International Society of Hymenopterists

#Hymathon2021 virtual symposium

6-7 May 2021

Organising Committee:
ISH Executive Committee, Jessica Awad, Erinn Fagan-Jeffries, Carly Tribull, Miles Zhang

- The symposium comprises three sessions (Americas - Australasia - Europe, Middle East and Africa) across three time zones
- All start times below are given both in GMT[1] (between brackets) and in the local time zone of the relevant session (in bold)
- Titles of talks with the name of the presenter only and Twitter handles when available are listed in the first part of the program; abstracts and full authorship + affiliations are listed in the second part of the program
- Zoom links to attend the sessions will be sent to registrants out shortly before the symposium (the symposium is free to ISH members but registration is essential)

#Hymathon2021 - Program

Americas Session - 6 May, local time: EDT (GMT -4)

Moderator: Miles Zhang; Victor Gonzalez Betancourt

(17:00 GMT) **13:00** **Introductory remarks**

(17:05 GMT) **13:05** **Keynote presentation:**
The use of museum specimens to perform phylogenomic studies: a case study in Braconidae
Presenter: Jovana Magdalena Jasso Martínez

(17:45 GMT) **13:45** **Break 1**

(17:55 GMT) **13:55** **Resolving the nightmare of the planidial clade!**
Presenter: John Heraty

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[1] GMT is equivalent to UTC - neither has a summer time

(GMT start time)	Local start time	
(18:10 GMT)	**14:10**	**The effect of early season temperature on adult life history traits of the wheat stem sawfly *Cephus cinctus* (Hymenoptera: Cephidae) and *Bracon cephi* (Hymenoptera: Braconidae)** Presenter: Dylan Sjolie - @bugboydyl
(18:25 GMT)	**14:25**	**Discovery of a putative troglomorphic ant (Hymenoptera: Formicidae: Leptanillinae: *Leptanilla* sp.) in southwestern Iran** Presenter: Zachary Griebenow
(18:40 GMT)	**14:40**	**Ants-extrafloral nectary associations in different growth stages of Bombacoideae (Malvales: Malvaceae) trees in a tropical urban ecosystem** Presenter: Aymer Andrés Vásquez Ordóñez - @VasquezAymer
(18:55 GMT)	**14:55**	**Down the bee-burrow: Unexpected diversity in the *Lasioglossum parvum* species complex (Halictidae: Halictini)** Presenter: Joel Gardner
(19:10 GMT)	**15:10**	**Break 2**
(19:30 GMT)	**15:30**	**Bees like flowers who knew? New Methods for Evaluating Foraging Choices in Bumble Bees (*Bombus impatiens*)** Presenter: Caleb Bryan - @bees_bryan
(19:45 GMT)	**15:45**	**Slicing the Gordian knot: A phylogenetic analysis of the subfamilial relationships of Aphelinidae (Chalcidoidea)** Presenter: Robert Luke Kresslein
(20:00 GMT)	**16:00**	***Diplolepis rosae* is more successful in North America than in Europe because of enemy release** Presenter: László Zoltán
(20:15 GMT)	**16:15**	**Wait, HOW many Hymenoptera are there? A global call for collaboration on estimating relative species richness** Presenter: Andrew Forbes - @Lord_Forbington
(20:30 GMT)	**16:30**	**An ethogram for the Comanche harvester ant, *Pogonomyrmex* comanche (Hymenoptera, Formicidae)** Presenter: Ann Mayo - @annbmayo
(20:45 GMT)	**16:45**	**Was it something I ate? Investigating how host order might affect body coloration Cirrospilini (Hymenoptera: Eulophidae)** Presenter: Ryan Perry - @chalcidcrusader
(21:00 GMT)	**17:00**	**Student prizes and concluding remarks**
(21:10 GMT)	**17:10**	**Social Americas**

Australasia Session - 7 May, local time: ACST (GMT + 9.5)

Moderators: Erinn Fagan-Jeffries; Alana Delaine

(GMT start time)	**Local start time**	
(04:00 GMT)	**13:30**	**Introductory remarks**
(04:05 GMT)	**13:35**	**Keynote presentation:** **Molecular phylogenetics, biogeography and evolution in spider wasps (Hymenoptera: Pompilidae)** Presenter: Juanita Rodriguez Arrieta - @juanita_rodr
(04:45 GMT)	**14:15**	**Break 1**
(04:55 GMT)	**14:25**	**The Chemical Ecology of Stink Bug Egg Parasitoids (Hymenoptera: Scelionidae)** Presenter: Tom Saunders - @TomSaundersNZ
(05:10 GMT)	**14:40**	***Psyllaephagus*, an important but problematic genus of Encyrtid wasps.** Presenter: Alana Delaine - @entoandbento
(05:25 GMT)	**14:55**	**The Consolidation of Long-Term Memory in *Diadegma semiclausum*** Presenter: Sung-Hsia Weng
(05:40 GMT)	**15:10**	**Systematics and host-parasitoid association of the Far Eastern velvet ants of the genus *Nemka* Lelej** Presenter: Juriya Okayasu - @mutillidologist
(05:55 GMT)	**15:25**	**Unravelling the life history of the wood moth parasitoid wasp, *Virgulibracon endoxylaphagus*** Presenter: Jessa Thurman - @jessa_thurman
(06:10 GMT)	**15:40**	**Break 2**
(06:30 GMT)	**16:00**	**To the next dimension - 3D cybertaxonomy of ants** Presenter: Francisco Hita Garcia - @Pangapaco
(06:45 GMT)	**16:15**	**Spatio-temporal distribution of bumblebee around Tolipir National Park, Azad Jammu and Kashmir, Pakistan** Presenter: Abu ul Hassan Faiz
(07:00 GMT)	**16:30**	**Interpretations drawn for over a decade of rearing butterfly-related parasitoid fauna in India** Presenter: Ankita Gupta

(07:15 GMT) **16:45** **Phylogenomics and biogeography of the parasitoid wasp family Gasteruptiidae (Hymenoptera: Evanioidea).**
Presenter: Ben Parslow - @ParslowBen

(07:30 GMT) **17:00** **Student prizes and concluding remarks**

(07:40 GMT) **17:10** **Social Australasia**

Europe, Middle East, Africa Session - 7 May, local time: CEST (GMT +2)

Moderators: Lars Krogmann; Jessica Awad

(11:00 GMT) **13:00** **Introductory remarks**

(11:05 GMT) **13:05** **ISH Awards ceremony**

(11:20 GMT) **13:20** **ISH 2020 Distinguished Research Medal recipient keynote presentation:**
Black and yellow, we all sting together
Presenter: Donald Quicke

(12:00 GMT) **14:00** **Break 1**

(12:10 GMT) **14:10** **Putting Afrotropical Ceraphronoidea back on the map**
Presenter: Tobias Salden

(12:25 GMT) **14:25** **Niche partitioning between *Eupelmus messene* and E. microzonus, parasitoids of *Aulacidea hieracii* (Hymenoptera: Eupelmidae, Cynipidae)**
Presenter: Vladimir E. Gokhman

(12:40 GMT) **14:40** **Buried for more than 54 million years – what does a wing of a fossil Darwin wasp tell us about its taxonomic placement?**
Presenter: Alexandra Viertler - @AViertler

(12:55 GMT) **14:55** **Evolution of the sting shape in ectaheteromorph ants**
Presenter: Alexandre Casadei-Ferreira - @ale_cferreira

(13:10 GMT) **15:10** **A first possible record of fossil *Toxares* (Hymenoptera, Braconidae, Aphidiinae) from Rovno amber**
Presenter: Maryna Kaliuzhna - @marinka_kma

(13:25 GMT) **15:25** **Break 2**

(GMT start time)	**Local start time**	
(13:45 GMT)	**15:45**	**The wasp as terrestrial indicator of environmental metal composition: Evidence from Zimbabwe** Presenter: Yasfir Tarif Nadat
(14:00 GMT)	**16:00**	**Cracking the code on cryptic species in *Trissolcus*** Presenter: Cristina Vasilita - @Nuga_Vasilita
(14:15 GMT)	**16:15**	**GBOL III: Dark Taxa and the figitids** Presenter: Jonathan Vogel - @J_Vogel_Hym
(14:30 GMT)	**16:30**	**Hidden in plain sight: Investigating the unknown diversity of German Pteromalidae (Hymenoptera: Chalcidoidea)** Presenter: Michael Haas
(14:45 GMT)	**16:45**	**Break 3**
(14:55 GMT)	**16:55**	**Fight or fright: Potential drivers of body size evolution in Cimbicidae (Insecta, Hymenoptera)** Presenter: Lars Vilhelmsen
(15:10 GMT)	**17:10**	**The evolutionary history of Chalcid wasps (Hymenoptera)** Presenter: Jean Yves Rasplus
(15:25 GMT)	**17:25**	**Hymenoptera genomes through Darwin Tree of Life** Presenter: Gavin Broad - @BroadGavin
(15:40 GMT)	**17:40**	**Using hybrid datasets to combine high support and deep taxon sampling in the phylogeny of Cryptini (Ichneumonidae, Cryptinae)** Presenter: Bernardo Santos - @bernardo_santos
(15:55 GMT)	**17:55**	**Break 4**
(16:05 GMT)	**18:05**	**Keynote presentation:** **Ants and trees – a myrmecological view on investigating patterns of diversity and evolution in Hymenoptera** Presenter: Bonnie B. Blaimer - @bblaimer
(16:45 GMT)	**18:45**	**Recap Student prizes and concluding remarks**
(17:00 GMT)	**19:00**	**Final Social**

#Hymathon2021 - Abstracts

Americas Session - local time: EDT (GMT -4)

(17:05 GMT) **13:05** **Keynote presentation:**

The use of museum specimens to perform phylogenomic studies: a case study in Braconidae

Jovana M. Jasso-Martínez (Colección Nacional de Insectos, Instituto de Biología, Universidad Nacional Autónoma de México, 3er Circuito Exterior s/n, Cd. Universitaria, Copilco, Coyoacán, Ciudad de México, Mexico), Robert R. Kula (Department of Entomology, National Museum of Natural History, Smithsonian Institution, Washington, 0560, DC, USA), Donald L. J. Quicke (Integrative Ecology Laboratory, Department of Biology, Faculty of Science, Chulalongkorn University, Pathumwan, Bangkok, Thailand), Bernardo F. Santos (Institut de Systématique, Évolution, Biodiversité. Muséum National d´Histoire Naturelle, Paris, France), Sergey A. Belokobylskij (Zoological Institute, Russian Academy of Sciences, St Petersburg 199034, Russia and Zoological Institute, Russian Academy of Sciences, St Petersburg 199034, Russia), José L. Fernández-Triana (Department of Integrative Biology and the Biodiversity Institute of Ontario, University of Guelph, Guelph, ON, Canada and Department of Integrative Biology and the Biodiversity Institute of Ontario, University of Guelph, Guelph, ON, Canada), Alejandro Zaldívar-Riverón (Colección Nacional de Insectos, Instituto de Biología, Universidad Nacional Autónoma de México, 3er Circuito Exterior s/n, Cd. Universitaria, Copilco, Coyoacán, Ciudad de México, Mexico)

Abstract

Natural history collections represent the main repository of information not only for conducting traditional taxonomic (i.e. morphology-based) research, but also for evolutionary, genetic, behavioural, ecological and conservation studies. In particular, specimens preserved in biological collections have become the most important source to obtain DNA sequence data, and phylogenetic studies that make use of next-generation sequencing (NGS) techniques are rapidly increasing to address the systematics and evolution of different biological groups. The use of these techniques also has allowed that the biological material employed in phylogenomic studies now includes extinct or rare species, as well as taxa that are otherwise extremely difficult to collect. Implementing NGS approaches for insect museum specimens is challenging, mainly because many of them are considerably small and their amount of DNA is considerably low. Recent studies, however, have shown that enrichment methods as ultra-conserved elements (UCEs) have a higher success rate compared to other methods when sequencing old and/or dried insect museum specimens with highly degraded DNA. Here we show the results of published and ongoing phylogenomic studies carried out for the family Braconidae. We have been able to obtain a substantial amount of genomic information from considerably old and pinned museum specimens, which has helped us to reconstruct robust phylogenetic relationships within the family at different taxonomic levels. Moreover, the UCE methodology employed has permitted us to generate mitochondrial information as a secondary product, making possible the assembly of partial and complete mitochondrial genomes that are being used for phylogenetic reconstruction.

(17:55 GMT) 13:55 Resolving the nightmare of the planidial clade!

John Heraty (University of California, Riverside, USA), Junzia Zhang (Hebei University, Baoding City, China), Austin Baker (University of California, Riverside, USA), Chris Darling (Royal Ontario Museum, Toronto, Canada), Jean-Yves Rasplus (INRAE, Montferrier-sur-Lez, France), Astrid Cruaud (INRAE, Montferrier-sur-Lez, France), Javier Torréns (CONICET, Anillaco, Argentina), Elizabeth Murray (Washington State University, Pullman, USA), James Woolley (Texas A&M University, College Station, USA).

Abstract

An active first-instar larvae (planidium) is restricted to one clade within Chalcidoidea that includes Eucharitidae, Perilampidae and Eutrichosomatinae (Pteromalidae). Phylogenomic approaches have helped to identify the clade and the relationships among groups, which will ultimately lead to a revised classification of families. The morphology and behavior of the planidia and other behavioral attributes across the different groups will be reviewed, and some anomalous results discussed.

(18:10 GMT) 14:10 The effect of early season temperature on adult life history traits of the wheat stem sawfly *Cephus cinctus* (Hymenoptera: Cephidae) and *Bracon cephi* (Hymenoptera: Braconidae)

Dylan Sjolie (University of Saskatchewan/Saskatoon/Canada); Meghan Vankosky (Agriculture and Agri-Foods Canada/Saskatoon/Canada); Christian Willenborg (University of Saskatchewan/Saskatoon/Canada)

Abstract

Wheat stem sawfly, *Cephus cinctus* Norton (Hymenoptera: Cephidae), is a long-standing pest of wheat Triticum aevstivum L. (Poaceae) in the northern Great Plains region of North America. Larval feeding damage within the wheat stems causes decreased head kernel weights, reduced photosynthetic capacity, and overall yield losses. Serious *C. cinctus* infestations can cause economic losses exceeding over $400 million annually. Recently, a bioclimatic model for *C. cinctus* was developed for the Canadian Prairie region, but the model lacks forecasting capabilities due to missing knowledge gaps of how early season weather patterns affect *C. cinctus* population dynamics. The purpose of the study was to measure the effects of different post-diapause development conditions on life history traits of adult *C. cinctus* and *Bracon cephi* (Hymenoptera: Braconidae), a native parasitoid of *C. cinctus*. Field-collected individuals were reared under two different temperature regimes to generate two distinct emergence groups for adult survivorship and longevity comparisons. With a better understanding of how early season weather can affect *C. cinctus* population dynamics, a forecasting model for *C. cinctus* can be developed.

(18:25 GMT) 14:25 Discovery of a putative troglomorphic ant (Hymenoptera: Formicidae: Leptanillinae: *Leptanilla* sp.) in southwestern Iran

Zachary Griebenow (University of California, Davis, USA); Majid Moradmand (University of Isfahan, Isfahan, Iran); Marco Isaia (University of Turin, Torino, Italy)

Abstract

Despite their diversity and ubiquity across terrestrial ecosystems, the ants (Formicidae) are rare in cave environments. At present, only two described species are regarded as exhibiting a cave-adapted phenotype, i.e. troglomorphism. Here, we report an undescribed species of *Leptanilla* (Leptanillinae: Leptanillini) collected from the milieu souterrain superficiel (MSS) near salt caves in Fars Province, Iran. The soma and appendages of this ant are bizarrely elongated, prohibiting the soil-dwelling behavior observed in its closest relatives. Therefore, this undescribed *Leptanilla* sp. is arguably troglomorphic. Preliminary morphological observations are here presented, along with predicted phylogeny. Its phenotype is not only remarkably distinct from all leptanilline ants heretofore known, but exceptional among ants as a whole. Future phylogenomic inference will resolve the evolutionary relationships of this remarkable leptanilline ant.

(18:40 GMT) 14:40 **Ants-extrafloral nectary associations in different growth stages of Bombacoideae (Malvales: Malvaceae) trees in a tropical urban ecosystem**

Aymer Andrés Vásquez Ordóñez (Universidad del Valle & Fundación Ecovivero/ Cali/Colombia), José Luis Criollo (Club de Observadores de la Naturaleza del Valle del Cauca/Cali/Colombia), Francisco López Machado (Independent Researcher/Cali/Colombia), Daniel Pereira (Universidad del Valle/Cali/Colombia).

Abstract

Extrafloral nectaries are relevant in the study of insect-plant interactions. Among insects, ants are the most frequent. This association has been little investigated in Bombacoideae trees, which are an important group in the tropics. In these trees, extrafloral nectaries are present, with the particularity of being the only group within the Malvaceae to have such a structure on the petiole. Moreover, it is not known how this interaction varies according to the developmental stage of the plant. For these reasons, we examined the extrafloral nectaries in 60 trees belonging to *Ceiba speciosa*, *C. pentandra*, *Pachira quinata*, *Pa. insignis* and *Pseudobombax septenatum* in Cali and Palmira, Valle del Cauca, Colombia. We reported the species and number of ants associated with the nectaries. In total, we recorded 679 ants associated with *C. pentandra*, P. quinata and P. septenatum. The ants belonged to seven species of the genera *Camponotus*, *Crematogaster*, *Nylanderia*, *Paratrechina*, *Pheidole*, *Pseudomyrmex* and *Wasmannia*. *W. auropunctata* and *Cr. longispina* were the most abundant on *C. pentandra*, while *Ca. planatus* was most abundant on *Pa. quinata* and *Ps. septenatum*. Nectaries were present in all stages of plant development evaluated, however, in *C. pentandra* and *Pa. quinata* the ant association was only present in small plants while in *Ps. septenatum* these were recorded in reproductive and tall plants. In conclusion, this is a more extensive report of ants associated with Bombacoideae in the world, it is also an approximation that this interaction in Bombacoideae is variable according to the stage of development.

(18:55 GMT) 14:55 **Down the bee-burrow: Unexpected diversity in the *Lasioglossum parvum* species complex (Halictidae: Halictini)**

Joel Gardner (University of Manitoba/Winnipeg/Canada), Jason Gibbs (University of Manitoba/Winnipeg/Canada)

Abstract

Historically, identifying species in the *Lasioglossum parvum* species complex was a simple matter of geography and metasoma colour. Under this system, only three names were commonly used: *L. tegulare*, *L. tegulariforme*, and *L. hunteri*. A previous revision of *L. tegulare* revealed that it actually included four "cryptic" species, and ongoing work in the western Nearctic region is revealing even higher diversity in both *L. tegulariforme* and *L. hunteri*. There may be as many as 21 western species, including 12 new ones.

(19:30 GMT) **15:30** **Bees like flowers who knew? New Methods for Evaluating Foraging Choices in Bumble Bees (*Bombus impatiens*)**

Caleb Bryan (University of Saskatchewan/Saskatoon/Canada), Sean Prager (University of Saskatchewan/Saskatoon/Canada)

Abstract

Bumblebees are important pollinators in agricultural and native habitats, and are faced with sorting through complex signal cues in the search for suitable forage. The motivation for these foraging behaviors is simple; gaining the highest reward for least calories expended. Recently, the search for understanding the complex choices involved in locating forage has taken investigations out of the field and into the lab. Traditionally, bumblebee foraging ecology studies have focused on large flight arenas where bees discriminate between single artificial cues, or field studies where bees interact with novel stimuli, or are simply recorded on which plants they visit. Utilizing choice assays allows the reduction of complex behaviors into bivariate situations where the effects of specific stimuli on behavior can be analyzed. Choice assays are ideal for this as they present a subject organism with an array of conditions that allows the organisms to make real world decisions. For most other animals, including terrestrial insects, we employ simple mazes, such as T or Y mazes, for measuring choice preferences. Few studies, however, use simple maze designs in understanding bumble bee foraging, while none have utilize whole intact plants. We propose a new system that approximates discriminant choices between patches of forage, utilizing a whole plants and a simple y-maze.

(19:45 GMT) **15:45** **Slicing the Gordian knot: A phylogenetic analysis of the subfamilial relationships of Aphelinidae (Chalcidoidea)**

Robert Luke Kresslein (University of California, Riverside), John Heraty (University of California, Riverside)

Abstract

Aphelinidae (Chalcidoidea) are a diverse group (1,385 species, 40 genera) of parasitoid wasps that exploit whiteflies, scale insects and aphids. They are among the most important taxa used in biological control and are the cornerstone of over 90 successful biocontrol programs. Resolving the phylogeny of Aphelinidae has proved to be a veritable Gordian knot: an intractable problem that morphological and traditional molecular approaches are unable to solve. Next-generation molecular analyses have shown promise for recovering phylogenetic hypotheses for challenging taxa. Here we use an expansive Anchored Hybrid Enrichment (AHE) dataset (1,013 loci, 447,698 bp) to recover a preliminary phylogenetic hypothesis for Aphelinidae, explore the influence of exonic and intronic regions on the resulting topology, and suggest a revised tribal classification. The conclusions drawn from our investigation will enable biocontrol specialists to evaluate species of Aphelinidae within a phylogenetic context, and to predict and evaluate traits that may influence the success of biological control programs. It will also provide a framework for future work into the phylogenetics of economically important parasitoids in Aphelinidae including the genus *Encarsia* Förster.

(20:00 GMT) 16:00 ***Diplolepis rosae* is more successful in North America than in Europe because of enemy release**

László Zoltán (Hungarian Department of Biology and Ecology, UBB Cluj, 400006, Romania); Chris Looney (Washington State Department of Agriculture, Olympia, WA 98504, United States); Hunor Prázsmári (Hungarian Department of Biology and Ecology, UBB Cluj, 400006, Romania); Joseph D. Shorthouse (Laurentian University, Sudbury, Ontario, Canada)

Abstract

The enemy release hypothesis predicts that introduced species in their new range are freed from natural enemies (e.g. predators, parasitoids) that control their populations. Robin's pincushion is an iconic widespread gall in the Western Palearctic induced by *Diplolepis rosae* (Hymenoptera: Cynipidae) on wild roses (Rosa sp.), that supports a robust "component community" of inquilines, parasitoids, and hyperparasitoids in its native range. *Diplolepis rosae* was introduced to North America by the mid-1800s. By the early 1900s the species was found across the continent, and has since become widespread and common. Galls appear notably denser in North America than in its native range, suggesting that some factor – such as enemy release – has contributed to greater abundance. We tested this hypothesis by comparing the insect communities associated with *D. rosae* galls from Canada and the US Pacific Northwest with those of Eastern Europe. Throughout its introduced range, gall-wasp abundance was higher and parasitism rates were lower than those of galls in their natural range. Component communities were also less diverse and species-rich. There was also a significant negative relationship between gall size and parasitism rates in its native range, but not in its introduced range. These results show that the component community in its introduced range is depauperate and provide support for the enemy release hypothesis. The spread of *D. rosae* and its host plants raises questions about whether they may disrupt the relatively rich Nearctic species of *Diplolepis* and their component communities.

(20:15 GMT) 16:15 **Wait, HOW many Hymenoptera are there? A global call for collaboration on estimating relative species richness**

Andrew Forbes (University of Iowa/Iowa City/USA)

Abstract

My colleagues and I published a paper a couple of years ago (Forbes et al. 2018, BMC Ecology) arguing that the Hymenoptera are likely the largest order of animals. We based our argument on ratios of specialist parasitic wasps to host insects that we calculated using hosts in four genera (*Rhagoletis* flies, *Neodiprion* sawflies, *Malacosoma* moths, and *Dendroctonus* beetles) as case studies. Though I would maintain that we tried to be extremely conservative in our final estimates of relative global species numbers, our estimates nevertheless depend on these four host genera and their associated parasitoids, which is a rather limited set of data. I would like to use this opportunity to ask if folks in the global #Hymathon community are interested in expanding this dataset to include additional host/parasite systems and to perhaps produce a follow-up to the first paper. The primary goal will be to identify additional host insect genera for which we know many or all of the associated parasitoids, and for which we know how specialized those parasitoids are on the species in that host genus. In this presentation, I will briefly review the methods of our previous study and make a call for folks to propose additional systems and to hopefully collaborate in this effort.

(20:30 GMT) **16:30** **An ethogram for the Comanche harvester ant, *Pogonomyrmex* comanche (Hymenoptera, Formicidae)**

Ann B. Mayo (University of Nebraska-Lincoln, Lincoln, USA)

Abstract

An ethogram is a catalogue of the behaviors of an animal species. Such a catalogue can provide important insights into the life of social insect colonies which are organized by reproductive castes and a division of tasks among workers. Several species in the genus *Pogonomyrmex* have been well studied, but the Comanche harvester ant, *P. comanche*, has not. In this project, I observed the Comanche harvester ant in the field, video recorded approximately 1200 minutes of behavior, and performed some simple experiments to construct an ethogram. While the catalogue is not complete, I was able to describe many behavioral units and sequences and to compare these among castes. I found evidence supporting the importance of visual orientation and that the use of visual cues varies with worker task. Worker ants switch task fairly easily and there is great similarity in the behaviors of workers and queens with marked differences in comparison with male alates. These observations raise many questions for further experimental investigations in behavior, neurology/physiology, developmental biology, and genetics.

(20:45 GMT) **16:45** **Was it something I ate? Investigating how host order might affect body coloration Cirrospilini (Hymenoptera: Eulophidae)**

Ryan Perry (UCR, Riverside, USA), John Heraty (UCR, Riverside, USA)

Abstract

A recent revision of Cirrospilini reveals patterns related to color and host specificity. When comparing phylogeny and host, it is found that those genera which are dipteran specific form a clade, and genera that attack multiple orders form their own clade. In addition, genera with broad host ranges had almost equally large amounts of variation in color, while those with a smaller host range exhibit almost no variation in color.

Australasia Session - 7 May, local time: ACST (GMT + 9.5)

(04:05 GMT) **13:35** **Keynote presentation:**
Molecular phylogenetics, biogeography and evolution in spider wasps (Hymenoptera: Pompilidae)

Abstract

Pompilids constitute a young radiation of behaviourally diverse solitary wasps. Females search for spiders, which they paralyze and oviposit to feed their larvae. With over 5,000 species, spider wasps occupy all continents and exhibit a high level of morphological convergence, which is a result of behavioural adaptations. Moreover, their venom produces one of the most painful effects on humans and contain hundreds of molecules yet to be characterised. In this talk, I will present recent advances on the use of Ultra Conserved Elements and whole-genome-sequencing to answer systematics and evolutionary questions within Pompilidae, ranging from higher-level-phylogenetics of the whole family, to systematics studies at lower levels, biogeography, and venom evolution.

(04:55 GMT) 14:25 The Chemical Ecology of Stink Bug Egg Parasitoids (Hymenoptera: Scelionidae)

Thomas E. Saunders (University of Auckland, Auckland, New Zealand), Gonzalo A. Avila (Plant & Food Research, Auckland, New Zealand), Gregory I. Holwell (University of Auckland, Auckland, New Zealand)

Abstract

Screening natural enemies for potential non-target risks is fundamental to safe and effective classical biological control programmes. Traditional methods, such as no-choice tests, provide compelling evidence of a candidate agent's physiological host range. However, once a biological control agent is released, a variety of sensory filters narrow the pool of attractive hosts to a list of species the agent will actually attack (its ecological host range). Understanding how and why a parasitoid chooses which hosts to attack would help to reduce uncertainty during pre-release host range testing. Here we present an overview of our work on the chemical ecology of three *Trissolcus* species in New Zealand, including *Trissolcus* japonicus Ashmead (Hymenoptera: Scelionidae), a biological control agent conditionally approved for release against brown marmorated stink bug (*Halyomorpha halys* Stål), should it establish in New Zealand. We conducted electrophysiological experiments (GC-EAD) to identify compounds associated with adult stink bugs which elicit antennal responses. We also exposed parasitoids to non-target egg masses to measure the outcomes of competitive interactions between adults and larvae. Finally, we observed arrestment responses in relation to both host and non-host odours. Incorporating chemical-ecological data in host range testing will support decision makers evaluating applications to release new organisms.

(05:10 GMT) 14:40 *Psyllaephagus*, an important but problematic genus of Encyrtid wasps.

Alana Delaine (University of Adelaide/Adelaide/Australia), Erinn Fagan-Jeffries (University of Adelaide/Adelaide/Australia), Juanita Rodriguez (Australian National Insect Collection, CSIRO/Canberra/Australia), Steven Cooper (University of Adelaide/Adelaide/Australia), Andy Austin (University of Adelaide/Adelaide/Australia)

Abstract

The host specific, parasitoid wasp genus *Psyllaephagus* (Encyrtidae) are the principal natural enemies of psyllids (lerps) in Australia. As such, they are important for regulating natural psyllid populations as well as the biocontrol of pest lerps. However, the taxonomy of the Australian fauna is in a state of confusion, with species being poorly described and mostly unidentifiable, partly because of their tiny size, morphological simplicity and associated cryptic appearance. Most Australian *Psyllaephagus* species are virtually unidentifiable due to their largely intractable taxonomy and historically poor descriptions. By rearing *Psyllaephagus* from known hosts, this project will develop a DNA barcode library, utilise sequence data, morphology and host associations to delineate species and develop tools for rapid identification of the Australian fauna, describe new taxa, and develop a molecular phylogeny to examine the evolution of the genus and associated tri-trophic host relationships.

(05:25 GMT) **14:55**

The Consolidation of Long-Term Memory in *Diadegma semiclausum*

Sung-Hsia Weng (School of Biological Sciences, University of Queensland),Michael J. Furlong (School of Biological Sciences, University of Queensland), Ralf G. Dietzgen (Queensland Alliance for Agriculture & Food Innovation, University of Queensland)

Abstract

Diadegma semiclausum (Hellén) are parasitic wasps which develop inside diamond back moth (DBM), *Plutella xylostella*. As previously shown, plant odour emitted by DBM-infested Chinese cabbage is more attractive to naïve *D. semiclausum* compared to DBM-infested common cabbage. However, such preferences can be overridden by experienced *D. semiclausum* which previously deposited eggs in DBM larvae on common cabbage. To improve the understanding of host-plant-parasitoid interactions, this study examined the formation of long-term memory (LTM) in *D. semiclausum* following different training regimes, so-called “conditioned stimulus (CS)”. Following CS where DBM and common cabbage were both present, the memory for the learned odour was assumed to consolidate in *D. semiclausum* brain. Experiments were done in olfactometer assays at a series of timepoints post CS. By examining attraction to DBM-infested Chinese cabbage and common cabbage, we assessed if *D. semiclausum* females retain formed memory and show stronger preference for DBM-infested common cabbage, also known as learned odour. The results show that three time-spaced oviposition events could contribute to a lasting 24h-memory in *D. semiclausum* females for the learned odour. In contrast, single oviposition and consecutive oviposition events both achieved a short 12h-memory. However, *D. semiclausum* females did not discriminate between originally oriented and learned odour in 48h- and 96h-memory and large proportions of individuals were found to be non-respondent. Although memory was sustained longer after time-spaced CS, the memory for learned odour waned after 48h. This clearly suggests that LTM did not completely consolidate in *D. semiclausum*.

(05:40 GMT) **15:10**

Systematics and host-parasitoid association of the Far Eastern velvet ants of the genus *Nemka* Lelej

Juriya Okayasu (Systematic Entomology, Graduate School of Agriculture, Hokkaido University, Sapporo, Japan)

Abstract

Velvet ants (family Mutillidae) usually exhibit extreme sexual dimorphism, with males usually winged and females wingless, resulting in reduced mobility in female individuals. Because of limited ability in host searching, mutillids utilize various host species that are found in a particular environment. Despite of large overlaps of host preference in closely related species, temporal and spatial co-existence of multiple congeneric mutillids is commonly observed. Species interactions in such mutillid communities are not understood at all. In this project, I attempted a systematic review of *Nemka* Lelej species of China, Taiwan and Japan, and recognized two species in Taiwan, and one species each in China mainland and Japan. Two Taiwanese species shared same geographical range. Those four *Nemka* species were considered a monophyletic group based on synapomorphies. I used this species-complex to determine if there is resource partitioning in mutillids by comparing the body size, because body size of mutillids correlate with that of their hosts. Additionally, I analyzed the phylogenetic relationships of those *Nemka* species based on morphological data. Phylogenetic analyses reconstructed non-sister relationships of *N. taiwanensis* and *N. wotani*. *Nemka* limi and *N. yasumatsui* exhibited wide variation

of body size in both sexes and bimodal distribution of it in males, suggesting utilization of multiple hosts. Contrarily, the body size of *N. taiwanensis* and *N. wotani* was less variable with unimodal distribution. *Nemka* taiwanensis was apparently larger than *N. wotani*. This implies those two species have strict preference to different sized hosts. This phenomenon is regarded as resource partitioning.

(05:55 GMT) **15:25** **Unravelling the life history of the wood moth parasitoid wasp, *Virgulibracon endoxylaphagus***

Jessa Thurman (University of Queensland, School of Biological Sciences/Brisbane/Queensland/Australia), Geoff Monteith (Queensland Museum/Brisbane/Queensland/Australia)

Abstract

The wood moth parasitoid wasp, *Virgulibracon endoxylaphagus* (Braconidae; Quicke & Ingram, 1993) parasitizes the Australian giant wood moth, *Endoxyla cinereus* (Tepper, 1890), which is the heaviest moth in the world, a culturally important food resource to indigenous Australians, and a major economic pests of Eucalpytus plantations. Despite the importance of its host, the wood moth parasitoid and its life history are poorly understood, with nothing written on this wasp since its description nearly thirty years ago. Here, we describe and discuss the complex natural history of the wood moth parasitoid wasp (*V. endoxylaphagus*) based the constraints posed by its host (*E. cinereus*). This compiled understanding of the wasp's natural history may then be used in future efforts to combat the pest status of Endoxyla spp. in Eucalyptus plantations, while also shedding light on a parasitoid of one of Australia's most enigmatic insects.

(06:30 GMT) **16:00** **To the next dimension - 3D cybertaxonomy of ants**

Francisco Hita Garcia (Okinawa Institute of Science and Technology, Biodiversity and Biocomplexity Unit, Onna-son, Okinawa, Japan)

Abstract

Recent technological advances have opened new possibilities for interactive and 3D imagery, of which x-ray microtomography (micro-CT) is the most commonly used. The technology enables non-invasive, high-resolution, detailed 3D visualization and analysis of morphological structures, as well as digitization of tissues, organs, or whole specimens, but it is also an excellent tool for the virtual examination and dissection of (often rare and valuable) material in order to evaluate and discover new morphological characters of taxonomic or phylogenetic significance. This extraordinary richness of morphological data, as well as novel ways to analyse and present it, opens up new possibilities to strengthen the role of morphology-based taxonomy within the field of systematics.

Based on examples of current taxonomic works on different ant genera, I will show the potential of 3D specimen data to greatly advance collections-based research in general and taxonomy in particular through new virtual and interactive possibilities of presenting, analyzing, and publishing morphological data. Combined with molecular data or stand-alone, 3D morphological data opens up a whole new dimension of opportunities for alpha taxonomy. Overall, 3D modelling offers great potential for a future of natural history museums that combines digitization of collections, usage of collections as biodiversity libraries, and creation of virtual and openly accessible 3D natural history collections.

(06:45 GMT) 16:15 Spatio-temporal distribution of bumblebee around Tolipir National Park, Azad Jammu and Kashmir, Pakistan

Abu ul Hassan Faiz and Lariab Zahra (Women University of Azad Jammu and Kashmir, Bagh, Pakistan)

Abstract

The present study was conducted to investigate the spatial and temporal behaviour of bumblebees around Tolipir National Park in (Ghorimar, Noor Kot, Kotari, Darak, Alisojal, Kahoo Kot, Dhahol Dhok, Hussain Kot, Pir Kot, and Panjal), Azad Jammu and Kashmir. Monthly Surveys were done from June 2019 to May 2020 to different localities of study area. Bumblee bees were monitored counted and sampled by line transect methods along roadside, crops, forest and marked with GPS (Global Positioning System).The collected data was analysed and presented graphically using Microl Origin software. Only one bumblebee specie (*Bombus haemorrhoidalis*) were found in my study area. Queen were observed in March, April and May while workers were recorded from June to November. Maximum population of (*B. haemorrhoidalis*) was found in August and minimum was recorded in March and November. There was no population from December to February at different localities including (Ghorimar, Noor Kot, Kotari, Darak, Alisojal, Kahoo Kot, Dhahol Dhok, Hussain Kot, Pir Kot, and Panjal). The present study provides the change in population fluctuation and possible distribution of bumblebees for future utilization in conservation programme for this pollinator in Azad Jammu and Kashmir.

(07:00 GMT) 16:30 Interpretations drawn for over a decade of rearing butterfly-related parasitoid fauna in India

Ankita Gupta (ICAR- National Bureau of Agricultural Insect Resources/Bengaluru/India)

Abstract

The present interpretation on the faunal diversity of parasitoids related to Indian butterfly species was drawn after pooling data which was accumulated over a period of 11 years (2009-2020) by the author during her studies and surveys conducted from all over India including Andaman & Nicobar islands with more biasness towards peninsular India (owing to feasibility). The following parameters were given emphasis− host & parasitoid species (possible taxa - wherever exact species identity could not be ascertained), stage of parasitism (egg, larval, pupal), host-parasitoid specificity/range, and parasitoid predominance. The survey sites were from different habitats (inhabited/ uninhabited): agroecosytems, dense forests/mixed forests, island ecosystem, etc. Mode of collection was manual scouting for parasitized hosts. More than fifty predominant species of butterflies were analyzed for host susceptibility and parasitoid predominance. Parasitism rate was highest for the following families in the descending order of parasitism: Hesperiidae>Lycaenidae>Nymphalidae>others. Percent parasitism in the descending order of dominance observed was: Braconidae>Eulophidae>Tachinidae (Diptera) and Ichneumonidae almost at par followed by others. This study indicated that butterflies of family Hesperiidae were most vulnerable to parasitism followed by Lycaenidae and Nymphalidae. Comparing various stages of butterfly life cycle, maximum encounters of parasitism were in larval stage followed by pupal and egg stage, respectively. Studies also indicated that host abundance was directly proportional to the parasitism rate. Hyperparasitism by many species of eulophids and eurytomids up to five trophic levels was observed.

(07:15 GMT) 16:45 Phylogenomics and biogeography of the parasitoid wasp family Gasteruptiidae (Hymenoptera: Evanioidea).

Ben A. Parslow (South Australian Museum, Adelaide, Australia), Michael P. Schwarz (South Australian Museum, Adelaide, Australia), Mark I. Stevens (Flinders University, Adelaide, Australia)

Abstract

The wasp family Gasteruptiidae (Hymenoptera: Gasteruptiidae) is an easily recognised, diverse group of wasps whose larvae are predator-inquilines of cavity nesting bees and wasps. Although they are readily collected and there is an abundance of material in collections, there is limited information on their systematic relationships, biodiversity and the evolutionary relationships with their hosts. The family exhibits an interesting distribution with the largest genus *Gasteruption* found across all biogeographical regions. The smaller genera are all restricted to specific regions (e.g. *Pseudofoenus* is restricted to a Gondwanan distribution, *Spinolafoenus* is only found in the Neotropical region). There has been no strong consensus for the phylogenetic relationships or biogeography of the family, with only two studies including more than singleton taxa in large scale family level studies. We used Ultraconserved Elements (UCE) from freshly collected and museum preserved material to infer phylogenetic relationships, estimate divergence dates and test biogeography boundaries for the family across the world. Our dataset recovered the most robust phylogeny for the family to date with almost unanimous support across the tree confirming the monophyly of the genera *Gasteruption*, Hyptiogaster and *Pseudofoenus*. We were also able to estimate the divergence age of the family during the Paleocene, coinciding with the divergence of their hosts but revealing a complex and confusing biogeographical history within this family.

Europe, Middle East, Africa Session - 7 May, local time: CEST (GMT +2)

(11:20 GMT) **13:20 ISH 2020 Distinguished Research Medal recipient keynote presentation: Black and yellow, we all sting together**

Donald Quicke (Chulalongkorn University, Bangkok, Thailand)

Abstract

Just wait and see…

(12:10 GMT) 14:10 Putting Afrotropical Ceraphronoidea back on the map

Tobias Salden (ZFMK/Bonn/Germany), Ralph S. Peters (ZFMK/Bonn/Germany)

Abstract

Ceraphronoidea is a small but globally distributed superfamily with a parasitoid lifestyle. They have a minute body size of less than 1 to 4 mm and are frequently collected in the field. However, the morphological identification on species level is challenging and the true species richness is unknown. Here, I am focusing on the taxonomy and species diversity of Afrotropical ceraphronoids. The superfamily is considered as a "Dark Taxon" and male genitalia have been suggested to provide reliable characters for species delimitation. Ceraphronoid specimens from Kakamega Forest, a threatened equatorial relict rainforest in Kenya, Mount Kilimanjaro in Tanzania and a forest in Gabon provide the basis of the study. The investigation is unique according to its large number of 423 examined male Afrotropical ceraphronoid specimens. By investigation of male genitalia it was possible to identify 102 species in total, of which 97 are new to science. These results contribute to the understanding of the hidden diversity of Kakamega Forest and would more than double the number of described Afrotropical ceraphronoid wasps. Furthermore, the study can lead to a broader awareness, that ceraphronoids are an important component of Afrotropical terrestrial ecosystems. This hopefully will increase their chance to be no longer ignored for concerns of general research and conservation.

(12:25 GMT) 14:25 Niche partitioning between *Eupelmus messene* and E. microzonus, parasitoids of *Aulacidea hieracii* (Hymenoptera: Eupelmidae, Cynipidae)

Vladimir E. Gokhman (Moscow State University, Moscow, Russia), Matvey I. Nikelshparg (Gymnasium no. 3, Saratov, Russia)

Abstract

In the southeast of European Russia, the gall wasp *Aulacidea hieracii* (Bouché) is attacked by ten parasitoid species, including *Eupelmus (Eupelmus) microzonus* Förster and *E. (Macroneura) messene* Walker. Although both members of the genus Eupelmus are idiobiont ectoparasitoids, they demonstrate different life-history strategies in respect to many bionomic features. Specifically, *E. messene* is represented by brachypterous thelytokous females which lay single eggs directly onto the host body. This species can parasitize both concealed and exposed larvae and pupae of *A. hieracii*, but fails to attack its primary parasitoids. On the contrary, arrhenotokous males and females of E. microzonus are fully winged. These parasitoids usually lay several eggs per host which are placed onto the wall of the host chamber and covered with a particular fibrous substance. E. microzonus never parasitizes pupae or exposed larvae, although it can readily attack concealed larvae of *A. hieracii* as well as of its primary parasitoids. In addition, hibernating individuals of *E. messene* undergo obligatory larval diapause, but those of E. microzonus are able to develop without exposure to subzero temperatures. All these data collectively suggest that the former species is highly specialized to exploit *A. hieracii* as a host, whereas the latter one mostly exhibits the so-called morphotypical specialization. These different strategies allow *E. messene* and E. microzonus to coexist on the same host species, as a local specialist and a more or less evenly distributed generalist respectively.

(12:40 GMT) 14:40 Buried for more than 54 million years – what does a wing of a fossil Darwin wasp tell us about its taxonomic placement?

Seraina Klopfstein (University of Bern, Bern & Natural history museum Basel, Basel, Switzerland), Alexandra Viertler (University of Bern, Bern & Natural history museum Basel, Basel, Switzerland)

Abstract

Darwin wasps (Ichneumonidae) are at the top of the insect food web, but despite their ecological importance, they are among the most poorly studied groups of organisms. Their fossil record is even more poorly understood than their extant diversity.

Compression fossils are the main source of information about the age and past diversity of Darwin wasps. We need to rely on interpretations of their morphology to taxonomically place them, but it is often difficult to interpret a fossil and its structures. Body parts that would be needed to identify a specimen are sometimes not well preserved, which often leads to several subfamilies remaining equally likely for placement.

Since wings are usually the best-preserved part of compression fossils, it is crucial to evaluate if there is subfamily-specific information in the wing venation of Darwin wasps. A geometric morphometric approach for fore wings has already been used to group Cretaceous species into their four extinct subfamilies. In my approach I will not only include fossil taxa but try to compare the fossil specimens with a large dataset of extant species, to find indications about their relatedness. Nevertheless, it is still not sure to what extent wing venation mirrors phylogenetic relationships in Darwin wasps and remains unknown until a better phylogeny of the entire family is at hand. But geometric morphometrics in the fore wings shows great potential to facilitate sound placement even of incompletely preserved fossils.

(12:55 GMT) **14:55** **Evolution of the sting shape in ectaheteromorph ants**

A. Casadei-Ferreira (Okinawa Institute of Science and Technology Graduate University, Onna, Okinawa, Japan); G.P. Camacho (California Academy of Sciences, San Francisco, CA, USA); W. Franco (Universidade Federal do Paraná, Curitiba, Paraná, Brazil); J.E. Lattke (Universidade Federal do Paraná, Curitiba, Paraná, Brazil); R.M. Feitosa (Universidade Federal do Paraná, Curitiba, Paraná, Brazil); E.P. Economo (Okinawa Institute of Science and Technology Graduate University, Onna, Okinawa, Japan)

<u>Abstract</u>

Changes related to female terminalia in Hymenoptera reflect adaptive radiation among its lineages. From the ground plan of an ovipositor adapted to place eggs inside soft plant tissues, hymenopterans experienced several significant changes that culminated in a sharp and stiff weapon, the sting. Besides the ‘weaponization’ of the ovipositor to capture prey, in social aculeates, the sting is used predominantly or exclusively for defense. Like other social aculeates, ants present a series of modifications in the stinging apparatus, including reductions and secondary losses. The dependence on live arthropods as a food source constrained a functional sting in ants since the acquisition of plant-product for their feeding is often associated with its simplification and loss. But many aspects of its morphology and functions are still not well known. In this project, we aim to investigate the morphology and evolution of the sting shape in predatory ants of the subfamilies Ectatomminae and Heteroponerinae, commonly known as Ectaheteromorphs. We will apply x-ray microtomography, 3D geometric morphometrics, and biomechanical approaches to investigate the realized morphological space and biomechanical responses associated with sting shape variation among and within Ectaheteromorphs genera. So far, our scanned database covers its main lineages, including six genera and 26 species, six of which have been preliminarily segmented. Our next steps involve enriching our database, increasing geographic coverage and taxa representativeness, and finally generating 3D models. We expect our results to provide valuable morphological information in a phylogenetic context, thus creating bases to illuminate our understanding of ants’ evolution and diversity.

(13:10 GMT) 15:10 A first possible record of fossil *Toxares* (Hymenoptera, Braconidae, Aphidiinae) from Rovno amber

Kaliuzhna M.O. (I.I. Schmalhausen Institute of Zoology of NAS of Ukraine, Kyiv, Ukraine), Perkovsky E.E. (I.I. Schmalhausen Institute of Zoology of NAS of Ukraine, Kyiv, Ukraine; A.A. Borissiak Paleontological Institute of the Russian Academy of Sciences, Moscow, Russia)

Abstract

Aphidiinae is a worldwide-distributed subfamily of Braconidae, which consists only of aphid parasitoids. For now, there are known 27 fossil species of 14 genera (Ortega-Blanco et al., 2009; Davidian et al. 2021, in press). Ephedrini seems to be the most ancient Aphidiinae with the oldest known species Archephedrus stolamissus Ortega-Blanco, Bennett, Delclòs & Engel, 2009, from the late Albian of Spain (Álava amber) (Ortega-Blanco et al., 2009). Most of fossil Aphidiinae were described from the early Oligocene (Alsace potash field, Anna pit); they are very common in middle Eocene Sakhalinian amber (Rasnitsyn, 1980); a few species are known from the late Eocene Baltic amber (Brues, 1933; Stary, 1970; 1973).

Rovno amber from northern regions of Ukraine is also of late Eocene age; Perkovsky et al. (2010) presented its characteristics in details. Rovno amber was studied in the last two decades; hymenopterans are represented by 135 species from 17 families (Perkovsky, 2018; Simutnik et al., 2020, and reference therein). Despite that, still only information about the presence of braconids in Rovno amber had been reported (Perkovsky et al., 2010; Kaliuzhna et al., 2020).

Here we discuss a new finding of Braconidae from Rovno amber. The studied specimen is a male, presumably belonging to the genus *Toxares* (Aphidiinae, Ephedrini), previously represented exclusively by extant species. The specimen is well preserved and having 17-segmented antennae, and complete venation. It clearly differs from other Ephedrini genera, however due to the lack of female specimen with plough-shape ovipositor we cannot be completely sure in ID.

(13:45 GMT) 15:45 The wasp as terrestrial indicator of environmental metal composition: Evidence from Zimbabwe

Yasfir Tarif Nadat (Research Unit: Environmental Sciences and Management, North-West University, Potchefstroom, South Africa), Henrik Kylin (Department of Thematic Studies – Environmental Change, Linköping University, Linköping, Sweden}, Rudo Sithole (Department of Biological Sciences, University of Zimbabwe, Harare, Zimbabwe), Velesia Lesch (Research Unit: Environmental Sciences and Management, North-West University, Potchefstroom, South Africa), Hindrik Bouwman (Research Unit: Environmental Sciences and Management, North-West University, Potchefstroom, South Africa),

Abstract

We investigated metal concentrations in Polistinae wasps from four sites near in Zimbabwe. We found increased concentrations at two presumed-polluted sites which were also located near a metal-enriched geological feature(The Great Dyke). A nature reserve served as reference. Only wasps from the two presumed-polluted sites had quantifiable Pt. For Cr, Ni, Mg, Se, Fe, Mn, and V we report the highest concentrations in wasps yet published. Wasps from polluted sites had significantly higher concentrations of most metals compared with wasps from the reference sites, suggesting pollution as a source. The geology of each site differs. It is probable that both geology and pollution contributed towards the differences in metal

concentrations. Due to its long and narrow dimensions (550 km long and 4 - 11 km wide), the Great Dyke offers opportunities for comparative studies. Wasps form parts of foods web and ecology, studies on the transfer of metals to wasps' predators are needed, especially given that some birds specialize in feeding on hymenopterans. The rich diversity of wasps (more than 145 000 species worldwide) occupying multiple different trophic levels, are good indicators, and has a rich potential to join other invertebrates as terrestrial indicators.

(14:00 GMT) 16:00 Cracking the code on cryptic species in *Trissolcus*

Cristina Vasilita (Alexandru Ioan Cuza University in Iasi, Iasi, Romania), Ovidiu-Alin Popovici (Alexandru Ioan Cuza University in Iasi, Iasi, Romania), Lucian Fusu (Alexandru Ioan Cuza University in Iasi, Iasi, Romania)

Abstract

Trissolcus Ashmead (Platygastroidea: Scelionidae) owes its fame to its utility in the biological control of pests like *Halyomorpha halys*, *Bagrada hilaris* and *Nezara viridula*. The need for reliable identification tools and a thorough understanding of the biology of this genus has led to *Trissolcus* being by far the most studied group in Scelionidae.

Searching for cryptic species and defining intraspecific molecular variation is now possible only because of the extensive work that has been done on the taxonomy of the genus in recent years. Our study is focused on what we define as the "*semistriatus* complex" comprised of a series of species from the previously established basalis group, some of which were placed in synonymy under T. semistriatus in 2017, but were eventually resurrected as distinct species.

The molecular dataset contains sequences for over 100 specimens from the western Palaearctic. We targeted four molecular markers: the mitochondrial protein coding COI, nuclear 28S rDNA and ITS2 region, and the nuclear protein coding Wingless gene. To test species delimitations we used the BPP (Bayesian Phylogenetics and Phylogeography) program on previously defined groupings from PTP and GMYC. The specimens were then examined and checked for morphological confirmation of the molecularly defined species boundaries.

(14:15 GMT) 16:15 GBOL III: Dark Taxa and the figitids

Jonathan Vogel (ZFMK/Bonn/Germany), Ralph S. Peters (ZFMK/Bonn/Germany)

Abstract

In July 2020, a both ambitious and unprecedented national barcoding and taxonomy initiative was launched - GBOL III: Dark Taxa. It is the successor of the successful first two phases of the German Barcode of Life (GBOL) which included animals, plants, and fungi. In phase III, the Central European so-called "dark taxa" in Hymenoptera and Diptera are in the focus. These had so far been – as in most larger biodiversity projects – widely excluded. With a project duration of three and a half years, funded by the German Ministry of Research and Education, 12 PhD candidates are involved, each tackling their own dark taxon. In Hymenoptera, the tackled taxa are various parasitoid wasp groups in Chalcidoidea, Ceraphronoidea, Platygastroidea, Diaprioidea, Ichneumonoidea, and Cynipoidea.

In this talk, the GBOL III: Dark Taxa project will be briefly introduced. Its structure, workflows and mission will be shown on the example of the Figitidae (Cynipoidea) sub-project. The status-quo of European figitid research, the current state of the project and an outlook to the planned projects will be given.

(14:30 GMT) 16:30 Hidden in plain sight: Investigating the unknown diversity of German Pteromalidae (Hymenoptera: Chalcidoidea)

Michael Haas (State Museum of Natural History Stuttgart, Germany), Carlos Monje (State Museum of Natural History Stuttgart, Germany), Tanja Schweizer (State Museum of Natural History Stuttgart, Germany), Hannes Baur (Natural History Museum Bern, Switzerland), Lars Krogmann (State Museum of Natural History Stuttgart, Germany)

Abstract

Despite their important role as key regulators in natural ecosystems, parasitoids like the Pteromalidae are somewhat neglected in nature conservation, mostly a result of their minute size and difficult morphological identification. With about 750 species in Germany, the family Pteromalidae accounts for every 14th species of Hymenoptera and it is believed that many more are to be discovered. Little is known about their biology, and the impact of the rapid insect decline on species that occupy such high trophic levels is not understood at all. Initiatives like the German Barcode of Life Project aim to ease the impediment of laborious morphological identifications by providing a molecular database for COI barcode identification in large scale biodiversity projects. Results show that barcode data, in conjunction with a tree-based approach, can aid in the discovery of previously unrecorded and undescribed species in Germany. Our integrative approach also resulted in the discovery of a species complex of one of the most abundant pteromalids in Germany, *Spintherus dubius* (Nees,1834). Molecular analyses suggest a minimum of two distinct groups within the S. dubius species complex, which can be characterized morphologically upon closer inspection. Through mass rearings, differences in the biology of the two groups could be observed, with different host ranges. This highlights the need for a deeper look into currently recognized species concepts, illustrating that our knowledge is severely lacking in this ecologically significant group.

(14:55 GMT) 16:55 Fight or fright: Potential drivers of body size evolution in Cimbicidae (Insecta, Hymenoptera)

Lars Vilhelmsen (Natural History Museum of Denmark, Copenhagen), Vasileia Chatzaki (Natural History Museum of Denmark, Copenhagen)

Abstract

Cimbicidae is a small family of Tenthredinoidea, containing the largest extant true sawflies. Body size evolution across the family is mapped on an existing phylogeny, and some potential drivers of body size increase are explored: intrasexual competition between males, and mimicry patterns. Body size varies substantially within Cimbicidae, the largest species being found within the subfamily Cimbicinae. The smallest species occur in Corynidinae; this subfamily has experienced an overall decrease in body size. Initially, body size increase in Cimbicinae is correlated with males being larger than females, increase in relative mandible size in both sexes but especially in males, and increased hind femur width/length ratio in males only. Relative mandible size decreases in *Cimbex* spp. + *Odontocimbex* and hind femur width/length in *Leptocimbex* spp., respectively. The record sizes obtained in *Cimbex* spp. + *Odontocimbex* is the result of a further increase in body size, coupled with increase in hind femur width/length ratio in males. Black and yellow body colouration and other potential mimicry patterns are observed in a number of genera of Cimbicinae, but are probably not ground plan features of the subfamily. Patterns vary across the other subfamilies, but are less clear than in Cimbicinae. Intrasexual

competition seems to be more likely to have influenced size increase in Cimbicinae than adaptations to mimicry.

(15:10 GMT) 17:10 **The evolutionary history of Chalcid wasps (Hymenoptera)**

Jean Yves Rasplus (INRAE, Montpellier France), Bonnie Blaimer (Museum für Naturkunde, Berlin, Germany), Seán G. Brady (National Museum of Natural History, Washington, USA), Roger Burks (USDA-APHIS, Washington, USA), Robert S. Copeland (International Centre of Insect Physiology and Ecology, Nairobi, Kenya), Skey Papilloud Natalie Dale (Natural History Museum, London, UK), Gérard Delvare (CIRAD, Montpellier France), Nicole Fisher (CSIRO, Canberra, Australia), Lucian Fusu (Alexandru Ioan Cuza University, Iasi, Romania), Michael Gates (USDA-ARS, Washington, USA), Gary A.P. Gibson (CNC of Insects, Arachnids and Nematodes, Ottawa, Canada), Alex V. Gumovsky (Schmalhausen Institute of Zoology, Kiev, Ukraine), Paul Hanson (Universidad de Costa Rica, San Pedro, San José, Costa Rica), C. Hansson (Lund University, Lund, Sweden), John Heraty (University of California, Riverside, USA), John T. Huber (CNC of Insects, Arachnids and Nematodes, Ottawa, Canada), Petr Jansta (Charles University, Prague, Czech Republic), Mircea-Dan Mitroiu (Alexandru Ioan Cuza University, Iasi, Romania), Sabine Nidelet (INRAE, Montpellier France), Aldrey José Luis Nieves (Museo Nacional de Ciencias Naturales Madrid, Spain), J.S. Noyes (Natural History Museum, London, UK), Andrew Polaszek (Natural History Museum, London, UK), Laure Sauné (INRAE, Montpellier France), Serguei Triapitsyn (Entomology Research Museum, Riverside, USA), Ekaterina Tselikh (Zoological Institute, St Petersburg, Russia), Simon van (Iziko South African Museum, Cape Town, South Africa), James B. Woolley (Texas A&M University, College Station, USA), Astrid Cruaud (INRAE, Montpellier France)

Abstract

Chalcidoidea is one of the most species-rich and morphologically diverse superfamily of Hymenoptera. Chalcid wasps encompass important ecological role by regulating insect populations in most ecosystems of the earth. However, the evolutionary history of the superfamily is still poorly understood. In our study, we used more than 1000 Ultra-Conserved Elements (UCEs) to reconstruct higher-level relationships within Chalcidoidea. We included members of all major lineages (701 species (692 ingroups + 9 outgroups), representing 23 families of chalcids, 93 subfamilies, 154 tribes and 582 genera). We will discuss, our main results and the difficulties we had to resolve the backbone of the chalcid radiation. Among the 23 families represented, 17 were recovered monophyletic (#75%); 6 poly- or paraphyletic (namely Chalcididae, Aphelinidae, Eulophidae, and Perilampidae; two families literally exploded respectively in 6 and 25 independent clades (Eupelmidae and Pteromalidae, the garbage can of the superfamily). Finally, we investigated the timing and patterns of diversification of chalcids wasps and propose a new time-scale for the evolution of the superfamily.

(15:25 GMT) **17:25 Hymenoptera genomes through Darwin Tree of Life**

Gavin Broad (the Natural History Museum/London/UK)

Abstract

Darwin Tree of Life is a programme aiming to sequence the genomes of the British biota. This brief overview outlines the challenges involved in maintaining the cold chain from field to genome, and knowing how to target and identify key taxa while validating identifications when the specimen is destroyed for sequencing. I willl present progress in sampling Hymenoptera and production of draft genomes, while exploring some of the difficulties we will face in obtaining genomes for thousands of Hymenoptera species.

(15:40 GMT) **17:40 Using hybrid datasets to combine high support and deep taxon sampling in the phylogeny of Cryptini (Ichneumonidae, Cryptinae)**

Bernardo F. Santos (Muséum National d'Histoire Naturelle, Paris, France)

Abstract

In the past few years, new techniques have enabled the collection and analysis of genomic data at an unprecedented scale. However, there are still troves of molecular data accumulated from past studies using either single or multigene Sanger sequencing. Combining both sources of data is an obviously appealing possibility, but it can also lead to inconsistency due to high levels of missing data, disparities in the scale of Sanger versus genomic datasets, and little overlap among characters across species. To investigate the potential of such “hybrid” datasets, I combined data from ultraconserved elements for 240 species of Cryptini (Ichneumonidae, Hymenoptera) with a previously existing dataset of 7 loci and morphological data including 370 species. In many cases, bioinformatics pipelines allowed recovery of Sanger loci data from the bycatch of UCE data, reducing the problem of limited character overlap. The resulting trees combining Sanger and UCE data are highly supported and include a dense taxon sampling of Cryptini, allowing for a much better understanding of the phylogeny of the group. However, some seemingly artifactual results were detected in the trees, showing that problems with missing data and character compatibility still need to be worked out.

(16:05 GMT) **18:05 Keynote presentation:**

Ants and trees – a myrmecological view on investigating patterns of diversity and evolution in Hymenoptera

Abstract

Knowledge of species-level insect diversity, distributions and evolutionary relationships is needed now more than ever in the light of global insect declines. Although much work remains to be completed, recent advances in ant systematics and evolution have put us in a position to address key biodiversity questions that thus far have been reserved to more well-known groups such as vertebrates. In this talk, I will provide an overview of collaborative projects that build on and add to progress in ant phylogenomics to study the diversity and evolution of the group. First, I will discuss the goals and current results of our project MAMI (Malagasy Ant Microendemism), which is aimed at a synthesis of diversity survey efforts for ants in Madagascar spanning two decades. Here, we use a phylogenomic approach in combination with species distribution modeling to investigate regional patterns of diversity and endemism of ants in Madagascar across different habitat types, climate and elevational factors. I present initial results from this project focused on two widespread ant genera, *Crematogaster* and *Pheidole*. An analysis of island-wide community patterns of all ants in progress will uncover general patterns and allow us to draw broad conclusions for conservation planning. In a second part, I will summarize the objectives and preliminary results of a recently started collaborative project on camponotine ants and their bacterial endosymbionts, and outline other ongoing and planned work. Hereby, I provide a myrmecological perspective on how Hymenoptera could become a model group for much-needed studies to support insect conservation.

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