7th Conference of the Asian Society of Arachnology

Program & Abstracts

Cuc Phuong National Park, Vietnam
October 17th - 22nd, 2022

Organized by:

Vietnam National Museum of Nature
(Vietnam Academy of Science and Technology)

Asian Society of Arachnology

PUBLISHING HOUSE FOR SCIENCE AND TECHNOLOGY

Celebrating 10 years of the ASA

2012-2022

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Asian Society of Arachnology

Preface

On behalf of the Organizing and Scientific Commitee, it is our pleasure to welcome you to the 7th Conference of the Asian Society of Arachnology. The ASA conferences are annual meeting of Asian and international arachnologists who are working on Asian and other regional arachnids. Past ASA conferences editions were held in Laos, Thailand, India and China. This year, the ASA conference is at Cuc Phuong National Park in Ninh Binh province, Vietnam.

The 7th ASA Conference is an important milestone, on the occasion of 10th anniversary of the Asian Society of Arachnology, the International year of Basic Science for Sustainable Development 2022. This is not only a significant scientific event but also a good opportunity to connect arachnologists in Asia and all other continents in the world.

Confirm delegates from eleven countries will be presenting their latest research on arachnids. The Conference program includes 42 oral and poster presentations divided into five major subjects: (1) Systematics, (2) Phylogeny and biogeography, (3) Ecology, (4) Behavior and (5) Molecular mechanisms.

Besides the stimulating scientific programe, with its up-to-date topics and recent dindings, we provide a multifaceted experience through complementary activities and supplementary side-trips.

A mong them, the main attraction will be the complemented visit to established in 1962, Cuc Phuong National Park which is the oldest national park in Vietnam. Cuc Phuong National Park is situated in the monsoon tropical climate region. At the height above sea level from 140 m to 648 m, topography, especially the limestone mountains interspresed with hills and valleys running from the northwest-southeat. Due to the terrain very intense fragmentation created several sub-clinate regions and different microclimates. This is premise of different vegetation formation, making Cuc Phuong biological diversity is very diverse, rich and its own particular character.

This is the ideal habitats of plants and animal species, and ancient people who lived in the forest some 7500 years ago are also to be found in the numerous mountain caves.

We belive these andeavors will provide excellent opportunities both to get in touch with international associates and to become acquainted with the coulture and history of this region.

We hope you will enjoy this exciting event.

Yours sincerely,

Nguyen Trung Minh

Chairman of the Organizing Committee
7th Conference of the Asian Society of Arachnology
Director General of Vietnam National Museum of Nature, VAST

ORGANISERS AND COMMITTEES

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Vietnam National Museum of Nature (VNMN), Vietnam Academy of Science and Technology (VAST)

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PARTICIPANTS

1. Attend in-person *(in alphabetical order)*

	Name	Affiliation	Country
1	Aneesh V. Mathew	Sacred Heart College	India
2	Anitha Abraham	Maharaja’s College	India
3	Aswathy S.	Sacred Heart College	India
4	Asima A.	University of Kerala	India
5	Anusmitha Domichan	Sacred Heart College	India
6	Bernetta Zi Wei Kwek	National University of Singapore	Singapore
7	Chaowalit Songsangchote	Kasetsart University	Thailand
8	Daiqin Li	National University of Singapore	Singapore
9	Darko D. Cotoras Viedma	California Academy of Science	USA
10	Domagoj Gajski	Masaryk University	Czech Republic
11	Dharmaraj Jayaraman	Sri Vijay Vidyalaya College of Arts and Science	India
12	Deeplaxmi Kulkarni	Bharatiya Mahavidyalya, Amravati	India
13	Gunasekaran C.	Bharathiar University	India
14	Hirotsugu Ono	National Museum of Nature and Science	Japan
15	Ibuki Hamamoto	Kyoto University	Japan
16	Katarzyna Mietus	Araneus	Poland
17	Kaya Szyszkowska	Araneus	Poland
18	Kotaro Mori	Kyoto University	Japan
19	Mathew M. Joseph	Sacred Heart College	India
20	Masahiro Miyashita	Kyoto University	Japan
21	Nishi Babu	University of Kerala	India
22	Ondrej Kosulic	Mendel University in Brno	Czech Republic
23	Patipan Sriranan	Khon Kaen University	Thailand

	Name	Affiliation	Country
24	Pedro de S. Castanheira	Murdoch University	Australia
25	Peter Jaeger	Senckenberg Research Institute	Germany
26	Paveen Piyatrakulchai	Khon Kaen University	Thailand
27	Pham Dinh Sac	Vietnam Academy of Science and Technology	Vietnam
28	Priyanka Hadole	Sant Gadge Baba Amravati University	India
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30	Reena Laharia	Brijlal Biyani Science College	India
31	Rio Shida	Kyushu University	Japan
32	Ryusuke Nakamichi	Kyoto University	Japan
33	Shoichi Sakai	Kyoto University	Japan
34	Shogo Noguchi	Kyushu University	Japan
35	Siegfried Jakob Huber	University of Freiburg	Germany
36	Stano Pekar	Masaryk University, Vice-President of the ISA	Czech Republic
37	Stephanie Frances Loria	Zoological Museum Hamburg	Germany
38	Sunil Jose K	Deva Matha College	India
39	Szymon Przebinda	Araneus	Poland
40	Tipakhon Michalko	Nonpang village, Lumphan, Mueang, Kalasin	Thailand
41	Valentin Lion Ehrenthal	University of Hamburg	Germany
42	Varat Sivayyapram	Chulalongkorn University	Thailand
43	Venus Saksongmuang	Prince of Songkla University	Thailand
44	Wan Xin Rachel Seah	National University of Singapore	Singapore
45	Warbota Khum	Mendel University in Brno	Czech Republic
46	Wasin Nawanetiwong	Chulalongkorn University	Thailand
47	Yuya Suzuki	Kyushu University	Japan
48	Yuumi Fujita	Kyoto University	Japan

2. Attend online *(in alphabetical order)*

	Name	Affiliation	Country
1	Amelia Joyce Philip	University of South Bohemia	Czech Republic
2	Chao Zhang	Hebei University	China
3	Evgeni M. Zhukovets	SSPA "SPC NAS of Belarus for Bioresources"	Belarus
4	Fan Zheng	Southwest University	China
5	Feng Lu	Shenzhen University	China
6	He Zhang	Hubei University	China
7	Honda Yoshiko	Fumakilla Limited	Japan
8	Huimin Sun	Hunan Normal University	China
9	Joseph K H Koh	National University of Singapore	Singapore
10	Jie Liu	Hubei University	China
11	Jinxin Liu	Hunan Normal University	China
12	Jingxia Zhao	Southwest University	China
13	Jieshi Luo	Southwest University	China
14	Jihe Liu	Jinggangshan University	China
15	Junxia Zhang	Hebei University	China
16	Keke Liu	Jinggangshan University	China
17	Long Yu	Hebei University	China
18	Lin Xiao	Southwest University	China
19	Luyu Wang	Southwest University	China
20	Na Li	Hunan Normal University	China
21	Mahammad Irfan	Southwest University	China
22	Mingqin Deng	Southwest University	China
23	Ping Jiang	Jinggangshan University	China

	Name	Affiliation	Country
24	Qing Zou	Southwest University	China
25	Rui Zhong	Hubei University	China
26	Supreet Kadakol	Mangalore University	India
27	Shuqiang Li	Institute of Zoology, CAS	China
28	Xiangbo Guo	Hebei University	China
29	Xiang Xu	Hunan Normal University	China
30	Xin-Ru Zhang	Hunan Normal University	China
31	Xin Xu	Hunan Normal University	China
32	Yannan Mu	Hebei University	China
33	Yang Zhu	Hubei University	China
34	Yaying Wu	Dali University	China
35	Yonghong Xiao	Jinggangshan University	China
36	Yun-E Tang	Hunan Normal University	China
37	Zhaoyi Li	Hebei University	China
38	Zhisheng Zhang	Southwest University	China
39	Zizhong Yang	Dali University	China

PROGRAM

Monday: October 17th 2022

Check in at Vietnam Academy of Science and Technology (VAST), 18 Hoang Quoc Viet, Cau Giay, Hanoi, Vietnam	
07:30-12:30	Conference participant arrivals: The registration
14:30	Leaving Hanoi to Cuc Phuong National Park by bus (provided by the organizer)
19:00	***Dinner***

Tuesday: October 18th 2022

Opening Ceremony		
09:00	Zhisheng Zhang	Opening remarks from ASA president
09:05	Nguyen Trung Minh	Director General of VNMN
Session: 10 years of ASA		
09:10	Zhisheng Zhang	President of ASA
09:40	Peter Jaeger	Respected initiator of ASA
09:45	Stano Pekar	Vice-President of the ISA
09:50	***Coffee break and Conference photo***	
Session: Systematics Chair: Li Daiqin		
10:30	Peter Jaeger	“Love bites” in Sparassidae - more usual than thought?
10:45	Rio Shida	Notes on the arboreal wolf spider *Hogna trunca* newly recorded from Japan (Araneae: Lycosidae)
11:00	Pedro de S. Castanheira	Taxonomy and systematics of the “backobourkiine” spiders, a new Australian subfamily of orb-weavers (Araneae, Araneidae)
11:15	*Poster*	
12:00	***Lunch***	
14:00	Visit to Cuc Phuong National Park	
19:00	***Dinner***	

Wednesday: October 19th 2022

Session: Systematics **Chair: Hirotsugu Ono**		
09:00	Anusmitha Domichan	On the spiders of subfamily Linyphiinae (Araneae: Linyphiidae) from Western Ghats, Central Kerala, India
09:15	Muhammad Irfan	Linyphiidae of China: past, present and future
09:30	Yuya Suzuki	Taxonomy, web architecture and habitat diversity in Japanese slingshot spiders (Araneae: Theridiosomatidae)
09:45	Deeplaxmi Kulkarni	Faunistic diversity of spiders (Arachnida: Araneae) in some agroecosystems at Amravati, Maharashtra, India
10:00	Wasin Nawanetiwong	Taxonomy of scorpions (Arachnida: Scorpiones) in Thailand
10:30	***Coffee break***	
Session: Ecology Chair: Masahiro Miyashita		
11:00	Ondrej Kosulic	Asian invader in Europe - threat or opportunity for biodiversity of European forests?
11:15	Nishi Babu	Diversity of ant-mimicking spiders and their morphological mimicking strategies in a low-lying agroecosystem of Kerala, South India
11:30	Darko D. Cotoras Viedma	Intraspecific niche partition without speciation: individual level web polymorphism within a single island spider population
11:45	Reena Laharia	A preliminary account of spider diversity in and around community gardens in Amravati, Maharashtra, India
12:00	***Lunch***	

Session: Ecology Chair: Stephanie Loria		
14:00	Radek Michalko	Landscape composition and climate affect web-building spiders - prey food-web in dry dipterocarp forests
14:15	Asima A.	Araneae of the Myristica Swamp Forests of Shendurney Wildlife Sanctuary in the Southern Western Ghats, Kerala, India
14:30	Warbota Khum	Effect of local and landscape factors on spider-prey-mango food webs in Cambodian mango orchards
14:45	Gunasekaran C.	Distributional patterns of Mygalomorphs with special reference to the genus *Poecilotheria* (Theraphosidae) in the Western Ghats of Tamil Nadu, India
15:00	***Coffee break***	
Session: Ecology Chair: Darko D. Cotoras Viedma		
15:30	Stephanie Loria	Assessing arachnid diversity in Eurasia during the Eocene
15:45	Aswathy S.	Lifestyle patterns and conservation challenges of mygalomorphs in the southern Western Ghats of India
16:00	Sunil Jose K.	Diversity of mygalomorph spiders of Western Ghats, India
16:15	Dharmaraj Jayaraman	Spider Diversity in a Selected Agriculture Area of Dharmapuri, Tamilnadu, India
16:30	Mathew M. Joseph	Pseudoscorpion Fauna of Peninsular India
17:00	**ASA meeting** Chair: Zhisheng Zhang	
19:00	***Dinner***	

Thursday: October 20th 2022

Session: Behavior Chair: Mathew M. Joseph		
09:00	Daiqin Li	Proportional mutual assessment of exaggerated chelicerae in male contests of an ant-mimicking jumping spider
09:15	Bernetta Zi Wei Kwek	Female preference for lower pattern contrast males follows Weber's law of proportional processing in an ornate jumping spider
09:30	Shogo Noguchi	Diet and prey-capture behavior in Japanese ant-eating spiders (Theridiidae: Hadrotarsinae)
09:45	Stano Pekar	Drivers of mimetic accuracy in ant-mimicking spiders
10:00	Venus Saksongmuang	Predation networks of common web-building spiders in rice ecosystems, Southern Thailand
10:30	***Coffee break***	
Session: Molecular mechanisms Chair: Stano Pekar		
11:00	Wan Xin Rachel Seah	A multi-level approach to opsins in jumping spiders
11:15	Shoichi Sakai	Bioactive peptides from the venom of the scorpion *Liocheles australasiae* inhabiting Japan
11:30	Anitha Abraham	Bioprospective studies of spider silk
11:45	Masahiro Miyashita	Chemical analysis of fluorescent substances in scorpion cuticles
12:00	***Lunch***	

Session: Phylogeny and biogeography Chair: Peter Jaeger		
14:00	Hirotsugu Ono	Mesothelae in East Asia, tracing their lineage from Japan to Vietnam and Myanmar
14:15	Varat Sivayyapram	Multi-locus phylogeny in the segmented spider genus *Liphistius* (Araneae, Liphistiidae) in Thailand
14:30	Domagoj Gajski	Development of a simple and cost-effective DNA barcoding protocol for spiders based on third-generation nanopore sequencing
14:45	Valentin Ehrenthal	First micro-CT scans of the scorpion brain
15:30	Szymon Przebinda	An exhibition and adventures
16:00	***Coffee break***	
16:30	**Conference Closing** Chair: Daiqin Li	
19:00	***Dinner***	

Friday: October 21st 2022

Visit to Tràng An Scenic Landscape Complex	
07:30	Breakfast
08:30	Departures
12:00	Lunch
19:00	Dinner at Cuc Phuong National Park

Saturday: October 22nd 2022

Congress participant departures	
07:30	Breakfast
08:30	Leaving Cuc Phuong National Park to VAST (Hanoi) by bus (provided by the organizer)

The comparative morphology of trichobothria in the phylogeny of Arachnida

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Trichobothria is a conspicuous type of mechanoreceptive sensilla represented by direct strongly elongated setae that are set in a deep cup-like socket, the bothrium. These sensilla are recorded in several lineages of terrestrial arthropods (hexapods, myriapods and arachnids), and seems arose several times independently. In the Arachnida trichobothria were found in majority of orders, except of Solifugae, Ricinulei and Opiliones.

Numerous publications were devoted to the thin structure of arachnid trichobothria; arrangement of trichobothria is an important character in the systematic of some orders; but there are no attempts to apply the comparative morphology of trichobothria to the phylogeny of Arachnida.

We studied by SEM trichobothria of Scorpiones, Araneae, Amblypygi, Thelyphonida, Schizomida and Pseudoscorpionida (3 suborders), as well as setae in Solifugae, Opiliones (3 suborders) and Ricinulei. Our conclusions on the structure of mite and palpigradan trichobothria based on literature data.

Bothria of all the studied orders, except of Araneae, including the Palpigradi and Acariformes, are highly uniform and presented by a simple open cup; the data on presence of trichobothria in Parasitiformes are controversial. In contrast, bothria of all the spiders, including Mesothelae, is a complex structure: proximal and distal plates, surrounding the alveolus, which sometimes fused into a single dome-like cover. Such advanced type of bothria is a doubtless synapomorphy of the order Araneae. On the other hand, in Acariformes the bothria are uniform, but the setae (trichs) are very diverse; in contrast to the rest orders, mites possess the trichobothria on the body (not only on the legs).

In Solifugae there is a continuous series of setal modifications up to strongly elongated (but still conical) setae which set in quite wide and deep cup-like socket with membranous bottom; such setae seem to be some sort of "functional trichobothria". Similar setae present in Ricinulei. In Cyphophthalmi such strongly elongated setae are absent, but some conical setae (a single to each leg joint) set in deep and wide sockets; the rest two opilionid suborders are lack any trichobothria-like structures. Such setae are very similar to ones of the tetranychoid and trombidioid mites, which are named by acarologists "bothridial setae" and estimated as a modified trichobothria.

The distribution of the abovementioned types of trichobothria between arachnid orders seems perfectly corresponding to a molecular phylogeny of Arachnida by Sharma et al. (2014). First of all it is a clade comprising Solifugae, Ricinulei and Opiliones, supported by presence of "bothridial setae" instead of trichobothria. Pseudoscorpions in this system are united with "pulmonate" orders (Scorpiones, Araneae, Amblypygi, Thelyphonida, Schizomida); the presence of the leg (not body) trichobothria is an important character of this branch. We are predicting that the further molecular data will nest the Palpigradi in the same lineage.

Notes on the arboreal wolf spider *Hogna trunca* newly recorded from Japan (Araneae: Lycosidae)

Rio Shida[1], Toshiya Hirowatari[1], Akio Tanikawa[2]

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The lycosid species, *Hogna trunca* Yin, Bao & Zhang 1996, is newly recorded from Japan. *H. trunca* was originally described from Zhejiang province (China) and was previously known only from China. During the field surveys, we confirmed its presence in Nara Prefecture and in the northern part of the Okinawa Island in Japan, reporting it as a new record for the country. The genus *Hogna* is also newly recorded from Japan.

Hogna species are medium to large-sized, ground-dwelling spiders that mainly inhabit grasslands and open habitats. Among them, only this single species, *H. trunca*, has been reported to present arboreal ecology. In both habitats in Japan, the species was found in forests along streams and was observed staying on tree bark or hiding in tree hollows mainly at night. Presumably, the species has not been discovered until recently because of its unique ecology different from common lycosid spiders.

References

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Yin, C., Bao, Y. & Zhang, Y. 1996. On two new species of wolf spiders from Zhejiang province (Araneae: Lycosidae). Acta Archnol Sinica, 5: 5-9.

Taxonomy and systematics of the “backobourkiine” spiders, a new Australian subfamily of orb-weavers (Araneae, Araneidae)

Pedro de S. Castanheira[1], Volker Framenau[1], Nikolaj Scharff[2], Dimitar Dimitrov[3], Abha Chopra[1] & Renner L. C. Baptista[4]

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The orb-weaving spider family Araneidae includes generally medium-sized to large spiders that are extensively studied in terms of, for example, behaviour (i.e. orb-web construction) or evolution (i.e. sexual size dimorphism) (e.g. Hormiga et al., 2000; Dahirel et al., 2018). A recent world-wide molecular systematic study showed a severely paraphyletic traditional “Araneinae” within the orb-weavers, indicating the existence of many new clades, including the Australian “backobourkiine” spiders, of which most species were misplaced in the genera *Araneus* Clerck, 1757 and *Eriophora* Simon, 1864 (Scharff et al., 2020). This is a largely Australian clade, including the common large-bodied Australian “Garden orb-weavers” species. However, some species were introduced to neighbouring countries as New Zealand; while the genus *Plebs*, for example, also occurs throughout south-east Asia and into India.

Two putative synapomorphies of the male pedipalp have been proposed: the presence of a single macroseta on the patella and the median apophysis forming an arch over the radix (Scharff el al., 2020; Framenau et al., 2021). Those key sclerites, including the terminal and median apophyses vary greatly, although appear to show some systematic signal at the genus level. Testing homology hypotheses of the various pedipalp sclerites within the “backobourkiines” and developing a generalized ground plan for this group will be a prerequisite to develop a sound taxonomic framework to finalise a genus-level revision.

The large majority of backobourkiine genera has now been described as hypotheses for future systematic work (in chronological order): *Novakiella* Court & Forster, 1993 (two species, one new), *Backobourkia* Framenau, Dupérré, Blackledge & Vink, 2010 (four species), *Lariniophora* Framenau, 2011 (one species), *Plebs* Joseph & Framenau, 2012 (22 species), *Hortophora* Framenau & Castanheira, 2021 (13 species, five new), *Socca* Framenau, Castanheira & Vink, 2022 (12 species, nine new), *Salsa* Framenau & Castanheira, 2022 (seven species, three new) and *Leviana* Framenau & Kuntner, 2022 (five species). We are currently finalising the revisions of other “backobourkiines” included in Scharff et al.’s (2022) study: *Acroaspis* Karsch, 1878 (around eight to ten species, three to five new), *Carepalxis* L. Koch, 1872 (estimates of 11 Australian species with around 6 new; in addition to two Papuan species and three Neotropical species, the latter being misplaced in *Carepalxis*). *Parawixia dehaani* (Doleschall, 1859), which is widespread from northern Australia into Asia, also represents a new genus. Scharff et al.’s (2020) phylogeny also included *Singa nitidula* C. L. Koch, 1844 in the backobourkiines, a Palearctic species requiring further investigation. If the genus is of Australasian origin, *Singa* putatively dispersed into South-East Asia and the Indian subcontinent after Australia collided with the Sunda shelf, as for example in the genera *Plebs* and *Hortophora* (Joseph & Framenau, 2012; Framenau et al., 2021a).

Future generic treatments include the Australian *Araneus arenaceus*-group (with at least four species, two new), and the circumscription of a new monotypic genus based on “*Araneus” necopinus* (Keyserling, 1887). In Scharff et al.’s (2020), the latter was placed basal in the Araneidae outside the “backobourkiines”, but their pedipalp morphology agrees with the putative synapomorphies of the clade. Finally, we also described the new genus *Mangrovia* Framenau & Castanheira, 2022, tentatively included it in the “backobourkiines” due to the presence of a single patellar spine on male pedipalp (Framenau & Castanheira 2022). However, the lack of the median apophysis' arch over the radix and the presence of a terminal pocket on the scape of the female's epigyne (character absent in other members of the clade) may indicate otherwise.

Following our genus-level revisions, we will conduct further phylogenetic work based on extensive morphological and molecular data to test these generic hypotheses and to clarify dubious relationships (i.e. *Acroaspis* was paraphyletic in Scharff et al. (2020) phylogeny with respect to *Socca*). Collection of fresh material for this study will be carried out in early 2023. The molecular analyses will have a UCE probe set component that targets more than 2,000 loci specific to spiders and has been used successfully on araneids, allowing us to use Museum specimens with degraded DNA (Kulkarni at al., 2019). This phylogenetic study aims to establish the new subfamily Backobourkiinae to make it better accessible for future ecological and evolutionary work.

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On the spiders of subfamily Linyphiinae (Araneae: Linyphiidae) from Western Ghats, Central Kerala, India

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Linyphiinae Blackwall, 1859 is a large subfamily with 510 species under 75 genera (Linyphiid spiders of the world, 2022). The species distribution extends over all geographical realms. Paleartic realm has the highest representation of Linyphiinae (Linyphiid spiders of the world, 2022). In this paper, we report four species belonging to three genera under Linyphiinae, namely, *Ketambea nigripectoris* Oi, 1960*; Neriene birmanica* Thorell,1887 *Prosoponoides idukkiense* Domichan & Sunil Jose, 2022 and *Prosoponoides sinense* Chen; 1991. Of these, genus *Ketambea* Millidge & Russell-Smith, 1992 is making its first report from India. Central Kerala, the collection area, being a part of Western Ghats, provide ambient habitat for these sheet web spiders. Photographs, descriptions and maps are provided.

Securing paternity in spiders (Arachnida: Araneae): A brief overview

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Mating plugs, mechanical deformation of epigynesare known in almost all spiders' families but only belonging to Entelegynae or in those who have complicated epigynes. In the presentation I will describe different methods used by males to prevent copulation with other males.

Taxonomy, web architecture and habitat diversity in Japanese slingshot spiders (Araneae: Theridiosomatidae)

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The family Theridiosomatidae Simon, 1881, also known as slingshot spiders or ray spiders, is composed of small-sized spiders that prefer dark and humid environments (Coddington, 1986). Web architecture of Theridiosomatidae varies among genera: severalgenera build conventional orb webs, while others constructconical-shape orb webs with radial anastomosis ordeformed webs called sparse networks. Webs of some genera are characterized by a tension line, a non-sticky thread that stretches from the center of the web and attaches to the substrates (Fig. 1). Spiders drag thetension line with forelegs and hold it into coiled conditions while holding the web with hind legs. Therefore, the web acquires a distorted conical shape. When flying insects approach the web, the tension line is promptly released, and the launched web captures the prey (Shinkai & Shinkai, 1985; Coddington, 1986).

Currently, ca. 130 species belonging to 19 genera of Theridiosomatidae are recorded mainly intropical and subtropical regions worldwide. After the revisionby Coddington, new genera and new species were described mostly from China and Southeast Asia. In Japan, however, taxonomic studies of Theridiosomatidae were less conducted andonly three species (*Theridiosoma epeiroides*, *Ogulnius pullus* and *Wendilgarda nipponica*) were known before 2018.

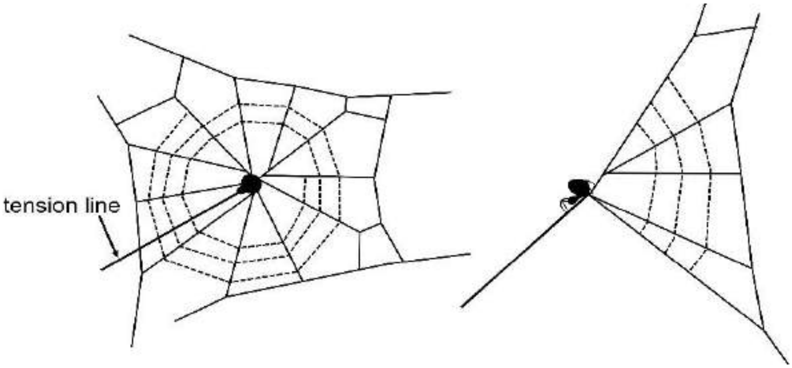

Fig. 1. Web architecture of *Theridiosoma* (Theridiosomatidae). Frontal (left) and lateral (right) views

As a result of morphological examinationon numerous specimens of the family collected from Japan, we found several undescribed species especially from Ryukyu Islands (Suzuki, 2019, Suzuki et al., 2020, 2022). Field observations also revealed their interspecific variations in habitat preference: some prefer forest floors andside of streams in forests, while others are exclusively collected from limestone caves, open habitat such as riverbeds, grasslandsand water surface of ponds and lakes. In addition, we discovered morphological variations in their web structures which may correspond to their habitat types.

In this presentation, we introduce recent taxonomic updates of Theridiosomatidae in Japan, which includes seven new species and a new genus. We also report morphological diversity and specializations in their webs and discuss the relationship between web architecture and their natural habitat.

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"Love bites" in Sparassidae Bertkau 1872 -more usual than thought?

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There are only few direct observations of male fang use during coercive mating of spiders. Indirect evidences are scars, e.g., in *May* Jäger & Krehenwinkel, 2005 or *Thunberga* Jäger, 2020. From their position, distance and their nature these scars are supposed to be caused by male spiders with their fangs when clinging to the female. When preparing a manuscript with 100 new species of the genus *Pseudopoda* Jäger (2000), more such cases became evident. A survey through published records and the collection of the Senckenberg Research Institute was conducted. Results are shown and an outlook for other families is given.

Taxonomy of scorpions (Arachnida: Scorpiones) in Thailand

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The taxonomic state of Southeast Asia (SEA) scorpions (Arachnida: Scorpiones) is largely elusive. The most current synoptic work on the species diversity in Thailand and neighboring countries by Kovarik (1995) proved to be unreliable and incomplete. Here, we provide a preliminary annotated checklist to scorpions found in Thailand through literature review and field collecting from 2017 to the present (n = 177). An updated taxonomic information, species number, distribution maps, and identification key to specific levelsare provided. We reported 5 scorpion families in Thailand, include Buthidae (4 genera, 8 morphospecies), Chaerilidae (1 genus, 7 morphospecies), Hormuridae (1 genus, 1 morphospecies), Scorpionidae (2 genera, 3 morphospecies) and Scorpiopidae (1 genus, 23 morphospecies). This fundamental data is essential to further the studies of SEA scorpions.

Asian invader in Europe - threat or opportunity for biodiversity of European forests?

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A new invasive alien disease from Asia affecting common ash (*Fraxinus excelsior*) trees has resulted in severe dieback and mortality throughout much of the natural distribution range of ash in northern and central Europe. In contrast to its aggressive behaviour of this disease in Europe, infection appears to be a benign associate of indigenous *Fraxinus mandshurica* without visible changes in infested Asian native forests. On the other hand, the ash dieback in Europe has resulted insignificant structural and environmental changes and in alterations of various biotic interaction, especially in low land flood plain forests. However, the forest successional theory would predict a positive impact on biodiversity due to the opening of forest canopies and increasing of habitat heterogeneity after forest dieback. Surprisingly, there is only a limited number of empirical studies investigating how thisdisease caused by fungus *Hymenoscyphus fraxineus* affectsmulti-trophic biodiversity of infested forestsin different successional stages. In this study, we hypothesized that the impact of ash declineon biodiversity will be strongest in young stands and will decrease with the succession stage due to the higher resilience of older stands. Further, we assumed that the strongest infestation homogenizes the habitat structure through the total opening of canopies and consequent spreading of ruderal and pioneer plant species. This reduces niche availabilities and ultimately overall multi-trophic biodiversity. As we hypothesized, the effect of ash

decline on diversity was strongest in the young plantations but surprisingly was stronger also in old forests more than in middle age forests. The relationship between biodiversity indicators and infestation was mostly hump-shaped or clearly negative in all successional stages. The ultimate impact of the ash-dieback was therefore highly contradictory because the strong infestation of the ash stands greatly reduced the multi-trophic biodiversity. We suggest that this Asian invasive disease could be seen as a serious threat rather than an opportunity for forest biodiversity.

Diversity of Ant-mimicking spiders and their morphological mimicking strategies in a low-lying ecosystem of Kerala, South India

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Myrmecomorphy often involves Batesian mimicry, which utilizes the morphological and behavioural characteristics of ants to deceive potential predators. However, there are significant differences in the similarity between mimics and ants. The present investigation discovered nine spider species which are mimicking ants, are collected from same locations of an agroecosystem. This investigation, conducted at a few key locations in Kuttanad, sought to identify the ant-impersonating spiders and their ant models. The study was conducted for a period of 6 months, from January 2022 to June 2022. Spiders that resemble ants include *Myrmaplata plateloides*, *Myrmarachne prava*, *M. uniseriata*, *M. ramunni*, *Indomarengo chavarapter*, *Myrmarachne* sp. 1, and *Myrmarachne* sp. 2, which are members of the Salticidae family, and *Corinnemma severum* and *Castineira zetes*, that belong to the family Corinnidae. It was discovered that these ant-mimicking spiders and their ant models are frequently coexisting in the same areas. Along with the morphological resemblances, morphometric analysis revealed similarities between the collected spiders and ants. Ants are eusocial insects that form large colonies with many individuals; hence, mimics should have a lower density than the model. Additionally, due to their aggressive behaviour, spiders from genus *Myrmarachne* may resemble some ant species. This demonstrates the necessity of simulating size and colour to reduce the likelihood of predation encountering the mimics.

Intraspecific niche partition without speciation: individual level web polymorphism within a single island spider population

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Early in the process of adaptive radiation, allopatric disruption of gene flow followed by ecological specialization is key for speciation; but, do adaptive radiations occur on small islands without internal geographical barriers? Island populations sometimes harbour polymorphism in ecological specializations, but its significance remains unclear. On one hand, morphs may correspond to “cryptic” species. Alternatively, they could result from population, developmental or behavioural plasticity. The spider *Wendilgarda galapagensis* (Araneae, Theridiosomatidae) is endemic to the small Isla del Coco and unique in spinning three different web types, each corresponding to a different microhabitat. We tested whether this variation is associated with “cryptic” species or intraspecific behavioural plasticity. Despite analysing 36 803 loci across 142 individuals, we found no relationship between web type and population structure, which was only weakly geographically differentiated. The same pattern holds when looking

within a sampling site or considering only Fst outliers. In line with genetic data, translocation experiments showed that web architecture is plastic within an individual. However, not all transitions between web types are equally probable, indicating the existence of individual preferences. Our data supports the idea that diversification on small islands might occur mainly at the behavioural level producing an intraspecific niche partition without speciation.

A preliminary account of spider diversity in and around community gardens in Amravati, Maharashtra, India

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Spiders are one of the most diverse groups of organisms that, like many invertebrates, receive little attention from the community; this may be due to fear and/or dislike of their appearance andbehavior. Creating community awareness for this invertebrate group is a necessary activity, that might work on reducing arachnophobia, promoting the subject, and encouraging scientific literacy through some outreach initiatives. Community gardens exist in various forms and are often positioned as spaces contributing a sense of association and relativity to the urban environment. Hence, a preliminary survey of spider fauna was carried out to examine five community garden landscapes in the central residential zone of Amravati - a region undergoing a considerable urban transformation in recent decades. The study period was brief, from June 2022 to August 2022. A total 457 number of spiders belonging to 28 genera from 10 families were identified. From this study, we propose that such assessments have greater potential to enlist further species from such urban landscapes that would be valuable for creating an extended database of this region.

Landscape composition and climate affect web-building spiders-prey food-web in dry dipterocarp forests

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Dry dipterocarp forest is a key dry forest type across South-East Asia. Despite dry dipterocarps being endangered with almost no protection, factors at local and landscape scales that may affect their functioning are unknown. We investigated how local habitat structure, land use, and climate affect the structure of web-building spider-prey food-web in dry dipterocarp forests to identify important factors for future conservation programs. We selected 21 dry dipterocarp forests across Northeast Thailand where we collected actual and potential prey of web-building spiders. Within each plot, we quantified the structural properties of the vegetation. Around each plot, we quantified the landscape composition within a 5 km radius as the proportion of agroecosystems, forests, water bodies, and urban areas. We further extracted climate data for each plot from a public database. The food-webs were affected mostly

by the composition of landscapes and the evenness of captured prey showed a hump-shaped relationship with the proportion of agroecosystems in each landscape. The observed change in prey composition between plots were caused predominantly by changes in web type composition between local spider communities. The total number of captured prey decreased with mean annual precipitation which mirrored the decline of total prey availability along this gradient. Our results indicate that the functioning of dry dipterocarps is threatened mostly by land-use change, specifically by agricultural intensification at the landscape scale, and changes in climate. The web-building spiders-prey food-webs seem to be relatively resistant to small changes in local habitat structure due to moderate human disturbances such as grass harvesting or tourist activities.

Araneae of the Myristica swamp forests of Shendurney Wildlife Sanctuary in the Southern Western Ghats, Kerala, India

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Myristica swamps are unique freshwater swamp forests that can be found in the low-lying valleys of the Western Ghats' evergreen tropical forests. Myristica swamps are now a rapidly disappearing, fragmented, and endangered ecosystem found only in a few small patches in southern Kerala, the Uttara Kannada district of Karnataka, Goa, and a newly discovered area in the northern Western Ghats of Maharashtra. Myristica swamps are rich in biodiversity and are distinguished by a prevalence of Myristicaceae tree species found in the Western Ghats, India, which is one of the most primitive families of flowering plants known for the species of the nutmeg tree. The spider fauna of Myristica swamps was largely unknown, and only very few studies are available in this regard. The present study was carried out in the Myristica swamps of Kattilapara, located in the northern part of the Agasthyamalai Hills of the southern Western Ghats, in Shendurney Wildlife Sanctuary, Kollam district, Kerala, India. Data on the spiders were collected over a period of three seasons, and spiders were collected using the standard protocols. spiders were identified based on relevant literature and keys available and using the World Spider Catalogue. We recorded 34 species of spiders belonging to 28 genera and 11 families. A checklist of spiders of the Myristica swamp is also provided.

Effect of local and landscape factors on spider-prey-mango food webs in Cambodian mango orchards

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Local management and landscape structure can concurrently impact trophic interactions in local communities, which may affect the ecosystem functioning and services such as biological pest control. However, the study of how these factors influence the changes of predator-prey interactions remains unclear. Here, we assessed the effect of landscape structure and farming management practices on spider-prey food webs in mango orchards in Cambodia. We performedthe arthropod sampling in 15 mango orchards of similar age (5-10 years) in different farming management (organic and conventional), landscape composition (habitat types) and configuration. During the season, we sampled arthropods with sweeping, sticky traps, and beating. We also collected leaves to estimate herbivory. We then measured the traits of spiders (body size and hunting strategies). Our study found that local factors and landscape components significantly affected the spider community with rather complex effects on herbivores and herbivory.

Distributional patterns of Mygalomorphs with special reference to the genus *Poecilotheria* (Theraphosidae) in the Western Ghats of Tamil Nadu, India

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Genus *Poecilotheria* of the family Theraphosidae is endemic to South Asia. Totally 14 species of *Poecilotheria* have been reported so far, among which seven are endemic to India, five are endemic to Sri Lanka and two are reported from both India and Sri Lanka. *Poecilotheria* is exclusively arboreal, nocturnal, largely found in dry deciduous and evergreen forests living in tree barks, holes and under the rocks (Nanayakkara, 2012) and hence their behaviour and food habitats are little known (Das *et al.,* 2012). These species are threatened by various factors like deforestation, habitat loss and pet trade. Due to their colouration, size and longevity, *Poecilotheria* are popular in the pet trade. Among the nine indigenous species, 2 are Critically Endangered, 2 are Endangered, 1 each of the rest are Vulnerable, Least Concerned and Data Deficient (IUCN, 2022). Population monitoring and documentation on the diversity of this genus are unknown. Preliminary investigation of the presence of *Poecilotheria,* documentation of their status and distribution and identifying the pervasive threat of exploitation and illegal trade, along the foothills of the Western Ghats in selected districts of Tamil Nadu, India was

attempted in our study. This helped us to design conservation strategy and to develop educational materials for awareness. Distributional patterns, associated threats, conservation action under taken are presented here. Thanks to USFWS for the financial support and Tamil Nadu Forest department for their support extended for the study.

Assessing arachnid diversity in Eurasia during the Eocene

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During the Eocene, the Earth experienced a greenhouse climate and large parts of the Northern Hemisphere were covered in humid, warm temperate forests. However, between the Oligoceneand Quaternary, global temperatures dropped by nearly ten degrees, leading to cooling and drying across the world. This drastic change in temperature resulted in range shifts and extinction of the flora and fauna in Eurasia and North America. The European succinite ambers, which include Baltic, Bitterfeld and Rovno ambers, preserve a large diversity of arthropod species, including arachnids. These ambers were deposited during the Paleogene, however, debate exists whether these ambers were deposited simultaneously or over a 30 million year period, and if they originated from adjacent paleo-locations or locations well-separated by geographical barriers. Multiple species are known to be shared across these amber deposits, yet the faunas of each of these ambers is thought to be distinct. In this project, we aim to test whether these three amber types represent the same ecosystem by sharing the same arachnid fauna and if Eurasian arachnid assemblages show a shift in adaptation from warmer to cooler climates from the Eocene until today. To accomplish this objective, we: (i) document species diversity in European succinite ambers; (ii) test whether species recorded across multiple amber deposits (Baltic, Bitterfeld and/or Rovno) are conspecific or distinct; (iii) map records of extant and fossil taxa to look for shifts in distribution; and (iv) synchrotron scan selected taxa to examine changes in morphological characters associated with adaptation to

particular environments. Preliminary results indicate that many arachnid taxa are found in all three ambers, providing support for a shared ecosystem among the European succinite deposits. Results also show that since the Eocene, several arachnid lineages have shifted their distribution from northern Europe to tropical and subtropical climates in the Southern Hemisphere. By comparing past changes with current diversity trends, we can better predict the future of our arachnid fauna given the ongoing climate crisis.

Lifestyle patterns and conservation challenges of mygalomorphs in southern Western Ghats, India

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The Mygalomorphae are an ancient lineage, considered the sister group of a more highly diverse and better-known group of spiders, the Araneomorphae. This diverse group of relatively large and long-lived spiders includes tarantulas, trap-door spiders, arboreals, sheet-web spiders, and others that build burrows with silk constructions. India has a rich mygalomorph fauna. Studies in the past have primarily focused on taxonomy, and there is very little information available on the ecology and natural history of Indian mygalomorphs. Although mygalomorphs are found all across the planet, tropical areas are where they are most diverse and numerous. Mygalomorphs inhabit undisturbed forest areas and woods. They have been documented in a variety of forest types, including moist deciduous woods, dry deciduous forests, mixed forests, and wet evergreen forests.

The Western Ghats, which make up 25 % of India's biodiversity, are a treasure trove for its outstanding biological diversity and endemism in India. The Western Ghats are considered one of the eight hottest hot spots of biodiversity in the world and an ecologically sensitive area. The vegetation has reached its highest diversity towards the southern tip of Kerala, with its high-statured, rich tropical rain forests. The study was mainly conducted in Kerala, which is the major part of the biodiversity hotspot of the Western Ghats. Kerala state in the southern Western Ghats is home to a wide variety of mygalomorphs. Seven genera, including *Annandaliella, Haploclastus, Neoheterophrictus, Poecilotheria,* *Thrigmopoeus, Sason,* and *Conothele* had their habitat and lifestyle documented throughout the study.

The female mygalomorph spiders of the genera *Haploclastus* and *Thrigmopoeu*s are sedentary and long-lived organisms that spend most of their lives inside their burrows lined with silken retreats. They are usually burrowing types, although there are a few exceptions to being arboreal. The study showcases different stages of the life of *Haploclastus kayi,* an endangered burrowing tarantula of the Western Ghats. The subfamily Poecilotheriinae is the only genus distinctively arboreal in habit, found in the dry deciduous and evergreen forests or wooded areas of peninsular India. They usually build their silk retreats out of vegetation, but they also build them out of human structures. The genera *Annandaliella* and *Neoheterophrictus* are found under boulders and rotting logs of mixed moist deciduous forest types, plantations, human habitation regions etc. The web made by females is messy with multiple entrances, which may lead to a silk-lined tunnel. The trapdoor spiders, *Sason* and *Conothele,* are two distinct solitary burrowers. The *Conothele* spiders construct simple, vertical tube-like burrows with closed, intact lids in a “D” shape on the ground, highly camouflaged with the surroundings. The inner surface of burrow lids is lined with hardened silk. Spiders of the genus *Sason* are arboreal and build their nests without lining in shallow depressions on tree trunks or bark. They are highly camouflaged with the bark texture, making it difficult to locate them in the wild. However, the habitat and the lifestyle followed differ among genera and families in response to the microhabitat preference, substrate characteristics (soil or deposits, for example), vegetation, resource availability, and slope. The difference in burrow architecture is also related to the sex and size of spiders.

Plant and animal life have suffered as a whole as a result of human activities (urbanization, roads, agricultural and touristic activities), which has resulted in the extinction of many species and the threat of others becoming extinct. Climate change is a global threat to the planet and must be considered. Natural phenomena like frequent rainfall, rise in sea level, and unduly seasonal changes can result in complete loss of the population in its natural range. Large theraphosids often form a key component of the exotic pet trade in many countries due to their exotic beauty, iridescent colors, ease of maintenance, and long life. In India, invertebrate conservation is often overlooked. The spiders of *Poecilotheria and Haploclastus* are in the commercial pet trade and the conservation of the species is necessary. Because of their limited distribution, these mygalos are vulnerable to habitat loss and fragmentation induced by ecosystem degradation. Misconceptions regarding tarantulas, such as the belief that they are incredibly dangerous and should be killed on sight, pose a serious threat. Ecology and natural history studies are critical for species conservation. The most essential conservation efforts identified across species include protecting their natural habitats through protected areas and developing management strategies for both the species and their environments. Basic taxonomic research, along with its distribution, ecology, and natural history, is strictly needed before the development of any appropriate conservation actions. Conservation actions and proper research plans are to be implemented for the survival of endangered species.

Diversity of mygalomorph spiders of Western Ghats, India

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Western Ghats belong to one of the 25 hot-spots considered with richest biodiversity in the world. The diversity of mygalomorph spiders are poorly known in India. Their primitive nature and poor distributional abilities makes them highly prone to extinction. The majority of mygalomorph spiders live on the ground, while a few species, such as *Poecilotheria,* are also arboreal. Several species belonging to genera like as *Poecilotheria* and *Haploclastus* are also included on the IUCN's Red List.

3106 species of mygalomorph spiders were described under 358 genera and 30 families worldwide (WSC, 2020). Only 118 species belonging to 32 genera and 9 families have been documented in India. During the course of my research, four families, including Ischnothelidae, Macrothelidae, Nemesiidae, and Theraphosidae, have been discovered in the Western Ghats. Additionally, around 18 genera belonging to various families have been discovered in various regions of the western ghats. The study also attempts to investigate their taxonomy and ecology in detail. Several new distributional records are made during the study. In addition redescription of many poorly described species are also made as a part of the study.

A few genera, including *Poecilotheria, Haploclastus,* and *Chilobrachys,* are dreaded by locals due to their poisonous nature. These spiders are currently threatened with extinction due to habitat loss caused by habitat degradation, commercial logging, floods, pet trade and climate change. In many regions of the world, there is also an increase in the prevalence of these spiders reared as pets. Several South American species belonging to the genera *Chromatopelma, Hysterocrates,* and *Brachypelma* are also smuggled into India, according to the personal observations shared by officials of customs department in India.

They are generally known as tarantulas and inhabit burrows. Their lifespan is significantly longer than that of other spiders. However, due to their evolutionary conservatism, the vast majority of species exhibit little variation between and within genera. Numerous species of tarantulas that are absent from other regions of the Western Ghats are still present in a number of Western Ghats regions. However, due to their secretive nature, the majority of India's species are poorly understood.

Spider diversity in selected agriculture area of Dharmapuri, Tamilnadu, India

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We estimated the spider diversity in agriculture area of Dharmapuri in different degree of agri lands at Dharmapuri, Tamilnadu, India. In general, spiders play an important role in pest control in agriculture. Spiders were recorded at different agriculture habitats between from May, 2021 to June 2022. During this study 25 species 17 genera and 11 families were documented. The results showed that human disturbance has an influence on spider communities: species richness was significantly higher in the preserved site as regards to the selected agriculture fields. Family Salticidae, was found to have 9 numbers of species which is the maximum as compared to the other families. The statistical analyses and diversity indices were calculated for each study sites. These types of studies are very important to study the distribution of spider population in selected habitats and to create a biodiversity database of arachnid fauna in the respective study site and to know its importance.

Pseudoscorpion fauna of Peninsular India

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Knowledge of biodiversity is pivotal for planning efficient conservation strategies. Conservation planning in India is largely based on higher vertebrates and invertebrates, and consequently, meso-diverse fauna have largely been neglected. Against this backdrop, a study was undertaken to understand the conservation aspects of invertebrates with an example of pseudoscorpions as they are carnivores of microarthropods and thus occupy a relatively top-level carnivore status amongst invertebrates. The scope of the study was limited to peninsular India and included the Western Ghats, Eastern Ghats and Tamil Nadu. The Western Ghats occupy the western Peninsular India, which is further divided into three divisions: a northern division comprising the Deccan trap area from River Tapti down to 16 degrees N latitude about the level of Goa, a central division, extending from 16 degrees N latitude southwards including Kudagu and Wayanad region of south Karnataka and Nilgiris and a southern division comprising the Anamalai, Palani and Cardamom hills of Kerala. The Eastern Ghats are a discontinuous range of mountains running along the east coast of India extending from Odisha and Andhra Pradesh to Tamil Nadu in the south passing some parts of Karnataka. Pseudoscorpion sampling was undertaken in all of these regions at representative site during May 2019 to May 2022. Sampling techniques included litter extraction, sifting, and visual search. The study yielded 32 taxa of pseudoscorpions belonging to 18 genera and 10 families. This account for 18.82 % of Indian pseudoscorpion species. Overall, the most abundant pseudoscorpion family across all sampling sites was Atemnidae (9 species), which was followed by Geogarypidae (5 species). The most abundant species was *Geogarypus angulatus* Chamberlin, 1930. New discoveries include *Metawithius keralensis*, Johnson et al., 2019, *Afrosternophorus longus* Mathew & Joseph, 2021 and *Metawithius gavi* Mathew &

Joseph, 2022. Among all the sites, the highest species richness, abundance and diversity indices were recorded from Northern Western Ghats. Among the 32 species collected, 68.75 % were tree dwelling and the rest are litter dwelling. A total of 18 species are endemic to India of which 8 species are endemic to Western Ghats and 4 species are endemic to Tamil Nadu. The study reported exceptional intra-specific variation in the species *Tyrannochthonius heterodentatus* Beier, 1930. The preliminary results provide baseline information for developing conservation strategies of pseudoscorpions of Western Ghats biodiversity hotspot and other parts of India.

Proportional mutual assessment of exaggerated chelicerae in male contests of an ant-mimicking jumping spider

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Perception of signals by receivers affects efficacy of communication and drives thee volution of the signals. According to Weber's law, the minimum change eliciting discrimination is proportional to thesignal magnitude, and the discrimination between two stimuli is depending on the proportional, but not the absolute, difference. The role of proportional perception has been recognized in foraging and female matechoices in a few animals, but whether its role in male-male competition remains unexplored. Using the ant-mimicking jumping spider, *Toxeus maxillosus*, in which males exhibits exaggerated chelicerae, we investigated whether males assess their opponent'sweaponized chelicerae and make contest decisions based on proportional perception. We found that males with larger chelicerae were more likely to win contests, and the proportional, but not the absolute, difference in chelicerae size between two males better predicted male contest outcomes. We also found that contest duration was negatively correlated with the proportional, but not the absolute, difference between the opponents'chelicerae size, which implies that the loser may persist for a shorter time and retreat earlier when the proportional difference in chelicerae size between the loser and winner is larger. This is the first study identifying the role of proportional perception in male contests, therefore highlighting its importance in intrasexual competition and weapon evolution.

Female preference for lower pattern contrast males follows Weber's law of proportional processing in an ornate jumping spider

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Weber's law of proportional processing is often observed in various sensory modalities and behavioural contexts where animals discriminate between stimuli based on proportional difference rather than absolute difference alone in their magnitudes to make behavioural decisions. However, whether female preference for colour patterns follows Weber's law of proportional processing remain largely unexplored. Here we addressed this using the jade jumping spider, *Siler semiglaucus*, which exhibits remarkable sexually selected colour patterns in males. By manipulating the dorsal abdomen colour patterns of *S. semiglaucus* males, we created males with varying pattern contrasts. We then tested female preference using dichotomous choice tests, in which we varied both the absolute and proportional differences in pattern contrast between two males. We found that females preferred males with lower pattern contrasts and discriminated between the males based on both proportional and absolute differences. However, discrimination based on proportional difference, coupled with absolute difference, had a greater influence on female mate preference than absolute difference alone. Our results suggest that *S. semiglaucus* female preference for lower pattern contrast males follows Weber's law of proportional processing.

Diet and prey-capture behavior in Japanese ant-eating spiders (Theridiidae: Hadrotarsinae)

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Today, 14 genera and 325 species of Hadrotarsinae Thorell, 1881 (Araneae: Theridiidae) are recorded in the world (WSC, 2022). Many species of the subfamily are known from tropical and subtropical regions such as Southeast Asia, Australia, and Central and South America (Yoshida, 2003). In Japan, 6 genera and 22 species are currently recorded (Tanikawa, 2022).

Although all the members of Hadrotarsinae may be specialized as predators of ants (Yoshida, 2002), there is little evidence to support this possibility. Only 13 species belonging to 4 genera are regarded as myrmecophages according to the publication (Pekár & Toft, 2015). Moreover, in the laboratory, *Euryopis episinoides* fed other prey types such as fruit flies, termites, springtails, crickets and bugs, suggesting that *E. episinoides* is euryphagous (Líznarová & Pekár, 2019).

Details of predatory behaviors in hadrotarsines are scarcely known. Although most theridiids build webs for prey capture, hadrotarsines except for *Dipoena* spp. do not build webs (Benjamin & Zschokke, 2003; Gastreich, 1999; Cathrine, 2018). Instead, *Euryopis* species capture the ant by throwing silk from spinnerets and then bite it on the leg or antenna (Carico, 1978; Porter & Eastmond, 1982; Líznarová & Pekár, 2019). However, little is known about prey-capture behavior in other genera in hadrotarsines.

To reveal the diversity in diets and prey-capture behaviors of hadrotarsines, we firstly investigated their prey in the natural habitat and in the laboratory for the eight species belonging to

Hadrotarsinae. The prey of six hadrotarsine species were identified for the first time. We also discovered some *Phycosoma* species alsofed non-ant prey (Psocoptera and Lepidoptera). Secondly, we observed prey-capture behaviors of the eight species using video camera recording in the field or laboratory. As a result, 5 species (*Dipoena*, *Euryopis* and *Phycosoma*) captured the prey by throwing adhesive-laden silk and then biting it on the leg or the antenna, while 3 species (*Lasaeola* and *Yaginumena*) captured it by only biting it on the leg or the antenna. Moreover, *Y. Castrata* was observed to steal ant prey from other hadrotarsine in the field. As far as we know, this is the first report of food stealing behavior in Hadrotarsinae.

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Drivers of mimetic accuracy in ant-mimicking spiders

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The evolution and maintenance of accurate Batesian mimicry has been explained by several hypotheses built upon relaxed selection. However, selection can be influenced by ecological factors, such as habitat type or geographical distribution, which have not been considered.

I gathered data on body size, geographical area of distribution (temperate, subtropical, tropical), and habitat stratification (ground, low vegetation, bush, tree) from literature on more than 400 ant-mimicking (myrmecomorphic) spider species from 18 spider families. I ranked them into four accuracy levels based on morphology, from poor inaccurate mimics to very accurate ones. I used regression to study the effect of body size, distribution, and habitat on mimetic accuracy while controlling for phylogeny.

Mimetic accuracy increased with spider body size but differently depending on habitat type. On the ground and in low vegetation, smaller species were inaccurate; whereas on shrubs and trees even smaller species were accurate. Accuracy increased from temperate to tropical locations, again differently depending on habitat. In the temperate zone, only species occurring on bushes were accurate, but in the tropical zone even ground-living species were accurate.

Higher accuracy at lower latitudes is likely due to stronger predation pressure from visually hunting predators. Lower accuracy in species occurring near the ground is presumably due to predation pressure by non-visually hunting predators. Inaccurate myrmecomorphy in spiders appears to be further driven by smaller body size due to lower profitability to predators; and higher latitude due to increased occurrence of generalist predators.

Predation networks of common web-building spiders in rice ecosystems, Southern Thailand

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Spiders are common predators in tropical rice ecosystems. They can feed on various kinds of insect and their populations can be fluctuated along the rice growing season. However, it is still unclear for the actual prey composition of web-building spiders along the rice growing period. Therefore, we examine prey composition of common web-building spiders in rainfed lowland rice ecosystem, southern Thailand and also investigate whether different three stages of rice growth (tillering, booting and flowering) and different field management (conventional and organic) affect the spider-prey interaction by using predation network model. The results showed that common spider species varied among the different stages of rice plant. In the tillering and booting stages, the most common spiders were *Tetragnatha maxillosa, T. javana* and *T. mandibulata,* while other two species including *Neoscona inusta* and *Larinia phthisica,* exhibited high abundance in the flowering stage. The most common prey of the common spiders were insects in order Diptera, Ephemeroptera and Hemiptera and all of these were the main captured prey along the rice growing period. We detected only a marginal effect of field management on the spider and prey abundance but rice development significantly affected the predation food web and network characteristics. The network

metrics; linkage density, interaction diversity, and vulnerability increased with rice development. A large number of prey from detritus and aquatic insects in early season may enhance the abundance of web-building spiders in rice fields and consequently the top-down control of insect pests. The trends in network characteristics suggest that the progressing of rice fields increases the predation pressure of web-building spiders on their prey. Therefore, to support biological control of insect pests in rice agroecosystems, we recommend the reduction of vegetation management intensity in rice field to enhance the supply of alternative prey and suitable web-attachment sites for web-building spiders.

A multi-level approach to opsins in jumping spiders

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Visual systems in animals are fundamental in discerning the world of light and colours that they live in. Opsins are visual pigmentsthat are found in retinas and they determine the light sensitivity and visual range of the organism. Studies have shown that the diversity, abundance and distribution of opsins can be influenced by variations in environmental lighting conditions. Among the invertebrates family, jumping spiders are known to possess remarkable colour vision due to their high visual acuity and high spatial resolution in relation to their body size. Additionally, they are able to detect ultraviolet (UV) light, a wavelength that is completely invisible to humans. In our study, we used *Cosmophasis umbratica*, a tropical ornate spider that is well known for using UV light for communication and sexual behaviour. In our study, our results suggests that the interaction between the life stage of *C. umbratica* and the lighting conditions that they are exposed to, influences the relative expression of the opsin gene *rh3*, the gene responsible for detecting UV light. Relative *rh3* expression is significantly decreased when *C. umbratica* juveniles are exposed to UV light for 1 week. In conclusion, these preliminary findings suggest the high plasticity of the UV visual systems in relation to the life stage and environmental lighting conditions of *C. umbratica*.

Bioactive peptides from the venom of the scorpion *Liocheles australasiae* inhabiting Japan

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Scorpions usevenom to capture prey and to defend themselves against predators. Major bioactive components in the venom are peptides, which have various activities such as insecticidal and antimicrobial activities. These various bioactivities are determined by the sequence and conformation of the peptides. In general, structures stabilized by multiple disulfide bonds are found in ion-channel blocking peptides, where as α-helical structures without disulfide bonds are found in antimicrobial peptides. We have been studying the components of the venom of the scorpion *Liocheles australasiae* inhabiting Japan. To date, we identified three insecticidal peptides, LaIT1, LaIT2, and LaIT3 (Fig. 1). LaIT1 is composed of 36 residues and shows insect-specific toxicity. LaIT2 is composed of 59 residues and shows insecticidal and antimicrobial activities. This peptide has two structural domains. The N-terminal domain of LaIT2 adopts an α-helical structure, where as its C-terminal domain has a structure stabilized by three disulfide bonds. Interestingly, the peptide with only the N-terminal domain also showed the activity, indicating that the activity is caused mainly by the N-terminal domain. LaIT3 is composed of 84 residues and has a similar two-domain structure to LaIT2. However, due to its limited amount isolated, LaIT3 is poorly characterized in terms of its activity. In this study, we established a method to chemically synthesize a sufficient amount of LaIT3 to evaluate its activity. Because of its long chain length, it is difficult to synthesize LaIT3 by the normal solid-phase synthesis method. Therefore, we synthesized LaIT3 by dividing it into two segments and then condensed them by a native chemical ligation method. After disulfide bond formation, LaIT3 was successfully obtained. We will evaluate various bioactivities of LaIT3 using this synthesized peptide.

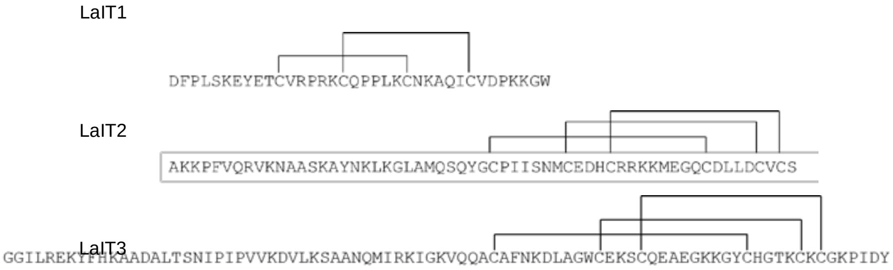

Fig. 1 Structures of LaIT1, LaIT2, and LaIT3

Bioprospective studies of spider silk

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Spider silk is a naturally occurring biomaterial with a diverse range of properties. Throughout history, spider silk has been utilized for a variety of purposes, but most notably for the healing of wounds. The current study focused on the antioxidant, antifungal and antibacterial properties of spider silk as part of the ongoing endeavour to identify the therapeutic benefits of different forms of spider silk. Web silk and egg case silk from *Cyrtophora moluccensis* (Family: Araneidae) were used in the investigation. The silk samples were hydrolyzed in acetone for two weeks. Using the DPPH (2, 2-diphenyl-1-picryl-hydrazyl-hydrate) assay, the antioxidant potential of silk was investigated at two different concentrations, and the results were conducive to the claimed property. It was observed that the antioxidant property improved as the concentration increased. Six bacterial strains (*Bacillus cereus*, *Staphylococcus aureus*, *Aeromonas hydrophila*, *Escherichia coli*, *Vibrio parahaemolyticus* and *Pseudomonas aeroginosa*) were chosen to evaluate the antibacterial properties of silk using the disc diffusion assay, and all except *B. cereus* showed results that were positive for inhibition. *E. coli* was identified asthe most sensitive strain. In every test, egg case silk fared better thanweb silk in terms of exhibiting antioxidant and antibacterial properties. *Aspergillus niger* and *Candida albicans* were used for the antifungal assay. *C. albicans* exhibited greater susceptibility to the tested silk samples than *A. niger*. Compared to egg case silk, web silk exhibited higher inhibitive activity. Among the three features assessed, the antifungal assay was the sole instance in which web silk outperformed egg case silk in relation to the inhibitory efficacy. The study was successful in unravelling the bio-prospective characteristics of spider silk and the promising findings could be actively pursued further for their potential therapeutic applications.

Chemical analysis of fluorescent substances in scorpion cuticles

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Scorpions are known to fluoresce under UV light. Although biological functions of the scorpion fluorescence remain unknown, it has been speculated that the fluorescent compounds play a role in protection from damage induced by UV radiation, as well as in interactive behaviors such as mating. To date, two compounds, β-carboline and 7-hydroxy-4-methylcoumarin, have been identified as fluorescent components in scorpion. However, it is possible that some other unknown fluorescent compounds with different chemical properties are present in the scorpion cuticle. In this study, we analyzed an extract of the exuviae of the scorpion *Liocheles australasiae* to examine the presence of novel fluorescent compounds.

The exuviae of *L. australasiae* were extracted successively with 90 % EtOH/H_2O, EtOAc, and 90 % MeOH/H_2O to obtain a crude extract. First, we examined the existence of the fluorescent compounds reported previously. However, both β-carboline and 7-hydroxy-4-methylcoumarin could not be detected from the extractby LC/MS analysis. This suggests that these compounds are derived from the body, not from the cuticle. Therefore, we searched for other unknown fluorescent compounds. The extract was partitioned between hexane and water, and the hexane layer was separated by a silica gel

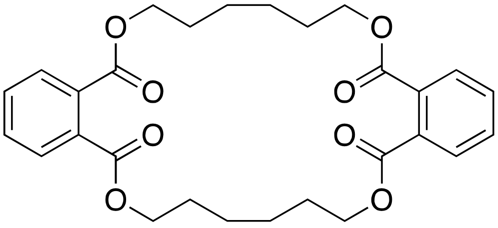

Fig.1. Structure of the fluorescent compound identified in this study

cartridge. Strong fluorescence was observedinone of the fractions, which wasfurther purified by HPLC.NMR analysis revealed that this compound has a cyclic dimeric phthalate ester structure (Fig. 1). Comparison of various analytical data with the synthesized compound confirmed that the structure obtained was correct. To examine its existence in other scorpion species, the same analysis was conducted using the exuviae of *Isometrus maculatus*. The result showed that this compound was also present in this scorpion. We also confirmed the presence of this compound in the extract of whole bodies of *Scorpio mauruspalmatus*, *Androctonusamoreuxi*, and *Buthacusleptochelys*. This strongly suggests that this compound is commonly present in the scorpion cuticle. Since fluorescent substances in the scorpion cuticle are thought to exist as macromolecules, this compound might be a constituent part of them.

Mesothelae in East Asia, tracing their lineage from Japan to Vietnam and Myanmar

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The story of the study of Mesothelae spiders began with the discovery of *Liphistius desultor* on the Malaysian island of Penang in 1849. Today, 173 years after, one genus and 67 species of Liphistiidae Thorell, 1869 and 7 genera and 107 species of Heptathelidae Kishida, 1923 are known in this suborder, and the numbers continue to grow. Considering only several species of the suborder were known in 1980 (!), the current development in this study field is amazing. Further development of the future is made possible by up-and-coming young researchers.

The National Museum of Nature and Science, Japan, has conducted zoological expeditions in Asia collaborated with researchers from various countries: Nepal Himalayas (1977-1982), the Philippines (1983-1984), Thailand and Malaysia (1987-1988), Taiwan (1989-1991) and Vietnam (1994-2003). The most recent project on the flora and fauna of Myanmar (2016-) is currently running. When I was 16 years old, I intrigued by the primitive, segmented spider (Kimura-gumo), which seems essential to unraveling aspects of the evolution of Araneae, and the spiders led me to the subtropic islands of Japan and to the fascinating unknowns of the Asian countries. Years later, after studying abroad in Germany, I took a job of the curator at the national museum, and concentrated on the study of Mesothelae. I participated in those joint studies in Thailand, Malaysia, Taiwan, Vietnam and Myanmar, and described some Mesothelan spiders including the local one (Fig.1). Looking close only at the ground for collecting trapdoor spiders, I often fell into a harvest less for other spiders as web builders and hunters.

On the occasion of this talk, I would like to share with colleagues the latest information on the study of Mesothelan spiders. The family Liphistiidae with a single genus is widely distributed in western part of East Asia, mainly Myanmar, Thailand and peninsular Malaysia (Schwendinger et al., 2019, 2022), while the range of heptathelids occupies its eastern part, namely Japan, China and Vietnam (Xu et al., 2015b). The more intense differentiation occurs in the latter family. Mesothelae spiders have recently diversified from an ancient lineage, and the genera show theirsharply allopatric habitat dominated by geological history (Xu et al., 2015a, 2016, 2021).

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Phylogenomic analysis of ultraconserved elements resolves the evolutionary and biogeographic history of segmented trapdoor spiders. *Systematic Biology*, 70(6): 1110-1122.

Fig.1. *Vinathela cucphuongensis*, female

Multi-locus phylogeny in the segmented spider genus *Liphistius* (Araneae, Liphistiidae) in Thailand

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Background: The segmented spider family Liphistiidae is the most basal family among living spiders. These spiders can be differentiated from other spiders by retention of several spider plesiomorphic characters, such aspresence of abdominal tergite plates and presence of spinnerets on the median area of the abdomen. *Liphistius* Schiödte, 1849 is endemic in southeast Asia. *Liphistius* includes 59 described species placedin seven species groups based primarily on genitalic characters. In Thailand, there are 34 *Liphistius* species in four species groups including the *birmanicus*-group, the *bristowei*-group, the *linang*-group, and the *trang*-group. In addition, the large *trang*-group has been subdivided into six species complexes. However, there is lack of consensus concerning phylogenetic relationships at the species and species-group levels.

Methods: In this study, we sampled 162 *Liphistius* specimens from 52 collecting sites in Thailand and Myanmar. We used five nucleotide loci (mitochondrial *COI* and *16S*, and nuclear *H3, 28S,* and *ITS2*) to reconstruct phylogenetic relationships and delimit *Liphistius* species. Bayesian Inferences and Maximum Likelihood phylogeny were analyzed using Mr. Bayes and IQTree 2 respectively.

Results: The concatenated alignments include 2,011 bps (*COI*:168 sequences, 550 bps, *16S*: 168 sequences, 316 bps, *H3*: 146 sequences, 241 bps, *28S*: 159 sequences, 630 bps, and *ITS2*:

161 sequences, 245 bps). Phylogenetic results aremostly congruent with morphology-based classifications, in supporting monophyly of the genus, the *bristowei*-group, and the *trang*-group. However, our results do not support the monophyly of the six species complexes within the *trang*-group. Molecular phylogenies suggest “Sibumasu origin” of the genus. The results group the taxa from Sibumasu terrain at the more basal clades of tree.

Discussion: Close relationship between the *birmanicus* group from the north and the *linang* group from the south at basal clade of the trees suggest widely distribution on the Sibumasu of *Liphistius* ancestor before diversifying into different species group. The migration to Indochina recently occurred in *Liphistius* phylogeny. There is only a recent clade within the *trang* group are found in the Indochina. In summary, molecular information is useful to reveal phylogenetic relationship and biogeographical history within *Liphistius.*

Development of a simple and cost-effective DNA barcoding protocol for spiders based on third-generation nanopore sequencing

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Taxonomic knowledge is an essential element of any effort to understand and diminish the effects of the current global biodiversity crisis. To effectively respond to this crisis, it is crucial to obtain detailed knowledge about the Earth's biodiversity and to routinely track its changes in ecosystems. However, the examination of biodiversity is labour-intensive, requiring extensive expertise on the taxa in question. Our need to accurately characterize the composition, relative abundance and interactions of biological communities is increasing. Fortunately, DNA barcoding using high throughput sequencing has greatly simplified taxonomic identification and become an essential tool in biodiversity research, as it allows rapid identification of taxa and speeds up community-level studies with large datasets. Despite its practicality, there are still limits to DNA barcoding. The commonly used single-locus barcoding approach is limited in its explanatory power and often does not give a precise species or genus level output from the analyzed sequences. Therefore, a DNA barcoding approach that increases the amount of available sequence data is needed. This should combine information from multiple non-associated loci across the genome and should be cost-effective, making it accessible to taxonomists. Therefore, in this project, we aim to develop a rapid multi-locus DNA barcoding protocol for obtaining long-read amplicons across the spider tree of life using

ONT (Nanopore) technology. We present the results of a pilot study in which we successfully generated ca. 5300 bp of data per specimen, using two simple PCR reactions to amplify established barcode regions (COI, Cytochrome B, and the nuclear ribosomal cluster) for fifteen spider families representing most of the major clades of Araneomorphae. Our results are congruent with recent phylogenetic hypotheses for the spider tree of life and demonstrate the efficacy of third-generation sequencing as a practical, cost-effective, and powerful tool for obtaining taxonomic knowledge.

First micro-CT scans of the scorpion brain

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The scorpion central nervous system includes four major components: the subesophageal ganglion, a pair of circumesophageal commissures, seven free ganglia (three mesosomal and four metasomal) and the brain. The brain, or supraesophageal ganglionic mass, is situated directly underneath the ocelli and is divided into the protocerebrum and tritocerebrum. From there, several nerves originate: one pair of tegumentary, one pair of stomatogastric, two pairs of ocellar, three pairs of cheliceral, and one pair of rostral. Apart from these, a pair of pedipalpal, four pairs of pedal and four pairs of mesosomal nerves with uncertain destinations rise from the subesophageal ganglion, which also posteriorly continues into the seven free ganglia. The earliest studies addressing the scorpion nervous system stem from the first half of the twentieth century, however, no recent research has been conducted. In this project, we optimize preservation techniques and scanning parameters to visualize the scorpion brain using micro-CT scanning and aim to determine whether structural differences can be observed across families. For this project, specimens were euthanized by placing in a freezer for 20 minutes. Legs were removed and specimens were fixed in Bouin's solution with time ranging from a few days to several weeks. Specimens were dehydrated in a graded ethanol series (70 %, 80 %, 90 %, 95 %, 100 % for at least 2 hours for each washing) and then stained in 1 % iodine solution and washed in 100 % ethanol again. Specimens were critically point driedwith an automated dryer (Leica EM CPD300) and micro-CT scanning was performed on a Yxlon FF20 CT scanner. Preliminary results indicate no major differences, suggesting the morphology of this structure is relatively conserved.

The Fauna portal web identification platform: A concept for the rapid documentation of undescribed species

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The majority of the world's invertebrate fauna remains undescribed and it is increasingly likely, that many species will remain undocumented before they go extinct. For example, approximately 70-80 % of Australia's invertebrate fauna, is undescribed. Some 4.000 Australian spider species are currently named and species estimates have place the true diversity of this order in Australia between 8.500 and 20.000 species. Over the last five years (2017-2021), an average of 56 species were named each year. Assuming a similar speed of discovery, it would take 90-276 years (depending on the species estimate) to describe the remaining Australian araneofauna (questionable with little recruitment in the taxonomic workforce in Australia). Meanwhile, it is virtually impossible to use spiders in environmental studies or assess their distribution patterns, particularly of rare species of conservation significance.

The Fauna portal Australia (www.faunaportal.org) aims to provide a stopgap for the documentation and identification of Australia's undocumented invertebrate fauna and is easily transferable to other geographic regions. It is based on a taxonomically stable nomenclatural system derived from proven zoological principals (reference specimen in public institutions and diagnosis) supported by an underlying database that provides genus- and species-level nomenclatural codes. Diagnostic images for each species allow for an identification of each species and these images are accessible via filters for projects, morphology, sex and/or developmental stage and distribution (either by state or a region selected via map). Documentation of a new species is fast due to the simple backend design of the website. User-restricted sections allow developing projects hidden to the public, for example research data can remain concealed until the they are published. We believe, the Fauna portal has the potential to speed up species discovery, documentation and identification in Australia and else where and support environmental and taxonomic research.

The effect of Bt protein to embryonic development and activity of metabolic enzymes in *Pardosa pseudoannulata*

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Pardosa pseudoannulata is a big, ferocious, and predatory spider, which is dominant in the rice paddies, and has an important role in the regulation of pest populations. Now the mechanism of Bt insecticidal proteins in the transgenic rice on the target pests is reported largely. Among those, all the spider biosafety researches are mainly on the enrichment of Bt protein by the food chain in the spiders instead of the effects.

Our study used the *Pardosa pseudoannulata* as the object, analyzed the enrichment of Cry1Ab protein and its effects on the activity of three detoxifying enzymes in this spider from the perspective of the food chain; furthermore, Cry1Ab protein could be detected in the spider oocyst, so we could investigate Cry1Ab protein transferred from parent to descendant, the chemical substance content and morphological characteristics in the embryonic development, and the activities of four protective enzymes in the eggs, and the features of the livetins. Therefore, it could provide a theoretical basis for the safety assessment of transgenic Cry1Ab protein rice.

Drosophila and planthoppers were fed with transgenic Cry1Ab protein medium and rice respectively, to enrich Bt insecticidal protein, and then we feed the spiders with the *drosophila* and planthoppers. We used the enzyme-linked immunosorbent (ELISA) for Cry1Ab protein content in the *Pardosa pseudoannulata* body , and then detected changes of SOD, AchE, and GSH-Px enzyme activity with the kit; besides, took the birth oocysts as the embryonic development materials, determined Cry1Ab protein content by ELISA; assayed SOD, AchE, GSH-Px and CAT enzyme activities in the eggs with the kit; moreover, utilized the related methods to investigate differences of the chemical substance content during the embryonic development; observed changes in the embryonic morphological features by use of paraffin sections and transparent liquid paraffin technique; finally, exploited the electrophoresis to study the chemical properties of livetin.

The results showed that: Cry1Ab protein enriched in the *Pardosa pseudoannulata* body (enrichment factor up to 24.38), GSH-Px activity in experimental group increased significantly compared to the control ($p < 0.01$), and reached the peak at 7th day; AchE activity in experimental group reached its peak at 3th day and was higher than the control group significantly ($p < 0.05$) and got to the bottom at 7th day with significance to the control ($p<0.05$); from the 3th to 11th day, SOD activity in experimental group was markedly lower than the control group ($p < 0.01$) and reached the bottom at 7th day with highly significance to the control ($p < 0.01$). During the embryonic development, Cry1Ab protein content in the eggs of experimental group was also higher than the control ($p < 0.05$), and the SOD, AchE, GSH-Px and CAT enzyme activity detection showed that GSH-Px enzyme activity increased higher than the control ($p<0.01$) but that of other three all showed lower than the control group ($p<0.01$).

As a contrast to the control, embryonic development duration in experimental group extended and embryonic development incompleted, observed by the liquid paraffin and paraffin sections. Through the determination of the chemical substances in the eggs, we found that the protein content in control group was significantly higher than the experimental ($p < 0.05$), but no significant differences in sugar and fat content. Than, we found that livetin of the *Pardosa pseudoannulata* is a glycolipid-binding protein, by its extraction and electrophoresis. Livetin molecular weight in the experimental group was 279.64 KD, and its subunit size was 85 KD and 69 KD the 63.5 KD and 50 KD, respectively; moreover, that of the control was 274.79 KD, and its subunit size was 85 KD, 72 KD, 65 KD and 51 KD, separately. The amino acid composition analysis showed that the content of glutamic acid and arginine in the control group was higher than that of the experimental.

Study on effect of cadmium on cold resistance of paddy dominant species of *Pirata subpiraticus*

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The accumulation of heavy metal cadmium has certain effects on the growth, reproduction, viability and other aspects of *Pirata subpiraticus.* There are many scientific studies related to it, but there are few reports on the effects of cadmium stress on the cold resistance of rice spiders. In particular, there is no literature on the cold resistance of spiders at the molecular level. In this study, the effects of heavy metal cadmium on its cold resistance were discussed based on the dominant species of *Pirata subpiraticus* rice fields. The main results of the study are as follows:

1. The cadmium enrichment in *Drosophila* in medium cultured with different concentrations of $CdCl_2$ was determined, and 1.00 ml/L $CdCl_2$ was determined as the best experimental concentration. The cadmium in *Drosophila* was determined under different cadmium stress days. The enrichment amount showed that the cadmium enrichment reached the maximum on the 8th day, and it was confirmed that the *Drosophila* sinensis was fed with the cultured fish for 8±1d in the subsequent experiment; the *Drosophila* treated with 1.00 ml/L $CdCl_2$ was determined. The cadmium enrichment of the feeding spiders at 7d, 14d, 21d, 28d, 35d and 42d showed that the concentration of cadmium in the spider reached a maximum of 7.15±0.418 μg/g on the 28th day, so the late transcription Samples were selected for sampling in groups of 28 to 29 days.

2. The data of developmental duration, carapace width, body length, weight and middle eye area of the spiderling under cadmium stress were recorded. The differences of these growth indicators at different instars were analyzed by SPSS software. The results showed: The total duration of cadmium-stressed spiderling

(57±1.8212) was significantly higher than that of the normal group (54.7±1.2103), and there was a significant difference ($p<0.05$). From other indicators, the instar of cadmium stress significantly affected the spiderling. The period is 5-7th instars. After comprehensive analysis of these indicators, it is concluded that short-term low concentration of cadmium stress has little effect on the growth and development of the *Pirata subpiraticus*, and the cadmium stress time and cadmium enrichment from the 5th instar , the growth and development of cadmium-stressed larvae began to be affected by the toxicity of cadmium. Cadmium stress can affect the survival rate of *Pirata subpiraticus* spiderling and the effect of 2nd-5th instar is less. The survival rate of experimental group and control group at 6th and 7th instar is significantly different ($p<0.05$).

3. The effects of cadmium stress on energy metabolism of *Pirata subpiraticus* at low temperature were investigated. The contents of protein, sugar and fat in the hemolymph of *Pirata subpiraticus* and spiderling at 25 ℃ and 4 ℃ were determined. The results showed that the hemolymph protein content of each group of *Pirata subpiraticus* at 25 ℃ was higher than that of the same group of *Pirata subpiraticus* at 4 ℃. There were significant differences in protein content between the Cd-X group and the Cd-D group under cadmium stress at two temperatures ($p<0.05$). The protein content of cadmium-stressed spider hemolymph was higher than that of normal spiders, and there was no significant difference. At 25 ℃, the hemolymph sugar content of spiders in each group was higher than that of the same group of spiders at 4 ℃, There were significant differences between Ck-X, Cd-X and Cd-D groups ($p<0.05$). At the same temperature, the content of sugar in the hemolymph of cadmium-stressed spiders was lower than that of normal spiders, and there was significant difference at 4 ℃ ($p<0.05$). At 25 ℃, the hemolymph fat content of each group was higher than that of the same group of spiders. There was a significant difference in fat content between the Cd-X and Cd-D groups at two temperatures ($p<0.05$). At 4 ℃, there was a significant difference in the hemolymph fat content of cadmium-stressed spiders ($p<0.05$).

4. Transcriptome sequencing, after splicing 257,559 Unigenes were annotated into seven databases, the screening parameters is padj <0.05 &$|\log2FoldChange|>1$, gene expression

analysis was performed, and the spideling at 4 ℃, a total of 807 genes were detected between the spiderling CdX_vs_CKX with significant differential expression levels, 779 up-regulated genes and 28 down-regulated genes. A total of 596 genes between the mature spider CdD_vs_CKD had significant differential expression levels, 337 up-regulated genes and 259 down-regulated genes. GO-enrichment analysis results: the up-regulation of CK and Cd in spiderling is mainly enriched in metabolic processes, oxidation-reduction processes, extracellular region and oxidoreductase activities in four channels, down-regulating gene enrichment in metabolic process. To mature spider CK and Cd, the up-regulated differential genes are mainly enriched in the cellar response to chemical substances, cell proliferation; down-regulated gene enrichment in hydrolase activity, hydrolase and peptidase activity, indicating that cadmium may have certain effects on the reproductive, sensory and nervous systems of the spider. The results of KEGG enrichment: the up-regulation of CK and Cd in spiderling is mainly enriched in antigen processing and presentation, apoptosis, lysosomes, and oxidative phosphorylation; down-regulation of differentially expressed genes is mainly enriched in steroid hormone biosynthesis, metabolism of linoleic acid into spider CK and Cd is mainly enriched in glycosphingolipid biosynthesis - lactose and neolacto series, cytokine-cytokine receptor interaction, tryptophan metabolism and so on.

Effects and mechanisms of cadmium and Bt protein on the development of *Pirata subpiraticus*

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Pirata Subpiraticus (Arachnoidea: Araneida), is a dominant species in rice fields of southern China, and plays an important role in the ecological control of pests. Cadmium (Cd) is a toxic heavy metal widely distributed in the environment, which not only seriously pollutes the ecological environment, but also poses a great threat to the survival of organisms. Bt protein is a kind of insecticidal protein produced by *Bacillus thuringiensis*, which has been widely used in the field pest control due to the transgenic technology. Since heavy metals and Bt crops are both hot issues in farmland environment research in China, while most of the research, focus on the impact of single stress on organisms. Therefore, the author selected the spider as the biomarker to explore the effects of the combined effect of heavy metal Cd and Bt protein on the growth and development, antioxidant enzymes, gene expression levels. The main results are as follows:

1. The transport and enrichment of Cd and Bt protein in *Drosophila melanogaster* and *P. subpiraticus* were revealed by the food chain “culture medium to fruit flies to spiders”. Both fruit flies and spiders were able to accumulate Cd and Bt protein, and the Cd content reached maximum after three weeks treatment, while Bt protein after two weeks treatment. Regardless of heavy metal Cd or Bt protein, the enrichment of Cd+ Bt group was higher than that of Cd and Bt single stress group, with significant difference ($p<0.05$).

2. After it was clear that Cd and Bt protein could be enriched in spiders, this experiment studied the combined effect of the two stresses on the growth and development of *P. subpiraticus* compared with the single stress of Cd and Bt protein. The results showed that Cd and Bt proteins may affect the development

indicators of spiders, leading to the decrease of body length and weight, especially the extension of developmental duration of *P. Subpiraticus*. And the comparison between the two groups showed that the combined effect of Cd and Bt proteins was more significant than the single stress.

3. Compared with the control group, Cd and Bt protein both increased the activity of peroxidase and glutathione peroxidase in the body of the adult and *P. Subpiraticus*, among which the combined effect of Cd and Bt had a more significant effect than the single stress ($p < 0.05$). Under the combined action of Cd and Bt protein, superoxide dismutase (SOD) activity of spiders was significantly higher than that of other treatment groups. SOD activity in junior spider changes with age, and Cd and/or Bt protein treatment group is lower than control group. In addition, the activity of glutathione S-transferase in the adult and young spiders under combined stress was significantly higher than that in other treatment groups.

4. Transcriptomic sequencing technology was used to analyze the influence of Cd and Bt protein stress on the gene expression of arachnids. A total of 251,373 and 123,858 high-quality transcripts and unigenes were obtained. In addition, 5,995 (Cd vs CK), 6,914 (Cd +Bt vs CK) and 3,942 differentially expressed genes (Cd +Bt vs Cd) were screened by gene expression levels and *p* values. The enrichment analysis of GO and KEGG showed that most of the annotation functions of differentially expressed genes included "structural components of the cuticle", “synapses”, “transport vesicles”, etc., and the annotation pathways included “oxidative phosphorylation”, “steroid hormone synthesis”, etc.

5. Through in-depth analysis of sequencing data, it was found that under the combined treatment of Cd and Bt proteins, biological functions such as “structural components of cuticle”, “RNA polymerase complex” and “RNA-directed RNA polymerase activity” were significantly down-regulated in gene clusters with similar expression trends. In addition, the expression levels of cytochrome enzyme system, heat shock protein, cuticle and chitin were significantly lower than those of normal spiders under the treatment of Cd and Bt. In this study, 40 genes with transcriptional

factor function were screened, and related protein interaction networks were constructed to analyze the potential mechanism of transcriptional translation of transcriptional genes related to ecdysis signaling pathway by transcriptional factors, thus affecting the developmental duration of spiders.

In summary, this paper discussed the effects of Cd and Bt protein on the growth of *P. subpiraticus* according to phenotypic indicators, enzyme activities and gene expression levels. Compared with the single stress of Cd and Bt protein, the combined effect of Cd and Bt protein on *P. subpiraticus* was more significant. Furthermore, the key genes of Cd and Bt protein affecting the development of *P. subpiraticus* and their regulatory mechanisms were revealed from the molecular perspective, which provide theoretical and experimental basis for the treatment of heavy metal pollution and the safety evaluation of transgenic crops.

Effect of cadmium on embryonic development of *Pardosa pseudoannulata*

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Heavy metal cadmium may cause various physiological effects on the post-embryonic development of spiders, but the effect on the development of spider (*Pardosa pseudoannulata*) embryos has not been reported in the literature. Therefore, this study investigated the effects of heavy metal cadmium on embryonic development. The specific results are as follows:

1. The cadmium content of the medium-drosophila-spider-embryonics was determined by ICP inductively coupled plasma spectroscopy. The concentration of cadmium in the medium was 3.78 mg/kg, and the content of cadmium in the fruit flywas 20 mg/kg. The cadmium content was 28 mg/kg, and the final cadmium content in the oocysts was 6 mg/kg.

2. Effect of cadmium stress on embryo vitellogenin (Vt) at 6 h, 48 h and 144 h of development. The Vt content (25.58±0.2590 ng/mL) in the experimental group was significantly higher than that in the control group (13.5±0.5987 ng/mL, $p<0.05$). Cadmium stress had a certain influence on the activity of detoxification enzymes in embryos. The activity of superoxide dismutase (SOD) in the embryos of the experimental group at 48 h was 3.24±0.4239 U/mL, which was significantly lower than that of the control group (9.02±0.9688 U/mL, $p<0.05$). But did not reach significant levels in other periods. The activities of glutathione peroxidase (GPX) in the embryos of the experimental group at 6 h and 144 h (29.34± 1.0934 U/L, 17.95±0.2911 U/L) were significantly higher than those of the control group (10.7±0.4113 U/L, 7.84 ±0.2941 U/L, $p<0.05$), but the GPX activity in the experimental group was significantly lower than that in the control group (13.6±0.9559 U/L, $p<0.05$) at 48 h after embryonic development. The results showed

that both SOD enzyme and GPX enzyme had an adjustment and adaptation mechanism for heavy metal cadmium during the embryonic development of spiders. Through self-regulation, the spiders could survive in a certain concentration of cadmium-contaminated environment.

3. Transcriptome sequencing was performed on embryos that developed at 6 h, 48 h, and 144 h using high-throughput sequencing technology cadmium. The results showed that 273,860 Unigenes with an average length of 1028 bp were obtained after splicing and the N50 was 1503. There were 146, 165 and 517 genes significantly different in the embryos of the experimental group at 6 h, 48 h and 144 h compared with the control group at 6 h, 48 h and 144 h. The gene expression of the embryos at different stages of development were also different. The normal group 6 h, there were 10977 genes significantly differently expressed at 48 h; 16260 genes were significantly differently expressed in normal group at 48 h compared with 144 h.

4. KEGG enrichment analysis was performed on the differentially expressed embryos of embryos (cadmium treated vs normal group) and normal embryos of different developmental stages at the same developmental stage. The results showed that in the T_48h_vs_ck_48h differential gene was enriched to the mTOR signaling pathway, glutathione metabolism, glycosaminoglycan biosynthesis, MAPK signaling pathway, ErbB signaling pathway, and apoptosis. In the T_144h_vs_ck_144h differential gene enrichment to proline, leucine and isoleucine degradation, cell cycle, AMPK signaling, pyruvate metabolism, dopaminergic synapses, peroxisomes, arachidonic acid metabolism, ribosome, Notch signaling pathway, mTOR signaling pathway. In CK_6h compared to CK_48h differential genes were enriched in ribosome, purine metabolism, oxidative phosphorylation, MAPK signaling pathway, to hedgehog signaling pathway, TGF-β signaling pathway, Hippo signaling pathway, circadian rhythm, aldosterone synthesis and secretion. In CK_48h_VS_CK_144h differential gene enrichment to mRNA surveillance pathway, ubiquitin-mediated proteolysis, TGF-β signaling pathway, hedgehog signaling pathway, progesterone-mediated oocyte maturation, fatty

acid elongation, calcium signaling pathway, GnRH signaling pathway, Olfactory transduction.

This study reveals the effects of cadmium stress on the enzymatic activity and gene function of embryonic development of *Pardosa pseudoannulata* from physiological and molecular levels. It also analyzes the changes in gene function at different stages of embryonic development under cadmium-free conditions. Functional research remains to be further explored.

Linyphiidae of China: past, present and future

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China’s great topological and climatic diversity has produced a vast array of natural habitats that harbor a wide range of fauna and flora. Spiders are a diverse group of arachnids, distributed in all kinds of habitats. About 5,617 species in 831 genera in 69 spider families have been recorded in China, of which 418 species in 163 genera belong to the family Linyphiidae. The Linyphiidae spiders from China are relatively well studied as compared to the adjacent countries in East Asia and the Oriental region. In China, most of the previous studies have been done in the east and north-eastern parts of the country. Recent studies in southern China have revealed about >300 new species and several new genera (in press). About 80 % of the newly described species are solely endemic to their type localities. The current fauna of Linyphiidae spiders from China does not represent the actual diversity that still needs an extensive study to be done to document and remove the deficiencies of previously known species.

About toponymic problems in Oriental Arachnology

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It is clear that some toponymic problems for faunistics arise over time due to political and cultural changes. The state borders are shifting, toponyms are changing their spelling. So, the geographical names used in old scientific papers nowadays might have an ambiguous interpretation and generate inaccuracies. In particular, it concerns the spider species described by Thorell, Simon, and Badcock from the area of modern Thailand or the neighboring countries about hundred and more years ago. For example, some species from Patani Kingdom of Malay Peninsula, consisting of seven states and being independent from Siam till 1906, were actually collected from Thailand but not from Malaysia as it assumed now. The states “Jalor” and “Raman” correspond to the modern Yala province of Thailand, “Ligeh” to Narathiwat, “Nawng-Chik” to Pattani. The locality “Biserat” was situated in Jalor, i.e., in Yala province “Paklat” is located near Paknam, i.e., in Samut Prakan province In Badcock (1918), “Ban Sai Kau” and “Nandock” were possibly referred to “Sai Khao” and “Nawngchik” of the modern Pattani province, K. Mahek, Jalor is [Kuala] Mabek, Jalor (Yala province).

However, some of old toponyms cannot be revealed for sure. Thus, the type locality of *Epeira paviei* Simon, 1886 known as “Snakes” has unclear coordinates and may lie either in the mainland Thailand, Cambodia, or southern Vietnam. The locality “Bachiou”, given by Simon (1886) without clarification, mentioned for the materials collected by A. Pavie from the area partly occupying the modern territories of Thailand, Cambodia, and Vietnam. In four descriptions, this name was set directly before the Cambodian locality: “Bachiou, Pnom-Penh (Cambodge)” (Simon 1886: pp. 143, 163, 164), which perhaps could be attributed to

“Bachiou” in Cambodia: e.g., in Gravely (1924: p. 591, *P. irretita*, Bachiou, Cambodia). In their checklist, Murphy & Murphy (2000) considered Bachiou to lie in Thailand. When using “Bachiou” for other eight cases separately, Simon (1886: pp. 137, 141, 143, 146, 158, 163, 164) specified nothing in brackets, as it should be if the site would have belonged to Cambodia or any other certain country. It seems that the author had no detailed information about the locality apart from its name. The final report for A. Pavie mission, published in 1904, contains one reference to the locality with a very similar designation: “*Rhacophorus maculatus* Gray. Bachieu (Saïgon). 1 exemplaire” (Mocquard 1904: p. 473). So, the sampling site labeled as “Bachiou” in A. Pavie’s collection and examined by Simon was highly likely to be situated in Saigon in Vietnam. This corresponds to Ono et al. (2012), who noted “Saigon” as the type locality for two of the species described by Simon (1886) from Bachiou (*Heteropoda pressula* and *Pycnaxis nigrostriata*).

Based on the above information, *Pronous affinis* and *Theridion subradiatum*, which are still known from the type locality only (“Jalor”: Simon 1901), should be assigned to Thailand rather than to Malaysia. As for the spiders from “Bachiou” (Simon 1886), this type locality was erroneously attributed by Murphy & Murphy to Thailand for the following species: *H. pressula*, *P. nigrostriata*, *Pardosa irretita*, *Oedignatha sima*. Actually, *H. pressula* and *O. sima* was only recorded from Vietnam, although Simon (1897: pp. 190-191) mentioned the latter species as Cambodian, while describing the genus *Oedignatha*. *P. irretita* was also reported from Thailand (“Ligeh”, Narathiwat) by Simon (1901). *Pycnaxis nigrostriata* has been only found in Vietnam (Simon, 1886 & 1904; Ono et al., 2012) and Malaysia (Pulau Pinang: Lehtinen, 2016).

Spiders from Cuc Phuong National Park

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Cuc Phuong National Park, Ninh Binh province, with an area 22,200 ha, is situated in the foothills of the northern Annamite Range. The park consists of verdant karst mountains and lush valleys. Elevation varies from 150 to 656 m. Cuc Phuong is the first National Park in Vietnam, established in 1962. It is home to unique communities of rainforest spiders. The basis of a small species list of spiders are taxa described from within the national park. For three of them, the specific name is given according to the type locality.

Agelenidae: *Coelotes acerbus* Liu, Li & Pham, 2010; *Draconarius cucphuongensis* Liu, Li & Pham, 2010; *D. longissimus* Liu, Li & Pham, 2010; *D. pseudopumilus* Liu, Li & Pham, 2010; *D. pumilus* Liu, Li & Pham, 2010; *D. rotulus* Liu, Li & Pham, 2010; *D. volubilis* Liu, Li & Pham, 2010; *Notiocoelotes pseudovietnamensis* Liu, Li & Pham, 2010 (Liu, Li & Pham, 2010a). **Caponiidae:** *Laoponia saetosa* Platnick & Jäger, 2008 (Liu, Li & Pham, 2010b). **Hahniidae:** *Hahnia himalayaensis* Hu & Zhang, 1990; *H. rimaformis* Zhang, Li & Pham, 2013; *H. zhejiangensis* Song & Zheng, 1982 (Zhang, Li & Pham, 2013). **Halonoproctidae:** *Cyclocosmia latusicosta* Zhu, Zhang & Zhang, 2006 (Zhu, Zhang & Zhang, 2006). **Heptathelidae:** *Vinathela cucphuongensis* (Ono, 1999) (Ono, 1999). **Mysmenidae:** *Gaoligonga taeniata* Lin & Li, 2014, *Mysmena maculosa* Lin & Li, 2014 (Lin & Li, 2014). **Ochyroceratidae:** *Speocera bulbiformis* Lin, Pham & Li, 2009 (Lin, Pham & Li, 2009). **Pholcidae:** *Belisana decora* Yao, Pham & Li, 2015; *B. vietnamensis* Yao, Pham & Li, 2015; *Khorata cucphuong* Yao & Li, 2018; *Kh. palace* Yao & Li, 2018; *Leptopholcus huongson* Huber, 2011; *L. podophthalmus* (Simon, 1893); *Pholcus zhaoi* Yao, Pham & Li, 2015 (Yao, Pham & Li, 2015; Nie et al., 2018). **Psilodercidae:** *Relictocera sigen* Li & Li, 2019 (Chang, Li & Li, 2019). **Salticidae:** *Bristowia heterospinosa* Reimoser, 1934; *Burmattus pococki* (Thorell, 1895); *Carrhotus sannio* (Thorell, 1877); *Chinattus tibialis* (Żabka, 1985); *Colopsus longipalpis* (Żabka, 1985); *Emathis sumatrana* Prószyński & Deeleman-Reinhold, 2012; *Evarcha flavocincta* (C. L. Koch, 1846); *Foliabitus scutigerus* (Żabka, 1985); *Harmochirus zabkai* Logunov, 2001; *Hasarius kulczynskii* Żabka, 1985; *H. orientalis* (Żabka, 1985); *Magyarus typicus* Żabka, 1985; *Menemerus bivittatus* (Dufour, 1831); *M. brachygnathus* (Thorell, 1887); *Myrmarachne angusta* (Thorell, 1877); *M. fredwanlessi* Logunov, 2021; *Neobrettus phui* Żabka, 1985; *Onomastus simoni* Żabka, 1985; *Pancorius magnus* Żabka, 1985; *Phintella accentifera* (Simon, 1901); *Ph. debilis* (Thorell, 1891); *Ph. vittata* (C. L. Koch, 1846); *Portia albimana* (Simon, 1900); *Ptocasius strupifer* Simon, 1901, *Rhene albigera* (C. L. Koch, 1846), *Siler bielawskii* Żabka, 1985, *Synagelides palpalis* Żabka, 1985; *Thiania abdominalis* Żabka, 1985; *T. bhamoensis* Thorell, 1887; *Telamonia caprina* (Simon, 1903); *T. elegans* (Thorell, 1887); *T. festiva* Thorell, 1887; *Toxeus maxillosus* C. L. Koch, 1846 (Żabka, 1985; Logunov, 2001, 2021; Phung, 2017). **Sparassidae:** *Heteropoda jasminae* Jäger, 2008; *Heteropoda zuviele* Jäger, 2008 (Jäger, 2008). **Symphytognathidae:** *Anapistula orbisterna* Lin, Pham & Li, 2009; *Crassignatha bispina* (Lin, Pham & Li, 2009) (Lin, Pham & Li, 2009). **Telemidae:** *Pinelema cucphongensis* (Lin, Pham & Li, 2009) (Lin, Pham & Li, 2009). **Tetrablemmidae:** *Lehtinenia bisulcus* Lin, Pham & Li, 2009 (Lin, Pham & Li, 2009). **Zodariidae:** *Heradion flammeum* (Ono, 2004); *Mallinella septemmaculata* Ono, 2004 (Ono, 2004).

In May 2019, zoologists from Belarus collected material on spiders in Cuc Phuong National Park. All material is stored in the collection of arachnids SNPO “SPC of the National Academy of Sciences of Belarus for Bioresources”, Minsk, Belarus. Collection points coincide with the routes to the main attractions of the Cuc Phuong National Park.

Araneidae: *Aoaraneus pentagrammicus* (Karsch, 1879)
1f, 20°20′53.3″N, 105°35′51.5″E, 364 m, 16 May 2019, A. V. Derunkov.
Argiope pulchella Thorell, 1881
1f, 20°20′53.3″N, 105°35′51.5″E, 364 m, 16 May 2019, A. V. Derunkov;
1f, 20°21′32.4″N, 105°34′42.5″E, 360 m, 16 May 2019, R. V. Novitsky.
Argiope vietnamensis Ono, 2010
1m, 2f, 20°21′05.3″N, 105°35′26.9″E, 360 m, 16 May 2019, S. V. Saluk.
Cyrtophora moluccensis (Doleschall, 1857)
1f, 20°21′01.6″N, 105°35′23.4″E, 361 m, 16 May 2019, S. V. Saluk;
1f, 20°21′05.9″N, 105°35′19.4″E, 360 m, 16 May 2019, R. V. Novitsky.
Gasteracantha diardi (Lucas, 1835)
1f, 20°21′01.6″N, 105°35′23.4″E, 361 m, 16 May 2019, S. V. Saluk.
Macracantha hasselti (C. L. Koch, 1837)
4f, 20°21′01.6″N, 105°35′23.4″E, 361 m, 16 May 2019, S. V. Saluk;
5 f, 20°21′06.4″N, 105°35′28.3″E, 363 m, 16 May 2019, R. V. Novitsky.
Neoscona jinghongensis Yin, Wang, Xie & Peng, 1990
1f, 20°14′46.7″N, 105°42′56.6″E, 155 m, 18 May 2019, R. V. Novitsky.
Parawixia dehaani (Doleschall, 1859)
4 f, 20°21′05.3″N, 105°35′26.9″E, 360 m, 16 May 2019, S. V. Saluk.
Oxyopidae: *Oxyopes sertatoides* Xie & Kim, 1996
1m, 20°21′32.4″N, 105°34′42.5″E, 360 m, 16 May 2019, R. V. Novitsky.
Pisauridae: *Hygropoda campanulata* Zhang, Zhu & Song, 2004
1f, 20°21′21.9″N, 105°35′33.6″E, 460 m, 17 May 2019, S. V. Saluk.

Salticidae: *Colyttus lehtineni* Żabka, 1985

2f, 20°21′27.2″N, 105°35′35.7″E, 510 m, 17 May 2019, S. V. Saluk.

Hasarius orientalis (Żabka, 1985)

1f, 20°20′53.14″N, 105°35′52.5″E, 375 m, 17 May 2019, R. V. Novitsky.

Pancorius magnus Żabka, 1985

1 m, 20°21′01.6″N, 105°35′23.4″E, 361 m, 16 May 2019, S. V. Saluk,

1 f, 20°21′21.9″N, 105°35′33.6″E, 460 m, 17 May 2019, S. V. Saluk;

2 m, 2 f, 20°14′54.7″N, 105°42′56.3″E, 154 m, 16 May 2019, R. V. Novitsky.

Ptocasius strupifer Simon, 1901

1f, 20°14′44.0″N, 105°43′07.1″E, 150 m, 19 May 2019, S. V. Saluk.

Sparassidae: *Heteropoda venatoria* (Linnaeus, 1767)

1f, 20°15′11.9″N, 105°42′39.3″E, 180 m, 17 May 2019, S. V. Saluk.

Thelcticopis severa (L. Koch, 1875)

1m, 20°20′53.1″N, 105°35′52.5″E, 375 m, 17 May 2019, R. V. Novitsky.

Tetragnathidae: *Leucauge tessellata* (Thorell, 1887)

5f, 20°21′01.6″N, 105°35′23.4″E, 361 m, 16 May 2019, S. V. Saluk;

5f, 20°21′06.4″N, 105°35′28.3″E, 363 m, 16 May 2019, R. V. Novitsky.

Theridiidae: *Argyrodes miltosus* Zhu & Song, 1991

1f, 20°21′27.2″N, 105°35′35.7″E, 510 m, 17 May 2019, S. V. Saluk.

Episinus nubilus Yaginuma, 1960

1f, 20°21′21.9″N, 105°35′33.6″E, 460 m, 17 May 2019, S. V. Saluk.

Theridion zonulatum Thorell, 1890

1f, 20°20′53.3″N, 105°35′51.5″E, 364 m, 16 May 2019, A. V. Derunkov.

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Faunistic diversity of spiders (Arachnida: Araneae) in some agroecosystems at Amravati, Maharashtra, India.

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The spider diversity and its affluence in agroecosystemsare usually established by the intricacies of the assembly of the plant and its environmental conditions. The present study aimed to outline preliminary community diversity, species richness, and relative abundances of spiders across the two Kharif (Monsoon crop) cropping seasons with variationinclimatic conditions. Amravati is one of the majorpigeon pea and soybean growing regions. Here, we undertook mixed crop fields that widely cultivated pigeon pea (*Cajanuscajan*) alongside soybean (*Glycine max*). The observations were carried out from July 2020 to December 2020 and July 2021 to December 2021. In total, 879 individuals were collected from the study area, which comprises 33 genera from 14 families. 21 taxa have been identified at the species level. Four dominant families were reported commonly from both cropping seasons. Though, the family Araneidae remained dominantly abundant in both seasons, followed by Lycosidae and Thomisidae; in terms of species diversity, the family Salticidaewas found much more diverse than all other families in both seasons. The maximum species diversity was noted from August to November, correspondingly there was a decline in orb-weavers after the soybean crop was harvested.

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