. Their theoretical molecular weights were 15.559, 25.154 and 24.657 kDa, and isoelectric points were 6.02, 6.48 and 7.86, respectively. The signature motifs GFHIHEFGDNT and GNAGARSACGVI were found in *TcSOD1* and the MnSOD signature DVWEHAYY were found in *TcSOD3*. Only *TcSOD2* had an N-terminus signal peptide of 17 aa. *TcSOD1* and *TcSOD2* both had four Cu^{2+} binding sites and four Zn^{2+} binding sites, and *TcSOD3* had four Mn^{2+} binding sites. The phylogenetic tree constructed using the maximum likelihood method showed that SODs were divided into three groups and three SODs in *T. cinnabarinus* were highly homologous with those in *T. urticae*.

Keywords: *Tetranychus cinnabarinus*, SOD genes, bioinformatics analyses, phylogenetic analysis

No. 74

The complete mitochondrial genome of *Blattisocius keegani* Fox (Acari: Mesostigmata) and the phylogenetic relationship among Parasitiformes

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Abstract: *Blattisocius keegani* Fox is a predatory mite that preys the flour mites on grain. It is an efficient natural enemies to harmful and insects in stored products. In this study, the mitochondrial genome of *B. keegani* was sequenced using long-PCR. The mitogenome of *B. keegani* is 17, 314 bp length. Like most other metazoan mitogenomes, it contains 13 PCGs, 22 tRNAs and 2 rRNAs genes. Among all genes, 9 protein-coding genes (PCGs) and 14 transfer RNA (tRNAs) are encoded on the majority strand (J-strand), while 4 PCGs, 8 tRNAs and 2 rRNAs are encoded on the minority strand (N-strand). All 13 protein-coding genes (PCG) are initiated by the canonical putative start codons ATN. Eleven PCGs share the complete termination codons TAR, while COII and ND4 use an incomplete termination codon T.

Among 22 transfer RNAs, 19 have the typical clover-leaf structure, while trnS1, trnR and trnC lack the dihydrouridine (DHU) arm. The tRNA genes are scattered throughout the circular molecule and vary from 53 bp (trnR) to 74 bp (trnT) in size. Two rRNAs and all tRNAs have obviously high AT content.

The sequencing of *B. keegani* mitochondrial genome can enrich mitochondrial genome database, also providing basic data for comparative genomics research. ML and BI analysis of the phylogenetic tree based on nucleotide and amino acid sequences from all mt PCGs of Acari confirm the evolutionary position of *B. keegani*, which agree with the morphological classification of the Parasitiformes.

Keywords: *Blattisocius keegani,* mitochondrial genome, phylogenetic analysis.

No. 75

Effects of the heavy mental lead on population ecology of *Aleurolyphus ovatus* (Troupeau) (Acari: Acaridae)

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Abstract: The heavy metal can affect demographic parameters of arthropod. In this study, *Aleurolyphus ovatus* was fed with artificial feed of four different concentrations of lead (Pb) (12.5, 25, 50 and 100 mg/kg). The developmental duration, sex ratio and fecundity of each developmental stages of the treated first generation and multi generation mite were determined. Life table technology was used to calculate the parameters, such as net reproductive rate (R_0), intrinsic rate of natural increase (r_m), finite rate of increase (λ), average generation cycle (T) and population doubling time (DT) of different groups.

The developmental duration of *A. ovatus* under other four lead concentrations were increased, compared with the control group (without lead). Under 25-100 mg/kg lead concentrations, the total immature period of the first generation were more constant than that of long-term stress. However, there was no significant change in the total immature period of the first generation and long-term stres generation.

The total egg production per female of the first generation under four concentrations were 257.074, 371.667, 168.818 and 284.654, respectively, whereas which were 176.652, 301.542, 281.913 and 285.667, respectively, when under long-term lead stress. There are no significant difference between the control group and the treated groups on pre-oviposition, oviposition, post-oviposition period, adult longevity and per female fecundity.

In the first generation, R_0, r_m, λ and T reached the highest values under the concentration of 12.5 mg/kg, while DT was the shortest (3.817 d) at 12.5 mg/kg. It indicated that female adult of *A. ovatus* may increase reproductive potential and the life span under low concentration lead. Under long-time lead stress, in contrast to control group, all demographic parameters have negative effects, R_0, r_m, λ were decreased and DT was increasd. It suggested that reproductive potential and population growth rate of *A. ovatus* were reduced during long-time lead stress.

Keywords: lead, *Aleurolyphus ovatus*, demographic parameters

No. 76

Mites of *Pyemotes* for biocontrol: research and application

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Abstract: *Pyemotes* mites are parasitoids of insects and are an important group of biocontrol agents. They are of cosmopolitan distribution, and have high reproductive potential. *P. zhonghuajia* Yu, Zhang *et* He is common in northern China and is found on many host species: *Sinoxylon japonicum*, *Phloeosinus hopehi*, Dermestidae, Buprestidae, *Stenhomalus taiwanus*, *Phloeosinus* sp., *Cryptolestes turcicus*, *Scolytus japonicas* and *S. seulensis*. They are parasitic on larvae, white pupae, sometimes eggs and adults. An efficient method for rearing this species with very high reproductive output was discovered, making mite's mass rearing a reality. So, *P. zhonghuajia* have been released in the fields for biocontrol of bore pests and others in China, especially wood bores and those living in large groups, such as bark beetles, flatheaded borer weevil (e.g. *Cryptorhynchus lapathi*), longhorn beetle (e.g. *Semanotus bifasciatus*), *Dioryctria rubella*, *Cydia trasas*, wood leopard, ermine moth, wood leopard, and some piercing-sucking pests. In general, the mites as biocontrol agents against pests need to be released at the rates of 20,000-40,000 per centimeter in tree diameter. In 21 days, the control efficiency is usually 80% to 91% or higher.

Keywords: Pyemotes, biocontrol, research, application

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