# Systematikdagarna 2022

November 21—22
Swedish Museum of Natural History

## Abstracts and participants

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# Keynotes

## Evolution and systematics of Fagaceae: Integrating morphology, fossils and molecular phylogenies.

**Thomas Denk**
*Deparment of Paleobiology, Swedish Museum of Natural History*

The plant family Fagaceae (beech family) comprises 10 extant genera and about 1,000 tree species with a wide distribution across the Northern Hemisphere and range extensions into the Southern Hemisphere. Fagaceae have been extensively studied using phylogenomic analyses and intra-familial relationships are now well understood. These phylogenetic frameworks of extant taxa are crucial for the study of character evolution and identifying phylogenetically informative morphological characters back through time. Applied to the rich fossil record they allow us to trace evolutionary histories of individual members of Fagaceae. I will summarize currently available evidence for Cenozoic radiations of modern Fagaceae during the past 66 million years using the fossil records of dispersed pollen and other reproductive structures, and leaf fossils. I will also discuss some recent biogeographic ideas about northern versus southern hemispheric dispersal routes of Fagaceae.

## Sperm evolution across the animal tree of life

**John Fitzpatrick**
*Department of Zoology, Stockholm University*

Explaining the extraordinary morphological diversity of sperm – the most diverse cell type known – has been a major goal of evolutionary biologists for more than a century. Male-male competition, female-sperm interactions and variation in fertilization environments are commonly hypothesized to be key selective forces shaping sperm evolution. However, most studies examining sperm evolution focus at the clade, family or genus level. Consequently, our understanding of the factors shaping sperm evolution across the animal tree of life remains limited. In this talk, I draw on examples spanning the animal tree of life to describe a general framework for understanding sperm evolution. I show that sperm competition, an extended for of male-male competition that occurs after mating, and female-sperm interactions, which allow females to exert selection on sperm after mating, are key drivers of sperm morphological diversification. However, the way that sperm competition and female-sperm interactions influence sperm evolution changes following evolutionary transitions in fertilization environments, from external to internal fertilization. I argue that evolutionary transitions to internal fertilization supercharge sperm evolution by increasing the scope for female-sperm interactions and changing the rules for how sperm compete to fertilize eggs. Using this novel framework, we can make sense of sperm diversity across the animal tree of life and can even explain cases of sperm ‘gigantism’. Together, this work highlights that understanding sperm evolution requires careful consideration of female reproductive biology.

## The Natural History of leeches: evolution, blood and collections.

**Sebastian Kvist**
*Head of Science, Swedish Museum of Natural History*

I will present two central themes in this talk. The first focuses on the research and ongoing work to enhance the collections at the Swedish Museum of Natural History. In this context, I will provide an overview of the current state and provide a vision for the future. In the second theme, I will provide a background of my own research into the evolution of blood feeding in leeches, which entails collection-based strategies coupled with deep sequencing. Results suggest that ancestral leeches were indeed capable of anticoagulation and that blood feeding as a strategy has been lost on several occasions over the millions of years of evolution that the group has undergone. I discuss the implications of this from the perspective of both leech natural history and the medical applications of these charismatic critters.

# Oral presentations

## Untangling the *Derogenes varicus* species complex: description of a new species of *Derogenes* (Trematoda: Derogenidae) from *Hippoglossoides platessoides* (Teleostei, Pleuronectidae) from Scandinavian waters and redescription of some poorly known *Derogenes* species

**Chahinez Bouguerche**, Mohammed Ahmed & Thomas H. Cribb
*Department of Zoology, Swedish Museum of Natural History*

*Derogenes varicus* (Müller, 1784) is a trematode with a lack of host specificity, a universal distribution, and a wide range of definitive hosts. Several studies suggested that *D. varicus* represents a species complex. During parasitological examination of trematodes parasites of fish from Scandinavian waters (Sweden and Norway), we found specimens of *D. varicus* in the stomach of *Merlangius merlangus* off Sweden, and in *Gadus morhua* and *Hippoglossoides platessoides* off Norway; we compared them to *D. varicus* from the type-host, the Atlantic salmon *Salmo salar*, to verify their conspecificty. All the newly generated sequences (28S, ITS2 and cox1) of *D. varicus* clustered within a single clade DV1. A sequence of *D. varicus* from *S. salar* from Norway, i.e., close to the type locality, Danish waters clustered within the DV1 clade without having a distinct branche. We consider thus that that the lineage DV1 is in fact *D. varicus sensu stricto*. Additionally, specimens from *Merlangius merlangus* had a similar morphology and anatomy to those of *D. varicus* from *Limanda limanda*, *G. morhua* and *M. scorpius* from T. Odhner's collection, which supports the presence of a single species in the DV1 lineage. However, the interspecific variations between *Derogenes* from *Hippoglossoides platessoides* and other congeneric species reached 8–9% in 28S and 19% in cox1 and it is described as a new species.

We also revise type specimens of *Derogenes minor* Looss, 1901 from the A. Looss collection that are currently preserved in the Swedish Museum of Natural History and provide redescription of the latter species and of the type species of the genus, *Derogenes ruber* Lühe, 1900 and highlight the fragility of characters used to distinguish *Derogenes* species. Our results suggest that a molecular re-evaluation and integrative taxonomy of other *Derogenes varicus*-like specimens from various fish hosts combining morphology, DNA barcodes, and museum specimens could reveal the existence of additional parasite biodiversity.

# Understanding the origin of the incongruence between phenotypic patterns and genetic diversity in the Yellow and Citrine Wagtails

**Ximena Alva Caballero**
***Student**, Animal Ecology, Uppsala University*

The Yellow Wagtail complex (comprising the *Motacilla flava* and *Motacilla tschutschensis* subspecies) is broadly distributed in Eurasia, north Africa, and Alaska. It is remarkably polytypic as it presents 13 recognized subspecies, most of which are notably different in adult male breeding plumage. Their phenotypic variation, the existence of multiple described hybrid zones, and the appearance of similar-looking phenotypes in widely separated geographic areas have given rise to numerous phylogenetic studies in order to shed light on their taxonomy. However, different molecular datasets have produced incongruent results. The most recent study done on the topic used mt-DNA, SNPs, and introns data, and it concluded that there is conflicting support for the monophyly of the Yellow Wagtail complex. The SNP data pointed to a monophyletic group, while the mt-DNA and introns data recovered the group as paraphyletic. When paraphyletic, the clade comprising the *M. tschutschensis* subspecies appeared as a sister clade to *Motacilla citreola* (Citrine Wagtail). *M. citreola* is broadly sympatric with the Yellow Wagtails and phenotypically, is quite distinct from the *M. flava* and *M. tschutschensis* subspecies. In this study, we have taken a deeper look at the dynamics among the Yellow Wagtails subspecies by carrying out population structure and evolutionary relationship analyses that suggest a discrepancy between phenotype and genetic relatedness. We found that one of the subspecies considered, *M. t. plexa,* appears to be a true hybrid between *M. t. tschutschensis* and *M. f. thunbergi.* We have also tried to resolve the phylogenetic relationship between the *M. flava* and *M. tschutschensis* subspecies and *M. citreola*, to gain some insight into their shared evolutionary history. Early results show that introgression events among subspecies of *M. flava* and *M. tschutschensis* with *M. citreola* might be behind the puzzling phylogenetic pattern.

# Assessing the molecular diversity of Sargassum (Phaeophyceae) in the NE Atlantic Ocean

**Daniel Álvarez-Canali** & Ana Tronholm
***Student**, Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de La Laguna*

The brown algal genus Sargassum is distributed worldwide and plays a key role as habitat-forming in tropical and subtropical regions where it can form dense submarine forests. Species have traditionally been classified under several subgenera, sections, subsections, and series to reflect the evolutionary relationships. However, these classifications were until recently based only on morphological characters that show high variability in response to environmental conditions. DNA-based phylogenies have proven critical in delimiting the species and we have a better understanding now of most clades with one exception: the Atlantic species of Sargassum, subgenus Sargassum. Recent molecular studies have tried to evaluate its diversity with poor results, where Atlantic species show little to no diversity for the markers that have proven useful in discerning Pacific and Indian taxa, probably due to a recent colonization and radiation of the Atlantic basin. Here, we aim to assess the species molecular diversity of Sargassum in the NE Atlantic Ocean, exploring traditional and new genetic markers to support the current morphological and ecological diversity.

# Playing golf in the deep-sea! A revision of golf-ball sponges (Demospongiae, Tetillidae) from the North Atlantic

**Paco Cardenas**
*Pharmaceutical Biosciences, Uppsala University*

The Tetillidae Sollas, 1886 are massive spherical sponges that can reach 20 cm in diameter and are found worldwide. Golf-ball sponges (genus *Craniella*) are deep-sea Tetillidae, with many North Atlantic species poorly described in the 18th and 19th century. Consequently, most of these species are poorly known and most taxonomists tend to overuse the single name *Craniella cranium* (Müller, 1976) for specimens collected in the North Atlantic. We have obtained new material from the Norwegian/Swedish coast, the Norwegian/Greenland Seas, Rosemary Bank (off Scotland), Iceland, off Newfoundland/Labrador/Baffin Island, Brittany and the Balearic Islands. The material has been used for the partial sequencing of the cytochrome c oxidase subunit 1 (COI) and 28S (C1-C2 fragment). Type material of most species and their synonyms was also examined. The World Register of Marine Species (WoRMS) currently lists 9 valid species in the North Atlantic region. The literature and our results indicate the presence of at least 17 valid *Craniella* species with four species resurrected, two species reallocated to this genus and five potential new species. The only *Craniella* found in Swedish waters is not *Craniella cranium* but *Craniella pilosa*, a species to be resurrected.

# Species identification and diagnosis with shape characters for females cephalothorax of the genus *Stylops* (Strepsiptera: Stylopidae) using geometric morphometrics and an illustrated key to Nordic species

**María Alejandra Álvarez Covelli**
***Student***, *Department of Zoology, Swedish Museum of Natural History*

Strepsiptera is an obligate endoparasitic insect order with a problematic taxonomy ever since its discovery. Most morphological characters from males were used in taxonomy and classification of the group. Later on, characters from female cephalothorax started to be taken into account. However, these characters are often not qualitatively easy to define but of quantitative nature, specifically variation in shape, outlines, and curvature. In addition, it has been shown that there is a morphological variation depending on the host that the species is parasitizing. On the other hand, geometric morphometrics is a powerful statistical method for species identification process for different insect groups when it comes to shape variation and therefore is a good tool to be used for species delimitation within Strepsiptera.

The genus *Stylops* (Strepsiptera: Stylopidae) is one of the most abundant genera in Europe and it is known to parasite hymenopterans from the genus Andrena only. Nevertheless, in the Nordic countries uncertainty remains as to how many species of *Stylops* are present, and therefore more information is needed to understand and assess the status of the diversity of *Stylops* and to clarify host-parasite relationships.

Because of the above, this project has four main goals i) evaluate the taxonomic value of morphological characters that have been used for the identification of species within the genus *Stylops*, ii) propose new morphological shape characters of females based on geometric morphometric analysis, iii) test if geometric morphometrics of standard landmarks or pseudo-landmarks can discriminate species that occasionally share the same host species, and, iv) map shape characters across a molecular phylogeny of the genus *Stylops*.

## To be or not to be a name-bearer - more or less untypical type examples

**Mattias Forshage**
*Department of Zoology, Swedish Museum of Natural History*

Species and groups in zoology are codified by names regulated by a book of rules (the code). But before the code, original specimens were treated in very different ways. And since the arrival of the code, rules have changed over time, and authors have not always lived up to best practice. A view of various problems involved is provided by a few highlights from the entomology collections at the Stockholm museum. A few fascinating oddballs from the history of zoology and a few happy rediscoveries will be presented in the process.

## Taxonomic and faunistic revision of Swedish big-headed flies (Diptera: Pipunculidae)

**Mihaly Földvari**
*Department of Zoology, Swedish Museum of Natural History*

Members of the family of big-headed flies are parasitoids of leafhoppers and they have large compound eyes to detect their host as well as to localize mating partners. Their identification has its difficulties and the Swedish fauna has been understudied and lacked information on the species currently reported from the country and the updated distribution lists with taxonomic changes. The Swedish Malaise Trap Program provided extensive material throughout the country with valuable time-series data on the occurrence of the species and this was extended by the study of museum collections and individual field trips to interesting habitats. More than 8000 specimens were part of the study and various new characters were found to ease the identification and connections to North American species were revealed using barcode data.

## Seasonal environments drive convergence in life-history traits across butterfly adaptive radiations

**Sridhar Halali**
*Department of Biology, Lund University*

Earth has repeatedly witnessed climate change events throughout its history. The global expansion of savannahs during the Miocene (23-5 MYA) is one such dramatic example of climate-driven biome evolution, and their colonization from forests has resulted in explosive diversification across the tree of life. However, what adaptations were required to colonize seasonal savannahs? I use hyper-diverse parallel radiations of Mycalesina butterflies from mainland Africa, Asia, and Madagascar to address this question. Firstly, ancestral state reconstruction revealed that early forest-linked lineages began invading savannahs around 10-3 MYA across radiations. Secondly, I show that the timing of the evolution of reproductive diapause, a key life-history strategy, matches with forest to savannah shifts, and this strategy evolved in a habitat-dependent manner. Finally, by performing common garden experiments, I show that savannah species consistently adopt a ‘faster ’life-history strategy compared to forest species across all radiations. These findings demonstrate that adaptations in a suite of life-history traits were crucial in allowing Mycalesina butterflies to colonize and persist in savannahs and resulting in rapid diversification.

## A crowd-sourced museomic project to assess hybrid content in a rare avian vagrant

**Martin Irestedt,** Filip Thörn, Per G. P. Ericson, Hein van Grouw, Alexander Hellquist, Frank Johansson & Johan Nylander
*Department for Bioinformatics and Genetics, Swedish Museum of Natural History*

For most birdwatchers it is important to identify the observed birds to species level to keep track of and count the observations. The current crowed-sourced project was initiated when two presumed azure tits (*Cyanistes cyanus*), observed by hundreds of Swedish birdwatchers, were rejected as hybrids based on minor plumage deviations assumed to indicate hybrid contents from the European blue tit (*Cyanistes caeruleus*). The aim with the project was to correlate morphological variation with the amount of genomic hybrid content, by re-sequencing the genomes of presumed hybrids specimens in museum collections with varying plumages. The results confirm that hybrids morphologically assessed as first generation backcrosses, so called Pleske's tits, are first generation hybrids (F1 hybrids). Individuals, whose plumages are similar to azure tits, but assessed as hybrids based on minor morphological deviations, all vary in their degree of hybrid content. However, also individuals morphological recognized as pure azure tits expressed similar degrees of hybrid content. The results indicate that hybrid content may be widespread in azure tits in the eastern part of its distribution area, and that all azure tits observed in Europe outside its natural distribution may have some degree of hybrid origin. Although studies like this have narrow scopes that may have difficulties attracting research funds, they can be of great interest for the public as keen birdwatchers in this case. We argue that decreased costs and improved analytical tools for museomic projects open the doors for genomic crowed-sourced projects that may not address outstanding biological questions but have a major interest for lay citizens such as birdwatchers.

## Phylogenetic relationships of Eomyidae to other clades within Geomorpha (Rodentia, Mammalia).

**Daniela Kalthoff,** Thomas Mörs
*Department of Zoology, Swedish Museum of Natural History*

The extinct family of Eomyidae comprises small- to medium-bodied mouse-like rodents with a Holarctic distribution. The phylogenetic relationships of eomyids not yet resolved. Craniodental characters place them as closest relatives to Geomyoidea in the infraorder Geomorpha including fossil and extant New World Pocket Mice (Heteromyidae) and Pocket Gophers (Geomyidae), and often also the extinct Heliscomyidae and/or Florentiamyidae. Here, we present results from lower incisor enamel microstructure analysis supporting the alternative view that Eomyidae should be placed outside Geomorpha. At a minimum age of late Eocene (Duchesnean/Chadronian), Eomyidae show a highly apomorphic schmelzmuster with longitudinally oriented, uniserial Hunter-Schreger bands (HSB) in a two-or three-fold portio interna (PI), not present in any of the other families. In fact, the three-fold PI in Eomyidae is a previous unknown feature and unique within Rodentia. Geomyidae and Heteromyidae on the other hand are unique in sharing modified radial enamel as biomechanical reinforcement of the lower incisors to prevent structural failure under increased reaction forces due to significant burrowing activities (including chisel-tooth digging), underground feeding, and feeding on abrasive, fiber-rich plants and plant parts. Modified radial enamel in Geomyoidea is present since the early Oligocene (earliest Arikareean) and a retained plesiomorphic character in some extant taxa. The extinct Heliscomyidae and Florentiamyidae show moderately derived schmelzmuster types, which are widespread among rodents and lack special adaptations as seen in Eomyidae and in Geomyoidea. From the enamel microstructure perspective, Eomyidae are very different, higher evolved, and should rather

be regarded as sister group to Geomorpha, possibly together with Pipestoneomyidae with whom they share longitudinal HSB already at Chadronian times.

## Morphology or DNA? Monitoring insects using a hybrid method

**Mårten Klinth,** Håkan Johansson, Harald Havnås, Dave Karlsson
*Station Linné*

With the current alarming publications on the decline of insect biomass and diversity the need for a national monitoring of the Swedish insect fauna has never been higher. Monitoring targets two main questions: which species are present and what is their abundance? Traditional morphological sorting can answer both questions but is time consuming. Modern metabarcoding methods are fast and can answer which species that are present but struggles with estimating their abundance. We propose a hybrid method where a subset of specimens from a sample are selected and barcoded using efficient MinION technology. The selection of putative species based on their morphology allows us to estimate their abundance, and identifying the species using barcoding is faster and more robust than relying on morphology alone. This method has been used to great success in an ongoing monitoring of insects in four county boards in northern Sweden, with over 1000 identified species in a single Malaise trap.

## Is the relationship in lichens Liberal or Traditional? and how much it is effected by the climate change?

**Alica Košuthová**
*Department of Botany, Swedish Museum of Natural History*

With rare exceptions, the shape and appearance of the lichen are determined by the fungal partner. Besides the morphology, also fungal DNA-barcoding marker is crutial for the lichen identification. However, we uncovered that photobiont identity and their different morphotypes can corresponded to the lichen phenotype and separate the taxa. Additionally, environmental factors, such as climatic factors, soil chemistry and geography are considered as major factors affecting lichen symbiosis. We are here to revise the lichen symbiosis as a network of relationships to be determine how environmental limit or support the associations between the symbiotic partners. We will discuss if fungal partners are able to widen their ecological niches through photobiont switching.

## Closely related Tephritis flies (Diptera: Tephritidae) have closely related host plants

**Emma Kärrnäs,** Zachary Nolen, Hamid Ghanavi, Severyn Korneyev, Rune Bygebjerg,
Niklas Wahlberg & Anna Runemark
***Student**, Biology, Lund University*

The interactions between insects and plants have rendered them among the most species rich eukaryotic species groups, making them an excellent system for studying processes driving diversification. The Tephritis peacock flies (160 described species) are one genus that has diversified following specialisation on different plant taxa in the family Asteraceae. The variation in the degree of specialisation within Tephritis makes the genus a great system for understanding how species colonise novel hosts, and the consequences of this process for diversification. However, to truly understand the diversification a solid understanding of the phylogeny of both the flies and the host plant taxa is needed.

Here, we present the first well-supported molecular phylogeny of the genus Tephritis based on whole genome shotgun sequencing. The results suggest that there is a clear phylogenetic component to host use, as more closely related Tephritis species tend to have more closely related host plants. Interestingly, my findings offer some support to the oscillation hypothesis, stating that repeated cycles of specialisation and generalisation can be important drivers of diversification.

## When taxonomists disagree: Resolving obscurities in genus *Stylops* (Strepsiptera) with phylogenomics

**Meri Lähteenaro**, Johannes Bergsten, Johan Nylander & Jakub Straka
***Student**, Department of Zoology, Swedish Museum of Natural History*

Species diversity estimates of the twisted-winged parasite genus *Stylops* in West Palaearctic region has varied drastically over the years, due to varying host specificity concepts used by taxonomist. Estimates of the diversity have ranged from over fifty species to a single species, *S.melittae*, in Europe. Though the supergeneralist concept has been discarded, discrepancies among taxonomist about the species diversity still persist. We used phylogenomic species delimitation methods to test the species limits of this morphologically challenging genus, as well as to establish new host associations for the species. Over 150 individuals from nearly 80 host species were whole-genome sequenced. Close to 3000 orthologous genes were used in the species delimitation analyses. Species limits were tested using BPP and SODA. Here we present the preliminary results from the species delimitation analyses as well as discuss the implications they may have on the taxonomy of the genus in Europe.

## Systematics through song: a look at *Mirafra cantillans* & *Mirafra javanica* vocalizations

**Alexia M'Bark**
***Student**, Animal Ecology, Uppsala University*

*Mirafra javanica* (Horsfield's or Australasian Bushlark) and *Mirafra cantillans* (Singing Bushlark) have been traditionally considered to be separate species, with ranges from western Africa to Bangladesh (*M. cantillans)* and from Myanmar to Australia (*M. javanica)*. Molecular studies (Alstrom et al. 2013) suggest they may be part of a single species instead. However, if their vocalizations are markedly different, these populations would likely not interbreed if they came into contact. By comparing the vocalizations of individuals within this complex throughout their broad range, this research used in this presentation aims to look into the evolution of the vocalizations of this species complex, and the implications they may have for the taxonomy of these species, including any reproductive barriers that might occur due to the differences in songs. The research in this presentation was conducted on over 160 individuals (1300+ Strophes) from this species complex, ranging from Senegal to eastern Australia. The program Raven Pro was used to produce sonograms, which were compared to one another and checked for mimicry. Measurements from these sonograms were then further analyzed in R. The results from a Linear Discriminant Analysis show little differentiation between the vocalizations for the measured songs, however, the Indian population does stand out. This supports the hypothesis that *Mirafra cantillans* and *Mirafra javanica* should be treated as a single species. Further analyses, including a confusion matrix, will continue to be made with this dataset.

## A museomics approach to determine population dynamics in an endemic New Guinean bird family

**Ingo A. Müller**, Mozes Blom, John P. Dumbacher, Gibson Maiah, Knud A. Jønsson
& Martin Irestedt
***Student****, Department of Zoology / Bioinformatics and Genetics, Swedish Museum of Natural History*

New Guinea, the largest tropical island, is hyper-diverse and harbours an avifauna with many endemic groups such as the family Melampittidae, which consists of two monotypic genera: *Melampitta lugubris* (Lesser Melampitta) and *Megalampitta gigantea* (Greater Melampitta). Both *Melampitta* species exhibit scattered and disconnected distributions across New Guinea. While the Lesser *Melampitta* is rather common and found in most mountain regions of the island, the Greater *Melampitta* is elusive and known from only a few localities in isolated pockets on New Guinea with very specific habitats of limestone and sinkholes. In this project we apply museomics and have resequenced the genomes of all known *Megalampitta* samples hosted in museum collections as well as 24 Melampittae across their distribution. We observed that *Megalampitta* appears as a panmictic populations while *Melampitta* consists of multiple distinct populations. This work sheds new light on the mechanisms which shaped the intriguing distribution of this family and is a prime example of the importance of museum collections for genomic studies of poorly known and rare species.

## On trees and vines – attempting to solve the phylogenetic relationships in Suberitida

**Raquel Pereira** & Mikael Thollesson
*Department of Organismal Biology, Uppsala Univeristy*

More than two decades have passed since halichondrids and suberitids were encountered together in a phylogenetic analysis. Since then, numerous studies have shown that families Halichondriidae and Suberitidae are paraphyletic with intertwining clades among them. These groups together with Stylocordyla became unified as the order Suberitida in 2015, but attempts to resolve the phylogeny within Suberitida has been wanting. Here we present a new phylogenetic hypothesis for the order using both museum and freshly collected material and three molecular markers (28S, 18S and coxI). The phylogeny shows, among other things, at least two separated clades with species currently assigned to Suberites: a) one containing *S. domuncula* and species form NE Atlantic and characterised by a confused skeleton while b) a second clade containing *S. massa* and species from e.g., Caribbean (*S. aurantiacus*) and Indonesia (*S. diversicolor*) have a radial skeleton near the surface of the sponge. Some implications are that Suberites is split into two genera and Protosuberites and Terpios will be part of Halichondriidae.

## Integrating over datasets to resolve the systematics of the spiny footed lizard *Acanthodactylus erythrurus*

**Loïs Rancilhac**
*Animal Ecology, Uppsala University*

The spiny footed lizard *Acanthodactylus erythrurus* is a widespread species in semi-arid habitats in North-Africa and the Iberian Peninsula. Recent studies based on multi-locus and morphometric data showed that this taxon is in fact a species complex, with two new species described from the Moroccan High Atlas. Especially, this study highlighted substantial genetic divergence among the remaining Moroccan populations, which can be divided into 11 candidate lineages. In order to determine whether these genetic groups represent vicariant units (and potentially candidate species), we analyzed nine nuclear loci from 330 samples covering all Moroccan populations. We found that part of this genetic diversity is the result of Isolation by Distance, and that the populations can be divided into four groups separated by barriers to gene flow. Using RADseq data, we investigated the contact zone between two of these groups and found a very steep transition, consistent with species level lineages.

## Can genomics unlock the evolutionary history of Myotis bats?

**Victoria Twort**, Veronika Laine, Flora Whiting-Fawcett & Fernanda Ito
*BatLab Finland, Finnish Museum of Natural History*

Myotis are a diverse and widespread genus that represents one of the most successful mammal radiations in the world, with recent studies highlighting rampant phylogenetic conflict. We seek to explore this discordance with an extensive genomic dataset (currently > 150 individuals from ~30 species). Phylogenetic hypotheses are being constructed using a variety of genetic markers to explore the conflict, biogeographic histories and diversification shifts. To date phylogenies have been constructed from mitochondrial genomes and single copy genes. Our results provide a first insight into the large-scale Myotis evolutionary history using a gene-based approach and highlights the confounding results based on mitochondrial data. By examining the evolutionary history of Myotis using a variety of datasets we aim to develop a better understanding of not only the relationships but also what factors have been driving their evolutionary, diversification and biogeographic patterns.

## What’s all the fuzz about? – The taxonomic value of capitulum characters of *Scorzoneroides autumnalis* (Asteraceae)

**Groa Valgerdur Ingimundardottir**
***Student**, Department of Biology, Lund University*

Hairs are often important characters in identification keys and in the description of vascular plant species and varieties. However, their taxonomic value is rarely evaluated. *Scorzoneroides autumnalis*, which grows in a wide range of habitats in temperate and subarctic climates, has been divided into several varieties, based to a large extent on the hairiness and coloration of the involucral bracts surrounding the capitula. We collected plants from over 70 populations throughout Scandinavia and Iceland and kept them in a common garden at Lund university, Sweden. In a temperature gradient experiment, we used plants from 20 different crossings, replicated in each of four climate chambers, to study the consistency of capitulum characters used to delimit varieties of *S. autumnalis*. Our results show that colour and hairiness of the involucral bracts, as well as size and number of capitula, are environmentally plastic and much affected by differing temperature, with capitula being darker, hairier, larger, and fewer in number under cool conditions. We therefore conclude that the taxonomic value of these characters is limited, at least in *S. autumnalis*.

## Small and hidden but not forgotten – the taxonomy, distribution, and identification of Swedish Thysanoptera

**Emma Wahlberg**
*Department of Zoology, Swedish Museum of Natural History*

Thrips (Thysanoptera) are minute insects often not larger than 3 mm, but larger species may reach 5 mm in size. They are found within flowers, seed pods, on bark or in soil and deadwood, feeding on pollen, spores, fungi, algae, or prey. The small size and secluded lifestyle might be reasons for the relatively few taxonomic studies of the order. Some has caught the attention not only from researchers but also from the commercial and private sector, due to some species that are considered as pests in agriculture and even as invasive species. Phlaeothripidae is a family not familiar to many people, even though they are found almost everywhere. Some species are found in flowers, but most of the known species in Sweden are found in soil, leaf litter and decaying wood. In this project I provide updated determination keys, checklists, and molecular data.

## Re-appraisal of *Anthrophyopsis* (Gymnospermae): New material from China and global fossil records

**Yuanyuan Xu**
***Student**, Department of Paleobiology, Swedish Museum of Natural History*

*Anthrophyopsis* Nathorst 1878 is a representative Late Triassic foliar genus with uncertain systematic affinities and poorly understood morphology and anatomy. Since its earliest report by Nathorst in 1878, 16 species have been documented worldwide. However, the taxonomic statuses of some taxa remain questionable. Out of 16 reported species, only three of them, including *Anthrophyopsis crassinervis*, *A. tuberculata* and *A. venulosa* can be retained as valid. Besides, four species, such as *Anthrophyopsis brancai*, *A. miassica*, *A. narulensis* and *A. vachrameevii* need further revision and investigation. The other nine species are invalid. In this study, the morphological diagnosis for genus *Anthrophyopsis* is updated, and a revision of its historical collections and reported occurrences around the world was undertaken. Stratigraphically, the occurrences of *Anthrophyopsis* are almost confined to the Upper Triassic. And its limited occurrences in the Southern Floristic Province of China during the Late Triassic indicate that this genus represents a sensitive stratigraphic and palaeoclimatic marker.

# Posters

## Node ages, relationships, and phylogenetic incongruence in an ancient lineage (*Ephedra*, Gnetales)

**Ruben Blokzijl**
***Student**, Department for Ecology, Environment and Plant Sciences, Stockholm University*

Both morphological and molecular characters have been used in attempts to understand the evolutionary history of the gymnosperms of the genus *Ephedra*. Hitherto, the information provided by these characters resolved some, but not all relationships and an explanation for this is the sparse variation among species present in the DNA fragments used. To overcome this information poverty and to resolve the *Ephedra* phylogeny, we produced ample molecular data in the form of entire chloroplast genomes and nuclear ribosomal regions from a majority of the species of the genus. Independent analyses of the data from the two genomes resulted in topologies that are partly incongruent, albeit statistically supported. Additionally, severe conflicts are found regarding the absolute age estimates of the *Ephedra* crown group, ranging from a few million years in some analyses to pre-Cenozoic ages in other analyses. The results left us with more questions than when we started.

## The Neotropical rainforest mimosoid genus Zygia P.Browne - Diversification and evolution based on phylogenomics and morphology

**Julia Ferm**
*Department for Ecology, Environment and Plant Sciences, Stockholm University*

This project will clarify evolutionary patterns and processes within the mimosoid genus Zygia (Caesalpinioideae, Fabaceae) in order to add to the understanding of tropical rainforest diversification in the Neotropics. The aims of this project are to investigate diversification and evolution in Zygia, and the first step is to a) resolve phylogenetic relationships and node ages in Zygia using massive amounts of nuclear DNA data produced by next-generation sequencing (NGS) methods, and b) conduct extensive morphological studies of Zygia and in combination with the phylogenetic results, update the taxonomy and classification of the genus. With a resolved, dated phylogeny in place, further aims of this project are to c) determine if Zygia has undergone a recent rapid diversification caused by highly effective dispersal, and d) investigate to what extent hybridisation, introgression and polyploidy may explain evolution and diversification within the genus.

## Non-target insects in wetlands with and without mosquito control treatments in the River Dalälven floodplains, central Sweden

**Sandra Holmgren-Molin**, Martina Schäfer & Jan O. Lundström
*Biologisk Myggkontroll, Nedre Dalälven Utvecklings AB, Department of Medical Biochemistry and Microbiology/Zoonosis Science Center, Uppsala University*

In Sweden, Bti-based floodwater mosquito control was commenced in 2002 in the River Dalälven floodplains. Bti may have some effects on non-target insects and this motivated long-term follow-up studies. In 2012 an extended follow-up study commenced in 12 wetlands, six experimental (treated) and six reference (untreated) areas. The results of the composition and weekly abundance on wetland insect fauna for 2012-2019 showed complete lack of detectable negative effects from order to family and that hydrology was the main structural factor. However, besides the expected significant reduction of Culicidae (mosquitoes), we also observed a significant abundance difference for the sub-family Chironominae (fam. Chironomidae) between the areas. A closer look at the data showed a strong increase of Chironominae in the reference areas without a simultaneous increase in the experimental areas. Our final interpretation of the results is still pending, and we appreciate input from the audience.

## Genomic diversity changes in a declining bumblebee species, *Bombus pascuorum*, using modern and historical DNA

**Ellen Karlsson**
***Student***, *Centre for Palaeogenetics, Department of Zoology, Stockholm University*

Bees are important pollinators for many wildflowers and crops. Bumblebees are so called buzz pollinators and are important for pollination of many food crops. However, because of an intensification of modern agriculture and increased use of chemical pesticides and herbicides bees are in decline worldwide. *Bombus pascuorum* is an example of a commonly occurring, long-tongued specialist bumblebee suggested to be in decline in Sweden.

The objective of my project is to study Swedish bumblebee population decline through time using complete genomes from historical specimens dating back 150 years, as well as modern specimens. This will allow me to assess how (or if) population decline in *B. pascuorum* has affected population genetic structure, genomic diversity, and levels of inbreeding in an important wild pollinator species.

For the analyses the samples will be divided into four time periods: <1900 – 1919, 1920 – 1949, 1950 – 1979 and >1980, which will serve as comparative time points to assess changes in genetic diversity.

The work is carried out at Centre for Palaeogenetics at Stockholm University and the sequencing is done at SciLifeLab, using Illumina. The sequences are analysed using the pipeline GenErode and Plink.

I expect to detect genetic changes associated with this decline. The change should be detected in samples collected well after the modernization of the agriculture, when large monocultive exploitations became more prevalent. I predict this will be reflected in changes in population structure through time, as well as generally declining genomic diversity and increased inbreeding in younger samples.

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## Taxonomy of the lichen family Teloschistaceae based on multigene phylogeny.

**Serhii Kondratiuk,** Mats Hansson, Ingvar Kärnefelt & Arne Thell
*Department of Biology, Lund University*

The lichen family Teloschistaceae (Teloschistales, lichenized Ascomycota) included ten genera and ca 500 species shortly before the molecular era (Kärnefelt 1989). Nuclear ITS sequences have successfully been used in phylogenetic studies since the turn of the millennium. A few years later, a multigene approach using nrITS, 28S nrLSU, and 12S mtSSU sequences became the common method in molecular phylogeny. The results have formed a basis for a new taxonomy, resulting in today's 112 genera and ca 1200 species. Most genera are divided on the four subfamilies of the Teloschistaceae. Seven genera still lack sufficient data for clarifying their systematic positions with certainty. New species and genera in the Teloschistaceae, based on recently discovered monophyletic branches, are presented and discussed below.

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## Perissodactyls from the early Miocene of Lanzhou Basin, Northwest China

**Zhaoyu Li**
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Two different taxa of perissodactyls, Aprotodon (Rhinocerotidae) and Borissiakia (Chalicotheriidae), are reported from the early Miocene Xianshuihe Formation of the Lanzhou Basin, Northwest China (Xiejian Stage). Aprotodon occurs in Asia from the late Eocene to the early Miocene, and includes four species. The mandible from Lanzhou has elongated, strongly curved tusk-like incisors, a peculiar mandibular symphysis which widens sharply anteriorly, and lacks p1. Those features are different from other species (A. smith-woodwardi, A. fatehjangensis, A. aralensis) and support its attribution to A. lanzhouensis, which has also been discovered in the Erlian Basin, Nei Mongol and in the Linxia Basin, Gansu. The other mandible is most similar to the schizotheriine Borissiakia betpakdalensis from Kazakhstan except for a much smaller body size which is hardly explained by intraspecific variation and may represent a smaller body-sized species of Borissiakia. However, it also shares common features with the type specimen of Phyllotillon huangheensis from the same strata of the Lanzhou Basin, i.e., in the lower cheek teeth and the anterior end of the ramus which tapers more than in other taxa. Differences between both are the height of the ramus, especially the level of the symphysis, which may be explained by sexual dimorphism. Therefore, the schizotheriine mandibles from the early Miocene of the Lanzhou Basin probably represent the same taxon and both are attributed to Borissiakia huangheensis.

## A new illustrated fauna for the Swedish species of Eupulmonata, Hygrophila and Pylopulmonata.

Ted von Proschwitz, **Kennet Lundin**, Jonas Roth & Ulf Bjelke
*Gothenburg Museum of Natural History*

A new Swedish Fauna is in production for the Gastropod superorders Eupulmonata (126 species), Hygrophila (34 species) and Pylopulmonata (33 species) within the subclass Heterobranchia. The book is planned for publishing in spring 2023 as the 21st volume in the series The Encyclopedia of the Swedish Flora and Fauna (Nationalnyckeln för Sveriges Flora och Fauna), produced by the SLU Swedish Species Information Centre (Artdatabanken).

This will be the first complete fauna for land and freshwater snails covering Sweden, that has been published for more than 100 years. The chapter on species of marine pylopulmonates will be the first ever published for the country. The volume contains detailed descriptions of the morphology, variation, and ecology of all species as well as distribution maps for the limnic and freshwater species, and photos of all species from several angles. Beside photos of shells, more than 90% of the species in Eupulmonata and Hygrophila are covered with live photographs. For Pylopulmonata this figure is 40%. In the introductory sections the systematics, anatomy, ecology, and reproduction et c. are treated and in appropriate cases, anatomical details are described and illustrated. Determination keys for adult specimens are presented in both Swedish and English. The limnic Valvatidae (four species) was treated in the first book volume on the Heterobranchia, published in 2022. Limnic, brackish and terrestrial species of the Caenogastropoda and Neritimorpha (nine species in total) are included in an appendix in the fortcoming second book, but will be treated in the future in the concluding third volume on Swedish gastropods.

## The real *Devario browni* from the Irrawaddy River basin, and the new *Devario ahlanderi* from the Salween River basin in Myanmar (Teleostei: Cyprinidae: Danioninae)

**Mikael Norén** & Sven Kullander
*Department of Zoology, Swedish Museum of Natural History*

The cyprinid fish genus *Devario* Heckel, 1843 comprises 42 species of small (typically 40-50 mm SL), colourful, shoaling fish in South and Southeast Asia, found mainly in small fast-flowing hill streams, but also in rivers and lakes. *Devario* has economic importance as food fish, and several species are popular aquarium fishes. Specimens of *Devario* from a tributary to the Salween River in Myanmar initially identified as *Devario browni* but with a different colour pattern, were subjected to a comparative morphological analysis with syntypes and other specimens of *D. browni* from near its putative type locality. The Salween sample was recognised as representing a distinct species, here named *Devario ahlanderi*. No significant morphometric differences were found between *D. ahlanderi* and *D. browni*, but adult *D. ahlanderi* differ from adult *D. browni* in the trunk colour pattern, the presence of 14 vs 12 circumpeduncular scale rows, and distinct genetics (minimum genetic distance between *D. ahlanderi* and congeneric species is >2.1%).

## A perspective on hidden Swedish mite diversity

**Victor Passanha** & Kjell Arne Johanson
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Many Acari groups are among the least known in Sweden compared to other taxa. Three families within the order Mesostigmata, the Ascidae, Phytoseiidae and Uropodidae, are of special concern because they are considered extremely poorly known, in Sweden as well as in the rest of Scandinavia and most parts of the World. In this project, we aim at exploring all material available from Swedish museums as well as freshly sampled from localities considered to have high species diversity, i.e. Skåne, Södermanland, Gotland and Dalarna, which comprise many of the potential nature types in Sweden inhabited by the mesostigmata groups. However, the high species diversity previously reported from these areas might be due to biased sampling efforts and a more realistic picture of the diversity will be obtained by us due to expanding sampling areas to include north-south and low-high altitude gradients. We will apply a multiple setup of traps, being Berlese traps, yellow- bows and twig samples of trees and bushes, pitfall traps, live-pitfall traps, manual collecting, entomological umbrella, Winckler extractor, and Vulcan traps. We will sort, determinate and publish our findings together with leading taxonomists on the world fauna of mesostigmata diversity. The collected material will be used in molecular studies to investigate the ascid phylogeny and biogeography, as well as creating a barcode data library for all species. As a result, the known diversity will likely increase by 300%.

## Towards a better understanding of Lepidoptera phylogeny

**Etka Yapar,** Jadranka Rota & Niklas Wahlberg
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Butterflies and moths comprise together the order Lepidoptera, the second largest group of macroscopic organisms on Earth. There have been several phylogenetic/phylogenomic studies focusing on Lepidoptera with datasets of varying size. However, one common theme to all these studies is that there are ambiguities in the backbone of the tree. Whether these conflicts arise from insufficient taxon sampling, the limitations of current inference methods, or the convoluted patterns of evolution inherent to the data at hand remains to be investigated. This work aims to arrive at a reliable backbone phylogenetic hypothesis using large-scale genomic data and to identify sources of these conflicts. Studying them will not only help resolving the phylogeny, but also yield highly useful and generalizable methodological information regarding phylogenetic best practices with the side benefit of having a core set of alignments from thousands of genes across more than 350 taxa.

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**Total registered: 100**
**Presentations and posters: 35**
**Registered students: 25**
**Presenting students: 13**