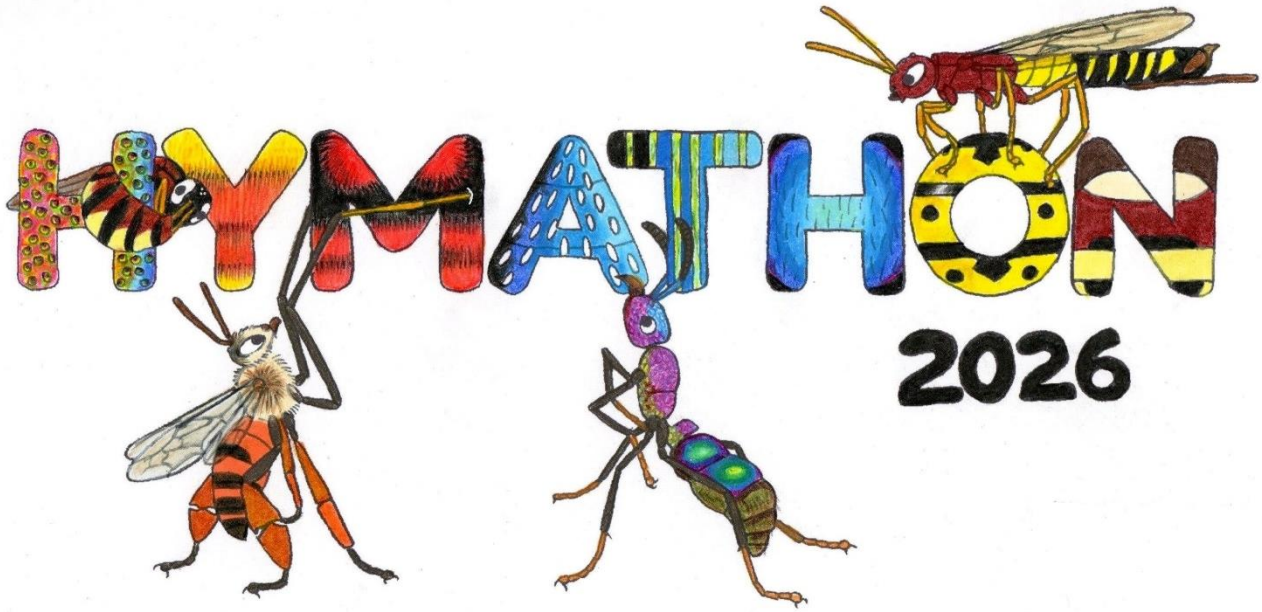


A 24 hour

virtual symposium from the

International Society of Hymenopterists

19 - 20 November 2026

Original artwork by Devon Henderson 2026

#HYMATHON2026

International Society of Hymenopterists virtual symposium

Organising Committee:

Natalie Dale-Skey, Erinn Fagan-Jeffries, Robin P. Marquez, Ana-Maria Chiosa, Maura Haas-Renninger, Luke Kresslein, Amelie Höcherl, Cristina Lupașcu-Vasilița, Alana McClelland, Miles Zhang, Thomas Hall, Jessica Awad, Gavin Broad, Emma Kärrnäs, Juanita Rodriguez

All start times in the program are given in UTC exclusively

All images in this program are the winning entries of last year's art competition

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ABSTRACTS

HYMENOPTERA SHOWDOWN

ART COMPETITION

HYMATHON AFTER HOURS

CODE OF CONDUCT



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Robin and Emma

17:05 **KEYNOTE: The Mind of a Bee**
Presenter: Lars Chittka



17:45 **Introduction of ISH Bingo**
Thomas Hall

17:50 **Evolution of social parasitism in Nearctic *Myrmecina* (Hymenoptera: Formicidae) (COMPETITION)**
Presenter: Benjamin Palm, benjamin.palm@pdmc.net

17:55 **Pteromalid tales of 2026**
Presenter: Koorosh McCormack kbrmccormack@gmail.com

18:00 **Clean up in aisle Eurytominae: revising a messy subfamily in light of phylogenomics**
Presenter: Miles Zhang, yuanmeng.zhang@gmail.com

18:05 **SHOWDOWN: Welcome to the dark side of Cynipoidea. Behold, the fiendish Figitidae!**
Presenter: Charles Davis, ckd.ento.eco.evo@gmail.com

18:10 **Break 1 S1**

18:20 **Integrative taxonomy of the *gibbus* species-group (Hymenoptera: Colletidae): Combining morphometrics, COI, and UCEs to resolve persistent taxonomic issues in *Hylaeus* (COMPETITION)**
Presenter: Martim Baptista, martimbaptista@hotmail.com

18:35 **Putting out the fire (ant): The phylogeography of an introduced *Wasmannia* parasitoid, *Orasema minutissima* (Chalcidoidea: Eucharitidae) in Hawai'i (COMPETITION)**
Presenter: Ashley Bui, abui052@ucr.edu

18:50 **Integrative taxonomy of *Leptacis* sensu lato (Hymenoptera: Platygastridae) (COMPETITION)**
Presenter: Konstantinos Kamoudis, k.kamoudis@gmail.com

19:05 **Taxonomy of Gall Wasp Parasitoids in genus *Ormyrus* (COMPETITION)**
Presenter: Robin Marquez, robinpmarquez@gmail.com

19:20 **On Unconfusing Species Concepts in *Anthophora* (Hym. Apidae) (COMPETITION)**
Presenter: Robert Zimmermann, robert.zimmermann@smns-bw.de

19:35 **Break 2 S1**

19:45 **I will tell the story of a mysterious collection of parasitoids in Baltic amber.**
Presenter: Elijah Talamas, elijah.talamas@fdacs.gov

20:00 **Discovery of two encyrtid parasitoids (Hymenoptera: Chalcidoidea) of invasive pasture mealybugs (Hemiptera: Pseudococcidae: *Heliococcus* Šulc) in Florida**
Presenter: Zachary Lahey, zachary.lahey@fdacs.gov

20:15 **The identity of *Megachile vidua* Smith, 1853 with implications on the status of *Megachile* (*Xanthosarus*) Robertson, 1903 (Hymenoptera: Megachilidae)**
Presenter: Cory Sheffield, cory.sheffield@gov.sk.ca

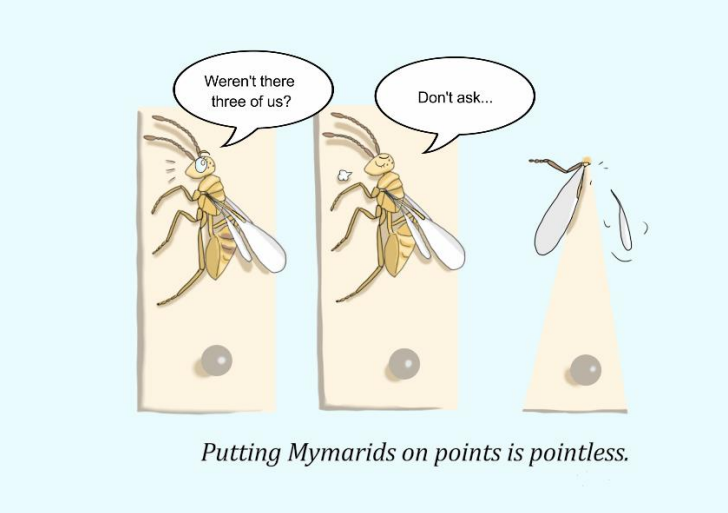
20:30 **An integrative taxonomic framework for *Inostemma* Haliday**
Presenter: Pierre Belloncle, bellonclep@gmail.com

20:45 **Concluding remarks**
Robin and Emma

20:50 **Break 3 S1**

21:15 **SOCIAL EVENT: ISH Trivia!!**
Presenter: Thomas Hall

21:35 **SOCIAL EVENT: Hamuli Live!!**
Presenters: Zach Griebenow and Philip Ward



2025 winner in the category '**Illustration – Fun & Artsy Hymenoptera'**: *Pointless* by Maura Haas-Renninger

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SESSION 2, chaired by Luke Kresslein and Maura Haas-Renninger

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00:00 **Introductory remarks**
Luke and Maura

00:05 **KEYNOTE: Old specimens, new questions: integrating curation, historical DNA and phylogenomics in Atlantic Forest ants**
Presenter: Gabi Camacho



00:45 **SHOWDOWN: Platygastroidea**
Presenters: Billy and Cassandra, elijah.talamas@fdacs.gov

00:50 **Break 1 S2**

01:00 **Four Families or 15? Phylogeny and Classification of Apoid Wasps (Sphecidae sensu lato) (COMPETITION)**
Presenter: Rin Krichilsky, eak2216@columbia.edu

01:15 **Phase IV: Discovering a new species of honey pot ant (COMPETITION)**
Presenter: Kai Jorda, k.l.jorda01@gmail.com

01:30 **Dive-bombing in bees: describing a novel behaviour and the effect of environmental and social factors (COMPETITION)**
Presenter: Breseya Clark, brie.yclark@protonmail.com

01:45 **An unexpected ally: *Hadronotus pennsylvanicus* (Ashmead, 1893) (Hymenoptera:Scelionidae) and its association with *Leptoglossus zonatus* (Dallas, 1852) (Hemiptera:Coreidae) in Mexican sorghum crops (COMPETITION)**
Presenter: Andrea Silva, amsm4934@gmail.com

02:00 **Big abdomen, bigger headache: untangling the *Pelecinus polyturator* (Hymenoptera: Pelecinidae) species complex (COMPETITION)**
Presenter: Allan Gabriel Cândido, allangabriel1402@gmail.com

02:15 **State of Hymenoptera research in Singapore: An abundance of specimens but a shortage of experts (COMPETITION)**
Presenter: Yu Fei Ng, yufei13579@gmail.com

02:30 **Break 2 S2**

02:40 **The first survey of parasitoid wasp diversity in Guam since the 1960s, sorted to morphospecies level**
Presenter: Karina Li, karinax1678@gmail.com

02:55 **Uncovering the evolution of Pompilidae venoms from fresh and museum specimens**
Presenter: Juanita Rodriguez, juanita.rodriguez@csiro.au

03:10 **An Australian goes to Peru: barcoding wasps at Manu Biological Station**
Presenter: Erinn Fagan-Jeffries, erinn.fagan-jeffries@adelaide.edu.au

03:25 **Who is living in the canopy of a Neotropical emergent tree, the case of Darwin wasps**
Presenter: Mabel Alvarado, malvaradog@unmsm.edu.pe

03:40 **Break 3 S2**

03:50 **The ongoing speciation of the *Ectatomma ruidum* species complex**
Presenter: Kenzy Ivveth Peña-Carrillo, kenzy.p@gmail.com

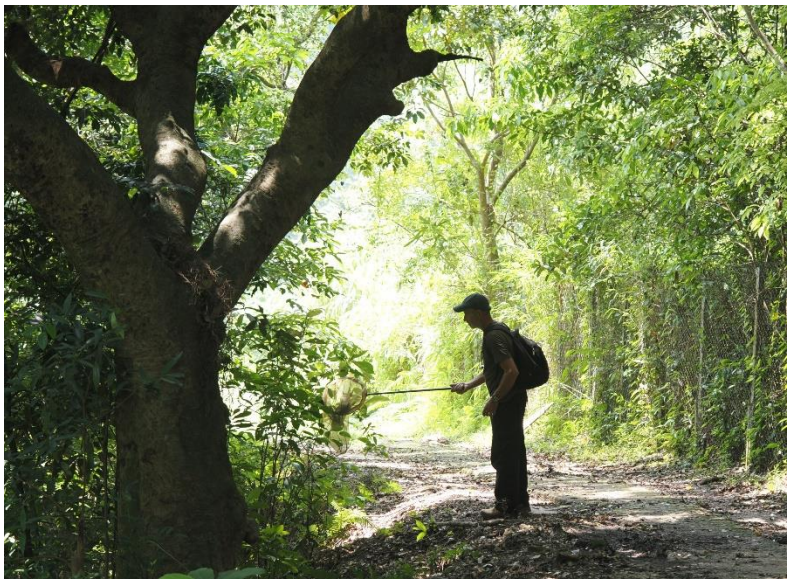
04:05 **The least known rose gallers: updates to *Liebelia* gall communities**
Presenter: Zoltan Laszlo, laszlozoltan@gmail.com

04:20 **Five years later: Observing the change in Encyrtid parasitoid population utilising *Heliococcus novovillei* (Hemiptera: Pseudococcidae) as a host from 2020-2026**
Presenter: Edward Bryans, edwardbryans@hotmail.com

04:35 **Chasing fairies: Unveiling the hidden diversity of fairyflies (Hymenoptera: Mymaridae) in Australia using Large-Scale Integrative Taxonomy**
Presenter: Maura Haas-Renninger, maura.haas-renninger@smns-bw.de

04:50 **Concluding remarks**
Maura and Luke

04:55 **SOCIAL EVENT: Gartic Phone**



2025 winner in the category '**Photography – Hymenopterists in action**: *A sunny day after typhoon passed* by Christophe Barthélémy

SESSION 3, chaired by Juanita Rodriguez and Gavin Broad

Session three abstracts here

06:30 **Introductory remarks**
Juanita and Gavin

06:35 **KEYNOTE: Evolutionary transitions in parasitoid wasps: Assymetry, reversibility, and constraints**
Presenter: Bernardo dos Santos, bernardofsantos@gmail.com



07:15 **SHOWDOWN: When I was a pteromalid**
Presenter: Natalie Dale-Skey, n.dale-skey@nhm.ac.uk

07:20 **Break 1 S3**

07:30 **Yes, we scan: Entomoscope and AI-based identification for Scelionidae (Platygastroidea) (COMPETITION)**
Presenter: Carmen Neuner, 23iglus.spitze@icloud.com

07:45 **It Takes Gall: Taxonomy and Systematics of the Gall-forming, Chalcid Family Tanaostigmatidae (COMPETITION)**
Presenter: Tareva-Chine Atkin-Zaldivar, a1804751@adelaide.edu.au

08:00 **Investigating the biodiversity and systematics of Australian rogadine parasitoid wasps using Phylogenomics and DNA barcoding (Hymenoptera, Braconidae, Rogadinae) (COMPETITION)**
Presenter: Mollie Slater-Baker, a1746992@adelaide.edu.au

08:15 **First micro-CT Reconstructions of the Male Genitalia of Two Species of the Nocturnal Darwin Wasp Genus *Netelia* (Hymenoptera: Ichneumonidae) and Their Functional Implications (COMPETITION)**
Presenter: Hsuan-Pu Chen, pooh890510@gmail.com

08:30 **The Grain Files: Uncovering the Hidden miRNA Repertoire of *Anisopteromalus calandrae* (COMPETITION)**
Presenter: Mariana Jimenez, mariana.jimenez80@gmail.com

08:45 **Ham or Jam? What can citizen science reveal about the feeding preferences of social wasps (COMPETITION)**
Presenter: Femi Benny, femi.benny.24@ucl.ac.uk

09:00 **Break 2 S3**

09:10 **Assessing the conservation status of Canadas bee (Apidae) fauna**
Presenter: Jennifer Heron, jenniferheron@gmail.com

09:25 **Bringing light (microscopy) to illuminating dark taxa: Cytogenetic analysis of parasitoid Hymenoptera**
Presenter: Vladimir Gokhman, vegokhman@hotmail.com

09:40 **Integrative Taxonomic Study of Chinese *Anastatus* (Hymenoptera: Eupelmidae) Based on Morphology and COI Barcoding, with Description of Eleven New Species**
Presenter: Ramzan Khan, ramzanpanwar158p@gmail.com

09:55 **North America bumble bees at-risk with atypical proventriculus morphology harbour distinct yeast communities in the digestive tract**
Presenter: Kirsten Palmier, palmieki@uregina.ca

10:10 **Digital biodiversity**
Presenter: Cristina Lupașcu-Vasiliță, cristina.vasilita@smns-bw.de

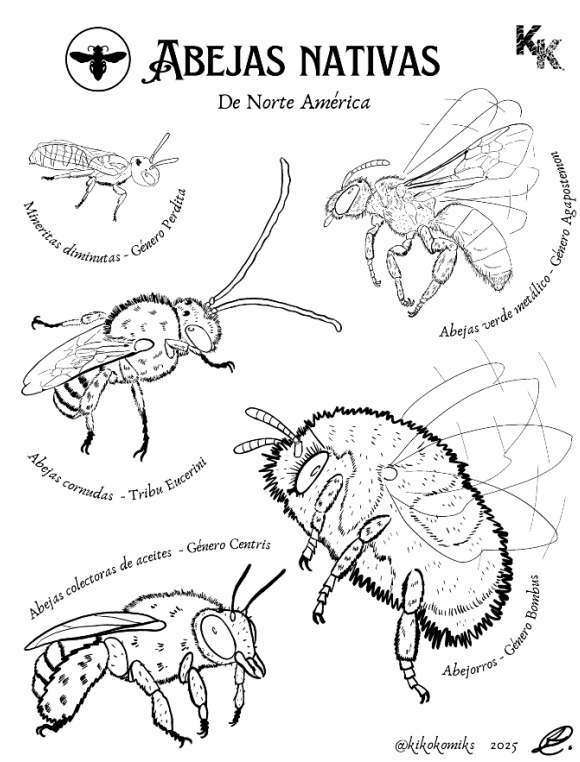
10:25 **Rapid detection of endogenized viruses in Ichneumonoidea reveals new viral lineages across disparate taxa**
Presenter: Barbara Sharanowski, barb.sharanowski@ucf.edu

10:40 **Concluding remarks**
Gavin and Juanita

10:45 **Break 3 S3**

10:50 **SOCIAL EVENT: ISH Business meeting**

11:50 **SOCIAL EVENT: Powerpoint Roulette!!**
Thomas Hall



2025 winner in the category '**Illustration – Scientific Illustrations**: *Abejas Nativas de Norte América* by *Kiko Kómiks*

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SESSION 4, chaired by Amelie Höcherl, and Cristina Lupașcu-Vasilița

Session four abstracts here

13:00 **Introductory remarks**
Amelie and Cristina

13:05 **KEYNOTE: High-throughput synchrotron X-ray microtomography of insects**
Presenter: Thomas van de Kamp, thomas.vandekamp@kit.edu



13:45 **DNA barcoding reveals hidden diversity of Microgastrinae (Hymenoptera: Braconidae) in Peru. (COMPETITION)**
Presenter: Lidia Sulca, lidia.sulca@gmail.com

13:50 **SHOWDOWN: Nomadinae (Apidae)**
Presenter: Tatiana Bush, tatiana.bush@wsu.edu

13:55 **Break 1 S4**

14:05 **Antennal Sensilla Morphology in Chalcididae (Hymenoptera: Chalcidoidea): Diagnostic Value and Phylogenetic Implications (COMPETITION)**
Presenter: Gwenivere Martin, gmart225@ucr.edu

14:20 **Uncovering Flat wasps from Northeast India: Challenges and Opportunities (COMPETITION)**
Presenter: Amritha Jaiprekash Kurup, jaiprekashamritha@gmail.com

14:35 **Revision of New World *Dyscritobaeus* Perkins, 1910 (Hymenoptera: Scelionidae). (COMPETITION)**
Presenter: Jamie Beach, jamiebeach@ufl.edu

14:50 **Host Identity, Ant Attendance, and Patterns of Host-Parasitoid Associations on Mo'orea, French Polynesia. (COMPETITION)**
Presenter: Willow Humphrey, willowhumphrey@berkeley.edu

15:05 **How Many Species Are We Missing? Large-Scale Integrative Taxonomy Reveals Unexpected Diversity in *Telenomus* (Scelionidae). (COMPETITION)**
Presenter: Anna Hauprich, anna.hauprich@gmail.com

15:20 **Small but mighty: Revealing the morphology and development of parasitoid wasps using Synchrotron X-Ray Imaging. (COMPETITION)**
Presenter: Pauline Pfeiffer, pauline-pfeiffer@hotmail.de

15:35 **Break 2 S4**

15:45 **Invisible gems: Phylogenomics of Tetrastichinae jewel wasps (Hymenoptera: Eulophidae) reveals cryptic taxa and rampant polyphyly**
Presenter: Emma Kärrnäs, emma.karrnas@biol.lu.se

16:00 **New species of Nearctic *Glyphomerus* Forster and the first records of the genus attacking woodbeauty galls induced by *Diastrophus* Hartig**
Presenter: Charles Davis, ckd.ento.eco.evo@gmail.com

16:15 **Lost in the Dark: Why we still don't understand parasitoid decline and extinction**
Presenter: Jessica Awad, jessica.awad@naturalis.nl

16:30 **The First Dated Molecular Phylogeny of Ceraphronoidea**
Presenter: Tobias Flores-Salden, to.salden@gmail.com

16:45 **EVENT: WISH Career panel**
Host: Cristina Lupașcu-Vasiliță

17:45 **Winners announcements**

18:05 **Concluding remarks**
Amelie and Cristina



2025 winner in the category '**Photography – Live Hymenoptera**: *Congregation* by *Jeong Jae Yoo*

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ABSTRACTS



All times given in UTC

SESSION 1, chaired by Robin Marquez & Emma Kärrnäs

17:05 KEYNOTE: The Mind of a Bee

Presenter: Lars Chittka

Lars Chittka FRS HonFRES MAE is the author of the book The Mind of a Bee and Professor of Sensory and Behavioural Ecology at Queen Mary College of the University of London. He is also the founder of the Research Centre for Psychology at Queen Mary. He is known for his work on the evolution of sensory systems and cognition using insect-flower interactions as a model system. Chittka has made fundamental contributions to our understanding of animal cognition and its impact on evolutionary fitness studying bumblebees and honeybees. He is the recipient of the 2026 International Society of Hymenopterists Distinguished Research Medal.

17:50 Evolution of social parasitism in Nearctic *Myrmecina* (Hymenoptera: Formicidae) (COMPETITION)

Presenter: Benjamin Palm @haplodiploid.bsky.social

Benjamin Palm (University of Hohenheim/Stuttgart/Germany); Daniela Mera-Rodríguez (University of Hohenheim/Stuttgart/Germany); Samyuktha Senthil (University of Hohenheim/Stuttgart/Germany); Stefan P. Cover (Museum of Comparative Zoology/ Harvard University/Cambridge, USA); Christian Rabeling (University of Hohenheim/ Stuttgart/Germany)

Social parasitism is a form of brood parasitism in which one social parasite species takes advantage of another social species for survival and reproduction. Social parasitism evolved repeatedly in ants through distinct evolutionary routes that often produce convergent parasitic syndromes. Currently, the ant genus *Myrmecina* includes a single recently described social parasite, *Myrmecina davisoni* MacGown, 2023, which parasitizes its host *M. americana*, a species widespread across much of the United States and southeastern Canada. Although rare, *M. davisoni* appears to follow its host throughout much of its range, with scattered records extending from Arizona to Massachusetts.

Here, we present the first phylogeny of Nearctic *Myrmecina* based on ultraconserved elements (UCEs), including all valid species, and reconstruct the evolutionary route to social parasitism. By resolving the relationships between *M. davisoni*, its host, and other Nearctic congeners, we assess whether the parasite originated directly within its host lineage or evolved from an independently diverged lineage. We also discuss the

expression of the social parasitic syndrome in *M. davisoni,* considering its morphology and natural history in the unusual ecological context of parasitizing an almost exclusively subterranean host.

17:55 ***Whatonearth isthis*** **McCormack, 2026: Pteromalid tales of 2026**

Presenter: Koorosh McCormack

Koorosh McCormack

For the past year I have been identifying large numbers of UK wasps, predominantly in the superfamily Chalcidoidea. Along with a few species new to the UK, I stumbled upon a wasp that is apparently not of Holarctic origin. Is it a new species? A new genus?? Where is it from??? I present to you, my hymenopteran friends, the temporarily named *Whatonearth isthis* McCormack, 2026.

18:00 **Clean up in aisle Eurytominae: revising a messy subfamily in light of phylogenomics**

Presenter: Miles Zhang, @ymilesz.bsky.social

Y. Miles Zhang (Birkbeck, University of London/London/UK)

Recent phylogenomic studies on Eurytomidae (Zhang et al. 2025; Park et al. 2026) have greatly clarified relationships within the subfamily Eurytominae, reaffirming previous morphological studies have suggested genera such as *Eurytoma, Bruchophagus, Gibsonoma*, and *Aximopsis* are not monophyletic. Resolving the Palearctic and Oceania fauna, however, remains difficult as much of the relevant type materials are hard to access. At the same time, new species are being discovered, often accompanied by detailed biological records that help anchor species limits. Here I briefly present my ongoing collaborative works toward untangling this messy subfamily, including revising bamboo gall associates, describing new species, and establishing new genera to accommodate aberrant lineages. I will also discuss the implications of these incremental revisions for a stable classification of Eurytominae.

18:05 **SHOWDOWN: Figitidae**

Presenter: Charles Davis

Welcome to the dark side of Cynipoidea. Behold, the fiendish Figitidae!

18:20 **Integrative taxonomy of the *gibbus* species-group (Hymenoptera: Colletidae): Combining morphometrics, COI, and UCEs to resolve persistent taxonomic issues in *Hylaeus* (COMPETITION)**

Presenter: Martim Baptista

Martim Baptista (Department of Zoology, Faculty of Sciences, Charles University/Prague/ Czechia; Museu Nacional de História Natural e da Ciência, Universidade de

Lisboa/Lisbon/Portugal; ce3c – Centre for Ecology, Evolution and Environmental Changes & CHANGE – Global Change and Sustainability Institute, Universidade de Lisboa/Lisbon/ Portugal); Romain Le Divelec (Laboratory of Zoology, Research Institute for Biosciences, Mons, Belgium); Francisco Hita Garcia (Center for Integrative Biodiversity Discovery, Museum für Naturkunde/Berlin/Germany); Joseph Monks (Insects Division, Natural History Museum/London/UK); Roberto A. Keller (Museu Nacional de História Natural e da Ciência, Universidade de Lisboa/Lisbon/Portugal; ce3c – Centre for Ecology, Evolution and Environmental Changes & CHANGE – Global Change and Sustainability Institute, Universidade de Lisboa/Lisbon/Portugal); Bernardo Santos (Center for Integrative Biodiversity Discovery, Museum für Naturkunde/Berlin/Germany)

The *gibbus* species-group has long been one of the most taxonomically problematic groups in Palearctic *Hylaeus*. Over time, the number of recognized species has varied greatly between authors, and inconsistent diagnostic characters have been used to differentiate between them. Here, we challenge the current species boundaries and employ morphometric analyses to demonstrate the limitations of some of the previously used diagnostic characters. Moreover, we present new characters and species boundaries supported by phylogenies inferred by both COI and UCEs. This improved framework supports the recognition of five valid species within this group.

18:35 Putting out the fire (ant): The phylogeography of an introduced *Wasmannia* parasitoid, *Orasema minutissima* (Chalcidoidea: Eucharitidae) in Hawai'i (COMPETITION)

Presenter: Ashley Bui

Ashley Y. Bui (University of California–Riverside/Riverside/USA); John M. Heraty (University of California–Riverside/Riverside/USA)

The first record of the parasitoid wasp *Orasema minutissima* Howard, 1894 (Chalcidoidea: Eucharitidae) was first found on the island of Hawaii in 2019, likely as an accidental introduction. The species is now well established across the island. Originally from northern regions in South America and the Caribbean, *O. minutissima* parasitizes the massively invasive Little Fire Ant (*Wasmannia auropunctata*). As *W. auropunctata* is among the most destructive and pervasive invasive species, particularly on the Hawaiian Islands, the establishment of *O. minutissima* could prove to be beneficial as a potential biological control agent. One major emphasis is determining the origin and phylogeographic pathway of the wasp in Hawaii. Utilizing samples of both *W. auropunctata* and *O. minutissima* from Dominica, Trinidad, Florida, Puerto Rico, and Hawaii, we will use low coverage WGS to determine variation and structure between the *W. auropunctata* and *O. minutissima* populations to investigate the geographic origins of both species. We also provide insight into the newly discovered behavioural shifts across the various populations of *O. minutissima*. Lastly, we assembled the first reference genome for not only the species, but the entire family (Eucharitidae) as well. We hope this project lays the groundwork for a future biological control program against the Little Fire Ant.

18:50 Integrative taxonomy of *Leptacis* sensu lato (Hymenoptera: Platygastridae) (COMPETITION)

Presenter: Konstantinos Kamoudis

Konstantinos Kamoudis (Wageningen University & Research/Wageningen/Netherlands); Elijah J. Talamas (FSCA/Gainesville/USA); Jessica Awad (Naturalis Biodiversity Center/Leiden/Netherlands)

Leptacis Forster, 1856, one of the largest genera of Platygastridae (300 described species), was recovered as polyphyletic in the ultraconserved-element phylogenetic analysis of Sosa-Calvo et al. (unpublished data). The substantial task of revising *Leptacis* and dividing it into monophyletic genera is therefore in the works. As a first step, *Leptacis tipulae* (Kirby, 1798), the type species of the genus and a natural enemy of wheat midges in Europe, was reassessed and redescribed. The ongoing work now concerns the world fauna of *Leptacis*, within which more than a dozen morphological species groups have so far been recognized yet still require further refinement and molecular phylogenetic testing. At the same time, genus-level identification of platygastrid BINs in BOLD Systems is being undertaken, aiming not only to retrieve barcodes and locate specimens relevant to *Leptacis*, but also to provide data for future large-scale studies of diversity and biogeography across the family.

19:05 Taxonomy of Gall Wasp Parasitoids in Genus *Ormyrus* (COMPETITION)

Presenter: Robin Marquez

Robin P. Marquez (University of Minnesota/Saint Paul/United States); Louis F. Nastasi (University of Nebraska-Lincoln/Lincoln/United States); Guerin E. Brown (University of Iowa/Iowa City/United States); MaKella J. Steffensen (University of Iowa/Iowa City/ United States); Andrew A. Forbes (University of Iowa/Iowa City/United States)

Oak gall wasps are a species-rich insect group that induce the formation of galls on widespread oak species. Galls provide putative protection to the young gall wasp but also recruit myriad other parasites and inquilines, thus becoming ecosystems unto themselves. The closed system offered by galls, and the associated arthropod diversity within and between galls, can be applied to address broader evolutionary and ecological questions. However, the continued exploration of gall wasp biology and ecology can be complicated by the presence of cryptic species among their natural enemies. The objective of this research is to contribute to a comprehensive taxonomic revision of the gall wasp parasitoid genus *Ormyrus*. Across 1,789 gall collecting events between 2015-2019 in the continental United States and British Columbia, we accumulated over 525,000 galls representing 201 different oak gall types from 32 oak tree species. From these, we reared over 151,000 gall wasps. We extracted DNA from a subset of these wasps, and amplified and aligned a short segment of the mtCOI gene to generate preliminary species hypotheses. We then validated these species hypotheses using morphological taxonomic work. This study clarifies species concepts for oak gall-associated *Ormyrus* and informs future taxonomic study of the genus, including new species descriptions and the development of morphological identification keys.

19:20 On Unconfusing Species Concepts in Anthophora (Hym. Apidae) (COMPETITION)

Presenter: Robert Zimmermann

Robert Zimmermann (State Museum of Natural History Stuttgart/Stuttgart/Germany); Michael C. Orr (State Museum of Natural History Stuttgart/Stuttgart/Germany); Thomas J. Wood (Naturalis Biodiversity Center/Leiden/The Netherlands)

The genus *Anthophora* Latreille (digger bees) is a speciose group of solitary, ground-nesting bees distributed over much of the world. Due to the application of unpublished and confused species group names, progress towards a sound taxonomic basis is hindered, especially in the subgenus *Paramegilla*. In this study, we traced the application of the historically misapplied name *Anthophora* inclyta Walker through the literature and museum collections and show that it has been used in three different species concepts. We clarify these concepts, establish new synonyms, and describe two species of *Anthophora* as new to science.

19:45 I will tell the story of a mysterious collection of parasitoids in Baltic amber.

Presenter: Elijah Talamas

Get ready for the story of a mysterious collection of parasitoids in Baltic amber, more than 75 years in the making.

20:00 Discovery of two encyrtid parasitoids (Hymenoptera: Chalcidoidea) of invasive pasture mealybugs (Hemiptera: Pseudococcidae: *Heliococcus* Šulc) in Florida

Presenter: Zachary Lahey

Zachary Lahey (Florida Department of Agriculture and Consumer Services/Gainesville/ United States); Nicole Benda (Florida Department of Agriculture and Consumer Services/ Gainesville/United States); Erin C. Powell (Florida Department of Agriculture and Consumer Services/Gainesville/United States)

Two hymenopteran parasitoids of invasive and damaging mealybug species, *Heliococcus novovillei* Powell and Miller and *Heliococcus summervillei* Brookes, are reported from Florida, United States. *Blepyrus saccharicola* Gahan is a primary, solitary endoparasitoid of *H. novovillei. Rhopus sp*. is a primary, gregarious endoparasitoid of *H. summervillei*. A species of *Prochiloneurus* Silvestri is presumed to act as a hyperparasitoid of *B. saccharicola.* Each species was reared from their respective mealybug host in quarantine at the Florida Department of Agriculture and Consumer Services, Division of Plant Industry, Gainesville, Florida, from material originating in central and southern Florida. In Florida, *B. saccharicola* is presently the dominant parasitoid of *H. novovillei* and has been reared from that species in four counties. These are the first Western Hemisphere records of any parasitoid attacking either species of pasture mealybug. Diagnostic characters, annotated images of each species, sequence data, and an illustrated key to the *Blepyrus* Howard of Florida are presented to allow for their identification to facilitate future biological control research on pasture mealybugs and provide early targets for potential rearing efforts.

20:15 **The identity of *Megachile vidua* Smith, 1853 with implications on the status of *Megachile (Xanthosarus)* Robertson, 1903 (Hymenoptera: Megachilidae)**

Presenter: Cory Sheffield @corysheffield.bsky.social

Cory Sheffield

Confusion exists on the identity of *Megachile vidua* Smith, 1853, the type species for *Megachile (Delomegachile)* Viereck, 1916. Prior to the early 1960s *M. vidua* was considered conspecific with *M. frigida* Smith, 1853 but was subsequently placed it into synonymy under *M. latimanus* Say, 1823, the type species of *Xanthosarus* Robertson, 1903; this should have resulted in *M. (Delomegachile)* being considered a junior synonym of *M. (Xanthosarus).* However, *Delomegachile* continued to be recognized as a Nearctic subgenus of *Megachile* until 2000. Though *M. (Delomegachile)* is currently treated as a junior synonym of *M. (Xanthosarus),* the true identity of *M. vidua* has important implications for the potential recognition of *Delomegachile* as a subgenus of *Megachile* as the concept of *Xanthosarus* globally is far from resolved. To address these issues, the type material for *M. vidua* was examined and its identity confirmed. To help address the latter issue, a comprehensive molecular phylogeny of *Xanthosarus sensu* Michener (2007) was completed that included taxa now considered part of the *Xanthosarus* and the *Megachiloides* groups of Gonzalez et al. (2019). The results will be discussed.

20:30 **An integrative taxonomic framework for *Inostemma* Haliday**

Presenter: Pierre Belloncle @perrydotite.bsky.social

Pierre Belloncle (Sorbonne Université/Paris/France); Jessica Awad (Naturalis Biodiversity Center/Leiden/Netherlands)

We often consider our lack of understanding of biodiversity through the number of yet-to-be discovered species. Yet, among those already described, some present a confused taxonomic history, making their identification at the species level obscure, sometimes even subjective. We call these taxa dark taxa *Inostemma* Haliday, 1833 (Hymenoptera, Platygastridae) is a genus of 1-2mm parasitic wasps targeting eggs of gall midges (Diptera, Cecidomyiidae). Due to their small size and parasitic nature, description quality of *Inostemma* species has been inconsistent. They are often based on one individual, lacking any ecological information on host association and focus on one character: the horn growing from the first metasomal tergite of most females. *Inostemma* currently is a dark taxa. This study aims at laying a stable basis for future *Inostemma* study, using integrative taxonomy. I used morphological and molecular data to assess species boundaries in *Inostemma*, along with checking the boundaries of the genus itself. I used my results to create a new diagnosis and redescribe the type species of the genus, *I. boscii* (Jurine, 1807), along with resolving the type status of two individuals among this species. Finally, I used ct-scans to look at the entire reproductive system in female *Inostemma,* in order to describe the whole complex.

21:15 **ISH Trivia**

Presenter: Thomas Hall

Hey ISHers! Do you think you're the smartest hymenopterist in the breakout room? Prove it in this edition of trivia! (A separate device [e.g. phone] will be required to play)

21:35 **Hamuli Live**

Presenters: Zach Griebenow and Philip Ward

Philip Ward is Professor of Entomology at the University of California, Davis. His research focusses on the systematics and evolution of ants (Hymenoptera:Formicidae) and encompasses both species-level taxonomy and phylogenetics. Taxa of particular interest include big-eyed ants in the subfamily Pseudomyrmecinae and carpenter ants and allies in the tribe Camponotini. Recent research attempts to integrate phylogenomic (UCE) and morphological evidence to clarify our understanding of species boundaries and evolutionary history.

SESSION 2, chaired by Luke Kresslein and Maura Haas-Renninger



00:05 **KEYNOTE: Old specimens, new questions: integrating curation, historical DNA and phylogenomics in Atlantic Forest ants**

Presenter: Gabi Camacho

Gabriela (Gabi) Procópio Camacho is an Assistant Professor and Senior Curator of Hymenoptera at the Museu de Zoologia da Universidade de São Paulo (MZUSP), Brazil. She completed a PhD with Rodrigo Feitosa at the Universidade Federal do Paraná, including a year as a pre-doctoral fellow with Ted Schultz at the Smithsonian Institution, and was a postdoctoral researcher with Bonnie Blaimer and Brian Fisher at North Carolina State University and the California Academy of Sciences, and later at the Museum für Naturkunde Berlin, prior to joining MZUSP. Her research is focused on the systematics, evolution and biogeography of Hymenoptera, especially ants, combining fieldwork, morphology and alpha taxonomy with phylogenomics based on ultraconserved elements. As curator of a collection of roughly one million Hymenoptera specimens, she treats museum collections as a genomic resource, and her lab uses historical DNA from specimens to revise Neotropical ant genera and to map phylogenetic diversity and endemism across the Atlantic Forest, one of the most species-rich and threatened biomes on Earth. Her group is also building museomics capacity at MZUSP to expand the use of tropical biological collections in evolutionary research.

00:45 **SHOWDOWN: Platygastroidea**

Presenters: Billy and Cassandra

Elijah Talamas (Florida State Collection of Arthropods); Jessica Awad (Naturalis Biodiversity Center); Jamie Beach (University of Florida)

Billy and Cassandra attended the ISH meeting in Mexico City. There they observed a talk that presented incorrect information. During this video presentation, you will find out what was misrepresented, how it was disproven empirically, and a new anthem for the International Society of Hymenopterists. But you don't have to take our word for it, just read the following testimonials.

"I was sick and tired of presentations that were full of hype. Billy and Cassandra know how to get to the truth" J. D. McDavidsworth

"This year, I was thinking of giving up on being an ISH member, but now I am inspired to be a part of the society forever" M. V. von Jenkins

"*It seemed like the society had become stagnant, then I heard Cassandra sing and I could not get her voice out of my head. I even visited a neurologist but still, I can't get her voice out of my head"* Ccedil Č. Řeynoldson

"*When I heard Cassandra sing, I knew that there was hope for many things, and these things represented a wide variety of things"* Scaron de Uumlmblars El Ribletharing

"Most presenters don't have the strength of character or strong enough vocal cords to sing during their presentations. But Cassandra does. She knows how to be strong and how to sing. I really like listening to her sing. Cassandra's voice will soothe your troubled mind, mend your broken heart, and save what's left of your soul. Maybe you should listen to her sing. Try it, you might like it!" R. J. F. Wiblucius

01:00 Four Families or 15? Phylogeny and Classification of Apoid Wasps (Sphecidae sensu lato) (COMPETITION)

Presenter: Rin Krichilsky @rin-krichilsky.bsky.social

Rin Krichilsky (AMNH & Columbia University/NYC/USA); Jessica Ware (AMNH/NYC/USA)

Sphecidae s.l. are hunting wasps in the superfamily Apoidea. Also known as apoid wasps, they comprise over 10,000 species and are predators to spiders, springtails, and more than half of all insect orders. Phylogenomic studies have recently changed their classification from four to thirteen families. More specifically, subtribes, tribes, and subfamilies of Crabronidae were elevated to family-level. We assessed these boundaries with UCEs and by increasing generic coverage with museum specimens. Greater taxon sampling revealed novel paraphyly and corroborated the instability of Crabronidae. With a more robust phylogeny we are able to explore broader questions about their evolutionary history such as their sister-group relationship to bees and the role of diet in shaping their diversity.

01:15 Phase IV: Discovering a new species of honey pot ant (COMPETITION)

Presenter: Kai Jorda

Kai L. Jorda (UC Riverside/Riverside/USA) and John M. Heraty (UC Riverside/Riverside/USA)

The genus *Myrmecocystus* Wesmael, famously known as honey ants or honeypot ants; are well known for their replete workers that act as living food stores. This New World genus spans through the majority of Mexico and north to the US-Canada border. Roy Snelling revised *Myrmecocystus* in 1976 and 1982, describing several new species, nominating three subgenera, and defining eight species groups. Little has changed in the systematics of this genus, with only one new species being described within the past 50 years. Each subgenus displays a distinct habit and habitus difference, with the subgenus *M. (Myrmecocystus)* containing the yellow nocturnal species, *M. (Endiodioctes)* consisting of diurnal species that are frequently orange and black, and *M. (Eremnocystus)* consisting largely of smaller concolor matinal/crepuscular species. Recent molecular studies utilizing UCEs have inferred the subgenera to be paraphyletic and revealed several punitive new species.
Collections in southern California have revealed a punitive new species that was previously represented by three prior collections totalling 18 specimens in varying states

of wear. Two of the locales no longer foster populations of this new form. The aim of this study is to diagnose and describe the species based on all castes (i.e. gynes, workers, and males), database and map all prior records of *Myrmecocystus* in the region with an emphasis on mapping population decline over time, COI barcode all known populations of the new species to analyze population differences, and explore the possibility of hybridization with *M. testaceus.*

01:30 Dive-bombing in bees: describing a novel behaviour and the effect of environmental and social factors (COMPETITION)

Presenter: Breseya Clark

Breseya Clark (University of Southampton)

Studying bee behaviour provides valuable insights into the mechanisms that enable pollination, plasticity, and sociality. Furthermore, the study of novel behaviours informs the way bees respond to unprecedented environmental pressures.
This study sought to define an undescribed novel behaviour first observed in 2025, named dive-bombing, and record the conditions in which it occurs across all bee species it happens in.
Over 17 weeks, behaviours were observed between 10am and 2pm, when pollinators were most active, and recorded. In total, 51 instances of dive-bombing were recorded across 12 species over 112 hours. This was done across three sites in 2025 to assess the effect of land use and biodiversity, and in one cathedral garden site in 2026, to further assess the effect of temperature and species.
Dive-bombing is defined as a rare behaviour with an instigator and a victim, involving a ventral or head-first collision between two individuals, in which the instigator does not engage further with the victim or its surroundings.
The results show a slight positive correlation between the behaviour and temperature as well as site biodiversity. Land use and humidity did not affect bee behaviour. Excluding *Anthidium* and *Anthophora*, whose aggression is well documented, the behaviour is not correlated with species. However, most of the species in which dive-bombing occurs are social. Therefore, though the reason for the behaviour is unknown, possibilities include nestmate recognition or resource guarding. Further research will involve strengthening understanding of the association between this behaviour and temperature and sociality in a controlled setting.

01:45 An unexpected ally: *Hadronotus pennsylvanicus* (Ashmead, 1893) (Hymenoptera:Scelionidae) and its association with *Leptoglossus zonatus* (Dallas, 1852) (Hemiptera:Coreidae) in Mexican sorghum crops (COMPETITION)

Presenter: Andrea Silva

Andrea Silva-Márquez (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/ San Nicolás de los Garza/ México); María de Lourdes Ramírez-Ahuja (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/ San

Nicolás de los Garza/ México); Mariana Jiménez-Martínez (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/ San Nicolás de los Garza/ México); Gerardo Trujillo-Rodríguez (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/ San Nicolás de los Garza/ México); Iram Rodríguez-Sánchez (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/ San Nicolás de los Garza/ México)

Leptoglossus zonatus (Dallas, 1852), commonly known as the leaf-footed bug, has become an increasingly important agricultural pest throughout the Americas due to its broad host range and dispersal capacity. This polyphagous species can damage numerous economically important crops, reducing fruit and seed quality and facilitating the transmission of plant pathogens. Conventional pest management strategies have relied heavily on chemical pesticides, however, concerns about pesticide resistance, environmental contamination, and food safety. In this study, we report for the first time the association of the egg parasitoid *Hadronotus pennsylvanicus* (Ashmead, 1893), with eggs of *Leptoglossus zonatus* collected from sorghum crops in Sinaloa, Mexico. *Leptoglossus* eggs were collected from sorghum crops and maintained until the emergence of the parasitoid or the bug. Some egg masses were parasitized, from which about 20 parasitoids emerged. Adult parasitoids were examined morphologically, and molecular identification was performed using the mitochondrial cytochrome c oxidase subunit I (COI) gene. The resulting sequences supported the identification of the emergent scelionid wasps as *H. pennsylvanicus*. This finding extends the known host associations and geographic distribution of *H. pennsylvanicus* and provides new insights into the natural enemy complex associated with *L. zonatus* in the Mexican sorghum agroecosystems. Although further studies are required to evaluate parasitism rates, seasonal dynamics, and field effectiveness, this record suggests that *H. pennsylvanicus* can contribute to the natural regulation of *L. zonatus* populations. These results provide a baseline for future studies on parasitoid-based biological control and integrated pest management strategies against leaf- footed bugs in Mexico.

02:00 Big abdomen, bigger headache: untangling the *Pelecinus polyturator* (Hymenoptera: Pelecinidae) species complex (COMPETITION)

Presenter: Allan Gabriel Cândido

Allan Gabriel Cândido de Oliveira (Universidade Federal do Paraná/Curitiba/Brazil); Gabriel Augusto Rodrigues de Melo (Universidade Federal do Paraná/Curitiba/Brazil)

The genus *Pelecinus* currently comprises only three valid species, contrasting sharply with its rich fossil record. Despite their unique morphology and pronounced sexual dimorphism, the groups evolutionary history and true diversity remain poorly understudied. This study presents the first molecular phylogenetic analysis for the family Pelecinidae. Using multi-locus sequence data (COI, 28S, and ITS2) analysed via maximum likelihood and Bayesian inference, we integrate newly generated data from specimens collected mainly along the Atlantic Rainforest of Brazil with barcode COI sequences available in open databases. Our results demonstrate that *P. polyturator* is not a single

widespread species, but a complex composed of several distinct species. Based on congruent morphological and molecular data, we formally describe seven new species from Brazil: *P. caracensis sp. nov., P. carinatus sp. nov., P. cearensis sp. nov., P. fulgidus sp. nov., P. marumbi sp. nov., P. pintoi sp. nov.,* and *P. tibialis sp. nov.* Male-female associations are presented for six of these new taxa.

02:15 State of Hymenoptera research in Singapore: An abundance of specimens but a shortage of experts (COMPETITION)

Presenter: Yu Fei Ng @criclom.bsky.social

Ng Yu Fei (National University of Singapore, Singapore)

Singapore is a city-state with high urbanisation density, and it has few remaining primary forests and mangroves. Despite urbanisation, there are more than 900 species of Hymenopterans reported in Singapore. Both bees and ants are relatively well studied, with 135+ and 400+ species respectively while all Symphyta and parasitoid wasp families remain poorly studied. The Lee Kong Chian Natural History Museum in Singapore has collected tens of thousands of Hymenoptera via malaise traps, yellow pan traps, etc. over the past decade from a wide variety of habitats. Hence, there is plenty of opportunity to discover new records and species along with examining ecological trends. I will explain the preliminary findings of what has been discovered in Singapore thus far.

02:40 The first survey of parasitoid wasp diversity in Guam since the 1960s, sorted to morphospecies level

Presenter: Karina Li

Karina Li (University of Guam); Erica Garcia (University of Guam); Segundo Garrido (University of Guam); Alfred Daniel Johnson (University of Guam)

Guam is a tropical island in Micronesia which suffers many newly introduced species every year. Invasive species disrupt agricultural production and native ecosystems. Parasitoid wasps are known to be helpful in managing pest species, but the last survey of parasitoid wasps in Micronesia was conducted in the 1950s and 60s. Specific groups, such as aphid parasitoids, have been studied more recently in detail. However, a comprehensive updated diversity of parasitoid wasps on Guam is currently lacking. To address this research gap, a malaise trap and four yellow pan traps were set up in a vegetated area on the University of Guam campus. Collected wasps were identified to family level and then compared to identify individuals as the same or distinct morphospecies. Over the course of only 14 collection days spread between early February and early March 2026, approximately 150 distinct morphospecies of parasitoid wasp were collected. Notable superfamilies collected under Apocrita (parasitica) include Mymarommatoidea, Platygastroidea, Cynipoidea, Ceraphronoidea, Diaprioidea, Ichneumonoidea, and Chalcidoidea. Trapping will continue into January 2027, leading to collection days spanning nearly an entire calendar year. This survey may reveal families, genera, or species previously unknown to Guam, and may even lead to the collection of

undescribed species. A clearer understanding of parasitoid wasp diversity will also support future biological control efforts for invasive pests.

02:55 Uncovering the evolution of Pompilidae venoms from fresh and museum specimens

Presenter: Juanita Rodriguez @juanita_rodr.bsky.social

Juanita Rodriguez (CSIRO/Canberra/Australia); Daniel Dashevsky (CSIRO/Canberra/Australia); Alicia Grealy (CSIRO/Canberra/Australia); Liz Milla (CSIRO/Canberra/Australia).

Spider wasp (Pompilidae) venom toxins are interesting, because they cause paralysis and intense pain. Pompilidae females hunt, paralyse, and lay an egg on a spider. When the larva hatches, it feeds on the paralysed spider. Some pompilid toxins have been shown to modulate voltage-gated sodium channels of the type 1.6, which are abundant in the human brain. Studying these venoms can help understand central nervous system (CNS) function and pain and developing new treatments for CNS conditions. One such toxin is Pompilidotoxin. Using a venomics workflow we obtained Pompilidotoxin sequences for various pompilid genera. With these sequences as reference we then obtained the Pompilidotoxin from a large number of whole genome sequencing assemblies from fresh and museum specimens. We demonstrate that genome-mining can be used as an alternative method for obtaining venom toxin gene data from rarely-collected taxa.

03:10 An Australian goes to Peru: barcoding wasps at Manu Biological Station

Presenter: Erinn Fagan-Jeffries

Erinn P. Fagan-Jeffries (Adelaide University/Australia)

Join this presentation for a show-and-tell of Erinn's post-Congress adventure to Manu Biological Station in Peru. Alongside Nick Volpe and Lucy Kania, who have been running the volunteer program at the station and documenting the invertebrate biodiversity through high quality images, the project aimed (in two weeks!) to DNA barcode hundreds of specimens from the station's collections to bring together DNA data, morphological identifications, images of the live animals, and iNaturalist observations to start building a connected reference database for the station's wasps.

03:25 Who is living in the canopy of a Neotropical emergent tree, the case of Darwin wasps

Presenter: Mabel Alvarado

Mabel Alvarado (Departamento de Entomología, Museo de Historia Natural, Universidad Nacional Mayor de San Marcos/Lima/Perú); Luis Figueroa (Departamento de Entomología, Museo de Historia Natural, Universidad Nacional Mayor de San Marcos/ Lima/Perú); Claire Villemant (Département Origines et Evolution, Muséum National d'Histoire Naturelle/Paris/France); Ángela Aristizábal-Botero(Biodiversity Monitoring and Assessment, Royal Belgian Institute of Natural Sciences/Brussels/Belgium); Barbara

D'hont (Q-ForestLab, Department of Environment, Faculty of Bioscience Engineering, Ghent University/Ghent/Belgium); Maurice Leponce (Biodiversity Monitoring and Assessment, Royal Belgian Institute of Natural Sciences/Brussels/Belgium; Evolutionary Biology and Ecology, Université Libre de Bruxelles/Brussels/Belgium)

I will talk about what ichneumonid wasps are living in the canopy of an emergent tree, collected in two national parks of Peru. We recorded 211 species belonging to more than 78 genera and 19 subfamilies, including remarkable records of the genera *Chirotica, Megastylus, Lanugo, Stilpnus, Syrphidepulo, Xorides* among others. I will discuss the implications of this unexpected diversity to our understanding of insect tropical faunas.

03:50 **The ongoing speciation of the *Ectatomma ruidum* species complex**

Presenter: Kenzy Ivveth Peña-Carrillo

Kenzy I. Peña-Carrillo (INIFAP, Campo Experimental General Terán/General Terán/ Mexico); Rubi N. Meza-Lázaro (Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México/Ciudad de México/Mexico); Chantal Poteaux (Laboratoire d'Ethologie Expérimentale et Comparée, UR 4443, LEEC, Université Sorbonne Paris Nord/Clément/France); Maria Cristina Lorenzi (Laboratoire d'Ethologie Expérimentale et Comparée, UR 4443, LEEC, Université Sorbonne Paris Nord/Clément/France)

Delimiting species through the integration of different traits helps to reveal cryptic lineages that evolve and diversify without showing morphological changes. A key advantage of this multi-trait approach is that it simultaneously provides insights into which traits have driven species diversification. In this study, we investigated the variation observed in some species of the *Ectatomma ruidum* species complex, as an evidence of different taxa. *E. ruidum* is a widely distributed ant from the Neotropics, previous studies based on mitochondrial sequences proposed this was composed of at least four different taxa. The geographic distribution patterns of the different species show that some of them are restricted to small areas, without any apparent geographic barrier separating populations, which raised the question about which mechanisms are separating them. Thorough the analysis of recognition cues, acoustic signals, morphological acoustic traits and DNA sequences (mitochondrial DNA COI gene, 3RAD and UCE), we provide evidence for the separation of the previously proposed species. Additionally, results unveiled that recognition cues may have had a very important role for the diversification of the species complex. Overall, this study adds evidence in favour of the use of a multi trait approach for the delimitation of closely related species.

The least known rose gallers: updates to *Liebelia* gall communities

Presenter: Zoltan Laszlo

04:05

Zoltán László (Hungarian Department of Biology and Ecology, Faculty of Biology and Geology, Babeş- Bolyai University/Cluj-Napoca/Romania); Alibek Ydyrys (Biomedical Research Centre, Al-Farabi Kazakh National University/Almaty/Kazakhstan); Avar-Lehel Dénes (STAR-UBB Institute of Advanced Studies in Science and Technology, Babeş-Bolyai University/Cluj-Napoca/Romania

The genus *Liebelia* (Hymenoptera: Diplolepididae) remains the most poorly studied group of rose-associated cynipid gall wasps, with fragmentary data on host associations, gall morphology, and the insect communities inhabiting their galls. Here we present new records and community-level data for little-known *Liebelia* taxa. Galls of *Liebelia montana* collected near Almaty, Kazakhstan, yielded a diverse assemblage of chalcidoid and ichneumonoid parasitoids, dominated by torymid and eurytomid parasitoids attacking the gall inducer. The resulting rearing data provide the first quantitative picture of parasitoid community structure for this species and underline the importance of Central Asian rose stands as an underexplored reservoir of cynipid-associated parasitoid diversity, relevant both to regional biodiversity assessment and to broader questions about the biogeography of host-parasitoid networks across the Palearctic. We further report updated distributional and morphological notes on several *Liebelia* species, clarifying diagnostic gall characters that distinguish them from congeners. Finally, we relate about an unusual, morphologically interesting species of *Liebelia, L. cavarae* from Sardinia, whose gall structure departs notably from the pattern seen in continental *Liebelia*, raising questions about insular divergence within this species and its relationship to mainland populations. Together these findings expand the known host and parasitoid associations of *Liebelia,* and highlight how regional surveys of understudied gall-wasp genera continue to reveal substantial hidden diversity in both gall inducers and their associated communities.

04:20 Five years later: Observing the change in Encyrtid parasitoid population utilising *Heliococcus novovillei* (Hemiptera: Pseudococcidae) as a host from 2020-2026

Presenter: Edward Bryans

Edward Bryans (Queensland University of Technology/Brisbane/Australia); Caroline Hauxwell (Queensland University of Technology/Brisbane/Australia); Brett Williams (Queensland University of Technology/Brisbane/Australia)

The pasture mealybug (PMB) causes pasture dieback, resulting in loss of productivity and death of affected grasses in over 4 million hectares of pastures across Queensland and New South Wales. Previously thought to be a variant of *Heliococcus summervillei*, the PMB has recently been described as a new species *H. novovillei.* In 2020, an undescribed species of *Parectromoidella* (Hymenoptera: Encyrtidae) was identified as the primary parasitoid of *H. novovillei* with extremely low parasitism rate. This research aims to illustrate the change in the encyrtid parasitoid population utilising PMB over the past 5 years. Eight sites of historic pasture dieback were surveyed every 6-8 weeks from October 2025 to June 2026. The surveys included collecting mealybugs to observe parasitoid emergence, mealybug abundance assessments and sweep nets for parasitoid seasonal abundance.

Of the over 1100 mealybugs collected, 110 showed signs of parasitism and 83 parasitoid wasps emerged across 3 species. The undescribed *Parectromoidella* species appears to be the primary parasitoid, with undescribed species of *Anagyrus* and *Rhopus* also utilising PMB. The *Rhopus sp*. was also observed emerging from the Rhodes grass mealybug (*Antonina graminis*) from the same location as PMB. An increase in parasitoid diversity and rates of parasitism in PMB parasitoids offers hope of improving the natural control of this serious pest.

04:35 **Chasing fairies: Unveiling the hidden diversity of fairyflies (Hymenoptera: Mymaridae) in Australia using Large-Scale Integrative Taxonomy**

Presenter: Maura Haas-Renninger

Maura Haas-Renninger (Adelaide University/Adelaide/Australia); Erinn Fagan-Jeffries (Adelaide University/Adelaide/Australia); Steven J.B. Cooper (South Australian Museum/Adelaide/Australia)

The family Mymaridae (Hymenoptera: Chalcidoidea) is a group of minute (generally <1 mm long), morphologically conserved parasitoid wasps. They are egg parasitoids of various insects, mostly of Auchenorrhyncha (Hemiptera), therefore playing a central role in regulating their host populations. There are approximately 270 species known from Australia but it is assumed that this is only a fraction of the actual number of species. In the past, Mymarids have been studied based on morphology and many species descriptions are based on single specimens with the distribution of many species being unknown. DNA barcoding for species identification of Mymarids is nearly impossible as they are highly underrepresented in reference libraries. For Australia, there are 2,698 records (518 BINs) of which only six are assigned to a species name representing two species (BOLD Systems, 20.10.2026). This shows the need to build up a reference library for Australian Mymarids with species names. In addition, the high number of BINs compared to described species known from Australia shows the high potential of DNA barcoding to reveal species that are new to science. The aim of this project is to use material from various expeditions all across Australia to assess the distribution and diversity of Mymaridae using DNA megabarcoding for the first time. This will result in a reference library including species names, enabling the identification of Mymarids through DNA barcoding in the future, and the description of species that are new to science.

04:55 **Gartic Phone**

Presenter: Thomas Hall

In this game of broken telephone, take turns illustrating prompts to the best of your ability while trying to best discern the chicken-scratch drawings of your fellow ISHers! This game is open to ISH members with a wide range of illustrative "talent".

SESSION 3, chaired by Juanita Rodriguez and Gavin Broad



06:35 **KEYNOTE: Evolutionary transitions in parasitoid wasps: Asymmetry, reversibility, and constraints**

Presenter: Bernardo dos Santos

Bernardo Santos is a systematist and evolutionary biologist based at the Museum für Naturkunde Berlin. He completed his B.S. and M.Sc. studies in Brazil before pursuing academic training and appointments in the U.S.A., France and Germany. His research focuses on the systematics, evolution and biodiversity of parasitoid wasps, particularly Ichneumonidae. Combining traditional taxonomy, molecular phylogenetics, phylogenomics, and large-scale biodiversity datasets, he investigates the evolutionary history of parasitoid wasps, the origins and diversification of their extraordinary species richness, and the ecological processes shaping their global distribution. His work spans topics ranging from species discovery and classification to macroevolutionary patterns and global biodiversity gradients.

07:15  **SHOWDOWN: Pteromalidae**

Presenter: Natalie Dale-Skey

When I was a pteromalid.

07:30 **Yes, we scan: Entomoscope and AI-based identification for Scelionidae (Platygastroidea) (COMPETITION)**

Presenter: Carmen Neuner

Carmen Neuner (University of Hohenheim & Stuttgart State Museum of Natural History/Stuttgart/Germany); Cristina Lupașcu-Vasilița (University of Hohenheim & Stuttgart State Museum of Natural History/Stuttgart/Germany); Ana-Maria Chiosa (University of Hohenheim & Stuttgart State Museum of Natural History/Stuttgart/Germany); Hossein Shirali (Karlsruhe Institute of Technology/Karlsruhe/Germany); Christian Pylatiuk (Karlsruhe Institute of Technology/Karlsruhe/Germany); Ecaterina Pirvu (University "Alexandru Ioan Cuza in Iași"/Iași/Romania); Elijah Talamas (Florida State Collection of Arthropods/Gainesville/USA); Ovidiu Popovici (University "Alexandru Ioan Cuza in Iași"/Iași/Romania); Lars Krogmann (University of Hohenheim & Stuttgart State Museum of Natural History/Stuttgart/Germany)

The identification of hyperdiverse insect groups, such as "dark taxa," is one of the greatest challenges in global biodiversity monitoring. Due to the taxonomic impediment, immense proportions of these organisms remain overlooked. This project investigates the potential of automated, image-based identification in the parasitoid wasp family Scelionidae. Serving as a methodological proof of concept, this study builds upon

approaches applied to the family Diapriidae and validates the transferability of digital classification models to megadiverse dark taxa.
The study utilized standardized image stacks from over 1,000 morphologically and molecularly validated specimens. Digitization was performed using the Entomoscope. A YOLOv8-Large classification model was trained on six abundant genera of Scelionidae. To evaluate model behaviour when encountering unseen categories, 14 additional genera were used as an evaluation dataset. Model decisions were examined for morphological relevance using a computer-aided heatmap analysis (Eigen-CAM).
The trained model achieved a top-1 genus accuracy of 96.66% (91.48% at the specimen level). The Eigen-CAM analysis confirmed that the artificial neural network primarily relies on diagnostically relevant body regions. Misclassifications occurred almost exclusively between closely related or morphologically convergent genera. When confronted with the evaluation dataset, the model exhibited overconfidence on out-of-distribution data, forcing unknown genera into known classes.
These results demonstrate the high reliability of AI-supported classification tools for robotic pre-sorting within integrative taxonomy pipelines. The presented workflow offers a practical approach to mitigating the dark taxon impediment, reducing the workload of taxonomists, and opening up scalable pathways for biodiversity monitoring.

07:45 It Takes Gall: Taxonomy and Systematics of the Gall-forming, Chalcid Family Tanaostigmatidae (COMPETITION)

Presenter: Tareva-Chine Atkin-Zaldivar

Tareva-Chine Corazón Atkin-Zaldívar (Adelaide University/Adelaide/Australia); Erinn Fagan-Jeffries (Adelaide University/Adelaide/Australia; The South Australian Museum/ Adelaide/Australia); Yuanmeng Miles Zhang (University of Edinburgh/Edinburgh/UK); Timothy Hammer (Adelaide University/Adelaide/Australia; State Herbarium of South Australia/Adelaide, Australia); Astrid Cruaud (INRAE, Centre de Biologie pour la Gestion des Populations/Montpellier/France); Jean-Yves Rasplus (INRAE, Centre de Biologie pour la Gestion des Populations/Montpellier/France)

From inducing eye-catching, fluffy galls to species featuring striking pink and orange patterns, the family Tanaostigmatidae is hard to miss, in theory. In reality, this family within Chalcidoidea is still largely a mystery when it comes to their systematics; the largest genus, *Tanaostigmodes*, was suggested to be paraphyletic in a previously conducted Chalcidoidea-wide phylogeny (Cruaud et al., 2024). With a focus on the Australian fauna, this project brings together Tanaostigmatidae specimens from across the globe, including representatives from six of the eight currently described genera. Specimens underwent low-coverage genome skimming and Ultraconserved elements (UCEs) were then extracted bioinformatically and used in the creation of a phylogeny of the family. This work contributes to a greater understanding of the relationships within the family Tanaostigmatidae, and the diversity of gall-forming hymenopterans in Australia. This project also marks the first family-wide phylogeny of Tanaostigmatidae and the first study in Australia on the family in over 20 years

08:00 **Investigating the biodiversity and systematics of Australian rogadine parasitoid wasps using Phylogenomics and DNA barcoding (Hymenoptera, Braconidae, Rogadinae) (COMPETITION)**

Presenter: Mollie Slater-Baker @molliersb.bsky.social

Mollie Slater-Baker (The University of Adelaide/Adelaide/Australia); Michelle Guzik (The University of Adelaide/Adelaide/Australia); Juanita Rodriguez (Australian National Insect Collection CSIRO National Research Collections Australia/Canberra/Australia); Erinn Fagan-Jeffries (The University of Adelaide & South Australian Museum/Adelaide/ Australia)

Rogadinae is a subfamily of parasitoid wasps within the megadiverse family Braconidae. Rogadines are commonly known as mummy wasps; due to their unique ability to mummify their caterpillar hosts. These wasps are found worldwide and are commonly collected throughout Australia, however only a fraction of their estimated diversity has been formally documented. A particularly interesting but poorly known tribe, the Betylobraconini, is endemic to Australia and surrounding regions, making it an important target for taxonomic revision and further study. This project uses DNA barcoding for rapid assessment of the diversity of Rogadinae in Australia, along with short-read whole-genome sequencing to obtain ultra-conserved elements (UCEs) and mitochondrial genomes for examining phylogenetic relationships within the tribe Betylobraconini. Molecular methods are used alongside efficient morphological examination to explore the diversity of the Australian Rogadinae, and provide a foundational taxonomic and systematic framework for the tribe Betylobraconini, and describe new species.

08:15 **First micro-CT Reconstructions of the Male Genitalia of Two Species of the Nocturnal Darwin Wasp Genus *Netelia* (Hymenoptera: Ichneumonidae) and Their Functional Implications (COMPETITION)**

Presenter: Hsuan-Pu Chen

Hsuan-Pu Chen (Laboratory of Systematic Entomology, Graduate School of Agriculture, Hokkaido University/Sapporo/Japan); Kazuhiko Konishi (Hokkaido University Museum/Sapporo/Japan); Kazunori Yoshizawa (Laboratory of Systematic Entomology, Graduate School of Agriculture, Hokkaido University/Sapporo/Japan; Botanical Garden, Hokkaido University/Sapporo/Japan)

Insect male genitalia often exhibit remarkable structural diversity, whereas female genitalia are generally more conservative in morphology. This disparity has been hypothesized to result from sexual selection through cryptic female choice. The nocturnal Darwin wasp genus *Netelia* provides a promising system for investigating this hypothesis, as its species exhibit relatively uniform external morphology, despite considerable interspecific variation in male genital structures, including a sclerotized brace and a membranous pad on the inner surface of gonostyles, the copulatory organ, but both of which are absent in some species. In contrast, female genitalia are relatively simple and uniform. The repeated evolutionary gains and losses of the brace and pad may reflect shifts in copulatory signalling, but their functions remain unclear. To

investigate their potential functions, we used micro-computed tomography (micro-CT) to examine the male genitalia of two *Netelia* species, *N. tarsata* and *N. bicolor*, representing elaborated and simplified genital forms, respectively. The reconstructions revealed differences in the gs-hrp muscle, conjunctiva on the inner surface of the gonostyles, and fat body development. The gs-hrp muscle and conjunctiva were observed in *N. tarsata* but not in *N. bicolor,* and the fat body was more developed in *N. tarsata.* The gs-hrp muscle may facilitate movement of the bracepad complex, while fat body development may be associated with the hypothesized secretory function of the pad. Although broader taxon sampling is needed, these findings provide insights into the potential functions of male genital structures in *Netelia.*

08:30 The Grain Files: Uncovering the Hidden miRNA Repertoire of *Anisopteromalus calandrae* (COMPETITION)

Presenter: Mariana Jimenez

Mariana Lizbeth JIMENEZ-MARTINEZ (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/Nuevo León/ México); Gerardo de Jesús Trujillo-Rodríguez (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/Nuevo León/ México o); Iram Pablo Rodriguez-Sanchez(Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/Nuevo León/ México); María de Lourdes Ramírez-Ahuja (Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Fisiología Molecular y Estructural/Nuevo León/ México)

Stored-grain ecosystems harbor complex interactions between insect pests and their natural enemies. Among these, *Anisopteromalus calandrae* is a parasitoid wasp with potential applications in the biological control of coleopteran pests, including *Sitophilus zeamais*. However, its molecular regulatory landscape remains largely unexplored. This study aimed to characterize the microRNA (miRNA) repertoire of *A. calandrae* and investigate its conservation across five hymenopteran species: *Apis mellifera, Dinoponera quadriceps, Nasonia giraulti, N. longicornis,* and *N. vitripennis*.
Adult wasps were obtained from stored maize infested with *S. zeamais* in Joscute; Azueta, Veracruz, Mexico. Following RNA extraction and quality assessment, small RNA sequencing was performed using Illumina/Solexa technology. Bioinformatic analyses combined miRDeep2, miRBase, BLASTN, RNAfold, UGENE, Intervene, and R to identify, characterize, and compare miRNA sequences.
Our investigation revealed 75 conserved miRNAs and 33 putative novel miRNAs, establishing the first miRNomic profile of *A. calandrae*. Based on previous studies in insects, several conserved miRNAs have been implicated in development, reproduction, metabolism, immune responses, and cellular signalling. However, their specific functions in this parasitoid remain unverified.
These findings uncover a previously unexplored component of *A. calandrae* molecular biology and establish a foundation for future functional validation, regulatory target

identification, and comparative studies of parasitoid wasps with potential applications in biological control.

08:45 Ham or Jam? What can citizen science reveal about the feeding preferences of social wasps (COMPETITION)

Presenter: Femi Benny @femi-benny.bsky.social

Femi Ezhuthupallickal Benny (Centre for Biodiversity and Environmental Research/ University College London); Cintia Akemi Oi (Centre for Biodiversity and Environmental Research/University College London); Seirian Sumner (Centre for Biodiversity and Environmental Research/University College London)

Social wasps are familiar summer visitors at picnics where their foraging often conflicts with people. The diet of a social wasp reflects the needs of the colony; workers collect protein to feed larvae and carbohydrates to fuel adult activity, and the balance between the two is thought to change as the colony grows. However, we know very little about how these preferences play out across a season.
Citizen science offers a powerful way to address such gaps in ecology, allowing observations to be gathered across far larger areas and longer periods than a research team could achieve alone, while engaging the public with often-misunderstood insects. Through the Ham or Jams urvey, which ran from June to October in 2025 and 2026, we asked members of the public to report the feeding preferences of social wasps at their picnics such as ham; aka any protein rich food or jam; aka any sugary food.
We hypothesized that wasps would favour sugar during the early and later periods of the colony cycle and protein during the middle period of rearing larvae, workers, and new sexuals. Here we present a first overview of the results, and how they relate to our predictions. This work will help explain how the colony life cycle shapes the ecosystem services of social wasps as both pest controllers and pollinators and provide ecology-based recommendations for managing human-wasp conflicts.

09:10 Assessing the conservation status of Canadas bee (Apidae) fauna

Presenter: Jennifer Heron

Jennifer M. Heron (British Columbia Ministry of Water, Land and Resource Stewardship/ Surrey/Canada); Cory S. Sheffield (Royal Saskatchewan Museum/Regina/Canada).

There are over 1,000 bee (Apidae) species recorded from Canada, and for most of these species there is little information about their distribution and natural history. Conservation status assessments are crucial to identify at- risk species, focus conservation efforts, inform policy under federal and provincial acts, and monitor the effectiveness of protection and recovery actions. These assessments also help prevent irreversible biodiversity loss by providing the probability of a species' risk of extinction or extirpation, allowing for timely intervention before species disappear entirely. As part of the General Status of Species in Canada Wild Species assessment, the conservation status assessments for Canada’s bee fauna were first completed in 2015 and updated in 2020 using NatureServe methodologies. Using this prioritized list, those species deemed

most at-risk are then prioritized for status report preparation and assessment by the Committee on the Status of Endangered Species in Canada (COSEWIC), which uses the International Union for the Conservation of Nature (IUCN) Red List Categories Criteria. COSEWIC uses scientific and Indigenous knowledge to assess a species conservation status, and the recommends species to the federal government for listing under the Species At Risk Act (SARA). This talk will focus on updates to assessing the conservation status of Canada's bee fauna, information and methods used where little data is available, knowledge gaps, challenges to applying both IUCN and NatureServe criteria, how species are recommended for national assessment.

09:25 Bringing light (microscopy) to illuminating dark taxa: Cytogenetic analysis of parasitoid Hymenoptera

Presenter: Vladimir Gokhman

Vladimir E. Gokhman (5 Nordau Str/Haifa/Israel)

Hymenopterous parasitoids represent one of the most species-rich, taxonomically complicated and economically important groups of insects. Millions of nucleotide sequences originating from various parasitic wasps are currently known, but these sequences often come from individuals, which are not assigned yet to any described species, i.e., they represent so-called 'dark taxa'. Since it is often very difficult, if at all possible, to distinguish between closely related parasitoids using morphological characters alone, application of various genetic techniques, including karyotype research, can be indispensable for investigating dark taxa of parasitic wasps. The present work reviews results and perspectives of chromosomal analysis of parasitoids, with an emphasis on the dark taxa. A brief historical outline of the karyotype research of parasitic wasps is given. The chromosomal study can be effectively used for detecting and distinguishing between cryptic species of parasitoids. Information about the karyotype structure helps preparing chromosome-level genome assemblies and assists in physical mapping of DNA sequences. The chromosomal study can detect particular pathways of karyotype evolution as well as create phylogenetic reconstructions based on chromosomal characters. At present, acquisition of new data is accompanied by the accelerating technical progress in analyzing preparations of parasitoid chromosomes. These techniques include morphometric study, use of DNA-binding fluorochromes, chromosome microdissection and fluorescence in situ hybridization (FISH) with various DNA probes, together with use of fluorochrome-conjugated specific antibodies. Karyotype research currently demonstrates an enormous diversity of parasitic wasps in terms of taxonomy and genome structure, and it will hopefully lead to further exciting discoveries in the future.

09:40 Integrative Taxonomic Study of Chinese *Anastatus* (Hymenoptera: Eupelmidae) Based on Morphology and COI Barcoding, with Description of Eleven New Species

Presenter: Ramzan Khan

Ramzan khan (Biological control Research Institute, College of Plant Protection, Fujian Agriculture and Forestry University/China)

Thirty-two Chinese *Anastatus* species (Hymenoptera: Chalcidoidea: Eupelmidae) are studied, comprising 20 previously described species and 11 new species. Ten of the new species belong to the subgenus *A. (Anastatus): A. (Anastatus) nozdormu sp. nov., A. (Anastatus) kryptos sp. nov., A. (Anastatus) napoleonis sp. nov., A. (Anastatus) yalini sp. nov., A. (Anastatus) battutai sp. nov., A. (Anastatus) beaglei sp. nov., A. (Anastatus) neltharion sp. nov., A. (Anastatus) tigrinus sp. nov., A. (Anastatus) huijuanae sp. nov., A. (Anastatus) ashrafi sp. nov*. One belongs to the subgenus *A. (Cladanastatus): A. (Cladanastatus) alexstrasza sp. nov.* One additional species is newly recorded from China: *A. (Anastatus*) mantoidae Motschulsky rec. nov. A new synonymy is also proposed: *A. (Anastatus) flavaeratus* Peng & Tang, 2020 syn. nov. under *A. (Anastatus) gastropachae* Ashmead, 1904. Morphologically similar species were assigned to three informal species groups (*formosanus, fulloi,* and *japonicus* groups) based on morphology. Of the already-described species of the Chinese *Anastatus*, 15 were newly recorded from different provinces of China; this was true for all species except *A. colemani, A. bifasciatus, A. polikiarkoudus, A. taibaiensis,* and *A. zdenekbouceki.* Molecular analyses based on the mitochondrial cytochrome c oxidase subunit I (COI) gene were conducted on a total of 34 species (26 species derived from the specimens collected from China and eight species sequences downloaded from the BOLD and NCBI). Multivariate morphometric analyses (PCA, LDA, MANOVA) were employed to distinguish morphologically similar species. A comprehensive diagnostic key to all Chinese *Anastatus* species is also provided, accompanied by photographs of diagnostic characters.

09:55 North America bumble bees at-risk with atypical proventriculus morphology harbour distinct yeast communities in the digestive tract

Presenter: Kirsten Palmier

Cory Sheffield (Royal Saskatchewan Museum/Regina/Canada); Andrew Cameron (University of Regina/Regina/Canada)

Gut microbial communities are fundamental to insect physiology, influencing nutrition, immunity, and resistance to parasites. In bumble bees, the bacterial microbiota has been well characterized, revealing conserved core taxa and clear functional roles in digestion and immune regulation. Yet, despite this progress, the diversity, ecological function, and host interactions of fungal associates, particularly yeasts, remain poorly understood. Yeasts can be mutualistic, commensal, or parasitic, but their contributions to gut ecology and host defence have received little attention. Unusual foregut morphologies in male Bombus species provide a rare opportunity to examine how structural variation in the digestive tract shapes microbial colonization, especially by yeasts whose roles in bee biology remain largely unexplored.

10:10 Digital biodiversity

Presenter: Cristina Lupașcu-Vasilița

Cristina Lupaşcu-Vasilița (Stuttgart State Museum of Natural History, University of Hohenheim/Stuttgart/Germany); Lars Krogmann (Stuttgart State Museum of Natural History, University of Hohenheim/Stuttgart/Germany); Thomas van de Kamp (Karlsruhe Institute of Technology, Institute for Photon Science and Synchrotron Radiation/ Eggenstein-Leopoldshafen/Germany)

Natural history collections are the world's largest repositories of biodiversity data, yet much of this information remains inaccessible. The digital transformation of research increasingly enables remote access to collection specimens and their morphology in 2D. More recently, high-throughput 3D digitisation using synchrotron micro-computed tomography (SR-µCT) has made it possible to capture both internal and external morphology of entire collections. However, morphology alone is often insufficient, as biodiversity and evolutionary research increasingly integrates phenotypic with genetic and genomic data. Existing workflows frequently compromise one source of data in favor of the other: standard DNA extraction protocols digest internal soft tissues, preventing subsequent imaging, while the effects of high-dose µCT radiation on DNA integrity remain poorly understood.
This study systematically evaluates the reciprocal effects of µCT scanning and DNA extraction on insect specimens to develop an optimized workflow that maximizes both phenotypic and genotypic data recovery. Our results show that all DNA extraction methods damage soft tissues to some extent, whereas µCT scanning enables non-destructive visualization of internal morphology prior to digestion. Although DNA yield and integrity decline with increasing irradiation time, both DNA barcoding and UCE sequencing remain feasible when scanning parameters are carefully optimized.
The proposed workflow provides a framework for integrating morphological and molecular datasets in natural history collections while preserving both phenotypic and genotypic information, even for fragile or rare specimens. Such digital vouchers create permanent, high-resolution records that can be revisited without further physical handling, facilitating remote analyses, strengthening collaboration, and accelerating biodiversity and evolutionary research.

10:25 Rapid detection of endogenized viruses in Ichneumonoidea reveals new viral lineages across disparate taxa

Presenter: Barbara Sharanowski

Barbara Sharanowski (University of Central Florida/Orlando/USA); Rachel Behm (University of Central Florida/Orlando/USA); Willow Humphrey (University of California/Berkeley); Ashley Noll (University of Central Florida/Orlando/USA) and Gaelen Burke (University of Georgia/Athens/USA)

We present a rapid screening pipeline for detection of core genes of the class Naldaviricetes, combining homology searches, rapid filtering, tree building and flanking sequence analyses to determine viral presence, affiliation, and endogenization. Here we

report multiple taxa carrying previously unknown viruses, mostly endogenized, and some with second viruses, suggesting multiple viral endogenizations are more common than previously recognized. In three different ichneumonid subfamilies we also found a novel divergent virus that falls between the Filamentoviridae and Hytrosaviridae.

11:50  **Powerpoint Roulette**

Presenter: Thomas Hall

Oh no! You are about to present your slides at Hymathon but you open the wrong folder and out comes powerpoint slides you've never seen before! Take turns presenting your slides while pretending that absolutely nothing is wrong...

SESSION 4, chaired by Amelie Höcherl, and Cristina Lupașcu-Vasilița



13:05 **KEYNOTE: High-throughput synchrotron X-ray microtomography of insects**

Presenter: Thomas van de Kamp

Thomas van de Kamp is an entomologist working at the Karlsruhe Institute of Technology (KIT) in Germany. In 2011, he obtained his PhD in Biology at the University of Düsseldorf. For his doctoral thesis he studied weevil functional morphology using synchrotron X-ray imaging and digital 3D reconstructions. Currently, he holds the position of Senior Scientist and Principal Investigator for morphological X-ray imaging at the Institute for Photon Science and Synchrotron Radiation of KIT, which operates the X-ray imaging beamlines of KIT's particle accelerator, the KIT Light Source. His research interests include insect functional morphology, evolution and diversity & X-ray imaging of biological and paleontological specimens. He is part of the core team behind the international "Antscan" initiative that focused on high-throughput 3D phenomics of ant biodiversity.

13:45 **DNA barcoding reveals hidden diversity of Microgastrinae (Hymenoptera: Braconidae) in Peru. (COMPETITION)**

Presenter: Lidia Sulca

Lidia Sulca (Museo de Historia Natural, Universidad Nacional Mayor de San Marcos/ Lima/Peru); Mabel Alvarado (Museo de Historia Natural, Universidad Nacional Mayor de San Marcos/Lima/Peru); Spencer Monckton (Centre for Biodiversity Genomics, University of Guelph/Guelph/Canada); Jose Fernandez-Triana (Canadian National Collection of Insects, Arachnids and Nematodes/Ottawa/Canada). Microgastrinae is one of the largest subfamilies of Braconidae and exhibits high diversity worldwide. As exclusive parasitoids of Lepidoptera, their diversity is closely linked to that of their hosts. Currently, a total of 49 species of Microgastrinae has been recorded in Peru; but the estimate number of Lepidoptera in Peru is ~45,000 species, suggesting that the Microgastrinae fauna is substantially underestimated.
We present a DNA barcode (COI-5P) library of 1,128 Microgastrinae specimens from 14 departments of Peru, of which 1,009 were assigned to 318 Barcode Index Numbers (BINs) in BOLD. A single montane cloud forest site in La Mar, Ayacucho, yielded 232 BINs, while the remaining localities, mostly high-Andean, yielded 87. More than half of the BINs were represented by a single specimen, showing that the diversity of Microgastrinae in Peru is still largely underestimated.

13:50  **SHOWDOWN:** Nomadinae (Apidae)

Presenter: Tatiana Bush

Tatiana Bush (WSU/Pullman/United States); Katherine Odanaka (Cornell/Ithaca/United States)

Subfamily (Nomadiane/Apidae)

14:05 Antennal Sensilla Morphology in Chalcididae (Hymenoptera: Chalcidoidea): Diagnostic Value and Phylogenetic Implications (COMPETITION)

Presenter: Gwenivere Martin

Gwenivere Martin (University of California Riverside/Riverside/California); John Heraty (University of California Riverside/Riverside/California)

The superfamily Chalcidoidea are a large diverse group of parasitoid wasps (with over 27,000 species and potentially more than 500,000 undescribed) that provide great economic value in biocontrol. Despite their importance, the evolutionary history of many families remains contentious as new genomic data emerges. The monophyly of the family Chalcididae has been placed in doubt in recent molecular studies, in spite of strong morphological support. Antennal morphology provides a rich but underutilized source of informative morphology for insect systematics, particularly within Chalcidoidea (Hymenoptera). In Chalcididae, antennal sensilla have received limited comparative study despite their potential phylogenetic and diagnostic value. This study aims to characterize antennal sensillum morphology within Chalcididae, with emphasis on the subfamily Cratocentrinae, and to assess its phylogenetic significance relative to selected chalcidoid outgroups. Using scanning electron microscopy, antennal sensilla are described and categorized by type and sex. Comparative analyses across chalcidid genera and outgroup families revealed both conserved and unique character states, including recessed multiporous sensilla, which are potentially diagnostic for Chalcididae. These observations were used to define novel morphological terminology and character states applicable across the family. Derived characters were subsequently mapped onto existing phylogenetic trees using ancestral state reconstruction to evaluate patterns of character evolution. This study establishes a foundation for future morphological and phylogenetic work on Chalcididae.

14:20 Uncovering Flat wasps from Northeast India: Challenges and Opportunities (COMPETITION)

Presenter: Amritha Jaiprekash Kurup

Amritha Jaiprekash Kurup (CMS College/Kottayam/India); Dr. Nisha P Aravind (CMS College/Kottayam/India); Dr. Ankita Gupta (ICAR-NBAIR/Bangalore/India)

Flat wasps are parasitic wasps having excellent biocontrol potential belonging to superfamily Chrysidoidea and family Bethylidae, parasitizing mostly concealed larvae of lepidoptera and coleoptera. With over 3300 species in the world described in 131 genera, they are classified into 5 extant subfamilies, namely, Bethylinae, Epyrinae, Scleroderminae, Mesitiinae and Pristocerinae. India hosts over 100 species across multiple genera, with limited references to its host biology and distribution in North-east

India despite being the biodiversity hotspots. One of the major and extensive work from India has been done by Dr. Santhosh from southern Western Ghats related with 44 species from Oriental region (unpublished). The current study was carried out as a preliminary attempt to uncover the hidden presence of flat wasps from North-east Indian regions. Systemic sampling was conducted at various sites resulting in capture of limited number of specimens using the standard entomological methods like pan traps, malaise traps, handpicking and sweeping. Analyzing the low capture rate, some of the main issues faced was found to be the rugged terrains, unpredictable climatic conditions, accessibility and efficacy of the already existing collection methods and protocols. With scant research comprising of either in region specific aspects or species, with shortfall of updated taxonomic keys, lack of species mapping across sampled regions, limited knowledge on their adaptations, behaviour and evolution, a comprehensive analysis of flat wasps seems a timely investigation idea addressing currently changing landscapes, agricultural practices and climate crisis.

14:35 Revision of New World *Dyscritobaeus* Perkins, 1910 (Hymenoptera: Scelionidae). (COMPETITION)

Presenter: Jamie Beach

Jamie Beach (University of Florida); Francesco Tortorici (University of Turin); Elijah Talamas (Florida Department of Agriculture and Consumer Services)

Dyscritobaeus Perkins (Scelionidae) in the western hemisphere is being revised with a key to species, including newly described species that expand the known distribution of the genus. The generic concept of *Dyscritobaeus* is presently problematic and will be evaluated with a combination of morphological and molecular data. Simultaneously, the tribal concept of Dyscritobaeini will be critically evaluated. The host of *Dyscritobaeus* is unknown, and efforts to identify the host in Florida will be discussed.

14:50 Host Identity, Ant Attendance, and Patterns of Host-Parasitoid Associations on Mo'orea, French Polynesia. (COMPETITION)

Presenter: Willow Humphrey

Willow Humphrey (UC Berkeley/Berkeley/USA)

Parasitoid wasps are important regulators of arthropod populations, yet their diversity, host associations, and ecological drivers remain poorly documented on tropical islands. I conducted a host-associated rearing study across multiple habitats on Mo'orea, French Polynesia, to characterize parasitoid emergence across host insect groups and identify the dominant parasitoid families. I also quantified ant attendance to examine its association with parasitoid emergence. Parasitism intensity varied amongst host insects, with Homalodisca vitripennis exhibiting the highest emergence rates. Ant attendance was negatively associated with parasitoid emergence, suggesting a potential role for ant-host interactions in shaping parasitism outcomes. The emerging parasitoids were primarily identified as members of Encyrtidae, Aphelinidae, and Mymaridae. These findings provide a baseline for documenting host-parasitoid associations on Mo'orea and

highlight variation among host groups and a potential relationship between ant attendance and parasitoid emergence.

15:05 How Many Species Are We Missing? Large-Scale Integrative Taxonomy Reveals Unexpected Diversity in *Telenomus* (Scelionidae). (COMPETITION)

Presenter: Anna Hauprich

Anna Hauprich (University of Hohenheim/Stuttgart/Germany, State Museum of Natural History/Stuttgart/Germany); Cristina Lupaşcu-Vasiliţa (State Museum of Natural History/Stuttgart/Germany, University of Hohenheim, KomBioTa/Stuttgart/Germany); Lars Krogmann (State Museum of Natural History/Stuttgart/Germany, University of Hohenheim, KomBioTa/Stuttgart/Germany)

Despite being one of the best studied regions in terms of insect diversity, Germany still contains undocumented biodiversity, particularly among groups with high species diversity, such as parasitoid wasps. Many of these organisms belong to the so-called "dark taxa" which are often small in body size and poorly studied by taxonomists.
The egg parasitoid genus *Telenomus* (Scelionidae) is one such group. With over 570 described species worldwide, *Telenomus* accounts for more than two thirds of all scelionid specimens in our Malaise trap material. However, only 17 species are currently recorded from Germany, and identification remains challenging due to conserved morphology and limited identification tools.
To estimate *Telenomus* diversity in Germany and assess Large-Scale Integrative Taxonomy (LIT) for parasitoid wasps, over 1,400 COI barcodes, generated within the German Barcode of Life projects, were analysed. Six delimitation methods yielded 85-127 mOTUs, which were combined into 101 consensus clusters and visualized as haplotype networks to guide morphological validation.
So far, morphology supported 44 consensus clusters (44%), with nine additional clusters considered preliminarily valid. Twelve clusters showed indications of oversplitting, while nine genetically distinct clusters could not yet be differentiated morphologically. The targeted examination also facilitated the discovery of rare morphotypes. Only six consensus clusters could be linked to existing species-level barcode records in BOLD.
These results suggest that *Telenomus* diversity in Germany is underestimated. By substantially reducing the morphological workload, LIT provides a scalable approach for documenting hidden diversity in dark taxa.

15:20 Small but mighty: Revealing the morphology and development of parasitoid wasps using Synchrotron X-Ray Imaging. (COMPETITION)

Presenter: Pauline Pfeiffer

Pauline PFEIFFER; Rebecca SPIECKER; Thomas VAN DE KAMP; Tilo BAUMBACH

Parasitoid wasps make up to 10-20% of all insect species on earth. Within them, Chalcidoidea is one of the most speciose superfamilies with estimated 500,000 predominantly parasitoid species. They parasitize a variety of host stages and insect

orders. Since they kill their host at the end of their development, they fulfil a key role as antagonists in natural and managed ecosystems and are therefore of great ecological and economic value as biological pest control. The evolution of the parasitoid lifestyle led to a great diversification, a wide range of life history strategies and miniaturization. Due to their small size and high diversity, there is still a lot of research to be carried out. One of the most interesting and known chalcid wasps is *Nasonia vitripennis* WALKER (Pteromalidae) due its scientific use as a model organism to study sex determination. Another species we studied is the chalcid wasp, *Trichogramma spp.* (Trichogrammatidae), worldwide the most commonly used biological control agent. To study their morphology and development, we used synchrotron-micro-computed tomography (SR-µ-CT) as well as in-vivo radiography. These non-invasive imaging techniques allowed high-throughput image acquisition of the external and internal morphology in a high resolution and a subsequent detailed virtual reconstruction as well as the observation of living organisms in a concealed environment. In detail we created a complete 3D -atlas of *N. vitripennis* to be available open-access to other scientists, and visualized the complete process of a *Trichogramma* wasp emerging out of their host egg using dose-efficient in-vivo imaging. In addition, we analyzed the sexual dimorphism of the cerebral structure in several *Nasonia* species to investigate morphological integration, relative investment and total size differences.

15:45 Invisible gems: Phylogenomics of Tetrastichinae jewel wasps (Hymenoptera: Eulophidae) reveals cryptic taxa and rampant polyphyly

Presenter: Emma Kärrnäs @ekarrnas.bsky.social

Emma Kärrnäs (Lund University/Lund/Sweden); Christer Hansson (Lund University/Lund/Sweden; The Natural History Museum/London/UK); Etka Yapar (Lund University/Lund/Sweden); Jadranka Rota (Lund University/Lund/Sweden); Niklas Wahlberg (Lund University/Lund/Sweden)

Parasitising over 100 families belonging to 10 insect orders, the ubiquitous jewel wasps in the subfamily Tetrastichinae (Chalcidoidea: Eulophidae) are vital to terrestrial ecosystems worldwide as key insect population regulators. Yet this important group, with nearly 2500 described species, is one of the most taxonomically neglected. Here, we present the most detailed phylogenetic hypothesis for the subfamily to date, sampling a third of the 115 currently described genera. By analysing three different datasets using both concatenated (IQ-TREE) and multispecies coalescent approaches (wASTRAL)- 3033 Benchmarking Universal Single Copy Orthologs (BUSCOs) for 163 taxa, 1820 Ultraconserved Elements (UCEs) for 219 taxa and 12 mitochondrial genes for 177 taxa - we reveal rampant para- and polyphyly at the genus level within Tetrastichinae. Our results also reveal the presence of many undescribed and cryptic species. Overall, we provide a robust phylogenetic hypothesis for the subfamily, highlighting our poor knowledge of the group and calling for a major taxonomic revision of Tetrastichinae at both the generic and species levels. We also present an alternative approach to conducting phylogenomic studies of minute Hymenoptera, using whole-genome shotgun sequencing instead of relying on a hybrid-target enrichment approach, demonstrating its efficiency for samples up to 60 years old at the time of extraction. As a product of our

bioinformatic workflow, we also provide 164 DNA barcodes and 164 draft genomes of varying completeness, laying the foundation for future genomic, evolutionary and biodiversity studies of Tetrastichinae.

16:00 New species of Nearctic *Glyphomerus* Forster and the first records of the genus attacking woodbeauty galls induced by *Diastrophus* Hartig

Presenter: Charles Davis

Charles Davis (Centre for Biodiversity Genomics/Guelph/Canada, Pennsylvania State University/State College/USA); Ahmad Dawood Aslam (Pennsylvania State University, State College/USA); Louis Nastasi (University of Nebraska/Lincoln/USA); Cecil Smith (University of Iowa/Iowa City/USA); Heather Hines (Pennsylvania State University/State College/USA); Andrew Deans (Pennsylvania State University/State College/USA)

Insect induced plant galls are miniature ecosystems that house the gall inducer as well as numerous species of parasitoids, hyperparasitoids, and inquilines. In recent years there has been a growing body of work dedicated to elucidating the biology of gall wasps (Cynipidae) associated with herbaceous host plants. Across their oak associated counterparts, there are numerous undescribed species of parasitoids exhibiting strong selection across gall wasps and their respective host plants. In herbaceous gall systems, the diversity of parasitoids within these is not understood, and it is unknown if these same evolutionary relationships observed in oak galls are maintained. In our efforts to revise the gall wasp genus *Diastrophus*, we discovered not only a new host plant genus in woodbeauties *Drymocallis* Fourreau ex Rydberg but also a new association of *Glyphomerus* Forster parasitoids across these galls. *Glyphomerus* are typically associated with rose galls of *Diplolepis* Geoffroy (Diplolepididae) and genetic data only supports the type species inclusion within the genus. This lineage is peculiar as developmental studies have shown *Glyphomerus* may be able to continue gall development even after their host's demise. Here we provide evidence for two new *Glyphomerus* species using an integrative species concept incorporating molecular and morphological data. We discuss the potential niche *Glyphomerus* may inhibit within *Diastrophus* galls and speculate what factors resulted in their species diversity.

16:15 Lost in the Dark: Why we still don't understand parasitoid decline and extinction

Presenter: Jessica Awad @parasitoidrex.bsky.social

Jessica Awad (Naturalis Biodiversity Center/Leiden/Netherlands); Cristina Vasilita (Karlsruhe Institute of Technology/Karlsruhe/Germany); Amelie Höcherl (State Museum of Natural History Stuttgart/Stuttgart/Germany); Lars Krogmann (State Museum of Natural History Stuttgart/Stuttgart/Germany)

Insect decline is a matter of serious concern to global biodiversity, yet most research is focused on a few well-studied groups. A significant portion of flying insects consists of the understudied parasitoid wasps, which are extremely high in species diversity and provide crucial ecosystem services, most notably regulation of host insect populations.

For reasons that include small body size and scant diagnostic resources, these wasps are difficult to study at even the most basic level and are often referred to as “dark taxa”. In addition to the taxonomic impediment, the lack of accurate and comprehensive knowledge of host-parasitoid associations, the ecological impediment, is a critical barrier to monitoring parasitoid decline or extinction. In Germany, where flying insect biomass has decreased by more than 75% since the 1980s, the apparent disappearance of the giant platygastrid wasp, *Isocybus grandis*, exemplifies the manifold challenges of parasitoid conservation. The complexities of assessing the status of this species are aired as a case study. The taxonomic impediment, the ecological impediment, and their interrelationships are discussed in the context of lost species and dark extinctions.

16:30 The First Dated Molecular Phylogeny of Ceraphronoidea

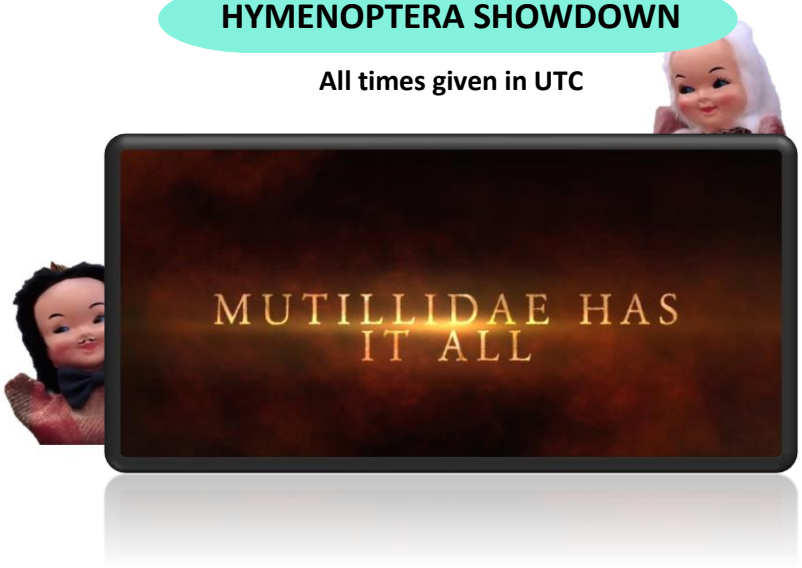
Presenter: Tobias Flores-Salden

Tobias Salden (Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn/Bonn/Germany); István Mikó (University of New Hampshire/Durham/United States of America); Jonathan Vogel (Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn/Bonn/Germany); Seán G. Brady (National Museum of Natural History, Smithsonian Institution/Washington DC/USA); Matthew L. Buffington (USDA-ARS Systematic Entomology Laboratory/Washington DC/USA); Bonnie B. Blaimer (Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Center for Integrative Biodiversity Discovery/Berlin/Germany); Ralph S. Peters (Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn/Bonn/Germany)

We present the first phylogenomic analysis of the superfamily Ceraphronoidea based on ultraconserved elements (UCEs), including 53 ingroup taxa and eight outgroup taxa representing 16 ceraphronoid genera that together encompass approximately 97% of the currently described species diversity. Three datasets with 50%, 60%, and 70% taxon occupancy, retaining 1,098, 829, and 456 UCE loci, respectively, were analysed. Maximum-likelihood and multispecies coalescent analyses recovered highly congruent topologies, providing the first robust phylogenomic framework for Ceraphronoidea. Our analyses strongly support the monophyly of Ceraphronoidea, the families Ceraphronidae and Megaspilidae, and the subfamilies Lagynodinae and Megaspilinae. Within Ceraphronidae, *Trassedia* and *Masner* form the sister group of the remaining taxa; *Pteroceraphron* represents the earliest-diverging lineage within the remaining Ceraphronidae. Species-rich genera, including *Aphanogmus, Ceraphron,* and *Conostigmus* were not recovered as monophyletic, indicating the need for substantial generic revision. We further present the first divergence-time estimates for Ceraphronoidea using three fossils as calibration points, including the oldest known ceraphronoid fossil. Results indicate a Middle Jurassic origin of Ceraphronoidea (~171 Ma). Both major family-level divergences occurred during the Early Cretaceous, including the split of Megaspilidae into Megaspilinae and Lagynodinae (~137 Ma) and the divergence of Ceraphronidae into *Trassedia + Masner* and *Pteroceraphron* + remaining Ceraphronidae (~134 Ma). Together, our results provide a basis for future systematic, taxonomic, and evolutionary research on Ceraphronoidea.

HYMENOPTERA SHOWDOWN

All times given in UTC



The showdown is a light-hearted opportunity for all ISH members to argue why their taxon of choice is the best (or at least the best loved…) in three minutes - backing up that assertion with a mix of fun, cool and (possibly un) scientific facts.

Billy and Cassandra are making their 2nd appearance to try and claim the crown, while last year's winners, the Mutilidae will not be defending the title. Come and see how these other groups have risen to the challenge:

SESSION 1, 18:05 UTC:

Welcome to the dark side of Cynipoidea. Behold, the fiendish Figitidae! represented by Charles Davis

SESSION 2, 00:55 UTC:

Platygastroidea, represented by Billy and Cassandra (AKA Elijah Talamas, Jessica Awad and Jamie Beach)

SESSION 3, 07:15 UTC:

When I was a pteromalid, represented by Natalie Dale-Skey

SESSION 4, 13:50 UTC:

Nomadinae (Apidae), represented by Tatiana Bush

Who will be crowned this year's winner? YOU DECIDE! All Showdown presentations will be available for you to vote **Here** throughout Hymathon

ART COMPETITION



Run by Ana-Maria Chiosa

Images entered in the four categories below will be available for voting throughout Hymathon:

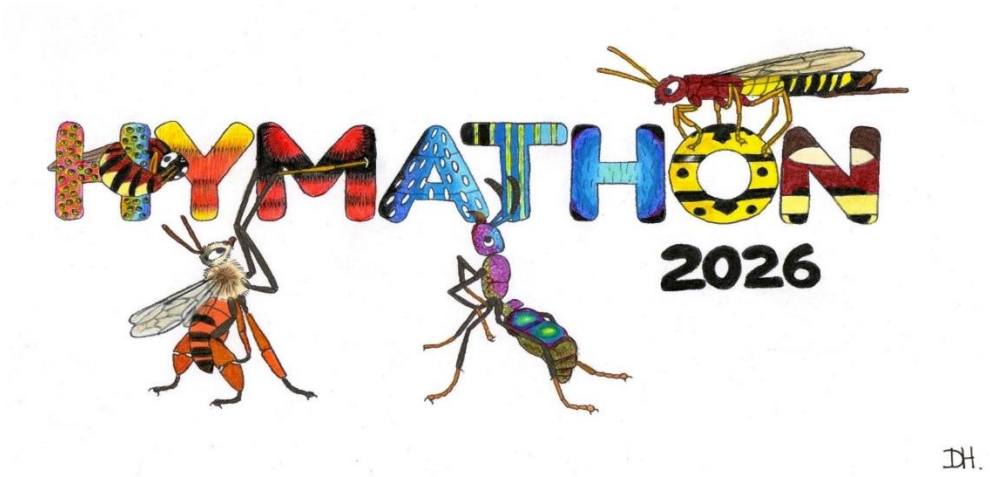
Vote here

Photography – Specimen: Specimen images of Hymenoptera.

Photography – Live Hymenoptera: Live Hymenoptera images photographed in the field or in the indoor studio.

Photography – Hymenopterists in action: Field work pictures, humorous or intriguing pictures of hymenopterists at work.

Illustration – Fun & Artsy Hymenoptera/Hymenopterists: Creative and imaginative artworks that showcase Hymenoptera or Hymenopterists in a playful, artistic, or unconventional manner. These can be abstract interpretations, cartoons, or any other artistic renditions that bring out the fun and whimsical side of Hymenoptera and their researchers.



HYMATHON AFTER HOURS



Join us for Hymathon social events organised and run by ISH Student Representative Thomas Hall

ISH BINGO (Introduced in Session 1 and to be played throughout Hymathon)
Picture this – you are sitting down at a conference, eagerly awaiting for someone's talk that you so graciously turned down your lab's mid-day karaoke outing for. And there it is again… Technical difficulties. You think to yourself: "Wow, this happens so often that if this were on a BINGO card, I would have won three times over." Well guess what: here is your chance to do just that!

Session 1: ISH Trivia
Hey ISHers! Do you think you're the smartest hymenopterist in the breakout room? Prove it in this edition of trivia! (A separate device [e.g. phone] will be required to play)

Session 2: Gartic Phone
In this game of broken telephone, take turns illustrating prompts to the best of your ability while trying to best discern the chicken-scratch drawings of your fellow ISHers! This game is open to ISH members with a wide range of illustrative "talent".

Session 3: Powerpoint Roulette
Oh no! You are about to present your slides at Hymathon but you open the wrong folder and out comes powerpoint slides you've never seen before! Take turns presenting your slides while pretending that absolutely nothing is wrong…

HAMULI LIVE!



ISH's new podcast series "Hamuli LIVE!" has come to Hymathon! During Hamuli Live, we interview a senior member of the Hymenoptera community and explore their research, their career progression, favourite collection methods, best stories from the field and more. We want to use this as an opportunity to communicate skills, techniques and narratives that traditionally are not fit to be published in academic settings. The interviews are held live, and audience members will have a chance to ask questions live or submit them ahead of time. Afterwards, the interviews will be transcribed and submitted for publication as a part of the Hamuli newsletter, and a recording of the interview will be made available on the ISH website.

Submit your questions here

CODE OF CONDUCT

The International Society of Hymenopterists (ISH) aims to encourage scientific research and to promote the diffusion of scientific knowledge concerning Hymenoptera.

ISH strives to be inclusive of the largest number of contributors, representing diverse backgrounds. We are committed to providing a friendly, safe, and welcoming environment that allows all members to participate in the society to the fullest extent, regardless of gender, sexual orientation, ability, ethnicity, socioeconomic status, and religion.

The society expects all participants at ISH functions to abide by our Code of Conduct policy (see link below), and in particular to exercise consideration and respect and refrain from demeaning, discriminatory, or harassing behaviour and speech

ISH Constitution and Code of Conduct – International Society of Hymenopterists

International Society of Hymenopterists

Journal of Hymenoptera Research