Evolution of host specialization and taxonomy of aculeate Hymenoptera parasites (Strepsiptera: Xenidae, Stylopidae)

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Twisted-winged parasites (Strepsiptera) are an obligate endoparasitic insect order with a cosmopolitan distribution. They have evolved many adaptations to the parasitic lifestyle in morphology, behaviour, physiology, and reproduction, and many complex adaptive traits that have no parallel in other organisms. In the basal groups of nocturnal Strepsiptera, the hosts are often unknown. In contrast, for the derived families that parasitise on aculeate Hymenoptera (Xenidae and Stylopidae), the hosts are known for almost all species, as they are often collected with them and the presence of endoparasitic females or male pupae can be easily detected. Both families are highly diverse and comprise almost half of all described species of Strepsiptera. For these reasons, they are an excellent group for studying the specialisation of parasites on hosts. Using molecular analyses, we created the first dated phylogenetic study of the family Xenidae. The original hosts of Xenidae were most likely social wasps, and the subsequent host switch from social to solitary wasps was secondary and probably occurred only once. A parallel host switch from solitary wasps to digger wasps (Sphecidae) occurred independently in the New and Old World. The constant rate in net diversification can be explained by the flexibility of this parasitic group, represented by their ability to colonise new host lineages combined with passive long-range dispersal by hosts. To analyse strepsipteran cryptic species diversity, we used three quantitative methods of species delimitation. Based on these results, we provide a taxonomic revision of Xenidae worldwide using morphological characters of female cephalothorax and male cephalotheca. We delimited 13 genera including 3 newly established. In addition, we are preparing a description of 3 new genera of Stylopidae that parasitise on Neopasiphaeinae bees, for which no Strepsiptera species have been previously described.

Reproductive isolation within a population of *Nasonia vitripennis* (Walker) (Hymenoptera: Chalcidoidea: Pteromalidae) caused by single and double infection with *Wolbachia* Hertig

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Wolbachia is a common endosymbiont in many arthropod species. It has multiple implications for the reproduction of its host, including cytoplasmic incompatibility (CI). CI a special form of postzygotic reproductive isolation marked by the absence of offspring from crossings of males infected with the endosymbiont and uninfected females. The genus *Nasonia* (Chalcidoidea Pteromalidae) currently comprises four described species of parasitoids of fly pupae in bird nest or carrion. CI caused *Wolbachia* represents one of the main reproductive barriers between some of the species. Here we report on the infection of *Wolbachia* in a local population of one *Nasonia* species, *N. vitripennis*, in the Park of Hohenheim University, Stuttgart, Germany. In 2012 and 2022, most wasps collected were infected with endosymbionts from the *Wolbachia* supergroup A. In addition, some wasps were also infected by a second strain from *Wolbachia* supergroup B. This caused unidirectional reproductive isolation, i.e., the absence of female offspring in crossings of *N. vitripennis* females infected only by the supergroup A *Wolbachia* strain and males infected by both *Wolbachia* strains. An infection with the second strain was found in 25% of the wasps tested in 2012, and 50% of wasps tested in 2022, respectively. This points to a spread of the second strain of *Wolbachia* in the studied population of *N. vitripennis*. Together these data provide additional evidence for the hypothesis that an infection with *Wolbachia* and associated CI can be the first reproductive barrier to arise in a population and therefore might be a starting point for speciation.

The encyrtids (Hymenoptera: Chalcidoidea: Encyrtidae) obtained from *Eriopeltis festucae* (Fonscolombe) (Homoptera: Coccidae) in Romania

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Encyrtidae were reared from females of *Eriopeltis festucae* (Boyer de Fonscolombe, 1834) (Coccidae) collected on *Agropyron repens* (L.) (Magnoliophyta, Liliopsida, Poales, Poaceae) from the localities Uzlina (the Delta of Danube) in Tulcea county, and Scobâlţeni and Breazu in Iaşi county. The following encyrtid species were collected from Uzlina: *Trichomasthus albimanus* (Thomson) (707 individuals), *Trichomasthus cyaneus* (Dalman) (223 individuals), *Trichomasthus cyanifrons* (Dalman) (26 individuals), *Metaphycus zebratus* (Mercet) (20 individuals), *Cerapterocerus pilicornis* (Thomson) (53 individuals), *Cheiloneurus paralia* (Walker) (50 individuals), *Discodes encopiformis* (Walker) (1102 individuals), *Discodes tamaricicola* (Sugonjaev & Babaev) (2 individuals) and *Mayrencyrtus imandes* (Walker) (34 individuals); from Scobâlţeni: *Trichomasthus albimanus* (39 individuals), *Baeocharis pascuorum* (Mayr) (12 individuals), *Trichomasthus cyaneus* (4 individuals) and *Metaphycus melanostomatus* (Timberlake) (1 individual); from Breazu: *Trichomasthus albimanus* (53 individuals), *Trichomasthus cyaneus* (2 individuals), *Trichomasthus cyanifrons* (1 individual), *Baeocharis pascuorum* (2 individuals) and *Metaphycus zebratus* (1 individual). The species *T. albimanus*, *T. cyaneus*, *T. cyanifrons, B. pascuorum*, *M. zebratus*, *M. melanostomatus, D. encopiformis*, *D. tamaricicola* and *M. imandes* are primary parasitoids, whereas *C. pilicornis* and *Ch. paralia* are secondary parasitoids. At Uzlina the percentage of parasitized females ranged from 33.1 to 45.5%, at Scobâlţeni 9.3% and at Breazu 16.2%. At Uzlina the important species were *D. encopiformis*, *T. albimanus* and *T. cyaneus*, whereas at Scobâlţeni and Breazu it was *T. albimanus. Discodes encopiformis* laid between 1 and 35 eggs in a female of *E. festucae,* with the average number 13.7 eggs; *T. albimanus* laid between 1 and 13 eggs, with the average number 5.2 eggs; *T. cyaneus* laid between 1 and 14 eggs, with the average number 4.8 eggs. Concerning emergence from the host, *T. albimanus* emerges in July, with a maximum emergence in the first half of this month, *D. encopiformis* starts emerging in the second half of July, with maximum emergence late in this month.

The parasitoid and inquilines complex (Hymenoptera: Ichneumonoidea, Chalcidoidea, Cynipoidea) of the cynipid gall wasp *Andricus curvator* (Hartig), sexual generation, (Hymenoptera: Cynipidae) in Romania

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The genus *Andricus* Harting, 1840 is represented in Romania by 56 species, including several recently recorded ones (I. Șchiopu, in press). For 27 of these, there are only disparate and partial data on the structure of the parasitoid complexes while only for 3 species there are publications on their parasitoid complexes. We focused on the structure and partly on the ecological functioning of the parasitoid complex of the gall wasp *Andricus curvator* (Hartig, 1840) ♀♂ in Romania. This species is a heterogonous cynipid wasp, the sexual generation inducing galls on very young branches and leaves of several oak species. The studied material consisted of 7 204 leaf galls collected in five forests in southern Dobrogea (South-Eastern Romania) from 1992 to 1997 and in six forests in the Moldova region (Eastern Romania) from 2004 to 2009. The material was reared and studied under laboratory conditions. So far only two inquiline and 6 parasitoid species of the complex were mentioned in Romania, without any other ecological or biological parameters. The present work adds 13 more parasitoid species that complete and configure the trophic network of this parasitoid complex in Romania. We found the following primary or secondary parasitoids: *Torymus auratus* (Müller, 1764), *T. angelicae* Walker, 1836, *Torymus cerri* (Mayr, 1874), *T. notatus* (Walker, 1833), *Ormyrus pomaceus* (Geoffroy, 1785), *Mesopolobus fasciiventris* Westwood, 1833, *M. fuscipes* (Walker, 1834), *M. tibialis* (Westwood, 1833), *Aulogymnus gallarum* (Linnaeus, 1761), *Aulogymnus* sp., *Ichneumonidae* species, *Braconidae* species. Out of these the association with *T. cerri* and *T. angelicae* are new for this parasitoid complex. Concerning the relative importance of species in this community, there is only one eudominant species, *Aulogymnus arsames* (Walker, 1838) in Dobrogea, while in Moldova it is *A. gallarum* followed by 5 dominant species: *O. pomaceus*, *Torymus flavipes* (Walker, 1833), *T. notatus*, *Eurytoma brunniventris* Ratzeburg, 1852 and *Mesopolobus fasciiventris*. All other species are subdominant and subrecedent: *T. auratus*, *T. angelicae*, *T. geranii* (Walker, 1833), *T. cerri*, *Mesopolobus fuscipes*, *M. tibialis* and *Mesopolobus sp*. This species complex is structured following a pattern like in other European countries, differing in the presence of two species of *Torymus* not found elsewhere (*T. angelicae* and *T. cerri*) and in the absence of some other species.

Egg parasitoids (Hymenoptera: Mymaridae and Trichogrammatidae) of rice leafhoppers and planthoppers in East Asia: reassessment of their diversity, identification, and host associations

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Surveys for fairyfly and trichogrammatid egg parasitoids (Hymenoptera: Mymaridae and Trichogrammatidae, respectively) of rice leafhoppers and planthoppers (Hemiptera: Cicadellidae and Delphacidae, respectively) known from Japan and Taiwan were conducted during 2016-2019 in mostly organic paddy fields. Using a variety of methods, egg parasitoids were collected, identified taxonomically, keyed, and illustrated. Their host associations are determined by rearings using sentinel eggs of mainly four key pest species of rice. The previously published records of such egg parasitoids in Japan and Taiwan were critically analyzed in the unfortunate absence of almost any voucher specimens from the prior studies. Four species of Mymaridae are shown to be the predominant egg parasitoids of one leafhopper and three planthopper major pests of rice in East Asia: *Anagrus* (*Anagrus*) *incarnatus* Haliday of the green rice leafhopper *Nephotettix cincticeps* (Uhler) and the delphacids *Laodelphax striatella* (Fallén) (small brown planthopper), *Nilaparvata lugens* (Stål) (brown planthopper), and *Sogatella furcifera* (Horváth) (whitebacked planthopper), as well as *Gonatocerus cincticipitis* Sahad (in Japan and Republic of Korea only), *G. saipanensis* (Doutt), and *Mymar taprobanicum* Ward of *N. cincticeps*. Among the Trichogrammatidae, *Pseudoligosita nephotetticum* (Mani) is shown to be the most common and widespread egg parasitoid of the two leafhopper and three planthopper pests of rice in Japan and Taiwan: the zig-zag leafhopper *Maiestas dorsalis* (Motschulsky), *Nephotettix cincticeps*, and the delphacids *Laodelphax striatella*, *Nilaparvata lugens*, and *Sogatella furcifera*; *Paracentrobia* (*Brachistella*) *andoi* (Ishii) was recorded as a common egg parasitoid of *N. cincticeps* in paddy fields in Japan. It was determined that many of the previously recorded species of egg parasitoids of rice leafhoppers and planthoppers in Asia were misidentified, and when possible, these misidentifications were corrected. Additions to the knowledge of biodiversity of other Mymaridae and Trichogrammatidae in paddy fields in Japan and Taiwan were also made and published.

Hitching a ride: a note on phoretic parasitoids (Hymenoptera: Chalcidoidea: Podagrioninae) of praying mantises (Mantodea)

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Chalcidoidea is an extremely diverse superfamily of Hymenoptera with majority of taxa being parasitoids, targeting a variety of invertebrates, mostly insects. One of the taxa, chosen by specialized members of Chalcidoidea as hosts, are praying mantises. The females of Mantodea lay the eggs in a specific structure, an ootheca, which encapsulates the eggs in hardy, often foamy protective layer, aiding in thermoregulation and defense against predators and parasitoids. Within Chalcidoidea, species of a few families are known to infect eggs in mantis oothecae. In Torymidae, Podagrioninae specialized almost exclusively on Mantodea, their ovipositor length being adapted to reach eggs in egg cases. On the contrary, two species of *Podagrion* and a few undescribed genera (from different regions – Africa, Australia and Southeast Asia) have the females search for mantises instead of clutches, attaching to the host and awaiting oviposition. Initially, phoretic podagrionines were found only on adult females of Mantodea. However, recently they were observed on adult males and juveniles as well. In primary rainforest of Cameroon, one immature male specimen of *Caudatoscelis caudata* (Mantodea) was observed to have a phoretic Podagrioninae sitting on its metathorax. The parasitoid female was found to belong to an undescribed genus, with one of the last tergites formed into spatulate structure, probably used for holding or attaching to host eggs during oviposition. Advantages of a phoretic behavior in this host-parasitoid pair are uncertain. The typical ootheca of Amorphoscelinae, to which *C. caudata* belongs, does not have a foamy layer and has relatively few (<10) egg chambers each having flat and thin outer walls. These chambers are probably accessible by a shorter ovipositor, seemingly eliminating the need for phoresy. On the other hand, as observed by us, *C. caudata* was found forming groups of individuals on the same tree trunks. As both sexes of *C. caudata* are macropterous, the parasitoids might use phoretic behavior to follow their host species in new areas or to other populations of the host. Moreover, the relatively small number of eggs observed in the ootheca puts additional pressure on the parasitoids to find hosts effectively, since there are very few eggs available to infect.

Laboratory biology and ecology of *Trichopria drosophilae* (Perkins) (Hymenoptera: Diapriidae) and its rival *Pachycrepoides vindemiae* (Rondani) (Hymenoptera: Pteromalidae), parasitoids of *Drosophila* flies

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The life history and immature stages of development of a diapriid wasp *Trichopria drosophilae* (Hymenoptera: Diapriidae), a biocontrol agent of drosophilid flies (Diptera: Drosophilidae), including the invasive *Drosophila suzukii*, were investigated. *T. drosophilae* is a solitary endoparasitoid that develops from egg to adult in 22-26 days under laboratory conditions at room temperature. The egg of *T. drosophilae* is broad ovate, with short petiole when fresh laid, but is getting more elongate later. There are three larval instars in *T. drosophilae*. The freshly hatched first instar has a narrow caudal part with bifurcated indentate abdominal appendage, the enlarged thoracic segments and the head with sclerotized sharp mandibles. The second instar is poorly sclerotized with peculiar everted (exodont) mandibles. The third instar is grub-like, with three pairs of thoracic spiracles and the stylet-shaped mandibles. The ratio of parasitoids reared in experiments on competitive interrelationships of *T. drosophilae* with a rival ectoparasitoid *Pachycrepoides vindemiae* (Hymenoptera: Pteromalidae) was biased by the ectoparasitoids, regardless of the priority of oviposition.

Traditional almond orchards in contrasting landscapes maintain extremely diverse parasitoid communities threatened by abandonment

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Hymenopteran parasitoids are an extremely diverse insect group, crucial for ecosystem functioning and pest control. Due to their high trophic level and high degree of specialization, parasitoids are particularly sensitive to perturbation and extinction events, being good indicators of arthropod diversity. While several studies have shown that parasitoids can be affected by management practices and landscape composition and configuration, few have evaluated the consequences of agricultural abandonment, a process that threatens the high biodiversity associated with European High Nature Value Farmland. In this context, we aimed to determine the effects of traditional almond orchard abandonment on the hymenopteran parasitoid community (at genus level), the role of the percentage of semi-natural habitats (SNH) in the landscape in mediating these effects, and the effect of the seasonality. We carried out four samplings between almond blooming and harvest (February – September 2019) in 12 orchards (6 abandoned) located in traditional landscapes with varying percentages of SNH (simple vs. complex landscapes). Abandoned and traditional almond orchards harbored different parasitoid communities but similar diversity measures, except in May, when traditional orchards clearly favored parasitoids. The landscape context conditioned the role of the farming system, abandoned orchards acting as a refuge in late summer only in simple landscapes, while complex landscapes favored parasitoid abundance irrespectively of the farming system. The strong seasonality drove a high turnover rate and conditioned community responses to our variables. Our results highlight the importance of traditional almond orchards and complex landscapes for parasitoid conservation and the relevance of working at high taxonomic resolutions to disentangle parasitoid responses to agricultural abandonment and landscape complexity.

Investigation of cryptic taxa within the *Cotesia tibialis* complex (Hymenoptera: Braconidae: Microgastrinae), a geometric morphometrics approach

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The phylogenetic lineage of European species from the genus *Cotesia* (Braconidae) that spin cocoon masses was investigated. Common cocoons are structures that are synchronously spun by parasitoid larvae that emerge from caterpillars. Cocoons are usually in the form of egg-shaped structures 1–2 cm long and about 1 cm wide. This study relies on a previously performed phylogenetic analysis based on the COI barcoding gene applied to the *C. tibialis* complex. As phylogenetically and behaviourally close relatives, *C. ofella* and *C. vanessae* were included in geometric morphometrics analysis of forewings as outgroups. More than 1000 forewings were analysed. The results of the analysis of the shape and size of the forewings displayed five entities. First, *C. vanessae* discriminated far from the rest of the four groups in the morphospace as defined by CV1 × CV2 axes. Then, *C. ofella* separated from the rest of the individuals. One putative new taxon appeared isolated between *C. ofella* and the *C. tibialis* complex, splitting them into one large group and a smaller one. Specimens belonging to the smaller group emerge from very white cocoons. Distinguishing two new morphotypes in this study according to the wing morphology confirms previous indication by molecular analysis, but the taxonomic problem of *C. tibialis* remains unresolved. The diversity of wing shapes is still great within the larger group. A closer look at the molecular analysis that divided this group into two phylogenetic lineages opens up possibilities for further research.

Monophyly of the subgenera of the genus *Netelia* Gray (Hymenoptera: Ichneumonidae: Tryphoninae)

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The genus *Netelia* is distributed all over the world, and 332 species in 12 subgenera have been recognized so far. As for the taxonomy of the subgenera, it has been suggested that most would not be monophyletic, as many of the defining traits would be likely to evolve in parallel. However, the subgenera *Apatagium* and *Monomacrodon* are characterized by the shape of hind tarsal claws and are considered to be a monophyletic group. Although the morphology of male genitalia is useful for identifying species in this genus, they have rarely been used to define subgenera. To evaluate the monophyly of the subgenera, phylogenetic analyses were conducted using 53 characters, including male genitalia and ovary-egg traits, for a total of 67 species: *Apatagium* (4 species), *Amebachia* (1), *Bessobates* (13), *Parabates* (3), *Netelia* (25), *Prosthodocis* (9), *Paropheltes* (7), *Toxochiloides* (2), *Monomacrodon* (2), *Protonetelia* (1). Furthermore, three species, *Tryphon* sp., *Phytodietus* (*Phytodietus*) sp., and *P*. (*Neuchorus*) sp., were included as outgroup taxa. Unfortunately, the subgenera *Toxochilus* and *Longiterebates* could not be included in the current study. Phylogenetic analyses were performed using the TNT software, employing either equal weighting of characters or implied weighting with varying values of k (5, 10, 15, 20, 25, 30). The results are as follows. *Apatagium* is polyphyletic and two species groups are monophyletic in all analyses. The *obesis* group is nested within *Prosthodocis* in the analyses employing implied weighting. *Amebachia* is a sister group of the *tristrigata* group of *Apatagium* in all analyses. *Bessobates* is monophyletic in all analyses. Its synapomorphies are presence of teeth of digitus, and strongly curved basal apodeme of aedeagus. *Monomacrodon* is monophyletic in all analyses and a sister group of all other species of the genus in the analyses employing implied weighting. *Netelia* is monopyletic in 6 out of 7 analyses or paraphyletic with respect to *Toxochiloides* (1/7). *Parabates* is monophyletic in all analyses. Its synapomorphies are the open areolet and the shape of basal apodeme of aedeagus. *Paropheltes* is monophyletic in the analyses employing implied weighting. *Prosthodocis* is paraphyletic with respect to the *obesis* group of *Apatagium* in the analyses employing implied weighting. Synapomorphies of this monophyletic group are broadened brace and flat clasping surface of paramere. *Protonetelia* is a sister group with all other species of the genus except *Monomacrodon* in the analyses employing implied weighting. *Toxochiloides* is monophyletic in all analyses and sister group of *Netelia* (6/7) or nested within *Netelia* (1/7).

Collection of Hymenoptera in the National Museum Prague

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The entomological collection of the National Museum in Prague, Czech Republic (NMPC) currently contains over 8 million specimens, including primary types of several tens of thousands of taxa. The majority of specimens and types belong to the order Coleoptera (beetles), but nearly all other insect orders are also represented by more or less numerous material, including types. The collection of the Hymenoptera is among the smaller parts of the collection being estimated to around 550,000 specimens. Despite that, it contains numerous primary types which are now being catalogued (so far, only the Formicidae and Braconidae types deposited in NMPC were properly catalogued). An important part of the history of the NMPC's Hymenoptera collection relates to its first curator-specialist, Zdeněk Bouček, whose collection of Chalcidoidea is one of the most important in the world and contains the largest amount of type material (more than 2,000 types). Among the most prominent workers were Oldřich Šustera and Vilém Zavadil, who determined and organized the collections already before World War II, and later they bequeathed their large collections of Hymenoptera, containing mainly material from former Czechoslovakia, to NMPC. Another important collection is that of František Gregor with approximately 70,000 specimens, mainly ichneumonid wasps, including types and historical specimens and together with the collection of Josef Šedivý, it is one of the most important collection of Ichneumonidae in the Czech Republic. Other important collections deposited in NMPC are Vladimír Balthasar's (Palaearctic Chrysididae, Sphecidae and Crabronidae) with approx. 7,500 specimens including type material and Augustin Hoffer's (Palaearctic Encyrtidae) containing approx. 16,000 specimens with more than one hundred types. The last significant acquisition was the collection of Vladimír Kalina, specialist on Eurytomidae and Eupelmidae, obtained in 2022 and containing approx. 35,000 specimens, also with types included. At present, the collection continues to be purposefully enriched and developed by the collecting activity of the present curator, Jan Macek (*1978). The greatest progress in the period of the last twenty years was in the Diapriidae, which, from the starting point of a small regional collection, has reached worldwide extent, and now is one of the largest in Europe. Besides the common material there are also included type series of newly described species from all over the world, but most of the material is from Europe.

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Microgastrinae mishmash: tackling a dark taxon in Germany

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There are substantial parts of the European and German fauna that are still largely unexplored, the so-called “Dark Taxa”. One such dark taxon are Microgastrinae wasps (Hymenoptera: Braconidae), a group of Lepidoptera parasitoids with 3,200+ species described worldwide. The known German fauna thus far consists of 251 species. Based on the host/parasitoid ratios and the actual diversity of 3,700+ Lepidoptera species recorded from Germany, it is very likely that the Microgastrinae diversity in the country is underrepresented. On the other hand, probably more than half of the German diversity of these wasps has been described by many different authors in the last 200 years. Hence, exploring this unknown diversity faces some challenges, such as missing holotypes, minimal historical descriptions and other similar problems that many European taxonomists are familiar with. That is in addition to the more standard challenges of dealing with a dark taxon in the first place, like cryptic species complexes, lack of host data, etc. As part of the German Barcode of Life Project GBOL III: “Dark Taxa” we attempt to tackle these challenges using a reverse and integrative taxonomy approach. We use DNA barcoding of the COI gene for molecularly clustering specimens in a first step and morphological examination of the voucher specimens in a second step. With 5,322 sequenced specimens available to us, we currently count 330 barcoding clusters mainly from southern Germany. Using this integrative taxonomy approach, we were able to report several species in Germany for the first time, uncover thus far unknown Holarctic connections, and find candidates for undescribed species.

Digitalization of type specimens of Hymenoptera deposited in the I. I. Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine (Kyiv, Ukraine)

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The collection of Hymenoptera deposited at I.I.Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine, Kyiv (SIZK), includes these groups of phytophagous, parasitic and predaceous Hymenoptera, collected in Europe, Asia, Africa, South and North America: Formicidae (about 2200 species), Ichneumonidae (1400 species), Braconidae (about 1000 species), Platygastridae (about 850 species), Eulophidae (500 species), Eurytomidae (about 500 species), Diapriidae (200 species), Encyrtidae (about 200 species), Pteromalidae (190 species), Torymidae (160 species), Trichogrammatidae (about 150 species), Cynipoidea (about 150 species), Chrysididae (138 species), Aphelinidae (about 100 species), Mymaridae (50 species), Ormyridae (50 species), Chalcididae (40 species), and Tetracampidae (15 species). The collection of type material (holotypes, paratypes) of Hymenoptera deposited at SIZK includes the groups: Formicoidea (Formicidae – 555 species and subspecies described by V.O. Karavaev and about 200 species described by O.G. Radchenko); Platygastroidea (Platygastridae – 368 species described by S.V. Kononova); Chalcidoidea (Eurytomidae – 221 species, Torymidae – 40 species, Ormyridae – 21 species, and Perilampidae – 2 species, described by M.D. Zerova and L.Ya. Seregina; Eurytomidae – 9 species described by M.D. Zerova and S.I. Klymenko; Eulophidae, Entedoninae – 40 species and Tetracampidae – 1 species, described by A.V. Gumovsky; Encyrtidae – about 40 species described by S.A. Simutnk; Trichogrammatidae – 14 species described by V.N. Fursov; Aphelinidae – 8 species described by O.M. Chervonenko; Ichneumonidae – about 100 species described by V.I. Tolkanitz, O.O. Varga, and A.D. Nuzhna; Braconidae, Microgastrinae – about 80 species described by A.G. Kotenko; and Cynipoidea, Cynipidae – about 60 species described by L.A. Djakonchuk). Current digitalization of type specimens includes digital photos of details of morphology (body, mesosoma, metasoma, antennae, head, face, wings, venation). Currently, the type specimens of 120 species of Eurytomidae and Torymidae, 17 species of Ichneumonidae, and about 250 species of Formicidae have been digitized. The digitalization of the collection of Hymenoptera is in progress and it is planned to include all other groups of Hymenoptera. All the digitized data will be openly available on web-site of Ukrainian Biodiversity Information Network (UkrBIN) and the database of Global Biodiversity Information Facility (GBIF).

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Nematinae sawflies (Hymenoptera: Tenthredinidae) in northern Europe

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Between 2012 and 2021 the Swedish Taxonomy Intiative (STI) and Senckenberg Deutsches Entomologisches Institut (SDEI) funded a collaborative project treating the Nematinae sawflies (Tenthredinidae) with particular focus on the fauna of Sweden. The nematines provide an example of reverse latitudinal gradient in species richness i.e increasing species richness towards higher latitudes. The Fennoscandian fauna includes more than 75% of the Western Palearctic Nematinae species which is currently about 440 of 575 species. The nematines tend to be more or less host plant specific, but less so than previously believed and a large proportion of the species actually feed on several species of plants such as willows. Initially, a new generic classification of the Nematinae based on recent molecular phylogenies was developed, resulting in synonymizations and a reduction of genera from 49 to 34 worldwide. Revisions of most genera of Western Palearctic Nematinae have been published or are currently in preparation. The largest remaining nematine genus *Euura* currently comprises more than 260 Western Palearctic species and a handful of new species are in the process of being described. Importantly, illustrated keys for the identification of adults and larvae have been provided for the revised taxa. An integrative approach combining morphological and molecular data from nuclear genes NaK and POL2 and the mitochondrial barcode COI were necessary to construct phylogenies and solving many of the difficult taxonomic problems in the group. In the course of the project a total of 10 000 Fennoscandian specimens of Nematinae were processed of which a great majority were collected during the project, greatly enhancing the collections at the SDEI and NHRS (Swedish Museum of Natural History) as well as our understanding of the evolution and systematics of the nematine sawflies. Finally, at least 73 species of sawflies, including 50 species of Nematinae were recorded for the first time in Sweden, which may be surprising as sawflies can be large and conspicuous insects and the Swedish insect fauna is considered to be relatively well-studied.

Genetic diversity and phylogenetic relationships among *Cotesia tibialis* and related species complexes: *C. xylina* and *C. yakutatensis* (Hymenoptera: Braconidae: Microgastrinae) revealed using COI barcoding sequence

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The parasitic wasp genus *Cotesia* Cameron, 1891 is one of the largest in the subfamily Microgastrinae. They behave as koinobionts of lepidopteran larvae from the "macrolepidoptera" group. The host spectrum includes some of the important pest species, therefore several *Cotesia* species have been used in biological control programs in agroecosystems. Under the shadow of hidden taxa within species, three related *Cotesia* were analyzed, namely *C. tibialis*, *C. xylina* and *C. yakutatensis*. All three species have the same cocoon architecture, spinning them in a form of a ball mass. Mitochondrial COI barcoding sequence was used to inspect genetic diversity and phylogeny among the three *Cotesia* complexes. In the first complex, 15 haplotypes of *C. tibialis* were detected, which are split in three clusters with an average genetic distance among them of 1.4%. Genetically, the most diverse is *C. xylina*, with 26 haplotypes that are also separated into three groups with an average genetic distance among the three groups of 1.7%. Finally, *C. yakutatensis* is divided into two distinct genetic lines with an average distance between them of 3.4% and with 13 detected haplotypes. Both *C. xylina* and *C. tibialis* segregates intertwine on the phylogenetic tree, forming a monophyletic group, while *C. yakutatensis* forms a separate branch. The preliminary results indicate the existence of eight entities. With additional morphological and morphometric analyses, as well as the discovery of missing hosts, it may lead to the description of new species.

Shaping diversity: A look into species limits in the *Eurytoma robusta* species group (Hymenoptera: Chalcidoidea: Eurytomidae) using genome sequence data

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Like in most parasitoid wasps, the diversity of Eurytomidae (Chalcidoidea) is generally underrepresented in species lists. This is mainly due to their small body size, uniform appearance, and often cryptic lifestyles as secondary phytophages or parasitoids on a wide variety of arthropod hosts. Increasingly fast and accessible molecular methods have allowed the detection of many more species and a better overview of natural diversity. But we can’t look at diversity in isolation: the phylogenetic patterns we observe are caused by complex interplay of biological processes. Ancient or recent hybridisation has been shown to be positively correlated with diversification in several taxa, and effective population size affects intraspecific genetic diversity, potentially obfuscating species delimitation. A large proportion of phylogenetic inconsistencies can be attributed to biological causes rather than methodological differences, so disentangling the role of these processes in diversification is becoming increasingly relevant in a taxonomic landscape where a slew of high output methods and sensitive analyses often leads to diverging results. We generated high quality genome sequence data from 90 individuals of the *Eurytoma robusta* species group along with six outgroup species from within the same family. Preliminary species delimitation using ASAP yielded 12 putative species based on COI barcodes. For female individuals these groups corresponded reasonably well with morphospecies identified previously. Male individuals were harder to sort morphologically and impossible to associate with conspecific females. Each putative species is represented in our dataset by multiple specimens from different localities in central Europe. We will investigate the species limits within the sampled taxa using universal single-copy ortholog genes, which have been shown to reliably partition even closely related species. Analysis of gene flow and estimation of effective population size will provide context in which to interpret the species limits and the evolutionary history of this group.

Megastigmidae (Hymenoptera: Chalcidoidea) – phylogeny, evolution, and reclassification of the family

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Megastigmidae, comprising about 250 species in 18 genera and 3 subfamilies (Keiraninae, Chromeurytominae and Megastigminae), is primarily found in the Australian region, although a few genera are present in other biogeographic regions. Megastigmidae exhibits diverse life-history strategies. Some genera feed on seeds of angiosperms or gymnosperms, while others are parasitoids, and one genus is suggested to be gall-maker. Our study is the first to: 1) produce a robust phylogeny for Megastigmidae; 2) use it to determine its biogeographic area of origin and identify its ancestral feeding strategy; 3) reclassify the family. We sequenced ca. 900 UCEs for >100 specimens from all known genera and species groups of Megastigminae, chosen to represent all feeding strategies and the world distribution of the subfamily, *Chromeurytoma* (Chromeurytominae) and *Keirana* (Keiraninae). For all taxa ca. 140 external morphological characters were scored and used to define genera of Megastigmidae. The family originated in the Australian region and colonized the world in several waves. Our analyses suggest that parasitoidism is the most likely ancestral feeding strategy of the family, with at least three subsequent shifts to phytophagy. Keiraninae and Chromeurytominae, sister clade to Megastigminae, are considered parasitoids. Megastigminae is subdivided into three subclades. The first clade comprises species that are primarily phytophagous, including gall-makers. The second clade likely consists exclusively of parasitoid species. Within the third clade, phytophagy has independently evolved at least twice. Using both morphological and molecular data, we almost double the number of genera of Megastigmidae and hence propose a new classification of the family.

Effect of seminatural habitats in agricultural landscapes on oilseed rape aphids (Hemiptera: Aphididae) and their parasitoids

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Seminatural habitats play an important role in biological control in agricultural landscapes because they can provide shelter, secondary food sources or overwintering sites for pests and their natural enemies. Aphids and parasitoids were collected from April to June 2021 in oilseed rape (*Brassica napus*) fields and field margins. Samples were collected by cutting leaves with aphid colonies and rearing the colonies in the laboratory until parasitoids emerged. A total of eight fields, four with seminatural margins (fallows, pastures, canals, shrubs, etc.) and four without, were sampled. We found 15 aphid species (Aphididae) and 15 species of their parasitoids (Braconidae, Aphidiinae). *Myzus persicae* was the only aphid species found on oilseed rape and it was parasitized by seven parasitoid species. Landscape composition surrounding the fields was characterized and mapped at three scales from 500 m to 1.5 km radius. Analyses were performed to detect relationships between landscape composition and aphid and parasitoid density, parasitism rate and species richness.

The biocoenotic parasitoid complex discovered in an endive culture (*Cichorium intybus* L. ssp. *sativum* (D.C.) Janchen var. *foliosum* Hegi) attacked by *Uroleucon cichorii* Koch colonies of aphids

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Pest control of an endive culture (*Cichorium intybus* L. ssp. *sativum* (D.C.) Janchen var. *foliosum* Hegi) was carried out at the request of the Bacău Vegetable Research Station. Most of the 100 second-year endives found in the culture (endives are biennial plants) were covered almost completely by *Uroleucon cichorii* Koch aphid colonies. In reality, those colonies were only the mummies left from the parasitic activity of their primary parasitoids *Aphidius funebris* Mack., *Ephedrus campestre* Stary and *Praon dorsale* (Hal.) (Braconidae: Aphidiinae) that were in turn parasitized by 2nd, 3rd, and 4th level parasitoids of other Hymenoptera. The 5521 collected mummies were transfered to the entomology laboratory of "Al.I.Cuza" University, Iasi, and allowed to grow under controlled conditions. A total of 5,023 adult parasitic Hymenoptera hatched from the mummies. These parasitoids belonged to Aphidiinae as primary parasitoids, as well as as hyperparasitic Cynipidae (Charipinae), Pteromalidae, Encyrtidae and Megaspilidae. A total of 34 parasitoids were identified. The trophic relations between these species were elucidated, and a specific food chain for the parasitoid biocoenosis was mapped. A synecological analysis of the biocoenotic complex of *Uroleucon cichorii* Koch was performed, in which the abundance, constancy, dominance, and the Index of Ecological Significance (IES) were monitored.

Mutualistic viruses in cyclostome subfamilies of Braconidae (Hymenoptera)

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Parasitoid wasps of the superfamily Ichneumonoidea have acquired both exogenous and endogenous mutualistic viruses multiple times independently. In the Braconidae, endogenous viral elements (EVEs) are represented by polydnaviruses (PDVs) and virus-like particles (VLPs), whereas exogenous viruses include entomopoxviruses, which help wasps to suppress the immune system of their hosts. These mutualistic viruses originated multiple times from dsDNA viruses that infect arthropods, and they have retained ancient core genes that are involved in viral transcription, replication and infectivity. EVEs have only been reported in two koinobiont endoparasitoid braconid lineages, the subfamilies of the microgastroid complex and Opiinae. We analyzed low-coverage genomic data of 42 endo- and ectoparasitoid species belonging to 12 cyclostome braconid subfamilies to search for mutualistic viruses through a homology search targeting six ancient core genes (DNApol, helicase, lef-5, lef-8, lef-9, p33) with HMMER and psi BLAST. The viral sequences were then confirmed through phylogenetic analyses. We found ancient core gene sequences in a member of the endoparasitoid subfamily Rogadinae (*Yelicones* sp.) that are related to an EVE identified as a filamentous virus found in species of Figitidae, the *Leptopilina boulardi* filamentous virus (LbFV). We also found ancient core gene sequences in a species of the ectoparasitoid subfamily Doryctinae (*Rinamba* sp.) that are closely related to the exogenous mutualistic virus *Diachasmimorpha longicaudata* entomopoxvirus (DlEPV). Our results provide the first evidence of mutualistic viruses within these two cyclostome subfamilies.

Metabarcoding to assess integrity of reared strains and efficiency of released strains of *Trichogramma* Westwood (Hymenoptera: Trichogrammatidae) or the biological control of insect pests

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Trichogramma (Chalcidoidea) are egg parasitoids of many insect species, primarily Lepidoptera. Hence, they are used for the biological control of economically important insect pests worldwide. The identification of these tiny wasps is obviously impossible on sight so that molecular quality control is necessary for (i) conservation of living strains for research purposes (see for instance: https://www6.inrae.fr/crb-eggparasitoids-coll/), (ii) field evaluation of promising (cocktails of) strains and/or (iii) prevention of any contamination during their mass-production. To enable rapid characterization of mixtures of strains, we developed a high-throughput approach based on two PCR steps followed by MiSeq sequencing of *COI*, the insect barcode. In the first PCR, the target gene region is amplified using specific primers flanked by tails. These tails allow for a second PCR reaction to add Illumina adapters and unique combinations of indexes to multiplex samples and track index hopping. A bioinformatic pipeline was also set up to analyze raw data. Nineteen bulks of samples made from 3 species were tested in triplicates in a preliminary analysis. All were well characterized, including the lowest ratio tested (1%; 1 sample from 1 species among 99 samples from another species). A real condition test was then performed with the release of cocktails of 7 species of *Trichogramma* to control pests of violets and jasmine in Southern France, the results of which (140 sterile egg patches of natural and substitution hosts) are currently being analyzed and will also be presented.

Parasitoid community of microlepidopteran species living on hops

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Interactions between parasitoids, phytophagous insects and their host plants play a major role in trophic relationships of all terrestrial food webs as they include more than half of all known terrestrial species (parasitoids-herbivores-plants). For many herbivores interactions with parasitoids have led to the evolution and diversification of various defense strategies. An example of a primary defense strategy against predators and parasitoids is the formation of shelters such as leaf mines, leaf rolls or even galls. Such strategies are a key factor influencing the composition of the parasitoid community. In our research, the spectrum of parasitoids of moth species *Caloptilia fidella* (Reutti, 1853) (Lepidoptera: Gracillaridae) and *Cosmopterix zieglerella* (Hübner, 1810) (Lepidoptera: Cosmopterigidae) living on hops (*Humulus lupulus*) in the Czech Republic was monitored. The larvae of *C. fidella* first mine the leaves, then switch to an exophagous feeding forming a leaf roll on leaf margin within which they feed. Pupation takes a place in a cocoon on the leaf surface outside the leaf roll. *Cosmopterix zieglerella*, on the other hand, mines inside the host hops plant throughout its life cycle. As part of this research, infested hops leaves with both herbivores and their parasitoids were collected and subsequently preserved under laboratory conditions. Detailed host bionomies were recorded and the spectrum of parasitoids of different developmental stages and host defense strategies (mine, cocoon life) were observed. For *C. fidella*, more than 12 species of parasitoids including hyperparasitoids have been newly recorded in our study. Most of them belong to the families Eulophidae, Braconidae and Ichneumonidae. No parasitoids are known for *C. zieglerella* to date. At least three species of parasitoids from the family Eulophidae and one species from the family Braconidae were reared from the collected material. Our results suggest that living inside the leaf (mine) appears to be a more convenient defense strategy for host species compared to rolling on the leaf margin.

Newly recorded hymenopteran parasitoids of invasive pests in the Czech Republic

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Invasive species are important pests of agricultural crops and forest trees worldwide with usually no natural enemies in the invaded area. Classical biological control is one of the most effective methods to decrease pests below an economic threshold with Hymenopteran parasitoids being the most commonly used regulators of invasive pests. Recently, we have found three parasitoids of alien species unintentionally spread to the Czech Republic (CZ). During monitoring of occurrence of galls of *Dryocosmus kuriphilus* (Cynipidae) on *Castanea sativa* in CZ in autumn 2022, we found *Torymus sinensis* (Torymidae) in galls on all localities with *D. kuriphilus*. Further, adults of *T. sinensis* were also observed ovipositing in May 2023. The origin of *T. sinensis* in the CZ is probably in south Europe and it was introduced by infested galls of *D. kuriphilus* with trees from a nursery. *Metcalfa pruinosa* (Flatidae) was first discovered in the CZ in Brno in 2001. However, its ectoparasitoid, *Neodryinus typhlocybae* (Dryinidae), was found for the first time at Zaječí train station in the summer of 2022. During a survey in the autumn of 2022, the parasitoids were found on other train stations southeast of Brno and in Prague as well. Larvae of *N. typhlocybae* arrived probably by train on nymphs of *M. pruinosa* to the CZ, possibly from Slovakia or Hungary. *Polynema striaticorne* (Mymaridae), an egg-parasitoid, was first introduced to Italy in 1966 against *Stictocephala bisonia* (Membracidae) from North America. Recently, we have found *P. striaticorne* in eggs of *S. bisonia* in a young apple orchard in 2016 and 2017. This tiny species is overlooked and may have a broader range of distribution in Europe. We suppose its origin in the CZ from Italy or elsewhere in Europe from where it was imported by trees from nurseries.

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Understanding the evolution of generalism and specialism in *Aleiodes* Wesmael (Hymenoptera: Braconidae)

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Ecological generalism and specialism are key concepts in ecology and evolutionary biology as they determine how organisms use and partition resources that are available to them. They help explain a variety of processes including adaptive radiations, speciation, community structure and adaptation to new environments. Understanding the mechanisms that shape generalism and specialism has never been more important, especially given that current environmental change is impacting how organisms interact with their resources. Host range identity and the degree to which a species is a generalist or a specialist are fundamental properties of parasitoid wasps, given that their entire life cycles revolve around their hosts. However, the evolution of specialism and generalism in parasitoid wasps remains poorly understood, despite consequences for biocontrol and ecosystem regulation. *Aleiodes* (Braconidae) is a species-rich genus which targets Lepidoptera and is known to vary in its degree of host specialism across species. Here, we attempt to improve our understanding of the evolution of host range specificity in the genus *Aleiodes*. We use a taxonomic approach to evaluate the host specificity of 28 *Aleiodes* species for which host data are available, and use this to uncover trends relating to the evolution of generalism and specialism. We pair this with an attempt to uncover the influences of host phylogeny, ecology, and life-history traits on the formation of *Aleiodes* species host ranges. Namely, we seek to understand whether generalists are more frequently associated with ecologically diverse hosts. This study will have implications for understanding how parasitoid wasps may adapt to environmental change in the future, but also to understand the high levels of ecological and behavioural diversity observed across the Hymenoptera.

What are the odds? – Notes on the frequencies of wing malformations in siricid sawflies (Hymenoptera: Symphyta: Siricidae) and their potential implications

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The wing venation represents the basic structure of the hymenopteran wing, through which the wing membrane is structurally reinforced. Its pattern is one of the most important character sets used for the classification and identification on different hierarchical levels of Hymenoptera. Despite this eminent role for the classification of the Hymenoptera, only few studies have focused on the abundance of malformations of the wing venation, and thus, on the reliability of this character set. This seems even more important, since fossil Hymenoptera, compression fossils in particular, are often described and classified based on their wing morphology only – the potential pitfalls are obvious. However, if published at all, malformations have often been reported as singular observations without a broader contextualization, which has lead to the (mis-)interpretation that they occur rather rarely and could therefore be neglected. Triggered by the finding of a cimbicid wasp (Cimbicidae) with an anomalous wing venation that did not key out to the family level, we searched for more specimens with an anomalous wing venation in the entomological collection of the Übersee-Museum Bremen (UMB) and found them in the siricid sawflies (Siricidae). Here, we present an account of the frequencies of wing malformations of the Siricidae in the collection of the UMB. Of 101 investigated specimens, 81 showed at least a minimal deviation of the normal wing venation, many specimens with multiple anomalies. Whilst anomalies showed up in different areas of the fore- and hindwings, sometimes symmetrical on both sides, they were most often observed in the regions of the submarginal cells – supernumerary cells (in more than 20% of all specimens) and defective veins in particular. Up to four irregularities in the wings of a single individual were rather common, with a maximum of eight in two individuals each. These preliminary results show that malformations may occur rather frequently in the wings of the Siricidae. Nevertheless, broader studies are needed to investigate whether similar patterns can be also found in other groups of Hymenoptera – other Symphyta in particular.

Structure and function of facial fovea in andrenid bees

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Andrena is a large genus of ground-nesting bees in the family Andrenidae, with approximately 1,500 described species. While *Andrena* species are well-documented for their pollination behavior and their importance as crop pollinators, their functional morphology remains largely unexplored. Specifically, the structure and function of the facial fovea, a critical cranial feature for *Andrena* systematics and species identification has yet to be explored. These foveae are velvety-like depressed patches just medial to the compound eyes and are especially prominent in females. Connected just below the surface of these foveae are secretory glands. For this project, *Andrena regularis* (regular mining bee) was selected due to its larger body size and availability. Specimens were dissected in RNAlater for transcriptomics and in phosphate buffer for chemical analysis. Specimens were also fixed for imaging. This research in progress aims to provide a baseline morphological, chemical, and genetic description of these facial fovea and the glands associated with them.

Hard exterior, soft core: characteristics of the Eucoiline scutellar plate (Hymenoptera: Cynipoidea: Figitidae)

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The evolution of the species rich parasitoid wasps has spurred numerous morphological and behavioral modifications of the Hymenoptera ground plan. Both morphology and behavior are closely linked, and their characteristics are the result of species adapting to their environment over time. Thus, understanding how and why certain structures and behaviors have been modified or added can help us shine light on the evolution of the respective taxa. One of these modifications is the scutellar plate of the figitid subfamily Eucoilinae. The scutellar plate is an intriguing, elaborate and apomorphic modification of the mesoscutellum found in all eucoilines. As endoparasitoids of cyclorraphous flies, such as the spotted wing Drosophila *Drosophila suzukii*, eucoilines play an important role in ecosystems and in agriculture as biological pest control agents. Nonetheless, eucoilines are still understudied and especially the function and detailed morphology of the scutellar plate remained a mystery. As eucoilines are the most species rich and usually the most abundant group within the whole of Cynipoidea, and since the scutellar plate is only found in eucoilines, we hypothesize that the function and the evolutionary success of the group are closely correlated. We examined the scutellar plate with a variety of methods, including scanning electron microscopy, micro computed tomography, histology, and chemical analyses to get a holistic understanding of the function and structure of this stunning modification.

Metatranscriptomics reveals unexpected diversity of *Ixodiphagus* Howard parasitoid wasps (Hymenoptera: Encyrtidae) in two sympatric Australian ticks

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Ticks are medically and agriculturally important invertebrate pests, representing a substantial threat to the livestock industry and a serious health concern for humans and companion animals. *Ixodiphagus* wasps (Hymenoptera: Encyrtidae) are known endoparasitoids of ixodid and argasid ticks, with potential utility as natural biocontrol agents. Two species, *I. brunneus,* and erroneously, *I. mysorensis*, are previously recorded from Australia. However, the Australian *Ixodiphagus* fauna lacks any formal revisionary work, and the validity and host-ranges of these species remain uncertain. A recent study using metatranscriptomic sequencing to examine the pathobiome of Australia's endemic ticks revealed the presence of *Wolbachia* sequences from ixodid tick samples, suggesting the cryptic presence of endoparasitoids wasps – while *Wolbachia* endosymbionts are common in hymenopteran hosts, they are not known to occur naturally in ticks. This initial finding prompted the current work where we utilised a quantitative PCR approach to screen 178 tick-pools containing questing nymph and adult *Ixodes holocyclus* (Australian paralysis tick) and *Haemaphysalis bancrofti* (common wallaby tick), from two sites in eastern New South Wales, for the presence of hymenopteran parasitoids. Using PCR primers specific to encyrtid wasps, *28S* rDNA and *COI* gene markers were amplified and sequenced. DNA sequences were also obtained from two of six pinned archival *Ixodiphagus* specimens from the Australian National Insect Collection, representing the only other known Australian *Ixodiphagus* wasps reared from ticks. Whole genome sequencing of these samples yielded a complete *Ixodiphagus* mitogenome and approximately 80% of the genome of their endosymbiotic *Wolbachia*. Our results suggest a previously undocumented *Ixodiphagus* diversity in two sympatric tick hosts, *I. holocyclus* and *H. bancrofti,* and demonstrates that the Australian *Ixodiphagus* fauna is distinct from the seemingly cosmopolitan *I. hookeri* found elsewhere, with a potentially significant diversity of tick-parasitoid Encyrtidae in Australia’s diverse eco-regions. The molecular data generated here represents the first-ever for the Australian *Ixodiphagus*, and doubles that of the world fauna, highlighting our extremely poor understanding of these important parasitoids. We call for an increase in publicly available *Ixodiphagus* molecular data, worldwide.

Systematics of Ceraphronoidea (Hymenoptera) and the evolution of pterostigma

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The monophyletic Ceraphronoidea is one of the most commonly collected parasitic Hymenoptera, with uncertain phylogenetic relationships as they share distinct traits with both sawflies and Apocritan taxa. The monophyly of the two ceraphronoid families has been challenged by morphological analyses of male genitalia and the recent rediscovery of the ceraphronid *Trassedia* Cancemi, 1996, which exhibits a pterostigma, megaspiline type female antenna, and Waterston's evaporatoria. We conducted a phylogenomic analysis using UCEs and generated a morphological data matrix of 145 characters for 55 ceraphronoid taxa. Our data was analyzed using the PARAMO approach. Our analysis reveals that the two families are monophyletic and consist of two distinct lineages each, one with a pterostigma and the other without it. The examination of the mesosomal skeletomuscular system and live specimens strongly suggests that the absence of pterostigma in ceraphronids is associated with their jumping behavior, while in Lagynodinae, it is linked to a shift in flight dynamics towards a low Reynolds number 'clap and fling' flight.

Genus *Aphidius* Nees (Hymenoptera: Braconidae: Aphidiinae): integrative taxonomy and implications for biological control

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The genus *Aphidius* Nees is the most speciose within the subfamily Aphidiinae, with over 100 species worldwide. Due to the frequent cases of cryptic speciation and the limited number of taxonomically reliable morphological characters, the species of this genus are among the most taxonomically problematic within the subfamily Aphidiinae. However, an integrative approach combining morphological characters, host range patterns, and molecular markers may lead to reliable identification of *Aphidius* species. The most useful taxonomic characters used for morphological identification are the venation pattern of the forewing (shape of the pterostigma and the ratio between pterostigma and metacarpus length) and the shape of the forewing analyzed by geometric morphometrics, shape of flagellomere 1 (ratio between length and width at midpoint), anterolateral area of petiole (rugose, costate or costulate), shape of petiole (ratio between length and width of petiole at spiracle level), number of antennal segments, number of maxillary and labial palpomeres. The barcode region of the mtCOI gene is informative for most *Aphidius* species and is very helpful in species delimitation. Several *Aphidius* species are used in biocontrol programs for aphid control worldwide. Among the most important are the species of the *Aphidius colemani* group, which is very commonly used as a biocontrol agent in greenhouses, and the species group *A. eadyi* (*A. eadyi* Starý, González & Hall, *A. smithi* Sharma & Subba Rao, and *A. banksae* Kittel), which is used worldwide to control *Acyrthosiphon pisum* Harris and *A. kondoi* Shinji in the field. Our studies confirmed the existing species groups and the unusual haplotype diversity within these species complexes. Valid identification is critical to the success of biocontrol programs. The highest diversity was detected within the *A. colemani* species group in Africa, while unusual haplotype diversity was detected within the *A. eadyi* species group in Asia Minor and Central Asia. Further studies should confirm the status of several populations within these two species groups.

New European initiatives on wild bees taxonomy and monitoring

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In the last two decades, high-profile reports have highlighted declines in wild bee abundance and species diversity, most clearly in Europe and North America. In response, the European Commission mandated a group of experts to develop a proposal for monitoring pollinators, to analyse the capacity for its implementation and to mitigate negative population trends. A report evaluating the possibility of an EU Pollinator Monitoring Scheme (EUPoMS) pointed out gaps for its implementation, including insufficient taxonomic resources for bees. A series of projects were therefore implemented (i) to strengthen taxonomic capacity in EU Member States regarding wild bees; (ii) to develop capacities to allow their effective monitoring and conservation; (iii) to better understand the causes of decline of wild bees on the continent. The first element is developed through ORBIT, a three-year project commissioned by the General Directorate for Environment (DG Env) of the European Commission aiming to develop taxonomic resources for facilitating bee inventory and monitoring. The second gap is tackled by the SPRING project, which is developing training of researchers on pollinator identification, refine sampling protocols to start a European-wide monitoring of pollinators in EU Member States, and support preparation for the implementation of the EUPoMS, by organizing training sessions for different level of expertise. The third point is covered by the PULSE project providing technical and scientific support in measuring the pulse of European biodiversity using the Red List Index, aiming to develop the new, updated IUCN Red List the European Red and the creation of the new checklist of European Bees, in collaboration with all the taxonomist members working in Orbit. Finally, SAFEGUARD is a Horizon 2020 project aiming to expand current assessments of the status and trends of European wild pollinators to safeguarding European wild pollinators. The first results of these activities at European scale are (i) the production of a new checklist of the European species, now recording 2,134 species in 77 genera; (ii) diagnoses for half of these European species and over 20,000 images for their identification; (iii) the updated key to genera to be translated in all European languages; (iv) the new re-assessment of European species; (v) national records for 3,000 European bee and hoverfly species, including their distributional status at the national level, achieved by incorporating both published and unpublished data, as well as expert knowledge. These projects represent an important step forward for future assessments of population trends and development of national and regional conservation actions.

Nomenclatural spring cleaning: tidying Aphelinidae (Hymenoptera) of taxa that do not spark joy

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Aphelinidae (Chalcidoidea) is a biologically diverse group of parasitoids containing ~1400 described species, 38 genera, 6 tribes and 4 subfamilies (Aphelininae, Coccophaginae, Eretmocerinae, and Eriaphytinae). Species in this family primarily target scale insects, whiteflies and aphids, though the family also includes many oophagous and hyperparasitoid species. Coccophaginae possess a unique life history called heteronomy in which male development differs from female development; they can act as primary parasitoids of a completely different host, ectoparasitoids on the same host, hyperparasitoids of a different species of parasitoid, or autoparasitoids of their conspecific females. The relationships within Aphelinidae are poorly resolved, leaving strong questions concerning the monophyly of genera, tribes, subfamilies, and the family itself. Analyses of sequence data from anchored hybrid enrichment (AHE) and ultraconserved elements (UCE) have begun to clarify these relationships. While there is variance between the phylogenies recovered by each dataset, both recover the same monophyletic subfamilies and tribes. Here we explore the recovered phylogenetic hypotheses for Aphelinidae based on UCEs and AHEs and their impact on tribal classification. We present a revised tribal classification of the subfamily Coccophaginae, including four new or re-established tribes (Euxanthellini, Eriaphytini, Prococcophagini and Prospaltellini), examine the implications of different recovered phylogenies of Aphelinidae for the establishment of putative new tribes and the reclassification of extant tribes which we recovered as non-monophyletic (Aphytini, Coccophagini). Finally, we discuss synonymy of four genera (*Allomymar*, *Metanthemus*, *Prophyscus*, *Prococcobius*) and the exclusion of three genera (*Noyesaphytis*, *Phtuaria*, *Verekia*) from Aphelinidae.

“Turbo taxonomy” based on COI to delimitate species does not agree with the biological species concept for *Lariophagus distinguendus* (Foerster) (Hymenoptera: Chalcidoidea, Pteromalidae)

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To speed up the current process of species discovery and the so-called “taxonomic impediment”, a number of studies working on parasitoid wasps have based species delimitation and description only on COI sequences. This approach was criticized for several reasons, but almost never for the fact that it neglects the biological species concept (BSC). Remarkably, this concept for species delimitation is used by most scientists working on evolution and ecology, but not by taxonomist which are describing species. Therefore, we tested if the commonly used divergence of 2% in the COI sequence is suitable to delimit species which are also separated based on the biological species concept. We studied different strains of *Lariophagus distinguendus* (Foerster), a pteromalid parasitoid of stored product pest beetles found in human storage facilities[1]. Most strains were collected within the larger area of Stuttgart (Germany) and therefore occur in sympatry. Total reproductive isolation (RI) according to the BSC was investigated in crossing experiments using strains from the same and different clusters recovered by COI. RI was virtually absent between strains separated by up to 2.8% COI difference, but strong or complete in pairs separated by at least 7.2%. Accordingly, all studied strains can be separated into three clusters, each representing one distinct species according to the BSC. This highlights cryptic diversity of this parasitoid species in direct vicinity to humans. These results also challenge the “turbo-taxonomy” practice of using 2% COI differences to delimit species, especially within parasitic Hymenoptera, as it might result in the separation of strains, which are not reproductively isolated according to the BSC. To reconcile the BSC and the species concepts based on molecular data including the barcode gap approach, we suggest using data on RI from crossing experiments with suitable candidate species to determine taxon-specific thresholds that can then be used for species delimitation.

Tetracampine and entedonine parasitoids (Hymenoptera: Chalcidoidea: Tetracampidae, Eulophidae): Afrotropical diversity and species delimitation based on behavior and biological traits

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The diversity of chalcidoid parasitoids in the tropics and their species delimitations are still poorly studied. Moreover, habitat degradation and transformation of natural biodiversity refugia in tropics jeopardize the existence of these and many other groups of animals, which may go extinct unknown and unnamed (i.e., so-called dark extinction). Our museum and field activities allowed description of new genera and species of entedonine (Eulophidae) and tetracampine (Tetracampidae) parasitoids, as well as to clarify the status of some other taxa, remained poorly understood since their description (beginning–middle 20th century). Some taxa have been described from areas that are currently war zones, suffer from unregulated gold mining and deforestation, and at the same time deserve conservation status (in particular in the DR Congo). A new species of the genus *Trisecodes* (currently in Systasidae) and the enigmatic tetracampine genera *Kilomotoia* and *Afrocampe* were described from DR Congo and Uganda, and South Africa, respectively, their phylogenetic position was later confirmed by molecular studies. The study on the very diverse genus *Pediobius* allowed not just describe peculiar new species, but also shed light on the related genera. The revisions of the 'taxonomically abandoned' Afrotropical genera *Colpixys* and *Xiphentedon* resulted in that three (one new) species were recognized in *Colpixys* and sixteen (thirteen new) species were assigned to *Xiphentedon*. The new species are distributed in a wide range of African regions. The revision of Afrotropical species of the cosmopolitan genus *Omphale* has revealed that the genus is numerous in tropical areas of the continent, chiefly in the primary and secondary forests. It is remarkable that many Afrotropical species are very similar to their Palearctic or Neotropical congeners, but still differ morphologically enough to be considered different species. Such challenging situation questions the mechanisms of species delimitation among parasitoids in general, entedonines and tetracampines, in particular. The question of the mechanisms of species delimitation may be considered on the examples of the European species of the tetracampid genus *Foersterella* and entedonine genus *Entedon*. Morphologically similar species of *Foersterella* differ in the pattern of mating behavior. Unlike them, the morphologically different and traditionally recognized species of *Entedon* occasionally appear just biological forms. Also, their congeners which differ poorly morphologically happen to have sound behavioral and embryological differences though parasitize same host.

Spotlight on the Figitidae (Hymenoptera: Cynipoidea): Studying their diversity and evolution with focus on the Western Palearctic fauna

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The Figitidae, close relatives of the gall wasps, are larval parasitoids of either cyclorrhaphous flies or aphid antagonists. Our knowledge of Figitidae has remained limited, with only 1,700 described species out of an estimated 14,000 extant species. Compounding this challenge is the scarcity of experts who can identify and study these often tiny wasps. In this talk, we embark on a journey into the world of Figitidae, shedding light on their intricate evolutionary adaptations and unveiling their hidden diversity and thereby showing exemplarily the efforts of the German Barcode of Life project's third phase, GBOL III: Dark Taxa. We have sequenced the CO1 barcode region of approximately 3,500 specimens, primarily from Germany, resulting in the preliminary identification of around 200 molecular species. Our findings, integrating morphological and DNA barcode data, show a significantly greater diversity within the subfamilies Anacharitinae, Charipinae, and Eucoilinae than previously known in the German fauna. Our project can be separated in three major sections: First, we conduct a taxonomic revision of the Western Palearctic eucoiline tribes Diglyphosematini and Kleidotomini, in the latter case for the first time and after a century-long gap in studies on the German fauna. Second, in addition to the state-of-the-art integrative taxonomy tools, we explore innovative approaches to integrate into the taxonomic process. As a case study, we delve into the anacharitine genus *Anacharis* Dalman, 1823 and show how wing interference patterns and other wing characters are used by artificial intelligence to make basic taxonomic decisions as well as we start tapping the potential of male genitalia morphology for taxonomy in a figitid subgroup. Finally, we sequence the genomes of multiple representatives from the Eucoilinae subfamily to reconstruct a phylogeny based on a novel set of single-copy orthologous genes in order to check tribal classification as well as to trace the evolutionary history of some intriguing eucoiline characters. In summary, GBOL III: Dark Taxa represents an exciting endeavour that advances integrative taxonomy, deepening our understanding of Figitidae's diversity, evolution, and biology.

Systematic study of Cremastinae (Hymenoptera: Ichneumonidae) in Japan

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Cremastinae, a group of Darwin wasps, is recognized as a monophyletic lineage characterized by a distinctive autapomorphy observed in the apex of the middle and hind tibiae. They are known as endoparasitic koinobionts of Lepidoptera and Coleoptera hosts. Globally, they are known from 844 described species in 35 genera. Conversely, from Japan, only 15 described species are documented in 3 genera: *Pristomerus* (7 species), *Temelucha* (7 species), and *Trathala* (1 species). Hence, it is anticipated that a substantially higher number of genera and species inhabit Japan. Until now, I found 49 species in 6 genera (1 species in *Cremastus*, 3 species in *Dimophora*, 13 species in *Pristomeurs*, 19 species in *Temelucha*, 12 species in *Trathala* and 1 species in an unidentified genus) inhabiting Japan. I will report in detail about species of *Trathala*, *Cremastus* and the unidentified genus. Furthermore, I will compare the morphology of male genitalia across these six genera found in Japan. *Trathala*, the fourth largest genus, has been known from 102 species, of which 3 species, *T. flavoorbitalis*, *T. hierochontica* and *T. striata*, have been known from Palearctic region. Only *T. flavoorbitalis* has been known from Japan, which parasitizes Lepidoptera such as Pyralidae and Tortricidae. I found 11 new species from Japan and one of the species hatched from *Intybia niponica* (Coleoptera: Melyridae). *Cremastus*, the second largest genus, has been known from 146 species, of which 30 species have been known from Palearctic region. I found 1 species from Japan. The unidentified genus exhibits certain shared characteristics with *Cremastus*, such as the presence of upper and lower lobes in male genitalia and the medially reduced upper portion of the occipital carina. However, they also exhibit distinct features. As seen in these genera, the morphology of male genitalia serves to diagnose some genera. Concerning the shared feature of male genitalia between *Cremastus* and the unidentified genus, the upper lobe is combined penis valve, digitus and cuspis, while the lower lobe is paramere. *Dimophora*'s penis valve in aedeagus has spines on mesad surface of subapical portion and ventral edge. Overall, the species richness of Cremastinae in Japan is comparatively lower than in other regions. This disparity can perhaps be attributed to the affinity of Cremastinae for arid and unobstructed habitats, such as grasslands and dunes, whereas Japan predominantly consists of forested areas. Additionally, certain genera within Cremastinae have exhibited a noteworthy phenomenon of host-shifting, extending beyond Lepidoptera and Coleoptera. Consequently, conducting phylogenetic analyses within these genera holds promise for unraveling the evolutionary dynamics associated with host-shifting.

Different or the same? Three species of the genus *Aphidius* Nees (Hymenoptera: Braconidae: Aphidiinae) sharing identical COI barcode region

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Due to their high economic importance, the subfamily Aphidiinae represents a well-studied group within the family Braconidae. All members of the Aphidiinae are obligatory koinobiont endoparasitoids of aphids (Homoptera). With more than 70 described species, genus *Aphidius* is one of the largest genera within the subfamily. Several *Aphidius* species are important biological control agents and have been successfully used against various aphid pest species. Some species exhibit almost cosmopolitan distribution, while others are found only in restricted microhabitats. However, there is confusion in the systematics and taxonomy of certain groups within the genus, with taxa being re-described several times and bearing numerous synonym names. Several revisions and identification keys have been made available over the last decades. Yet, high interspecific and low intraspecific morphological variability between species makes identification difficult. Considering that the majority of species are specialized parasitoids, data on their trophic interactions (plant – aphid host – parasitoid) often represents key information during the identification process. In recent decades, insect DNA barcoding has been used as a molecular tool to identify species or reconstruct phylogenetic relationships. The molecular marker cytochrome oxidase c subunit I proved reliable for most species in previous studies on the subfamily Aphidiinae. However, in several instances, the COI region failed to discriminate between certain species belonging to the genus *Aphidius*. This could be due to gene flow between closely related species or recent divergence. Such is the case for *Aphidius ervi* Haliday and *Aphidius microlophii* Pennachio & Tremblay where the genetic distance of the COI region is 0.0. Similarly, our preliminary analysis of the COI region of the *Aphidius funebris* Mackauer, *A. absinthii* Marshall and *A. tanacetarius* Mackauer couldn't differentiate between the species, despite their distinct morphological differences and different aphid hosts. With the aim of establishing the taxonomic validity of these three species, we have conducted additional molecular analyses as well as extensive morphological examination of material collected over the past decade. Furthermore, we compare their biology and discuss their taxonomic position.

Cuckoo wasps from the past: the unparalleled fossil record of Chrysididae (Hymenoptera)

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The Chrysididae are the second most diverse family within the Chrysidoidea and, due to the metallic shiny and colorful integument of their individuals, among the most appreciated insects by collectors. However, there is still much room for improvement in our understanding of this group. As an example, recent molecular data brought to light a partially artificial classification at the generic level. From a paleontological perspective, although fossils of Chrysididae are not particularly rare, many specimens are yet to be studied in order to better embrace their past diversity. Moreover, considering the unequal proportion of extinct over extant genera across the fossiliferous deposits around the world, the fossil record of the family is a rather unique case within the Hymenoptera. The most common evolutionary patterns for many hymenopteran families acknowledge the arising of modern generic lineages during the Paleogene, simultaneously with an increase in the number of available specimens, with some fossil lineages surviving up to 30 Ma. This is not observed for Chrysididae. Indeed, among the thirty or so known species during the Cretaceous, Paleogene and Neogene, only one of them is unquestionably attributable to a modern genus: *Ceratochrysis dominicana* Engel, 2006, from the Miocene amber of the Dominican Republic; and a substantial number of exclusively fossil taxa are still present by the upper Eocene. Three specimens from the Eocene and Oligocene compressions of Florissant (USA) and Brunstatt (France) have also been proposed to belong to *Chrysis* Latreille, 1802 but this attribution can be questioned due to the absence of preserved diagnostic characters. The scarcity of robust calibration points likely results in an underestimation of the generic divergence times proposed in 2018, using morphological data and tip-dating, and in the present study, using molecular data and node-dating, both under a Bayesian framework. This discrepancy is also highlighted by our discovery of an upper Eocene specimen belonging to the genus *Primeuchroeus* Linsenmaier, 1968, from Baltic amber, which becomes the oldest indisputable chrysidid belonging to a recent genus.

Illuminating a dark taxon: Exploring the German diversity of Ceraphronoidea (Hymenoptera) with an integrative taxonomic approach

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Like most dark taxa of parasitoid Hymenoptera, the superfamily Ceraphronoidea has been vastly understudied in the past. To counteract this gap in taxonomic knowledge, the German Barcode of Life (GBOL) III: Dark Taxa project aims to not only expand the German DNA barcode reference library but also to foster the study of dark taxa such as Ceraphronoidea and to raise public awareness for their ecological importance. Until recently, Ceraphronoidea has been remarkably resistant to COI barcoding efforts, yielding very low success rates when processed with standard protocols. As a first step in making Ceraphronoidea accessible for research, we developed a new DNA barcoding protocol specifically for this superfamily. Further, we discovered a new species of *Aphanogmus* (Ceraphronidae) in southwestern Germany that is highly distinctive through unique modifications to the ventral edge of the 7th metasomal sternite. Based on µ-CT scanning data, we reconstructed a 3D model that serves as cybertype and that yielded insights into the functional morphology of the ovipositor mechanism of this highly distinctive species. Entry into Ceraphronoidea research is very steep: the superfamily's previous resistance to barcoding has led to the use of unconventional morphological characters and literature is disjointed and not easily accessible. Therefore, we are currently developing an interactive key for the Palearctic genera of Ceraphronoidea to provide a starting point for future research. This key will be fully illustrated and available in multiple languages. At the same time, a comprehensive overview of reported host associations is compiled that will provide insight into the vast range of host taxa of this superfamily. It will also identify and highlight the most severe knowledge gaps in the current knowledge of Ceraphronoidea biology. In addition to scientific publications and presentations, we communicate the results of our research and our passion for microhymenoptera to a wide audience in various outreach activities. Our science communication includes a special exhibit with interactive elements, media coverage, popular science talks and join-in activities at public events.

The first step towards the unification of the Palaearctic fauna of the Pteromalidae (Hymenoptera: Chalcidoidea)

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Pteromalidae (new sense) is one of the most diverse families of chalcid wasps and therefore difficult to apprehend. The family comprises 424 genera in 8 newly redefined subfamilies. Despite their huge diversity and their great ecological importance, Pteromalidae remain poorly known, even in relatively well-sampled regions such as the Palearctic. Indeed, over the last 50 years, taxonomic studies have analysed separately Western and Eastern Palearctic diversity of Pteromalidae. Moreover, while in-depth studies were published for parts of the Western Palearctic, revisions of genera and reviews of local faunas were carried out in the Eastern Palearctic without reference to previous studies. Until now, there is no study covering the Palearctic fauna globally, at least at generic level. In order to fill this gap, we are carrying out a critical revision of the genera occurring in both areas and plan to propose a key to the genera of the Palearctic region. Our work first analyzed pteromalids sampled in poorly studied regions of the Palearctic, which may have the greatest biodiversity in this region (South Korea, China, Japan, Russian Far East). Additionally, we are reconstructing a global phylogeny of the family, using Ultra Conserved Elements, which may contribute to better redefine the status of atypic and widespread genera. Our very first results suggest that more than 10 East Palearctic genera must be synonymized, four genera sampled in the East Palearctic appear new to science and several others (such as *Merismomorpha* Girault, 1913 and *Uniclypea* Bouček, 1976) are recorded for the first time for the Palearctic fauna. As a result, out of the 414 world genera of Pteromalidae, 215 valid genera have been identified so far in the Palaearctic. A first important step towards the unification of the Palearctic fauna of Pteromalidae!

A revision of the *Encarsia mexicana* species-group (=*Dirphys* Howard) (Hymenoptera: Aphelinidae), gregarious endoparasitoids of whiteflies (Hemiptera: Aleyrodidae) in the Neotropical region

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The genus *Dirphys* Howard 1914 (from Greek Διρφυς, type species *Dirphys mexicana*) has long been considered highly unusual, due mainly to the unique rugose sculpturing of the mesosoma common to all species. It has long been known to be closely related to *Encarsia* Förster 1878, sharing also one of its host preferences, Aleyrodidae, but always considered distinct. Analyses of more than 300 28S-D2 sequences of a broad and more or less comprehensive range of Coccophaginae genera consistently recovered *Dirphys* as nested within *Encarsia*. *Dirphys* is therefore synonymized with *Encarsia*, and treated as a species-group of it, referred to henceforth as the *Encarsia mexicana* species-group. The *Encarsia mexicana* species-group is recovered as strongly monophyletic within *Encarsia*. All species of the *Encarsia mexicana* species-group are revised. The group includes six previously described species, and fourteen newly described species. All species are described (or redescribed) and illustrated. Detailed distributional data, and, where available, plant associate and host records are provided for all species. *Encarsia myartsevae* Kresslein & Polaszek is proposed as a replacement name for *Encarsia mexicana* Myartseva, now preoccupied by *Encarsia mexicana* (Howard). A dichotomous identification key, supplemented by an online multiple-entry key, is provided for all species.

World revision of *Piogaster* Perkins (Hymenoptera: Ichneumonidae: Pimplinae), a rare, but widespread Holarctic genus that parasitizes jumping spiders (Araneae: Salticidae)

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Piogaster (Hymenoptera: Ichneumonidae: Pimplinae) belongs to the *Polysphincta* group of genera that are koinobiont ectoparasitoids of spiders. The genus is widespread in the Holarctic, but relatively rare in collections and males are only known for one of ten species. A revision was undertaken following discovery of a single specimen collected from Alberta, Canada that represents a very distinctive second Nearctic species. Following this, a specimen representing a third Nearctic species from British Columbia, Canada was re-discovered, having been lost for several decades. The only described Nearctic species is from California, USA. All three of these species are known only from the holotypes. DNA barcoding of unidentified specimens and metabarcoding of bulk arthropod samples have led to the discovery of additional Palaearctic specimens of *Piogaster* and expansion of the geographic ranges of the described species. This talk will summarize our knowledge of the genus in terms of morphology, sequence divergence, biogeography, and what little is known of its biology.

The ant-parasitic Eucharitidae (Hymenoptera: Chalcidoidea): past, present and future

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Eucharitidae are one of the more interesting families of Chalcidoidea. Where known, all of the species are parasitic on ants, attacking the ant larva and developing on the ant pupa. There are major differences in how they enter the ant nest, and also how the adults exit the nest. Currently, there are 66 genera and 528 described species. An estimate of 784 species was made in 2002, and something less than 1000 species still may be realistic. Four subfamilies are recognized; we have no biology known for Akapalinae, but there is circumstantial evidence that it may be an ant parasitoid. Molecular analyses of the group have included traditional Sanger genes (18S, 28S, COI, COII) and targeted enrichment approaches (Anchored Enrichment and Ultraconserved Elements). While these methods retrieve the same subfamily and tribal level relationships, dramatic differences in relationships within the Eucharitini are indicated. The impact of these relationships on interpreting behavioral and geographic evolution across the family will be discussed, along with a discussion of the remaining mysteries to be uncovered in the family.

Illuminating a dark taxon: Central-European Eurytomidae (Hymenoptera: Chalcidoidea)

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Eurytomidae, a family within the Chalcidoidea, comprises over 1400 known species worldwide. In Germany, there are records of 101 species from six different genera. Eurytomids exhibit a wide variety of life histories, with many species acting as parasitoids of various insect taxa and life stages, while others are secondarily phytophagous, feeding on seeds or stems, or inducing galls on different plant taxa. As a result, eurytomids play diverse and abundant roles in two crucial ecological niches within natural food webs, namely as specialized herbivores and parasitoids. Generally, distinguishing eurytomids from other parasitoid wasp families is relatively straightforward. However, despite efforts to enhance our understanding of the family, species-level identification remains problematic, and the actual number of species in Germany remains unknown. The GBOL III: Dark Taxa project aims at shedding light on various families, including Eurytomidae, through an integrative taxonomy approach to species delimitation. We focus on two groups of the Central European fauna, the species-rich genus *Eurytoma* and the *Bruchophagus gibbus* species group. Species within *Eurytoma* are remarkably similar, and species limits are often not well defined. In addition, males have never been reliably associated with females. We employ both morphological and molecular approaches (mostly based on COI barcode data) to delimit species within our target groups and to match females with the morphologically even more challenging males. Automated species delimitation methods using the COI nucleotide sequence data that now can be generated at high success rate using a newly designed primer, yielded promising preliminary species delimitations, indicating a significant increase in the recorded number of *Eurytoma* and *Bruchophagus* species in Germany.

A first step towards a revision and phylogeny of *Oomyzus* Rondani and *Quadrastichus* Girault (Hymenoptera: Eulophidae: Tetrastichinae)

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Despite their immense ecological and economic importance, parasitoid wasps are one of the very least known groups of insects. They exhibit an astonishing species diversity and whenever studied taxonomically, new species are discovered. The jewel wasp family Eulophidae is no exception – new species are frequently being discovered and described from all over the world, even from relatively well-studied regions such as North-western Europe. Since the recent split-up of the family Pteromalidae, Eulophidae is now probably the largest family of jewel wasps (Chalcidoidea), a group of generally small mainly parasitic wasps that is thought to encompass as many as 500 000 species, of which 22 500 have been described to date. Out of these, 5300 are eulophids. Eulophids can be found in essentially all terrestrial habitats on Earth and are ecologically very diverse – solely the species in the subfamily Tetrastichinae have hosts in no less than 100 families belonging to ten insect orders, and some are even phytophagous. Using both morphological and whole genome sequencing data, we are working on a much-needed systematic revision of the two tetrastichine genera *Oomyzus* Rondani and *Quadrastichus* Girault. For this project, genomic data are particularly useful as these groups are morphologically difficult, i.e. displaying small interspecific morphological differences. Focusing on the species in Sweden and Northern Europe, we expect a doubling of the number of recorded species. Here, we present the first preliminary results of the number of species in *Oomyzus* and *Quadrastichus*, based on barcoding data. These data will form the foundation for selecting specimens for whole genome sequencing and the concluding revision and phylogeny hypothesis of *Oomyzus*, *Quadrastichus* and related groups in the "*Tetrastichus* group" of genera.

Revision of the historical type collections of long-horn bees (Hymenoptera: Apidae: Eucerini) preserved in the Muséum national d'Histoire naturelle, Paris - better 200 years late than never

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French entomologists were among the first to describe and document the enormous biodiversity of insects during the 19th and early 20th centuries. Historical collections, which include numerous primary types, are preserved today in the Muséum national d'Histoire naturelle (MNHN, Paris), yet many of them remain poorly studied. This talk presents a recently published first taxonomic revision of the MNHN historical type collection of West Palaearctic longhorn bees (Eucerini, Apidae). A total of 72 species names were revised, 147 type specimens were recognized, and 33 synonyms were newly proposed (the full details can be downloaded from https://doi.org/10.1080/00379271.2023.2192693). Unexpectedly, some of the oldest bee names were found to be misinterpreted and incorrectly used for nearly 200 years, demonstrating a substantial gap in our knowledge. Examples of long taxonomic confusion in this group of bees entail species such as *Eucera longicornis* (Linnaeus, 1758), and *Eucera rufa* Lepeletier, 1841, that are widely distributed in the Euro-Mediterranean region, together with some other names that are less well known or which were put in synonymy and were not used for many years (e.g., *Eucera grisea* Fabricius, 1793). The sequence of historical events that lead to the persistence of these taxonomic errors, and the actions that have been taken to resolve them will be presented. This study demonstrates how basic taxonomic research is essential to improve the understanding and communication of species names, which are continuously being used in biodiversity studies and databases.

Eleven years after: Revisiting the New World *Olixon* Cameron (Hymenoptera: Rhopalosomatidae) adding DNA barcodes reveals at least six cryptic species and a new host record

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Rhopalosomatidae are an unusual family of ectoparasitoid wasps (Hymenoptera: Aculeata) currently comprising less than 100 species found in the tropics and subtropics of all continents except Europe and Antarctica. Whereas some species of the family resemble nocturnal Ichneumonidae, others, i.e., members of the brachypterous genus *Olixon*, might be mistaken for spider wasps or different groups of brachypterous Hymenoptera. Despite their reduced wings, the genus *Olixon* is the most widespread rhopalosomatid genus, occurring in Australia, Africa, India, and the Americas – obviously a classic Gondwanan relict. In the Americas the genus is currently represented by six described species, e.g., *Olixon testaceum* being one of them. The broad distribution of *O. testaceum* throughout Meso- and South America coupled with the recent discovery of sympatric cryptic species of *Rhopalosoma nearcticum* in the USA made *O. testaceum* an excellent candidate for a species delimitation study. Our search in the Barcode of Life Database revealed 221 sequences from specimens (adults and larva) tentatively identified as *O. testaceum*. Given the biological significance of new host records for Rhopalosomatidae, our objectives were to 1) identify the unknown larvae to species, 2) identify their host species, and 3) explore the genetic diversity of *O. testaceum* for evidence of cryptic species. The results of our analyses revealed at least six distinct lineages, implying six or more cryptic species within *O. testaceum*. Furthermore, *Anaxipha* cf. *calusa* (Orthoptera: Trigonidiidae) is identified as the first known host of one species of the *O. testaceum* complex which provides further evidence that Trigonidiidae may be the ancestral host for rhopalosomatid wasps.

Cytology meets molecular biology: recent advancements in the cytogenetic study of parasitoid Hymenoptera

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Nowadays, the cytogenetic study of parasitoid Hymenoptera represents a rapidly developing research field, mainly due to the advent of molecular techniques. Phylogenetic reconstructions based on the results of DNA studies can provide a firm basis for identifying directions of the chromosomal change. Moreover, morphometric analysis can suggest possible chromosomal rearrangements, which can be confirmed using molecular approaches. The latter studies show high diversity of DNA sequences in the order Hymenoptera, including parasitic wasps, and advanced cytogenetic techniques also can demonstrate this diversity. Most of these considerations can be exemplified by the cytogenetic study of the *Lariophagus distinguendus* (Förster) species complex (Pteromalidae). This clade harbors two cryptic species, which also have different haploid chromosome numbers (n), i.e., n = 5 and 6. Furthermore, a molecular phylogenetic analysis demonstrated that n = 6 is ancestral for this complex, and thus a particular chromosomal fusion occurred. A morphometric analysis identified an acrocentric and a smaller metacentric chromosome in the karyotype with n = 6, which correspond to the arms of the largest metacentric chromosome of the species with n = 5. This assumption was later confirmed using microdissection and whole chromosome painting. A study of telomeric repeats in the order Hymenoptera can become another example of the interaction between classical cytogenetics and molecular biology. Specifically, the motif TTAGG, which is characteristic of many other insects, was initially detected using fluorescence *in situ* hybridization (FISH) in a few members of the Formicoidea and Apoidea. This repeat was also found in the family Tenthredinidae (Symphyta), thus showing its ancestral nature in this order. So far, subsequent studies did not reveal this motif in any other group, including parasitoids; however, research involving FISH and bioinformatic approaches demonstrated an unprecedented diversity of telomeric repeats in the Hymenoptera. For example, the motif TTAGG was also found in other sawflies, i.e., Cephidae and Orussidae, whereas most Chalcidoidea have another characteristic motif, TTATTGGG.

Repeated shifts in and out of phytophagy within the seed chalcids: UCE phylogenomics of the family Eurytomidae (Hymenoptera: Chalcidoidea)

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Eurytomidae is associated with a wide variety of plants and can often be found within galls or seeds feeding as an herbivore, parasitoid of phytophagous insects, or both. Because of their diverse biology, some members are important agricultural pests such as Almond Seed Wasp and Citrus Gall Wasp, while others such as Arundo Gall Wasp are used as biocontrol agents. Despite their diversity, eurytomid taxonomy is poorly understood due to their small size and being morphologically conserved. These challenges result in many para- or even polyphyletic genera, greatly hampering our understanding of their biology and evolution, as well as their economic impacts. With the rapid development and increased availability of tools designed to capture genomic DNA, there has been an increase in the use of such methods to unveil the complex evolutionary relationships of taxonomically challenging groups. Here we present a deep level phylogenomic study across the family, and the taxonomic changes to multiple genera. We also explore the evolutionary history of eurytomids in terms of shifting between phytophagy, entomophagy, and entomophytophagy.

Eco-evolutionary outcomes of floral specialization in bees

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How and why animals specialize on resources are fundamental questions in biology. In the case of bees, the answers to these questions have important consequences cascading throughout ecosystems via the invaluable pollination services they provide. Studies have investigated patterns of floral specialization in bees previously, but many questions remain. Primary among these are whether specialization or generalization are ancestral, and whether specialization might be associated with accelerated diversification rates. Here, we leverage the largest bee phylogeny to date to explore the diversification dynamics of bee-flower relationships.

Changes in the wild bee community over 100 years in relation to land use: A case study in a protected steppe habitat in Eastern Austria

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The wild bee community of a sand steppe habitat in Eastern Austria was surveyed in the years 2018 and 2019, complemented with historical data from over 100 years, and analyzed in relation to land use change. The mapping of land use categories was based on historical aerial photographs and orthophotos. Changes in bee community composition were analyzed by a multivariate statistical approach and took ecological traits into account (lecty, nesting type, habitat requirements, flight period, parasitism). In total, 310 bee species were recorded in the area, with the oldest records dating back to 1882. The bee species composition differed significantly among four defined timespans. Across the two most intensively sampled time periods (1931–1966 vs 2001–2021), a decline in species richness of over 50% was observed. We observed a disproportionally high decline of steppe- and sand-associated species, and a distinct shift from ground nesting species to above-ground nesting species. The oligolectic species assemblage was specialized on Dipsacaceae, Brassicaceae and Fabaceae in the two earlier periods, and on Asteraceae and specifically on Carduoideae during the two later ones. Possible measurements to improve the value of the site for the bee community and strategies to improve the value of the site for the wild bee community are discussed. Specifically, stronger reference to historic land management practices as short time periods of intensive grazing and small-scaled, staggered mowing would be desirable to improve the habitat quality. More drastic measures, such as removal of the topsoil in some parts and changes in the landscape re-establishing exposure to wind erosion, might be necessary to restore the area to its condition 100 years ago.

Revising the hyper-diverse genus *Andrena* Fabricius (Hymenoptera: Andrenidae) in the Iberian Peninsula: problems and advances

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The Iberian Peninsula is a global hotspot for bee diversity due to its large number of different habitats, particularly Mediterranean scrubland, mountains, and hot and cold steppe. As part of the Holarctic biogeographic region, the bee fauna of the peninsula contains a large *Andrena* element. The genus *Andrena* is the second largest genus of bees with approximately 1,700 species and is distributed predominantly throughout the Holarctic with the highest species richness in areas with a Mediterranean climate. Though well-known as a hotspot for bee diversity, the Iberian *Andrena* fauna has received surprisingly little attention, with few dedicated studies and the most recent focused revision published in 1976. The fauna therefore remains incompletely studied, particularly with reference to genetic investigation. Following comprehensive inspection of museum specimens, type material, and genetic investigation, the Iberian *Andrena* fauna is comprehensively revised, producing a total of 228 species, and confirming the Iberian Peninsula as a global hotspot for this bee genus. Due to previous incomplete or incorrect study of original type material, several changes to species concepts are necessary, though where possible existing concepts are preserved through the designation of new lectotypes and neotypes. Five new subgenera and four new species for science are also described. Overall, the revisions revealed a pattern of high endemism, including micro-endemism in Iberian mountains, supporting the hypothesis that *Andrena* have particularly high speciation rates due to rapid adaptation to local environmental conditions. Perspectives obtained from this faunal level revision are presented, including on the potential utility of this hyper-speciose bee genus as a model for answering evolutionary questions.

Toward building a DNA barcode database for Asian bee pollinators

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Bees (Apoidea; *Anthophila*) are widely acknowledged as the most important terrestrial pollinators. Their conservation depends on our knowledge of all facets of their life history and distribution. Asia holds 15% of total bee diversity, with many unique lineages, but these species comprise only 1% of public global bee specimen data, in part because identification of the fauna is extremely difficult and requires referencing type specimens often stored on the other side of the world. Many groups also require taxonomic revision due to cryptic species complexes. A primary solution for this taxonomic impediment is to integrate molecular resources with morphology to build foundational knowledge on Asian bee diversity. Here, we present preliminary results on the assembly of a DNA library based on more than 1000+ DNA barcode sequences (COI) from verified bee specimens collected across Asia, mainly from China, India, Singapore, and Thailand. Topics inferred from the generic-level phylogenies of various bee groups are discussed: taxonomic status, species identification and diagnostic characters, cryptic species, and gender matching. This standardized method will provide a reliable backbone of data for future research and bee conservation programs in Asia.

Lost in the dark: Potential declines in the German platygastrid fauna (Hymenoptera: Platygastridae)

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Germany is at the forefront of research on insect decline. Drastic losses in flying insect biomass over the past thirty years are well documented, but changes in species composition remain to be understood. Although parasitoid wasps constitute a large portion of insect monitoring samples, a lack of identification resources for “dark taxa" impedes further research. The Platygastridae are one such dark taxon, with a “superficial species impediment” due to the proliferation of names with vague concepts. Within the German Barcode of Life III: Dark Taxa project, we applied integrative taxonomic methods to examine the diversity of German Platygastridae in the context of insect decline. DNA barcodes indicated the presence of 178 species of Platygastridae in Germany, with an improved Chao1 estimate of 290. Another model based on Hill numbers estimated that our sampling captured 93.7% of total species richness, but only 45.8% of rare species. Historical specimens and ecological data suggest that species in the genus *Isocybus* Förster may be at particular risk of extinction due to their sensitive gall midge hosts and wetland habitat. One species, *Isocybus grandis* Nees, has not been collected in decades, and other species appear to have decreased in abundance since the early 20th century. However, taxonomic confusion continues to hinder progress. Conservation implications and future avenues for parasitoid decline research are discussed.

Fennoscandian sawflies (Hymenoptera: Symphyta)

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Work on the handbook of Fennoscandian sawflies (Hymenoptera: 'Symphyta') has resulted with 789 species treated. Known females and males of all species have been photographed (dorsal and ventrolateral aspect) and arranged into plates. Photo plates of mostly live larvae for 505 species have also been prepared. The book will also include introductory chapters, identification keys, and brief fact sheets for each species. Nearly half of the Fennoscandian sawfly species (46%) belong to the subfamily Nematinae (Tenthredinidae) and 29% (226) of species belong to the genus *Euura*. Host plants are now known for 92% of the species, most of which are mono- or oligophages (97%). The larvae feed mainly on Salicaceae (195 species), Rosaceae (111), Betulaceae (76), Pinaceae (68), Poales (58), Polypodiopsida (33), and Fabaceae (21). 168 species feed on *Salix*, which is largely driven by the northern genus *Euura* (144 species on *Salix*). Mitochondrial COI sequence data is available for 95% and nuclear data (at least one gene) for 70% of the species. During the project about 1000 specimens (about 800 adults and 200 larvae) were sequenced for COI and up to nine nuclear genes, which was critical for species delimitation as well as for associating males and females in Nematinae (especially for the genus *Euura*). Simultaneous sequencing of the larvae and their gut contents enabled reliable association with adults and identified previously unknown host plants for three species (*Salix* for *Euura malaisei* and *E. leptostigma*, *Betula* for *E. sordidiapex*). The Funding for the book project was provided by the Finnish Ministry of Environment through the Putte programme (2021–2022).

Biodiversity research on hyperdiverse Hymenoptera, exemplified by the GBOL project

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Elucidating the diversity of hyperdiverse Hymenoptera is a challenging task to undertake, especially considering the “dark” nature of most of those taxa and the lack of taxonomic expertise. The German Barcode of Life III: Dark Taxa (GBOL) project strives to alleviate these problems by training young taxonomists, developing and implementing new methods to integratively approach lesser-known taxa in Germany. Another project aim is to raise public awareness for Dark Taxa by various outreach activities. Further, GBOL aims to establish a DNA barcode database, to provide the means for public molecular identifications of those taxa that play a vital role in nature and are often extremely abundant in environmental samples. Information on life histories of species is often scarce, which hinders their utility as potential indicators for nature conservation and ecological studies. They could be good indicators given their often highly specialized and therefore informative biology. GBOL examples from “Pteromalidae” (Chalcidoidea) show that even in comparatively well investigated areas like Central Europe, their biodiversity is grossly understudied, highlighted by the discovery of numerous new species records with unknown life histories and undescribed, often cryptic diversity. In fact, one of the most abundant pteromalid species in open grassland, *Spintherus dubius* (Nees, 1836), was revealed as a cryptic species complex through DNA-barcoding efforts. The case of *S. dubius* also shows the value of integrative approaches to disentangle synonymies with morphological methods and rearing efforts to gain life history information, ultimately resulting in solid species hypothesis. Although highly informative, such complex approaches are time consuming, which is why more streamlined methods need to be explored in the race against time to shed light on species-rich taxa.

"Dark Taxa" discovery in Ceraphronoidea (Hymenoptera), with focus on Biodiversity Hotspots

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Parasitoid wasps are a megadiverse group of Hymenoptera with ecological and economic importance. The number of currently described species of parasitoid wasps does not reflect their true diversity. Our studies on Ceraphronoidea – a prime example of a parasitoid wasp "dark taxa" group – from the biodiversity hotspots in the central-eastern Afromontane regions (Kenya, Tanzania) and the Caucasus (Armenia, Georgia) support this hypothesis. So far, we described 88 new species, i.e., more than doubling the number of Ceraphronoidea species known from the Afrotropical mainland. In addition, we made the first ever targeted efforts to collect Ceraphronoidea from the Caucasus, a hotspot virtually unstudied for the superfamily with only five unconfirmed species records. The collected specimens are treated in an integrative species diversity exploration approach, combining morphological examination with focus on male genitalia and nanopore sequencing data of CO1 barcodes. Preliminary results indicate a high diversity in both Ceraphronidae and Megaspilidae, with more than 100 species, many of which are likely to be new to science. In summary, our results highlight that it is necessary and also possible to illuminate the grossly understudied parasitoid wasp fauna of biodiversity hotspots. We hope that our studies will bring the necessary momentum for the exploration of the diversity of small-bodied and megadiverse insect groups by providing the basic taxonomic knowledge that is much needed for protecting biodiversity and understanding evolution and the networks of life on earth.

A framework to integrate species with variable molecular, morphological and biological data into turbo taxonomy revisions, with a focus on Braconidae parasitoid wasps

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As part of the current global biodiversity crisis, a large number of species remain undocumented. Rapid, economically and scientifically feasible methods, such as turbo taxonomy, are needed to accelerate the pace at which taxonomic work is done. For example, species recognition, diagnosis and descriptions can be facilitated by extensive use of molecular data (e.g., DNA barcoding), but that should also be combined with other approaches (e.g., morphology) to increase the accuracy, quality, and usability of the results. However, in practice this is complicated because species have variable amounts of information associated with them, ranging from taxa well characterized by many available specimens and a wealth of data (molecular, morphological, biological, etc.) to taxa very poorly understood, with one/few specimens known and barely any information. The disparity of data prevents treatment of all species in a uniform manner, especially when preparing dichotomous keys and diagnoses; the difficulties are even higher for hyperdiverse taxa such as parasitoid wasps (Hymenoptera), and for groups with many species described in the historical literature. A framework is here proposed to rank all species based on the accessibility and quality of name-bearing types, availability of other specimens, possibility to assess morphological and biological traits, and availability (or potential availability) of molecular data. Based on the ranks assigned, species are then diagnosed and integrated into the taxonomic work at different levels, as allowed by the available data. Actual examples on how to implement this framework are provided for several genera of Braconidae parasitoid wasps, but the approach could be implemented in other groups of Hymenoptera and potentially other insect groups.

Mining the black gold – studying the phenology of parasitoid Hymenoptera from mass samples

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Parasitoid Hymenoptera play a major role in ecosystems as they are natural enemies of their hosts and prevent populations from taking over. Therefore, they are essential for the resilience of an ecosystem, which in the face of insect decline is more important than ever. In order to study insect population trends, many biodiversity monitoring projects were launched in the last years resulting in large numbers of mass samples especially from Malaise traps which contain huge numbers of Hymenoptera specimens. In parallel, there is a taxonomic impediment which means that taxonomic experts are rare and the focus of monitoring projects is set on less problematic taxa than parasitoid Hymenoptera or use biomass as only indicator. In this case, a lack of knowledge can lead to hidden extinctions of many parasitoid species which are still unknown to science. Extracting as much information as possible on parasitoid Hymenoptera from mass samples is the goal of my doctoral project. As parasitoid Hymenoptera are potential indicators for biodiversity, I study the phenology of parasitoid families by using malaise trap samples from a whole study year. I use the fractionator to separate the specimens of the complete sample by size and use the small sized fraction, the so called “black gold” to sort out and identify parasitoid specimens on the family level. Interestingly, the different families show population peaks in varying times of the season which gives hints on their biology and host preferences. Further, I could find a strong correlation between parasitoid number and daily biomass gain, which is unexpected as the small sized parasitoid specimens make only a small amount of the whole biomass. My work on extracting Hymenoptera specimens from mass samples shows the huge potential of these samples for studying parasitoid Hymenoptera and contributes to surpassing the taxonomic impediment.

Impatient barcoding for accelerated species discovery

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Six out of the 20 top most species-rich and abundant families of flying insects are within Hymenoptera. In the vast majority of hymenopteran families, the estimated diversity surpasses by far the documented species count. In the midst of a mass insect decline, the epitome of “We can only conserve what we know” is more relevant than ever. The German Barcode of Life III: Dark Taxa (GBOL) project strives to alleviate those problems by training young taxonomists in developing new methods to integratively approach hyperdiverse and highly abundant “dark taxa”. DNA-barcoding is a useful, albeit imperfect tool due to laborious and repetitive procedures, high costs, the need for highly trained staff and designated sequencing facilities. To overcome these shortcomings, we developed the Express Barcoding protocol at the Centre for Integrative Biodiversity Discovery at Museum für Naturkunde, Berlin, which allows for the fast, reliable and cost-efficient species-level sorting of ecological samples for biodiversity research. We combined the quick and cheap HotSHOT extraction method with the performant technology of a NextGenPCR for rapid amplification and nanopore sequencing with ONT’s MinION sequencer. We demonstrate the power of the approach by obtaining 250 barcodes for 285 specimens in less than a day (6 hours). Express barcoding can revolutionize the way we acquire data for biodiversity research, making mass-barcoding of individual specimens available in a time and cost-efficient manner. With the express barcoding approach we have the framework to accelerate biodiversity discovery and aid biodiversity monitoring - anywhere, anytime, by anyone.

Assessing parasitoidism strategies and life history traits as promoters of diversification rate shifts in the parasitoid wasp family Braconidae

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Some biological and ecological attributes have a significant evolutionary impact on lineages, triggering speciation and thus influencing diversification rates. The study of how specific features influence diversification rates is particularly interesting in megadiverse groups. Within Insecta, the order Hymenoptera has perhaps the greatest species richness, mainly due to the extraordinary diversity found among the parasitoid wasps. The family Braconidae represents one of the most diverse of all parasitoid wasp lineages in terms of life history strategies and associated traits. Within this family there are marked differences in species richness among its lineages (e.g. some subfamilies having fewer than 50, others a few hundred, and yet others with more than 3,000 described species). Understanding the evolutionary history of parasitoidism strategies (ecto- and endoparasitoidism, koino- and idiobiosis) and associated traits such as host use, viral endogenization and host mummification has been a common theme in braconid-related research; nevertheless, whether and how parasitoidism strategies could influence diversification rates among braconid clades remains unexplored. Here we provide the largest time-calibrated phylogeny of Braconidae based on genomic ultra-conconserved element data (UCEs) to investigate the possible correlation of biological traits with diversification within the family.

Rogue sawflies: Eocene amber fossils in the phylogeny of Tenthredinoidea (Hymenoptera)

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True sawflies (Tenthredinoidea) have a substantial fossil record but are rarely encountered in Eocene ambers. We report †N. gen. & sp. from Rovno amber. Based primarily on characters in the fore wing venation, we assign the new taxon to Tenthredinidae: Allantinae: Allantini; it is similar in many ways to the extant genus *Taxonus* Hartig, 1837. We report an additional specimen of †*Eodiprion* Schedl, 2007 (Diprionidae) from Baltic amber. We integrate †N. gen. & sp., †*Eodiprion* and †*Sambia* Vilhelmsen & Engel 2012 (Tenthredinidae: Tenthredininae) previously described from Baltic amber in a combined data set assembled from previously published morphological and molecular data sets. We analyze the combined data set in a Bayesian framework, implementing RoguePlots to evaluate the positions of the fossils. †N. gen. & sp. is placed inside Allantinae, but not particularly close to *Taxonus*; RoguePlots reveal some uncertainty as to its position. †*Sambia* is placed near the base of Tenthredinidae, but again RoguePlots flags possible alternative positions. †*Eodiprion* is unequivocally retrieved inside Diprionidae, but not among the Monocteninae as some of the characters observed in the fossil would suggest. The evaluation of the phylogenetic position of the fossils treated here will make them available for future dating analyses of Tenthredinoidea, helping to further elucidate the evolutionary history of this significant lineage of herbivorous insects.

Phylogeography and population structure of the Mediterranean ant *Crematogaster sordidula* (Nylander) (Hymenoptera: Formicidae)

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The Mediterranean area is characterized by extensive changes in climate and geology over the past few million years, resulting in high environmental and topographical heterogeneity, making it an ideal stage for investigating population dynamics and biogeographical patterns. Here, we present the results of a population-level phylogeny for *Crematogaster sordidula,* one of the most abundant ant species across the Mediterranean region, and discuss lineage diversification within *C. sordidula* along with geological events. In this study, we analyzed ultraconserved elements (UCEs) from 123 individuals to estimate maximum likelihood trees with concatenated and coalescent reconstruction methods. We also called SNPs from UCEs to infer the population structure across the wide range of *C. sordidula* in the Mediterranean region. Additionally, we calculated a time-calibrated phylogeny to investigate the biogeographical history and major divergence events in correlation with geographical and climatic changes. We found four major clades of *Crematogaster sordidula* with full support in all analyses, distributed from south-western Europe over the Tyrrhenian- and Adriatic coast and the Balkan Peninsula to the Aegean region and Anatolia. Population divergence started during the Pliocene-Pleistocene transition, leading first to a split into a western and eastern Mediterranean clade. The most recent common ancestor of the western lineages occurred in Morocco, from where lineages moved north colonizing south-western Europe in the late Pliocene. In the following cycles of glacial and interglacial periods, *C. sordidula* populations further diverged and colonized almost all parts of the Eastern Mediterranean from the Aegean region. Our results demonstrate the important role of the Mediterranean geological history and the potential influence of climate changes and sea-level fluctuations for the evolution of a widely distributed Mediterranean ant species.

Integrating genomic and fossil evidence to elucidate the evolutionary history of psenid wasps (Hymenoptera: Apoidea: Psenidae)

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The Apoidea include bees and several groups of predatory wasps known as apoid wasps, totaling more than 30,000 living species. Inferring the phylogenetic relationships of such a diverse group has been a challenge for the past 30 years. Most results indicate that apoid wasps are paraphyletic in relation to bees. Among the living apoid taxa, Psenidae is one of the lineages indicated as a possible sister group to bees. Psenidae includes 18 genera, approximately 488 living species and at least six fossils from the Cretaceous and Paleogene. The crown group of Psenidae arose in the Cretaceous, most likely during the Late Cretaceous, with divergence time estimates ranging from Middle Aptian to Early Cenomanian. Although they are frequently represented in phylogenetic analyses of Apoidea, there are no previous works that aimed at resolving the phylogenetic relationships of this family in detail. The main goal of this study is to reconstruct the evolutionary history of Psenidae by investigating their phylogenetic relationships and estimating the time of divergence of fossil and recent lineages using tip-dating in a total evidence approach. To achieve the objectives, phylogenomic data of ultra-conserved elements (UCEs) were generated from museum specimens for a large sample of extant taxa of psenids. In parallel, morphological data were produced for all genera and major species-groups of psenids including fossil taxa. The main phylogenetic results are discussed, as well as the main challenges and advantages of this innovative phylogenomic study.

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Combining morphological and genomic data to unravel the evolutionary history of Agaonidae (Hymenoptera: Chalcidoidea) and a proposed renewed classification

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Fig wasp (Chalcidoidea: Agaonidae) are well known for their mutualistic interaction with fig trees (*Ficus*, Moraceae). Recent studies have either proposed a high level of co-diversification between figs and wasps, or alternatively, multiple introgressions within fig trees at shallow and/or deep levels of divergence. This last scenario implies a high level of pollinator exchange which is contradicted by the strong host conservatism of fig wasps. In addition, the taxonomical framework of Agaonidae is still weak, with polyphyletic genera (*Blastophaga*, *Platyscapa*), a poor circumscription of most genera and subfamilies and some doubts about inter-generic relationships. Therefore, a strong phylogenetic hypothesis of fig wasps to be compared with that of fig trees is highly desired. This requires comparing morphology and molecules to better assess putative systematic biases in phylogenomic analysis as well as the interplay of rampant homoplasy and character reduction and transformation. Using about 150 morphological characters and 950 Ultra-Conserved Elements and their flanking regions, we analyzed 145 ingroup species comprising nearly all type species of the 20 described genera and their synonyms. We proposed 1) a reassessment of all genera and subfamilies, the description of 7 new genera, the synonymy of 3 others and a new taxonomic framework for the family, and 2) a new phylogenetic hypothesis for Agaonidae that was used for re-assessing the temporal and biogeographical contexts in which they evolved. Finally, we compared morphology- and molecule-based hypotheses of both wasps and figs and discussed their implication for the Agaonidae / *Ficus* co-speciation and co-diversification debate as well as for the evolutionary history of the mutualism in space and time.

Awareness of systematic biases in the phylogenomics of Hymenoptera

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Each stage of the assembly of a phylogenomic data set can affect the accuracy of the final result. In addition, compositional and evolutionary rate heterogeneity among loci, nucleotides and taxa may drastically affect topologies that nevertheless appear strongly supported because of misleading high values of node support. In parallel, our overall knowledge in morphology to enable reality checks of molecular results is vanishing. The disappearance of expert taxonomists in many groups makes alternative hypotheses based on morphology frequently unavailable or inaccurate. Furthermore, building morphology-based phylogenetic hypothesis requires lengthy acquisition of character matrixes, which makes them uncompetitive with the fast acquisition of huge (but sometimes dirty) molecular data sets. Another issue is the high level of adaptative transformations in some groups, with possible convergence, which casts uncertainty on the closest relatives of some groups. This situation has opened the door to the publication of molecule-based only and, therefore, possibly biased, phylogenetic hypotheses. These molecular hypotheses could in turn suggest multiple and unnecessary taxonomic changes and may affect the inference of biogeography or traits leading to wrong assumptions. By presenting a series of examples from Hymenoptera, we will highlight how phylogenomic hypotheses can be misled by several artefacts. We will suggest a set of good practices and advocate integration of morphological and molecular phylogenetic hypothesis to cross-validate topologies and better identify areas of the topologies affected by biases.

Evolution of host association in *Torymus* Dalman (Hymenoptera: Chalcidoidea: Torymidae) is not constrained by ovipositor length

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Torymus Dalman, 1820 is one of the most species-rich genera of chalcid wasps (Hymenoptera: Chalcidoidea: Torymidae) with females having interspecific variance in length of the exerted part of ovipositor. Most species are larval ectoparasitoids of various Cecidomyiidae (Diptera) and Cynipidae (Hymenoptera) that cause galls on several plant families. However, some species have unique host strategies and attack wood-boring beetles (Coleoptera), gall-making chalcid wasps (Hymenoptera) or are secondarily phytophagous. This diversity in species and in host and host plant associations makes the genus particularly interesting for the study of the evolution of tri-trophic interactions and of the morphological adaptations to hosts and host plants. Here we use a strongly supported phylogeny of *Torymus* based on the analyses of target DNA enrichment data to test whether ovipositor length, host plants or parasitoid life histories play a role as possible drivers of *Torymus* diversity. Interestingly, the ovipositor length is a plastic character that is not constrained neither by parasitoid host range nor by host life-history and can easily adapt to very different hosts across its evolution. This may explain why *Torymus* is such a hyperdiverse genus with quite a broad host range. Our results also show that while phytophagy evolved only once, host switches between gall wasps (Cynipidae) and gall midges (Cecidomyiidae) occurred repeatedly. The plasticity of the ovipositor allowed for several switches between different hosts with different gall sizes. The presented study is the first one that combines a well-supported phylogeny with extensive comparative phylogenetic analyses to test the role of various traits in the evolution of host associations in the parasitoid wasp genus *Torymus*.

Whole-genome sequencing, aTRAM, and the classification of Platygastroidea (Hymenoptera: Proctotrupomorpha)

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The field of phylogenetics is experiencing a Renaissance. Traditional Sanger sequencing strategies have been all but abandoned for phylogenetic reconstruction methods that utilize hundreds to thousands of genetic markers mined from next-generation sequencing data. The methods used most widely in hymenopteran systematics are genome reduction approaches that target genomic regions typically associated with protein-coding genes. While useful for phylogenetics, these techniques (i.e., UCE, AHE, RNA-seq) generate data that have limited application for addressing additional questions related to organismal biology. Enter aTRAM (automated Target Restricted Assembly Method), a genome reduction approach to phylogenetics that leverages whole-genome sequencing (WGS) reads to assemble large phylogenomic datasets. Here, we document the utility of WGS and aTRAM by constructing nuclear phylogenies for the parasitic wasp superfamily Platygastroidea. The application of this sequence data to test hypotheses related to host shifting and diversification within Platygastroidea will be discussed and the implications of this phylogenetic reconstruction method will be highlighted.

Multilocus molecular phylogenetic assessment of species-groups of the Darwin wasp genus *Enicospilus* Stephens (Hymenoptera: Ichneumonidae: Ophioninae)

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Nocturnal ichneumonoid parasitoid wasps (*e.g.*, *Netelia* of Tryphoninae, Ophioninae, and Homolobinae) often exhibit convergent morphology, characterized by testaceous body color, large ocelli, and slender bodies. These morphological similarities have sometimes led to misunderstandings of their relationships. With over 700 valid species and an estimated 1,000 species, the genus *Enicospilus* Stephens (Hymenoptera, Ichneumonidae, Ophioninae) is one of the most species-rich genera of Darwin wasps. Most members of the genus exhibit typical nocturnal morphology. Their enormous diversity has been subdivided into about 60 species groups. However, the majority of these groups are complex and difficult to understand in terms of their relationships and morphological criteria, due to the lack of both morphological and phylogenetic evidence. Therefore, to address the classification and evolutionary history of *Enicospilus*, we reconstructed a molecular phylogenetic tree for the first time, based on a concatenated sequence of six gene fragments (cytochrome oxidase 1, long wavelength rhodopsin, sodium-potassium adenosine triphosphatase, NADH dehydrogenase subunit 1, wingless, and D1–D5 domains of 28S rRNA). Although the reconstructed tree is robust in places, some other parts are poorly supported. This indicates that the data generated by Sanger sequencing alone is not sufficient to establish comprehensive relationships within the hyper-diverse *Enicospilus*. A phylogenomic approach should be employed to achieve a fully resolved tree. However, some phylogenetically supported results demonstrate many incongruencies between traditional morphology-based classification and molecular phylogeny-based groupings. Therefore, we revised some species groups based on morphological and phylogenetic evidence. This study represents the first steps in the integrative taxonomic revision necessary for understanding the correct systematics and evolutionary history of the morphologically challenging and hyper-diverse genus *Enicospilus*.

Phylogenomics and taxonomy of the genus *Leioproctus* Smith (Hymenoptera: Colletidae)

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The bee genus *Leioproctus* (Colletidae) is the largest bee genus in Australia, comprising over 300 species. Despite its ubiquity, the monophyly of the genus and its subgenera has not been established, and numerous species remain undescribed. In this study, we aim to determine the boundaries of *Leioproctus*, closely related genera, and subgenera using Ultra Conserved Elements (UCE) extracted from fresh and museum specimens. We extracted DNA from 40 specimens, including 34 species, 11 subgenera, and 3 genera. For 36 of these extracts, we employed a miniaturized version of a hybrid capture approach to obtain UCEs, using the Hymenoptera v2 ant-specific UCE bait set, which includes 2590 loci. For the remaining samples, we utilized a whole-genome sequencing approach. UCE data were retrieved, aligned, and concatenated from the assemblies derived from these two approaches using Phyluce. On average, we recovered 1,609 loci with a mean length of 576 bp. A 75% complete matrix contained 1487 loci. We generated a maximum likelihood tree using iqtree2 and employed the ultrafast bootstrap method to obtain node support values. The resulting phylogeny does not support the monophyly of *Leioproctus s.l.* or *Leioproctus s.s.* However, the monophyly of all subgenera sampled is supported. Further sampling is required to establish the accurate classification of this ubiquitous bee genus, including a wide specimen sample within *Leioproctus* s.s., which could potentially lead to the description of hundreds of new species.

Collecting for genomes: Darwin Tree of Life and collection enhancement

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Darwin Tree of Life (DToL) is a Wellcome-funded consortium project contributing towards the Earth Biogenome Project, aiming to produce genome assemblies for the eukaryotic fauna of some islands in North West Europe: Britain and Ireland. The pilot phase aims to produce assemblies for as many families as possible, and many more genomes in particular groups. I will briefly update progress in sampling Hymenoptera, how we are tackling challenges such as collection and identification of parasitoids, and how DToL is stimulating a new phase in collecting and understanding the British and Irish fauna. Some examples are given, from *Vespa*, *Bombus* and *Netelia*, of how change in the UK Hymenoptera fauna can be detected through museum collections and how genomic data can help us interpret these changes. It will be very useful to find out what sort of genomic data the Hymenoptera research community wants and how DToL can help, including prioritising sampling.

Transposable elements of ichneumonoid genomes (Hymenoptera: Ichneumonidae)

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Transposable elements are mobile genetic units that are diverse in structure and transposition mechanisms. They are major determinants of genome size in insects and are highly influential in shaping structure and evolution of the eukaryotic genome. An annotation pipeline for repeat content and transposable elements is used on all currently available ichneumonoid genomes of high completeness to investigate the distribution of different types of transposable elements, as well as their correlation to genome size in these taxa.

UCE Phylogenomics of the Australasian Sphaeropthalminae (Hymenoptera: Mutillidae)

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The Mutillidae (velvet ants) are a diverse, and often-times abundant, aculeate family of solitary ectoparasitoids, characterised by their extreme sexual dimorphism. Females of the group are apterous and often exhibit a suite of defensive adaptations, namely: a painful venomous sting; the largest sting-to-body ratio of any hymenopteran; a thick and slippery exoskeleton; large cuticular spines; olfactory and auditory aposematism; and striking visual aposematism, leading to their participation in one of the largest known Müllerian mimicry complexes. Despite their diversity, abundance, ecological importance, and evolutionary significance, the Mutillidae are often underrepresented in our collections and severely understudied, especially in the Australasian region. Due to the challenging nature of mutillid taxonomy, a robust molecular phylogeny of the Mutillidae is key to providing a systematic framework for testing evolutionary hypotheses and to assess how evolutionary and ecological processes shape their present-day patterns of diversity. Here, we utilise a large morphometric and phylogenomic dataset (UCEs, and mitogenomes), spanning all currently described Australian genera, to reconstruct the phylogenetic history of the Australasian Sphaeropthalminae, and elucidate genus and species boundaries – a rather daunting and difficult task with morphology alone. Using colour-trait data from 5000 female mutillid wasps (approximately 200 species from 10 genera), we document the presence of four putative mimicry rings in Australia, with strong colour-pattern similarities not due to shared ancestry. However, each mimicry ring exhibited widespread geographic distribution across mainland Australia and significant overlap with all other rings – an unexpected finding given that mimicry signals are often subjected to purifying selection. This study builds on evidence of velvet ants forming large mimicry complexes and provides a potential new complex in which to study evolutionary hypotheses regarding Müllerian and Batesian mimicry systems.

Progress by reduction – the impact of the reduction of wings on the mesosomal morphology

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With over 150.000 described species, Hymenoptera is one of the four mega-diverse insect taxa. Aculeata, the most species-rich lineage in Hymenoptera, is traditionally divided into Chrysidoidea, Vespoidea and Apoidea. By far the majority of ants, bees and wasps have well-developed wings and are agile flyers. Nevertheless, a number of species in Aculeata possess brachypterous or wingless females as part of a sexual dimorphism due to a parasitic lifestyle. The frequency of flightless females ranges from a few taxa in Pompilidae to all of the taxa in the highly derived Mutillidae. There were discussions in the past that such a reduction occurs because of energy savings. Such energy savings result in early reproduction times and enhance the fecundity translating into a higher fitness. Usually, the reduction occurs in long time period stable habitats, in which the specimens can reach their destinations by walking, hopping or phoretic transport. Such a reduction belongs to major conversion processes impacting on the morphology of the locomotory center. Hence, the aim of this research is to study these major changes of the mesosoma. To follow the reduction process, we want to compare flying males of selected species to the corresponding brachypterous or wingless females. This comparison will culminate in an evolutionary morphological approach of several flightless aculeate taxa. The visualization will be carried out via micro-CT scans and 3D reconstruction software. These technologies enable the 3D visualization of the antagonistic system of sclerites and musculature and allow us to point out the differences of the locomotive apparatus of the specimens. The presentation on site will reveal the first findings of this approach.

Multiple independent modifications of apoid wasp ocelli: Common themes and striking differences

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Our study investigates the modified ocelli of apoid wasps, which, while of great taxonomic interest, remained enigmatic regarding their inner morphology and possible function. Ocelli were thought to form a simple light sensitivity sensor, but recent studies showed their intricate inner morphology aiding flight control and navigation. Thus, it is surprising that apoid wasps developed strong modifications to this vital organ. Even more so, as comparable modifications are otherwise unknown in pterygote insects but have been developed multiple times independently within apoid wasps. The drastic visible shape modifications range from slight elliptic deformations to C- or comma shaped lenses. While these are often described as “scars” and “reductions” in the literature, our study is the first to show that, despite these strong modifications, the ocelli are still fully functional. We found a translucent lens, an iris and retina, the form of the latter corresponding to the shape of the lens. To this end, we are using a combination of classical histology, electron microscopy and 3D reconstruction from high resolution micro-CT as well as synchrotron scans. Implementing all three methods on the same specimen greatly enhances comparability and allows for a comprehensive morphological insight from few samples if needed. While we found differences within and between the clades that evolved reductions independently, especially regarding pigmentation and the presence of a bipartite retina, there are astonishing similarities between genera from different apoid wasp clades. The unique formation of rhabdomers in uniform, distinct lines following the shape of the retina with little to no space between individual cells is shared by genera in Bembicinae and Crabronidae. This retinal organisation likely allows for the detection of celestial polarisation patterns. The degree of uniformity in organisation seems to succeed unmodified ocelli of different genera and families.

Morphology of Mymaridae (Hymenoptera: Chalcidoidea) as seen using scanning electron microscopy

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Although cleared and good quality slide-mounts of Mymaridae are necessary for species identification and are suitable for illustrating identification keys to genera and species, the external morphology of these small to minute egg-parasitic wasps is best studied and understood using scanning electron micrographs. About 900 micrographs of critical point dried and dissected specimens, and a few photographs of slides of the head, mesosoma and metasoma have been prepared and partly published, together with about 180 morphological terms used for the different structures. The terms are those used in Chalcidoidea generally except for a few, e.g., trabecula, that are unique to Mymaridae. In this talk, I give an illustrated overview of the external morphology of Mymaridae, with illustrations of some of the more unusual structural features that occur in various species of the family.

From words to data: using phenoscript to unleash the potential of taxonomic descriptions for phenomic research

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Over the past 250 years, taxonomists have described an impressive 1.2M species, with approximately 15–20K new species being found each year. Half of these new species are insects, with a significant proportion belonging to the Hymenoptera order. While this collective effort has generated a wealth of phenotypic data, most descriptions remain in Natural Language (NL). Due to this limitation, it is impossible to automatically extract and compare traits, or to reutilize existing descriptions, thereby preventing phenomic-scale research in biology. In this presentation, we will introduce Phenoscript, a user-friendly computer language (https://github.com/sergeitarasov/PhenoScript) that enables the creation of computer-readable species descriptions and automated phenotype comparisons. In Phenoscript, the descriptions are represented as a knowledge graph composed of terms from predefined biological ontologies. While Phenoscript descriptions resemble NL descriptions, they follow a specific language grammar that facilitates machine comprehension. To convert Phenoscript descriptions to NL and enable subsequent phenotypic comparisons, we offer Phenospy — a collection of Python-based tools specifically designed for this purpose. During this presentation, we will discuss how Phenoscript descriptions can be generated for Hymenoptera using the Insect Anatomy Ontology (AISM) and the Hymenoptera Anatomy Ontology (HAO). In addition, we will provide an overview of how ontology-driven methods may enhance phenotype analysis and species comparison in the near future.

The evolutionary dynamics of the labiomaxillary complex of bees (Hymenoptera: Apoidea: Anthophila)

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The labiomaxillary complex of bees is a key anatomical system mediating multiple interactions with the environment. Bees use their mouthparts to gather floral resources such as pollen, nectar, and nest building materials, but also to engage in behaviors such as building, provisioning, and defense. The mouthparts also play an important role in bee systematics, as expressed by several key characters employed in the high-level classification to separate major lineages and in phylogenetic reconstruction. However, in macroevolutionary terms, the overall structure of mouthparts differs substantially between the two main clades of the bee phylogeny: the long-tongued (LT-bees) and short-tongued bees (ST-bees). Such differences may reflect underlying genetic, developmental, and/or functional differences that could have impacted how bees in these two main lineages have interacted with angiosperm plants. In this study, we employ new ontology-informed phylogenetic methods to reconstruct the evolutionary dynamics of the labiomaxillary complex of bees. We produced an initial dataset of 73 characters from the mouthparts of 93 species representing all major lineages of bees. Then we employed our new R package "*ontophylo*" to estimate evolutionary rates on tree branches and reconstruct the dynamics of morphospace occupation through time. Our results indicate that there is strong phylogenetic signal in characters from the mouthparts, especially the labiomaxillary complex, justifying their use in phylogenetic inference. The early evolution of the LT-bees is characterized by exceptionally higher rates for characters of the labium, particularly the distal elements, such as the glossa and labial palps. The ST-bees show a more complex evolutionary dynamics with bursts of higher rates in different lineages for characters from the postmental area, cardo, and stipes. The pattern of morphospace occupation indicates that the evolution of the labiomaxillary complex seems to be less constrained in the ST-bees and highly constrained in LT-bees possibly reflecting two distinct structural morphotypes.

Flexible mandibles in Chalcidoidea revealed by a bizarre "antler wasp" (Hymenoptera: Pteromalidae: Colotrechninae)

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We present a new pteromalid genus from South Australia with bizarre mandibles with antler-like processes. The genus is morphologically and molecularly (UCE data) placed into Colotrechninae. Synchrotron µCT revealed that the mandibles of the bizarre wasp are monocondylic and allow for flexible movement. A comprehensive study of Chalcidoidea revealed that they all have this unique monocondylic mandibular articulation. Contrastingly, all other Hymenoptera have the dicondylic condition, the defining feature of Dicondylia, which comprise 99% of insect species. We hypothesize that flexible mandibles contributed to the evolutionary success of Chalcidoidea and facilitated its diversification. Flexible movement of mandibles is a particularly useful adaptation to parasitism of enclosed hosts, which poses different challenges to the emerging parasitoid wasps. We also show how flexible biting is used by egg parasitoids exhibiting the putative ground plan biology of Chalcidoidea. Our study highlights the need for comprehensive anatomical studies even of putatively well-known character systems to identify major steps in insect evolution.

ANTSCAN or how to generate 3D morphology data for the whole ant tree of life

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The molecular and computational revolution of last two decades have greatly transformed our understanding of evolution, whereas the study of phenotypes has remained comparatively slow and unable to benefit from advances in bioinformatics and computation. While solid knowledge of morphological modifications through time and space is vital for the reconstruction of evolutionary scenarios, presently, such data is rare and unavailable for most taxa, and if it exists, then only for very few taxa. Recently, some technological advances have opened new possibilities for interactive, and three-dimensional (3D) imagery of internal and external morphology, of which x-ray microtomography (micro-CT) is the most prominent. Micro-CT enables high-resolution, non-invasive, detailed 3D analyses of morphological structures and the digitization of tissues, organs, or whole specimens. However, the low-throughput nature of most micro-CT scanners greatly restricts large-scale data generation. ANTSCAN is new project performed by the Okinawa Institute of Science and Technology (OIST) and the Karlsruhe Institute of Technology (KIT), in which we use a robotic, high-throughput synchrotron-CT scanning pipeline to generate a large-scale dataset of organismal phenotypes across a diverse, ecologically dominant, and functionally important group, ants (Formicidae). Once published, the ANTSCAN dataset will comprise 3D full anatomical datasets of nearly 2200 specimens from 900+ species covering 210+ genera from throughout the ant tree of life, plus a small but representative number of Hymenoptera outgroups. This project represents the first open source, large-scale, “big data” 3D library of internal and external morphology of an ecologically important and very species-rich clade and opens the door to a new era of high-throughput studies in evolution, structure, and function of organismal phenotypes.

Past, present, and future: the morphology of Platygastridae (Hymenoptera)

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The limited status of Platygastridae systematics is in part attributed to a need for detailed knowledge in regard to evolutionarily significant anatomical structures. *Synopeas* is a particularly propitious biocontrol agent of several economically significant pests but lacks robust characterization beyond its well-known synapomorphic "fusion" of the first and second metasomal segments. In this study, we explored the functional consequence of this unique trait by analyzing the skeletomuscular and exocrine gland systems of the metasoma with comparative analysis to sister clade *Leptacis*. Guided by sixty-year-old unpublished drawings by Lubomir Masner, we have rediscovered unique evolutionary adaptations of *Synopeas* in both the male and female terminalia, including the presence of a biaxial joint between the cupula and the aedeago-volsellar shaft and the concealment of digiti. We propose a novel method of detecting class III exocrine glands in proteinase K digested specimens using SEM, revealing sclerotized gland canals. We provide a description of these characters via cutting edge microscopy and classical dissection in an effort to enhance the body of knowledge surrounding platygastrid morphology.

Evaluating wasps as indicators of metal pollution in Zimbabwe

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Wasps are highly diverse, occupying multiple different trophic levels, and therefore have good potential as terrestrial indicators of pollution. We investigated wasps from four sites in Harare, Zimbabwe, for metal content. Two genera of Vespidae, *Polistes* and *Belongaster* were sampled. Two sites were presumed polluted as they were near a mine and a heavy polluted lake. The mine is located on a metal-enriched geological feature, The Great Dyke, running north-north-east in a narrow band, 550 km long and 4-11 km wide, that can clearly be seen on Google Earth. An urban site and a nature reserve site served as two reference sites. Wasps from the two presumed polluted sites had statistically significant ($p<0.05$) elevated concentrations of many metals compared with the reference sites, including Pt that were only quantifiable from the mine site. We also found the highest concentrations yet published for Cr, Ni, Mg, Se, Fe, Mn, and V in wasps. This suggests the mine as a source of pollution. The geology, however, differs between the sites, implying that both geology and pollution may contribute to the differences measured. The Great Dyke harbours many mines and is rich in platinum-group metals, as well as Mg, Cr, Fe, Au, Ag, Co, Ni, and Cu, which offers opportunities for comparative studies. Possible effects due to pollution, such as wing asymmetry, could be investigated. Wasps are also food for other animals such as birds, and these might accumulate metals such as mercury. The ecotoxicology of metals in wasps need more study, but many opportunities and avenues of investigations are available. We also found that a good understanding of the biology of each wasp species is needed for a more informed interpretation of data. We conclude that the rich diversity of wasps (more than 145 000 species worldwide) occupying multiple different trophic levels, are good terrestrial indicators.

Successful parasitism of a specialist endoparasitoid *Cotesia kariyai* (Watanabe) (Hymenoptera: Braconidae) in a "non-host" caterpillar through multiparasitism with another parasitoid

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Female parasitoids often encounter non-host species that are sympatric with their usual host. They respond to chemical or physical cues of non-host species and oviposit onto or into them. This behavior is typically regarded as an "accident" or a "mistake" of female parasitoids, as the survival probability of their eggs in non-host species is very low. Kraaijeveld (1999) proposed the kleptoparasitism hypothesis, suggesting that parasitoids can develop into non-host larvae once those larvae are parasitized by another parasitoid. However, this hypothesis has not been thoroughly examined. In this study, I tested the kleptoparasitism hypothesis through laboratory experiments using two parasitoid wasps, *Cotesia kariyai* and *Meteorus pulchricornis* (Hymenoptera: Braconidae), that parasitize caterpillars of *Mythimna loreyi* (Lepidoptera: Noctuidae). Caterpillar of *Mythimna loreyi* is the usual host of *Me*. *pulchricornis* but non-hosts for *C*. *kariyai*. Caterpillar of *My*. *separata*, which is the typical host of *C*. *kariyai*, and *My*. *loreyi* coexist in grasslands across East and Southeast Asia. Oviposition and rearing experiments demonstrated that females of *C*. *kariyai* can oviposit into *My*. *loreyi* caterpillars. However, *C*. *kariyai* could not develop into this host. Interestingly, when *C*. *kariyai* oviposited into *My*. *loreyi* caterpillars already parasitized by *Me*. *Pulchricornis* (multiparasitism), *C*. *kariyai* successfully emerged from 10-20% of the caterpillars. Cage Experiments in cage containing both species of parasitoids confirmed that *C*. *kariyai* can emerge from *My*. *loreyi* caterpillars. These results suggest that the acceptance and oviposition into "non-host" species by parasitoid wasps may be adaptive behaviors in certain situations, such as when female wasps cannot find their usual host species in nature.

Phenomenal drilling behavior of the tiny parasitoid *Eupelmus messene* Walker (Hymenoptera: Eupelmidae)

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Insects, particularly the order Hymenoptera, possess evolutionary uniquely developed structures to provide highly effective reproduction. Namely, the ovipositor of parasitoid wasps is capable of drilling a hole in different natural materials, such as plant galls and woody tissue, to attack the hidden hosts and lay eggs. The morphology of this specific organ is studied in several species, while its functionality and capabilities are much more challenging to reveal. In this research we discovered an unusual behavioral pattern of oviposition in the female parasitoid *Eupelmus messene* Walker, 1839 (Hymenoptera: Eupelmidae): females drill through the wall of a polystyrene Petri dish with her ovipositor and then lay their egg outside the dish. Generally, *E. messene* attacks the gall wasp larvae *Aulacidae hieracii* Linnaeus, 1758 (Hymenoptera: Cynipidae), which form galls on the hawkweed *Hieracium x robustum*. *Eupelmus messene* drills into the wall in a gall with her ovipositor and upon finding the gall wasp larva, lays an egg next to it. However, in our case we were able to observe oviposition that was not associated with the host and any natural substances. The transparency of the plastic allowed us to describe the technique of ovipositor movement, which we divided into three types: pushing, rotational, and ejection. Moreover, we found that *E. messene* seals the perforation after the oviposition with a specific substance. Also, we studied the structure of the ovipositor focusing on the stylet, as well as the perforation made by it, using scanning electron microscopy. We propose that detailed analysis of structure and function of the ovipositor may contribute to the development of minimally invasive guided probes and advance methods of vertical and directional drilling.

Taxonomic observations on *Monorthochaeta* Blood (Hymenoptera: Trichogrammatidae) in Ukraine, and biological notes on *Monorthochaeta nigra* Blood

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Two species of egg parasitoids of the trichogrammatine genus *Monorthochaeta* Blood, 1923 are recorded in Ukraine: *M. nigra* Blood, 1923 and *M. galatica* Nowicki, 1940. *Monorthochaeta adanaensis* Doğanlar, 2002 is considered a junior synonym of *M. nigra* based on examination of the type specimens of *M. adanaensis*. The ovipositing behavior, egg and larva of *M. nigra*, a parasitoid of eggs of tortoise beetles (*Cassida rubiginosa*) (Chrysomelidae: Cassidinae), were studied. The eggs of tortoise beetles were collected on thistles in Poltava Oblast, Ukraine, in late June 2021 and a laboratory colony was established. Freshly laid host eggs were proposed to the parasitoid females for oviposition. The parasitized eggs were dissected immediately after oviposition and within each hour during the next 7–10 hours to trace immature development of the parasitoid. The mated females of *M. nigra* are attracted by the host eggs: either uncovered or covered by the host's faeces. Once the female locates the egg, it stops walking, drums the egg surface with the antennae and eventually bends its gaster and hooks the ovipositor saw into the egg chorion. Then it pushes the gaster down, punctures the chorion and starts twisting the gaster. The drilling of the host egg lasts for about 30 sec and ends up with either host feeding or egg deposition. The biology of *M. nigra* demonstrates the presence of only one larval instar. The existence of only one instar is supported by the possession of the mandibles of the same shape and length, and also by the lack of any signs of molts. Similar to *Trichogramma* species, the integuments of *M. nigra* larva are soft and distensible, so the body shape of the larva changes along with larva's feeding. It is remarkable, that there are no sutures which may suggest segmentation of the larva. However, the subdivision of the anterior part of the larval body into three swollen sections at about 48–72 hours after oviposition, suggests at least vestigial segmentation of the thoracic part.

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Diversity patterns and pollination interactions of wild bees (Apoidea) in the Western Himalaya, Uttarakhand

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The Himalayan Region is a fragile biological hotspot, facing multiple threats including habitat fragmentation, overexploitation, and climate change. Being part of the ecosystem, these menaces impact Himalayan wild bees. Worldwide, bees pollinate more than 90% of the angiosperms and ensure nearly 35% of food production. Nevertheless, the diversity and ecology of Himalayan wild bees are not well documented. Thus, this study is being conducted along the elevational gradient of Kedarnath Wildlife Sanctuary and aims to: (1) elucidate diversity and distribution patterns of wild bee communities across different forest types and elevations; (2) reveal their pollination interactions; and (3) partake in their conservation through spreading awareness about their significance. We conducted forest-type-wise bee inventories using sweep nets and coloured pan traps on different elevations. To document pollination interactions, along with visual observations, we also used CHDK-enabled Canon PowerShot® cameras on tripods as flower-pointed camera traps. We found an association of bee species diversity with forest types and elevations. The species diversity is highest in moist temperate mixed deciduous forests of mid-elevational zones (1800–2400 m asl). In contrast, alpine meadows of high elevation zones (above 3600 m) and gregarious pine forests of lower elevation zones (below 1800 m asl) represent low species diversity. We have also observed species specificity with elevations and forest types. For instance, most of the bumblebee species only occur in higher alpine zones, whereas species of genera like *Ceretina*, *Amegella* and *Xylocopa* are only found at lower elevations. Mid-elevation zones, on the other hand, are dominated by species of *Andrena*, *Ceratina* and by the families Halictidae and Colletidae, along with a few species of higher and lower elevations. Thus, the mid-elevation zone has the highest species diversity. This structure results in pollination interdependency between bees and the plants; for instance, the high-elevation plants (*Bistorta*, *Potentilla*, *Taraxacum*) are majorly (perhaps only) pollinated by bumblebees. Further, we are disseminating our findings to the forest department, native people and tourists to explain the role of bees in sustaining natural forests. As wild bees contribute immensely to the sustainability and regeneration of natural forests, this study will contribute towards their taxonomy, conservation and, ultimately, the resilience of the Himalayan ecosystem.

Oviposition behaviour of *Diplolepis rosae* (L.) and *Diplolepis mayri* (Schlechtendal) (Hymenoptera: Cynipidae)

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Gall wasps induce astonishing structures on plants to provide shelter and food for their breeds. Between the many species of gall wasps those belonging to genus *Diplolepis* cause galls only on feral roses (*Rosa* sp.). Females of *Diplolepis* wasps are minute and are characterized by a ploughshare-shaped hypopygium with which they deposit their eggs in the fresh rose buds. The genus *Diplolepis* consists of six closely related species in Europe from which, two, namely *D. rosae* and *D. mayri* cause usually large, multichambered galls being widely distributed among different feral rose species. Our knowledge regarding the oviposition habits and behaviour of *D. rosae* has been based on only a few observations, while for *D. mayri* there are none. We observed under laboratory conditions (constant humidity and 20°C) females of *D. rosae* and *D. mayri* ovipositing on expanding *Rosa* buds on plants covered by tulle meshes. The aim was to assess the *Diplolepis* ovipositing preferences considering different host plant species (*R. gallica*, *R. canina* and *R. rubiginosa*), presence of siblings (one or two females); and to evaluate their life-span related oviposition frequency. Observed females usually oviposited at first encounter with the host plants, then the oviposition activity declined. Ovipositing periods ranged between a few to more than ten minutes. Altogether 20% of roses paired with gall inducer females grew galls on their leaves and buds. Moreover, from the selected rose species only one was prone to produce galls.

Bodyguard manipulation or a parasitoid-induced stress sleep

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Some parasites can manipulate their host's behaviour and physiology to enhance their own survival and successful reproduction. In bodyguard manipulation, the manipulated host protects the manipulators' offspring from biotic threats. Bodyguard manipulation is induced by koinobiont parasitoids. The parasitoid juvenile pupates near the live host. The host ceases feeding and locomotion and exhibits a defensive response which wands off the approaching hyperparasitoids and predators. There are a handful of case studies of bodyguard manipulation, but the mechanism of how manipulation is induced is still unclear. One study suggests that the manipulation is induced by the symbiotic virus associated with the parasitoid wasp, which is transferred into the host during oviposition. Another study pointed out the role of the host immune mechanism in inducing some of the behavioural changes. A few others suggest that some parasitoid siblings stay behind within the hosts to do the manipulation while their kin pupate outside. In our study, we investigated the behavioural and physiological changes in a host, induced by a bodyguard manipulative parasitoid. We used the braconid parasitoid *Microplistis pennatulae* and its host, *Psalis pennatula*. We found behavioural changes to the host, including cessation of feeding and locomotion, which are like the stress-induced sleep of other invertebrates. We also found elevated octopamine concentration in the host after the parasitoid pre-pupal egression which may contribute to the guarding behaviour of the host. Based on our studies and several others, we propose a new hypothesis that parasitoid egression drives the host into a stress-induced sleep state. The observed behavioural changes can be a side effect of this state. Acknowledgements: Prof. Saskya van Nouhuys and Prof. M. Nasser for guidance and encouragement, Central University of Kerala for facilities, CSIR and DST-SERB for funding.

Nutritional ecology of tropical parasitoid wasps in dry evergreen forest, Thailand

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Nutritional ecology is a multidisciplinary integrative of science that explains organism's nutrition in relation to its ecology. In natural habitats and agroecosystems, parasitoid wasps are one of the most diverse groups of insects. The availability of sugar food sources in agroecosystems can positively influence a parasitoid wasp's abilities to shape insect communities. Adults of koinobiont parasitoid species require energy sources for survival, while the life history of idiobiont species strongly forces the adult to consume sugar not only for survival, but also for reproduction. However, there is no information on nutritional profile of parasitoid wasps in natural tropical forests, including in Thailand. Therefore, in this study wild parasitoid wasps were collected from natural habitats in dry evergreen forest at Sakaerat Environmental Research Station. In the laboratory, the metasoma of parasitoids were removed and crushed to prepare an extract solution for analysis of their dietary nutrition using the anthrone test. The output sugar profiles were compared between their sexes, life histories, and seasons on the percentage positive on the anthrone test. High-performance anion-exchange chromatography with pulsed amperometric detection (HPAEC-PAD) was used to describe the sugar profiles of each parasitoid wasp specimen for both quantitative and qualitative analysis and possible sugar feeding sources of parasitoid wasps in the natural habitat. The preliminary results showed that both the anthrone test and HPAEC-PAD analysis could detect the gut sugar contents of tropical parasitoid wasps; however, for those of a smaller size, there are some limitations for sugar detection using the anthrone test. The HPAEC-PAD analysis revealed that the three dominant sugar contents, fructose, glucose, and sucrose, can be found in both idiobiont and koinobiont species, while the amount of sugar components was different depending on the parasitoid wasp species. Furthermore, it can be concluded from these sugar dietary profiles that wild tropical parasitoid wasps feed on the sugar from a natural habitat (such as nectar and honeydew). This work is the first nutritional ecology study of the tropical parasitoid wasps' sugar in their natural habitats, which can be applied for biological control programmes and conservation management.

Cotesia Cameron (Hymenoptera: Braconidae) as an effective natural biocontrol agent for the Painted Lady outbreaks

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The Painted Lady, *Vanessa cardui*, is a well-known migrant butterfly of the family Nymphalidae, which is known for significant periodic outbreaks. In the summer of 2019, several waves of immigration of the Painted Lady from southern regions were recorded in Poltava Oblast, the Hlobyne Raion. Considerable damage of early shoots was observed on all soybean fields in early June. Further monitoring revealed the plants recovered due to strong natural suppression (up to 100%) of immature stages of *V. cardui* by parasitoids, including *Cotesia vestalis* (Braconidae) in July–August. Painted Lady monitoring and studies of its natural enemies during 2022 demonstrated that, as in 2019, the pest was suppressed by parasitic braconid wasps. The initial damage to soybeans by the Painted Lady caterpillars was detected on June 9–10, 2022. Also, the presence of natural enemies of the Painted Lady was recorded in the field, in particular white cocoons belonging to *Cotesia vestalis*. The number of cocoons was 0.74% to 5.17% of the number of detected caterpillars, however, dissections of the Painted Lady caterpillars have shown that true parasitism rates can be up to ten times higher than apparent. Observations of population dynamics and assessment of the ratio of the number of caterpillars of the Painted Lady and braconid cocoons in the fields showed that the number of braconids increases rapidly in July and exceeds the number of caterpillars by 59–330%. This change in abundance ratio illustrates the effectiveness of natural control of *V. cardui* caterpillars by *Cotesia vestalis*. Moreover, another natural enemy of the Painted Lady, *C. vanessae*, was found. Further studies on ecological interactions of *Cotesia* spp. and *V. cardui* caterpillars are required to understand the mechanism and efficacy of natural pest control of this soybean pest better.

Investigating the potential distribution and biocontrol prospects of *Metcalfa pruinosa* (Say) (Hemiptera: Flatidae) in Ukraine

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Metcalfa pruinosa (Say) is a highly significant invasive species in Europe. This insect originates from North America, where it is distributed in different climatic zones. The first record of *M. pruinosa* in Ukraine was documented in 2011 and, since then, it has been reported in nine regions across the country. The presence of *M. pruinosa* in Ukraine and its considerable potential for causing harm, necessitates the identification of suitable territories for its further spread and establishment. Furthermore, it is crucial to explore the prospects of implementing effective biocontrol measures against this pest in Ukraine. Using advanced GIS software and climate predictors, we assessed the potential distribution of *Metcalfa pruinosa* in Ukraine in light of global climate change. Our analysis revealed that Ukraine offers a favorable habitat for the species, with suitable climatic conditions and a diverse range of host plants. Notably, regions such as Zakarpattia, Crimea, and the Forest and Forest-Steppe zones show the highest suitability. However, current phytosanitary measures are insufficient to effectively curb the spread and mitigate the negative impact of *M. pruinosa*. To address this, we propose the development of a pest control system, potentially employing the introduction of *Neodryinus typhlocybae* (Ashmead), a North American parasitoid. GIS modeling identified suitable areas, particularly in southern Ukraine, for introducing this biocontrol agent. Additionally, we recommend including *M. pruinosa* in Ukraine's list of Regulated Non-Quarantined Harmful Organisms to improve risk management strategies.

Evolution of parental care and sociality in small carpenter bees (*Ceratina* Latreille)

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Knowledge about the natural history of Hymenoptera with simple social structures is crucial for understanding the evolution of eusociality. *Ceratina* bees (Apidae) serve as an excellent taxon for conducting comparative studies due to their extensive species diversity and behavioral variations. The high local population densities and convenient nest processing enable the collection of large datasets within a relatively short time frame. In my research, I conducted a comprehensive analysis of the nesting strategies of 30 species of *Ceratina* bees, based on the examination of over 14,000 dissected nests. Among the species studied, the majority exhibit facultative social behavior, although strictly solitary species were also identified. Even in facultatively social species, solitary nesting prevails, with social nesting occurring at a frequency ranging from 1% to 30%. Social nests typically contain only two females, although nests with up to seven females were observed. It is worth noting that social nests often contain more brood cells than solitary nests. In the European subgenus *Euceratina*, adult females in social nests can be mother and daughters, but also full sisters. Additionally, associations between unrelated females were also detected. Only one female in a social nest reproduces, while the other female(s) do not have any offspring. Interestingly, males can also participate in brood care. Males were detected in many species at the stage of nest provisioning, however, true biparental care, wherein a male and female form a pair, has evolved once within the Palearctic subgenus *Euceratina*. This biparental care strategy persists despite the low paternity of guarding males, as they still enhance their fitness through long-term guarding. Biparental care appears to be an alternative strategy that evolved in response to multiple mating conditions, serving as an alternative to eusociality based on single-mating.

DNA (meta)barcoding of bee and wasp collected food sources resolves quantitative multi-trophic interaction networks

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Bees and wasps are tremendously important for our ecosystems as pollinators or as natural enemies of other arthropods. This group is in decline even though it is one of the most species rich taxa within insects, and has an enormous taxonomic, behavioral and functional diversity. To understand population drivers, comprehensive knowledge about top-down and bottom-up interactions, including all interaction partners, is needed. Investigating nests of trap-nesting bees and wasps enables us to shed light simultaneously on multi-trophic interactions between bees, wasps, their collected food resources and their natural enemies. However, until now, not all trophic interactions are included in trap nest research because of the challenges of identifying the food used by nesting bees and wasps. We reconstructed quantitative three- and four-trophic interaction networks of species in three apoid wasp families, using DNA barcoding. The obtained tripartite- and quadripartite networks encompassed natural enemy-wasp-spider and natural enemy-wasp-herbivore-plant interactions. Moreover, we identified so far undescribed Hymenoptera-prey interactions including prey species known as agricultural and forest pests. By establishing a workflow for accurate (meta)barcoding using nanopore MinION sequencing we intend to gain even deeper insights into bee and wasp multi-trophic interaction networks. The latter can provide valuable insights to better understand responses to environmental and biodiversity change, to investigate ecological theory and to reveal so far unknown feeding connections.

Recurrent genomic dynamics linked to parallel evolution of secondary phytophagy in Hymenoptera

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Repeated reversals towards secondary herbivory have occurred multiple times across the hymenopteran phylogeny and have been linked to increased rates of species diversification. This phenomenon indicates the significance of studying the genomic basis of dietary shifts in insects, as it can provide valuable insights into evolutionary innovation and adaptation mechanisms. In this project, we aim to investigate the genomic characteristics of specific groups within the order Hymenoptera, namely Aculeata and Chalcidoidea which descend from zoophagous ancestors but exhibit repeated reversals towards secondary phytophagy. Notable examples of such transitions are observed in gall-wasps and pollen-collecting bees, which have adopted a phytophagous lifestyle, while their closely related lineages have retained their zoophagous nature. This project builds on already available high-quality reference genomes and will be enhanced by newly sequenced genomes of species with high taxonomic relevance. To enhance our understanding of the evolutionary processes underlying the nutritional capabilities of Hymenoptera we use comparative genomics and transcriptomics to uncover genomic underpinnings of macroevolutionary dietary adaptations linked to e.g., the metabolism of plant secondary compounds, the composition of odorant receptors, gustatory receptor families, or carbon dioxide receptor genes. Further, we study genomic changes underlying evolutionary dietary shifts, testing the repeatability of gene gain and loss, and rapid evolution in regulatory sequences, transposable element dynamics, and gene copy numbers.

Faunistic revision of Estonian bees (Hymenoptera: Anthophila) and solitary wasps (Hymenoptera: Pompiloidea, Thynnoidea, Tiphioidea, Vespoidea) and regional extinction risk assessment

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Despite the importance of bees and wasps in the ecosystems, these groups have remained relatively poorly studied in Estonia. For instance, the most recent and only checklist of Estonian bees was published more than hundred years ago and checklists of only a few groups of Estonian solitary wasps have been published. Moreover, the specific situation (distribution, abundance, population trends) of each species remains unknown. Currently, insects and especially pollinators receive a lot of attention and awareness of their importance has increased significantly. Evidently, better understanding of Estonian bees and solitary wasps is needed. To overcome this deficiency in the knowledge of Estonian insect fauna, we reviewed all bee and solitary wasp specimens in public collections. Additionally, we collected new data during extensive fieldwork throughout Estonia. Precise data of all studied collection specimens as well as accumulated novel occurrence data is published using the web-platform PlutoF and is available at GBIF (Global Biodiversity Information Facility). Based on all available occurrence data we assessed extinction risk of all investigated Estonian species based on IUCN criteria and regional guidelines. Our study revealed that there are 281 bee and 101 solitary wasp species of the examined groups in Estonia. Until annotated species checklists are published, all the original data is available at the regional and global biodiversity databases named above, enabling its usage in various studies or simply the generation of species occurrences maps. Newly proposed red list categories enable to draw attention to the species that are threatened in Estonia. Altogether, 57 species of the studied taxa belong to the threatened categories, and 72% of the species were categorized as lower risk categories (Least Concern and Near Threatened). Notably, a high number (28) of species was not assessed because these were found in Estonia only recently and therefore can be considered as recent colonisations. However, this could also be at least partially explained by the intensified research of Estonian Hymenoptera fauna.

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Thelytoky in *Haplogonatopus oratorius* (Westwood): ecological traits and trans-Pacific distribution (Hymenoptera: Dryinidae)

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A pincer wasp, *Haplogonatopus oratorius* (Hymenoptera: Dryinidae) is a flightless parasitoid of planthoppers (Hemiptera: Delphacidae). It occurs mainly in the Palaearctic region but it is also known from the Pacific Islands. In Asia, males are common in rice paddies, however, an unknown asexual population was discovered, which does not inhabit rice paddies. This study aims to compare the ecological and genetic traits between the sexual and asexual populations and to investigate the role of host dispersal in their distribution. Fieldwork was conducted throughout Japan, and museum collections were used for morphological observations. The host and reproductive type were confirmed by breeding and COI gene sequencing, while 16S bacterial ribosomal RNA gene metabarcoding was conducted to analyze endosymbiotic bacteria. Phylogenetic relationships were reconstructed using COI, ITS, and genome-wide SNP data obtained through MIG-seq analysis. The results confirmed that the sexual and asexual populations were genetically isolated, with *Rickettsia* causing thelytokous parthenogenesis. The female of the sexual lineage attacks *Laodelphax striatellus* in rice paddies, while females of the asexual lineage prefer *Sogatella kolophon* and are abundant in grasslands and pastures, particularly in the southern Ryukyus. Morphologically, *H. oratorius* is very difficult to distinguish from *H. apicalis*, however, some surface sculptures indicate the species-specific difference and the asexual female of *H. oratorius* is slightly different from the sexual female. Thereby females from the Ogasawara and Pacific Islands in the museum collections were identified as asexual lineage of *H. oratorius* and no male was found. The asexual lineage of *H. oratorius* is common in the Oriental part of Japan, possibly because *L. striatellus* is a temperate species and *S. kolophon* is more abundant in tropical and subtropical regions, including the Southern Hemisphere. This planthopper has high dispersal ability and possibly carries dryinid larvae like other long-dispersal planthoppers. Although both populations are found in Japan, the oceanic distribution and the host preference suggest that the current distribution of the asexual lineage likely reflects the host dispersal, originating further southward.

Encounter with Indian parasitic wasps: discovering, deciphering host-parasitoid interactions and demarcating potential ones for biological control

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India is one of the 17 megadiverse countries of the world. Hymenoptera is one of the super-speciose taxa and includes many species of agricultural importance. Being associated with an agricultural organization gave me the opportunity to study parasitoid taxa associated with diverse agroecosytems. An overview of interesting discoveries from India is presented in this abstract. Many genera were reported for the first time from India and some novel biological information provided—*Coccygidium* (Braconidae), *Klabonosa* (Pteromalidae), *Pambolus* (Braconidae) from the Oriental region, *Tanaostigma* (Tanaostigmatidae) from the Old World, and *Doddifoenus* (Pteromalidae) from India. Many native parasitoid complexes of invasive pests (fall armyworm, cassava mealybug and South American tomato pinworm) have been discovered. With the help of specialist experts, diagnostic keys of many genera have been developed—*Megaprosternum* (Bethylidae), *Cassidibracon* (Braconidae), *Diolcogaster* (Braconidae), *Pambolus* (Braconidae), *Halticoptera* (Pteromalidae), *Anisopteromalus* (Pteromalidae), etc. Some species of rare braconid genera with not more than two or three species known from India have been recorded—*Asobara*, *Paroligoneurus,* etc. The first species descriptions for some genera were done—*Paroplitis* (Braconidae) and *Callocleonymus* (Pteromalidae). *Ooencyrtus xenasteiae* Hayat & Gupta (Encyrtidae) was discovered and described as the first parasitoid from *Xenasteia* sp. (Xenasteiidae, an extremely rare family of Diptera). The first comprehensive integrated study of 26 provisional *Glyptapanteles* species was made based on 60 populations reared from 35 host species, including 100+ individual caterpillar rearings (1100 wasp specimens pinned and 2000 in alcohol) from 12 different geographical locations of India (11 states and one Union territory). Protocols for laboratory mass rearing of housefly parasitoids, namely *Nesolynx thymus* (Eulophidae), *Spalangia cameroni* (Spalangiidae) and *Nasonia vitripennis* (Pteromalidae) were standardized and the technologies were commercialized in order to encourage organic pest control in poultry farming and managing housefly menace in garbage areas. I have prepared and submitted a national status report on the absence of primary parasitoids of invasive cassava mealybug in India in 2020 and instrumental in the importation of *Anagyrus lopezi* (De Santis) (Encytidae) into the country. I have contributed to the global biocontrol initiative, and since 2014, I have been involved with CABI-UK on the biological control of some of the world's 100 worst invasive plant species – *Hedychium* spp. and *Rubus* spp. Presently I am also involved in digitizing the types and vouchers in the museum in our institute.

First record of Eulophidae (Hymenoptera: Chalcidoidea) from Laos

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For many years, our attention has focused on the study of Eulophidae in Vietnam, Cambodia, Thailand, and Myanmar (Yefremova, 1994, 2009, 2013, 2015, 2016, 2017, 2018). To date, no species of Eulophidae have been recorded in Laos. Our work took place in the north of Laos in Xiankhung province, near Phonsavan, 19º29' N; 103º17' E, elevation 1130 m. Methodology: Three collection methods were used, namely: 1) collecting with Malaise traps for one year (October 2018 to September 2019), 2) rearing of parasitoids from mines of *Phyllonorycter acutissimae* (Kumata) (Gracillariidae) and *Coptotriche* sp. (Tischeriidae) on oaks (October 2018–February 2019), and 3) sweeping with nets (October–November 2018). In terms of percentage of species obtained from each method, the results were Malaise trap (54%), rearing (29%), and sweeping (17%). In terms of the number of specimens, collecting by Malaise trap and sweeping both yielded around 35% of the total specimens collected, with 30% obtained by rearing. In total, 90 species of Eulophidae were collected, consisting of the following subfamilies: Eulophinae (14 genera/40 species), Tetrastichinae (17/33), and Entedoninae (12/16). The percentages of specimens collected were Tetratsichinae (47.4%), Eulophinae (30.4%), and Entedoninae (22.2%). Among Eulophinae, the most numerous genus was *Elasmus* (13 species), collected by Malaise trap, with other genera in this subfamily yielding 1–4 species. Among Entedoninae, only *Pediobius* included 4 species, with other genera including 1–2 species. *Pleurotroppopsis japonica*, reared from the tischeriid *Coptotriche*, was the species with the highest number of specimens. Tetrastichinae were mainly collected with nets and Malaise traps. Within this subfamily, *Aprostocetus*, *Neotrichoporoides*, and *Tamarixia* contained the most species (5-6), with the remaining genera containing 1-2 species. Conclusion: The genera *Kolopterna*, *Pronotalia* (Tetrastichinae), and *Ophelimus* (Eulophinae) are the first records in the Oriental region; previously, the first two mentioned had been found in the Palearctic, and the latter only in Australia. New species found in Eulophinae belong to the genera *Pnigalio*, *Elasmus*, and *Diglyphmorphomyia*, and in Tetratsichinae belong to the genera *Aprostocetus*, *Kolopterna*, *Neotrichoporoide*, and *Pronotalia*. Rearing allowed identification of new hosts for Eulophinae (*Sympiesis*, *Diglyphomorphomyia*), Entedoninae (*Pleurotroppopsis*, *Closterocerus*) and Tetratsichinae (*Neotrichoporoides* and *Chouioia cunea* Yang).

The updated checklist of gall-wasps (Hymenoptera: Cynipidae: Cynipinae) of Romania including rare and new species for this area

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The present paper is a synopsis of gallwasp species (Cynipidae), including inquiline species, recorded in Romania from the first citation until now. For this review, data available in the literature were used, to which results from the author were added. All taxa were presented in alphabetical order; each species is followed by current synonyms, host plant, gall type and references arranged chronologically. The most recent nomenclature and taxonomic classification were adopted. The first list of species of gallwasps and inquilines – Cynipidae from Romania, was published by Ionescu (1957), who listed 26 genera (22 gall-makers and 4 inquiline) and 108 species (96 gall-makers and 12 inquiline). Later, the same author (Ionescu, 1973) quoted 27 genera (23 gall-makers and 4 inquilines) with a total of 124 species (112 gall-makers and 12 inquilines). In both lists, the author considered the genus *Synophrus* (with the species *Synophrus politus* Htg.) as belonging to the gall-making cynipid and not to the group of inquiline species. With increasing research and samplings, the old list became outdated. In a period of more then 50 years since these lists, numerous new data have been reported; e.g. *Endocaulonia bicolor* Ionescu & Roman, 1960 was synonymised with *Panteliella fedtschenkoi* (Rübs.) and *Weldiella aequalis* Ionescu & Roman, 1962 was synonymised with *Cecconia valerianellae* (Thoms.) (both in Melika, 2006); new species for the Romania's fauna - e.g. *Aulacidea follioti* Barb., *Andricus burgundus* Gir., *Andricus glutinosus* (Gir.), *Andricus trotteri* Kieff., *Dryocosmus kuriphilus* Yasumatsu, 1951 etc.; a new genus was also reported: *Iraella* Nieves-Aldrey, 1994, with the description of a new species for science, *Iraella ionescui* Pujade-Villar & Șchiopu, 2015. Thus, the updated list of Romanian gall-wasps includes 30 genera (25 gall-makers and 5 inquilines) for a total of 130 species (113 gall-makers and 17 inquilines). Genera and species: *Andricus* (56 species); *Cynips* (7); *Neuroterus* (6); *Aulacidea* and *Diplolepis* (5); *Cerroneuroterus* and *Phanacis* (4); *Aylax*, *Callirhytis*, *Diastrophus*, *Dryocosmus*, *Isocolus*, *Liposthenes*, *Pseudoneuroterus* and *Trigonaspis* (2); *Aphelonyx*, *Barbotinia*, *Biorhyza*, *Cecconia*, *Chilaspis*, *Iraella*, *Neaylax*, *Panteliella*, *Pediaspis*, *Xestophanes* (1). Inquilines: *Synergus* (12); *Periclistus* (2); *Ceroptres, Saphonecrus, Synophrus* (1). Compared to the ca. 280 species of Cynipidae from Europe (Nieves-Aldrey, 2001) or the ca. 300 species from the Western Palaearctic (Dalla Torre & Kieffer, 1910; Melika, 2006; Abe *et al*., 2007), the current number of Romanian species represents 46 % and 44% respectively.

Getting a grasp on the diversity Diapriidae (Hymenoptera): a case study

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Diapriidae (Hymenoptera, Proctotrupoidea) is a highly abundant and megadiverse group of parasitoid wasps. Despite occupying all terrestrial habitat types worldwide, they are immensely understudied because they are challenging to identify due to their small size, huge distribution areas and similar appearance. The unknown diapriid diversity even in Germany is estimated to be 50% of all species. Since 2020, the German Barcode of Life (GBOL) initiative has launched its third phase, where several challenging groups of Diptera and Hymenoptera (one of which being Diapriidae) are tackled. These so-called dark taxa are studied using a wide range of innovative approaches (e.g. AI, DNA-barcoding, high-resolution imaging methods etc). Here, we highlight the research that is being conducted on Diapriidae, and present interesting findings obtained from a single sampling site in Bavaria. Although we are analyzing and presenting just a fraction of our data, we have recovered an exceptionally high number of first records for Diapriidae.

The Finnish National Pollinator Monitoring Scheme – Results of the first year

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Long-term monitoring of insects is important to detect population trends and assess the effects of land use and conservation efforts. In 2022, a wide-scale monitoring program, the National Pollinator Monitoring Scheme (PÖLYSEURA), was launched in Finland. It focuses on the most important pollinator groups, bees, hoverflies, and day-active Lepidoptera, as well as social wasps. The scheme is funded by the Finnish Ministry of Environment and coordinated by the Finnish Environment Institute SYKE. During the first year, pollinators were sampled at 134 sites around the country. The study sites represented the main habitat types for pollinators in Finland: meadows (28 sites), commercial forests (20), protected forests (16), forest road verges (20), cultivated field margins (40) and alpine fells (10). Two 250 meter transect-lines and four standard pan traps with blue, white and yellow bowls were placed in each site, with some exceptions. Transect counts were made four times and the pan traps were emptied three times during the two-month sampling period of June and July. A total of 4,207 bumblebees of 29 species and 491 honeybees were observed in the transects. The number of individuals and species in the pan trap material was 5,172/31 for bumblebees, 3,391/106 for solitary bees, 617/1 for honeybees and 449/10 for social wasps. The most abundant bumblebee, solitary bee and social wasp species were *Bombus pratorum*, *Lasioglossum rufitarse* and *Dolichovespula norwegica*. On average, 9.9 solitary bee, 6.9 bumblebee and 1.6 social wasp species were observed per site. Species richness was highest on field margins for bumblebees and on meadows for solitary bees, while forest road verges had the highest average abundances of both bumblebees and solitary bees. Bumblebee abundance was also high in alpine fells and protected forests. The results of the first year of monitoring are promising and provide important knowledge on the current state of pollinators in Finland. In the future, the scheme will also produce quantitative data on the yearly fluctuations, long-term trends, and habitat requirements of many previously poorly studied taxa.

Why are there so few species of Ichneumonidae?

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A major endeavor in evolutionary endeavors concerns understanding how highly speciose clades have attained their current levels of species richness. A common assumption is that remarkably diverse groups have undergone accelerated rates of speciation and/or enjoyed particular ecological success. However, clades are not uniform units and therefore their current levels of species richness need to be taken in phylogenetic and chronological context. For instance, while the Hymenoptera are undoubtedly one of the most speciose groups of animals on Earth, evidence suggests that they are sister to all other holometabolous insects. Therefore, their diversity is not particularly impressive when compared to that of their sister clade, i.e. Lepidoptera, Diptera, Coleoptera and other small orders *combined*. Recent diversification analyses suggest that putative “key innovations” in Hymenoptera, such as the wasp waist or parasitoidism, did not immediately cause large spurts of diversification in the order. Similarly, recent analyses indicate that Ichneumonoidea may be sister to all other apocritans. If that is the case, even though Ichneumonidae are the most species-rich family of Hymenoptera, their diversity may be considerate relatively depauperate compared to other comparable clades. In this talk we will explore major aspects about ichneumonid evolution and diversification that are beginning to be elucidated and some that have still eluded researchers. One relevant aspect is the importance of phytophagy in the diversification of Hymenoptera, as evidenced by recent research, and how ichneumonids seem to have poorly explored the phytophagous niche. Additionally, I will present evidence showing that koinobiont lineages have accelerated rates of diversification within Ichneumonidae when compared to idiobiont groups, as well as higher rates of phenotypic evolution. Finally, I will discuss the elusive latitudinal gradients of diversity in the global ichneumonid fauna and how this may (or not) relate to their current levels of species richness.

Contributions to our knowledge of the Mutillidae (Hymenoptera) of the Texas Hill Country (U.S.A.)

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Our understanding of the velvet ant diversity in North America is likely greater than it is for more diverse areas in South America, Africa, or Australia. However, we still have much to discover about this charismatic family of wasps, even in regions where the fauna is presumptively better-known. In May 2021, I established a Townes-style Malaise trap in Gillespie County, Texas, with the dual purpose of documenting the entomofauna of the region as well as creating what I hope will become a long-term insect dataset from this biodiverse region. The trap has been running continuously for two years and has yielded over 600 velvet-ant specimens to date. Periodic hand-collecting efforts have produced dozens of additional specimens, primarily females. Nine genera and 25 species have been recorded so far from this 1,500 acre site. I summarize the diversity of mutillids collected and discuss my findings in the context of published mutillid records in the United States. I also highlight some of the other Hymenoptera found at this site.