# The southwestern Baltic Sea–Kattegat area: a hotspot for the lichen genus Xanthoria s.l.

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# Systematikdagarna 2025

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Swedish Museum of Natural History

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# Keynote speakers

## Causes and consequences of higher host specialisation in the Tropics

**Mariana Braga**
*Department of Ecology, SLU Uppsala, Sweden*

This talk will focus on a project we have recently started to work on. The goal of this project is to provide an unbiased assessment of host plant specialisation in butterflies, investigate its causes and consequences in terms of risk of local coextinction. For that, we will combine field observations, rearing experiments, transcriptomics, interaction prediction, and phylogenetic reconstruction. Our goal is to deliver comprehensive understanding of the evolution of host specialisation, enough to propose an explanation for the latitudinal specialisation gradient. The frameworks for efficient data gathering based on interaction prediction and for quantification of vulnerability to coextinction will hopefully be valuable tools for many researchers studying ecological interactions.

## Evolutionary plant biogeography: grasses, Madagascar, and global patterns

**Jan Hackel**
*Department of Ecology, Environment and Plant Sciences, Stockholm University, Sweden*

My research focuses on understanding plant biogeography from an evolutionary perspective: How have speciation, extinction and dispersal driven distribution patterns and the emergence of biomes? What are the relative contributions of selection versus chance? I will present some of my past and present work, starting with a taxonomic focus on the grass family (Poaceae). Then I will talk about how phylogenetic/systematic approaches can help us understand the emergence of biomes in Madagascar, a global biodiversity hotspot. I will end the presentation by zooming out and talking about (lineage) dispersal and global geographic disjunctions in seed plants.

# Oral presentations

## A Collection without Catalogue: Unpacking botanical exhibition material from the first half of the twentieth century

**Anna Svensson**
*Department of Botany, Swedish Museum of Natural History, Sweden*

A set of c. thirty boxes containing material once exhibited in the entrance hall of the Botany Museum (Botanhuset, NRM) presents both classification challenges and possibilities. Unpacking the boxes revealed contents that mirror the probable exhibition design along thematic groupings of either vegetable products (fibre, dyes, spices, etc.) or macro plant/fungi parts such as pinecones and wood samples. Some of the object labels cover the essential data for incorporation into the herbarium, and there is already considerable material from previous exhibitions in the macro collections. At the same time, many are ethnobotanical objects covering about a century up to the mid-1900s, and could constitute a separate collection. After basic conservation interventions, especially removing tape from both objects and labels, the question now is where the objects/specimens belong? How should they be classified, registered, and preserved?

## AI for species identification and beyond

**Steffen Kiel**
*Department of Paleobiology, Swedish Museum of Natural History, Sweden*

Many systematic, evolutionary, and biogeographic studies are based on molecular data, which are unavailable for the large number of species based on dead skeletal material, including fossils. Here I explore two ways to use Artificial Intelligence to estimate phylogenetic relationships among taxa from specimen images, with bivalves as a model group. First, taxonomic hierarchy and genetic distances were included in the training of an AI for image classification. This improved the accuracy of the predictions overall and also of predictions of the higher taxonomic levels of a given taxon, thereby providing a means to indicate closely related species. Second, the output of a similarity-learning technique was compared to the molecular phylogenetic relationships of the involved taxa, which yielded a reasonable congruence for orders and subclasses. This method could be used to match a taxon’s close relatives and potentially to estimate the genetic distances based on that similarity.

# An unexpected gills roommate from museum collections: unveiling a new *Microcotyle* from T. Odhner's legacy and revisiting *M. donovani* Van Beneden & Hesse, 1863 in Swedish waters

**Chahinez Bouguerche**
*Department of Zoology, Swedish Museum of Natural History, Sweden*

Natural history museums preserve invaluable biodiversity records that support ecological and taxonomic research. The Swedish Museum of Natural History houses important collections of parasitic Platyhelminthes, including unstudied material collected by Theodor Odhner. Examination of this historical material revealed new morphometric and anatomical data for *Microcotyle donovani* Van Beneden & Hesse, 1863, the type species of *Microcotyle*, from its type host *Labrus bergylta* off Sweden, and led to the description of *M. odhnaturiks* Bouguerche, 2025 from the same host. The new species differs from Atlantic and labrid *Microcotyle* spp. by clamp structure, caeca extension, and an inverted question mark–shaped germarium. We also propose a clarified nomenclature for *Microcotyle*-type clamps and introduce new anatomical characters to refine species delineation within the genus. This study confirms two *Microcotyle* species on *L. bergylta* and provides the first record of the genus from Sweden and Scandinavian waters.

# Conservation gap analysis for *Erica* (Ericaceae)

**Michael D. Pirie**, Stoffel P. Bester, Robbie Blackhall-Miles, et al.
*University Museum, Department of Natural History, University of Bergen, Norway*

The flowering plant genus *Erica* (Ericaceae) includes well over 800 species and numerous formally described subspecies and varieties. Many of these are threatened in the wild. The Global Conservation Consortium (GCC) for *Erica* was established under Botanic Gardens Conservation International (BGCI) in order to collaboratively prevent species extinctions. To target this work, we need fundamental information on species distributions, conservation status in the wild, and representation in ex situ collections. In large, complex groups like *Erica*, such data are not necessarily available or easily accessible. Here, we document the current state of ex situ and in situ conservation of threatened Erica species, identify knowledge and resource gaps, and set out priorities for future work.

# Crossing the biggest ocean in the world – the phylogeography of how plant genus *Wikstroemia* colonised the islands of the Pacific

**Ruben Cousins-Westerberg**, Matthew L. Knope, Clifford W. Morden, et al.
*Department of Biology, Lund University, Sweden* **(Student)**

We present the first ever genus level phylogeny of *Wikstroemia* (Thymelaeaceae), a medically and culturally significant genus of flowering plants found throughout East, South, and Southeast Asia, as well as on most major Pacific islands. Using this phylogeny as a backbone, we discuss the biogeographic history of the genus: its origin in a common ancestor in Asia and subsequent dispersal across the Pacific region. Was each island colonised only once, or several times? Is the occurrence of several species across several islands the result of repeat colonisation events, or a taxonomic error caused by plasticity and parallel evolution? We address these questions as well as the “logistics” of cross-ocean dispersal and the challenge of defining species across vast geographic distances. We put specific emphasis on the colonisation of the Hawaiian archipelago – arguably the most isolated island group in the *Wikstroemia* range and the most notable instance of rapid species radiation. We also discuss future prospects, such as why the *Wikstroemia* colonising Hawai’i kicked the evolution of novel sexual systems in the otherwise hermaphrodite genus into overdrive?

# Cyclostomatida (Bryozoa) in Norwegian and adjacent waters

**Maria Grankvist**
*Department of Natural History, Norwegian University of Science and Technology, Norway*
**(Student)**

Despite their ecological importance, bryozoans remain largely overlooked in Norwegian and global marine biodiversity research. Within the phylum, the order Cyclostomatida represents one of the most neglected groups. This study addresses the knowledge gaps by applying an integrative taxonomic framework to assess the diversity, distribution, and systematics of Cyclostomatida in Norwegian and adjacent waters. Morphological analyses were complemented by molecular barcoding and geographic data, and combined with a comprehensive review of taxonomic literature and occurrence records spanning the past 200 years. By integrating historical knowledge with modern data, the study produced an updated regional species checklist showing a 50 % increase in recorded species richness relative to biodiversity database baselines, including two species not formerly found in Norway. The findings provide an updated reference framework for Cyclostomatida in northern marine ecosystems and outline key priorities for future taxonomic, biogeographic, and ecological research on this understudied group.

## Genomic approaches to resolving difficult taxonomic groups

**Andrii Tarieiev**
*Institut für Biologie, Martin-Luther-Universität Halle-Wittenberg, Germany*

In the current study we performed a genome-wide SNP analysis of Ukrainian endemic *Betula klokovii* and related species, based on low-coverage whole-genome sequencing. Additionally, we extracted and assembled complete plastomes, and investigated B*. klokovii*'s relationships with other birch taxa by reconstructing plastome-based phylogenies. These approaches revealed a clear separation between *B. klokovii* and the other analysed taxa. Therefore, *B. klokovii* is likely a distinct taxon that is closely related to *B. pubescens*, yet morphologically and genetically different. Genomic approaches could provide significant new insights for resolving difficult taxonomic groups. There is a need for reference-grade, chromosome-scale genome assemblies, especially for polyploid species. Long-read sequencing makes assembly easier and provides additional epigenetic information. We are currently testing ONT sequencing for phylogenomic studies on selected species within the genera *Betula* and *Saxifraga*.

## Genomic insights into the evolutionary history of *Berardius* beaked whales: speciation driven by resource specialization, gigantism and thermal barriers?

**Morgan L. McCarthy**
*Population monitoring, Swedish Museum of Natural History, Sweden*

Beaked whales (family Ziphiidae) are among the most poorly understood marine mammals. The ziphiid genus *Berardius* is comprised of three extant species, however a lack of genomic data results in uncertainties of their phylogenetic relationships. Our genome-wide comparisons support an initial divergence of *B. minimus* from the *B. bairdii* - *B. arnuxii* common ancestor ~ 4 mya, and a divergence between *B. bairdii* and *B. arnuxii* ~ 1.5 mya. Gene flow was detected between species pairs for at least 75% of their post-divergence branch lengths. Strong levels of introgression (~8%) were detected between the non-sister but geographically overlapping *B. bairdii* and *B. minimus* species, despite their significant differences in body size. Our results show that the *Berardius* speciation process goes beyond simple bifurcating divergences. We hypothesize that resource specialization and an increased body size in the *B. bairdii* - B*. arnuxii* ancestor may have been an incipient driver of speciation.

## Incredibly important yet rarely seen: new species of *Piloderma* from the Nordic countries

**Sten Svantesson**, Karl-Henrik Larsson, Lowie Tondeleir, Matti Kulju, Reda Iršėnaitė, et al.
*Enheten för Botanik, Swedish Museum of Natural History, Sweden*

Through two recent taxonomic studies we have tripled the number of species in the ectomycorrhizal, globally distributed fungal genus *Piloderma*. We utilised several large fruiting body datasets from ecological studies, conducted extensive field-work in a novel

approach informed by eDNA data from soil and assembled a multi-gene dataset to delimit 13 new species to science, based on Nordic material. Three of the new species are among the 100 most common in Swedish soil and hence likely very important symbionts of trees, while another species showed a clear association with old growth forests and will be nationally Red Listed this year. One previously described species was epitypified and a semicryptic species was split from it – their morphological separation made possible seemingly only by the presence of mites!

## Large scale megabarcoding using Oxford Nanopore Technology enables fine scale mapping of Terebellides (Annelida, Trichobranchidae) in Sweden

**Maël Grosse**, Paul Ampblard Rambert, Erica Leder & Arne Nygren
*Marine Sciences, Gothenburg University, Sweden*

Species of the genus *Terebellides* (Annelida, Trichobranchidae) are common and abundant in marine benthic communities. They are also morphologically homogeneous, and molecular studies have revealed the presence of many undescribed species. The number of species actually occurring in Swedish waters, their distributions and relative abundance are unclear. 521 specimens of *Terebellides* were gathered for molecular analyses. Two methods were used and compared. The first one used individual Sanger sequencing to obtain a 313 bp fragment of COI. The second method combined tagged primers and multiplexed sequencing with Oxford Nanopore Technology (ONT).

191 sequences were obtained with Sanger sequencing and 413 sequences with ONT. Sequences were obtained with both sequencing methods for 174 specimens. 17 specimens could be sequenced only with Sanger, while 239 specimens could be sequenced only with ONT. Six species were found in the dataset, including two undescribed species.

## Less is more in intraspecific herbarium genomics

**Yannick Woudstra**, Patrick Meirmans, Anne-Sophie Quatela, Niels Wagemaker, et al.
*Department for Ecology, Environment and Plant Sciences, Stockholm University, Sweden*

Target capture sequencing has enhanced the study of plant systematics through unlocking DNA sequences from herbarium specimens. A non-trivial consideration is whether to invest time and funds into targeting variable loci (the customised approach) or using a cheaper "off-the-shelf" universal kit with highly conserved genomic targets. There is growing evidence that universal kits can also capture considerable intraspecific genetic variation. This study presents a direct comparison between universal and customised kits at the limits of intraspecific variation: near-identical genotypes within apomictic lineages of Taraxacum officinale. Although exons from universal kits yield less intraspecific genetic variation than customised approaches, they still provided enough to discriminate between near-identical genotypes of the same apomictic lineage. Given that universal kits save time, money, and the need for genomic reference data, this approach is recommended to increase the number of samples under budgetary constraints while still capturing considerable levels of intraspecific genetic variation.

# No single road to extreme climate adaptation: macroevolutionary pathways to drought and cold resistance in desert plants

**Marc Fradera-Soler** & Aelys M. Humphreys
*Ecology, Environment and Plant Sciences, Stockholm University, Sweden*

Hot and cold deserts impose multiple abiotic stresses, making them ideal systems for studying the evolution of stress polyresistance in plants. Using time-calibrated phylogenies, georeferenced occurrences, and climate data for 769 species across eight globally distributed desert plant groups, we tested macroevolutionary relationships between drought and cold resistance to understand polyresistance evolution. Results reveal no single evolutionary route: several groups show patterns consistent with facilitation, while some exhibit evidence of trade-offs producing either drought or cold specialists, and several display shifts in evolutionary correlations across desert and non-desert regimes. Reconstructions indicate that cold resistance often preceded or co-evolved with drought resistance, consistent with late Cenozoic cooling and aridification. Together, these findings reveal multiple evolutionary pathways to abiotic stress polyresistance, depending on lineage and ecological context.

# Past meets present: from archival documents to FAIR biodiversity Data

**Britt Andermann**
*Evolutionsmuseet, Uppsala University, Sweden*

Natural history museum archives hold vast, untapped biodiversity data—field notes, journals, and donation records with detailed species observations across centuries. At the Museum of Evolution, Uppsala University, we explore how these analog materials can be transformed into interoperable biodiversity datasets. Our pilot study centers on the Kullenberg Excursion Journals (1948–1996), documenting c. 100,000 insect occurrence records with rich ecological metadata. In collaboration with the Biodiversity Data Lab, we are digitizing and structuring these data into interoperable datasets to recover historical biodiversity baselines and integrate them into global infrastructures. Aligned with global initiatives such as the Disentis Roadmap, and a focus on mobilizing taxonomic treatments and FAIR biodiversity data, this work highlights how archival sources can provide data for revealing long-term species trends and connecting past observations to modern biodiversity knowledge networks.

## Patterns and drivers of floristic discovery in Ukraine: lessons from three decades of vascular plant records

**Mykyta Peregrym**, Ihor Olshanskyi & Svitlana Zhygalova
*Ecology and Genetics, University of Oulu, Finland*

Despite centuries of botanical exploration, new vascular plant taxa continue to be discovered in Ukraine. We analyzed 330 floristic discoveries made between 1997 and 2024, including 56 taxa newly described for science, to identify ecological and methodological factors promoting such findings. Synanthropic habitats yielded the highest number of new records, followed by grasslands and forests, while the Crimean and Carpathian Mountains remained key centres of endemism and hybridization. More than a quarter of discoveries were based on historical herbarium specimens, and citizen science platforms increasingly supported new records. These results highlight the ongoing incompleteness of floristic knowledge, even in well-studied regions, and demonstrate how targeted surveys, herbarium research, and public participation can accelerate biodiversity discovery and documentation.

## Phylogenomics of Tetrastichinae (Hymenoptera: Eulophidae) demonstrate a need for a revision of genera

**Emma Kärrnäs**, Christer Hansson, Jadranka Rota & Niklas Wahlberg
*Department of Biology, Lund University, Sweden* **(Student)**

Despite their immense ecological and economic importance, jewel wasps (Hymenoptera: Chalcidoidea) are one of the very least known groups of insects. They exhibit an astonishing species diversity – the group is thought to perhaps encompass as many as 500 000 species – and whenever studied taxonomically, new species are discovered. The largest jewel wasp family Eulophidae is no exception. The 6 000 species described to date most certainly only represent a fraction of the true species diversity, and little is known about the phylogenetic relationships of many groups within Eulophidae. The family Eulophidae is divided into five subfamilies of which the largest one, Tetrastichinae, has long proven notoriously challenging for taxonomists because of the lack of defining morphological characters of many groups within the subfamily. Currently, no large-scale detailed phylogeny of the generic relationships within Tetrastichinae has been published. To remedy this gap of knowledge, we extracted the whole genomes of 180 tetrastichines for reconstructing the first detailed phylogeny at the genus level, with an emphasis on the *Tetrastichus* group within Tetrastichinae. By extracting mitochondrial genes, ultra-conserved elements and BUSCO genes from the genomes, we show that several of the genera within Tetrastichinae are para- or polyphyletic, questioning the validity of the current classifications within the subfamily.

# Re-visiting phylogenetic relationships in Erebidae (Lepidoptera, Noctuoidea) with genomic data

**Etka Yapar**, Hamid Ghanavi, Reza Zahiri, Nicolas J. Dowdy & Niklas Wahlberg
*Department of Biology, Lund University, Sweden* **(Student)**

Erebidae includes approximately 25,000 described species with diverse diets and life history traits, some of those species being pests of economically significant plants. As the genomic-scale molecular data have become available for other Noctuoids, several studies revisited the systematics of the entire superfamily; however, to our knowledge, systematics of Erebidae with genomic data remains largely unexplored. Here, with the help of our in-house data and the published high-quality reference genomes, we take a closer look at phylogenetic relationships within the family based on an extensive dataset from 1490 nuclear protein coding genes across ~100 ingroup taxa, sampling all of the 18 currently recognized subfamilies of Erebidae. We find Eulepidotinae to be the sister group to the rest of Erebidae, and discover two recurring clades —of the "erebine" and the "arctiine" subfamilies— between our results and the results from the previous molecular work on the group.

# Sloth moths and relatives: first molecular phylogeny of Chrysauginae (Insecta: Lepidoptera: Pyralidae)

**Jadranka Rota**
*Biological Museum, Lund University, Sweden*

Sloth moths are moths living in a very close association with sloths. Much is known about their habits, the fact that the adults live in sloth fur, while the larvae develop in sloth faeces, but very little is known about their evolutionary history. There are three genera of sloth moths. Together with about 130 other genera, they belong to the pyralid moth subfamily Chrysauginae, having about 400 species in total. Chrysauginae are mainly distributed in the Neotropics, with several lineages in the Nearctic, and possibly also a separate lineage in Australia. The group is in dire need of study – more than half of the genera are monotypic! In this Master's thesis project, we inferred a first molecular phylogeny of Chrysauginae, including ca. 60 genera, using a museomics approach and sequencing whole genomes. From three different datasets (11 mitochondrial genes; legacy and LepTree genes; and ca. 1000 BUSCO genes) we inferred well-resolved phylogenetic trees that largely agree in topology.

## Structured phylogeographical patterns in the heterosporous spikemoss *Selaginella selaginoides* indicate dispersal limitations

**Annelie Svanholm**, Stina Weststrand & Petra Korall
*Organismal Biology (& Department of Botany), Uppsala University (& Swedish Museum of Natural History)* **(Student)**

A family of plants still underrepresented in the field of phylogeography is the spikemosses (Selaginellaceae). They are spore-dispersed and heterosporous – they produce two types of spores with different sizes, and both spores are needed for successful reproduction. Spikemosses have therefore been believed to be poor dispersers and historical long-distance dispersal events are rare in the family. From this premise we study the phylogeographical patterns of *Selaginella selaginoides* (northern spikemoss). The species has a large geographical distribution across the northern hemisphere and is therefore interesting in the context of long-distance dispersal. We aim to investigate if the large-scale evolutionary dispersal patterns of the family are discernible also on an intraspecific level. With the use of both RAD-seq data and Sanger sequence data, we see a geographically structured pattern in the species' genetic variation – an indication of dispersal limitation.

## Surviving abundance: Contrasting proteomic responses to vastly elevated CO2 levels in conifers, magnoliids and modern angiosperms

**Stephanus Francois Du Toit**
*Department of Biology, Lund University, Sweden*

Plants transitioned onto land a long time ago (approximately 500 million years). Since then, land plants have undergone profound morphological, functional, and molecular adaptation, making them fit for the terrestrial environment. During their long history on land, the Earth has also experienced numerous changes to its climate and atmosphere, suggesting that the morphological and physiological process optimizations observable in plants today have experienced numerous rounds of non-parsimonious experimentation, to extremes in plant growth conditions, i.e. not taking the simplest path to the current situation. We have grown a variety of species, with a wide range of phylogenetic distribution, in chambers which mimic the extreme atmospheric CO2 concentrations estimated to have resided in Earth's prehistory, specifically the Mesozoic. After allowing adequate acclimation to these conditions, we report our findings of contrasting physiological and proteomic steady-state responses. Our findings highlight how molecular processes, such as photosynthesis, are altered in vastly different ways in response to greatly elevated CO2 and suggest an evolutionary history component to a species' ability to adapt to extreme growth conditions.

# Vilesida, a new order of demosponges revealed by molecular phylogeny and abundant 24-isopropylcholesterols (24-ipc sterols)

**Julio A. Diaz** & Paco Cárdenas
*Evolutionsmuseet, Uppsala University, Sweden*

Sponges (phylum Porifera) are highly plastic organisms with few reliable morphological characters for classification, and consequently, several order-level relationships remain unresolved. Here, we establish Vilesida ord. nov., a new order of demosponges, initially identified through mitochondrial (COI) and nuclear (18S and 28S) markers. Most of the species now grouped within Vilesida were previously scattered among the orders Suberitida, Bubarida, and Axinellida, with which they share overlapping morphological features. Species of this new order possess monactinal and diactinal megascleres arranged in a confused halichondroid pattern. Importantly, all species analysed within Vilesida share a unique chemical synapomorphy not observed in any other eukaryotic lineage: the presence of distinctive C30 sterols as their major membrane sterols. In particular, 24-isopropylcholesterol and structurally related analogues dominate their sterol profiles. These compounds are lipid precursors of the sterane biomarker 24-ipc, which is abundant in certain Neoproterozoic rocks and oils and has been hypothesized to represent one of the earliest animal biomarkers. We propose the resurrection of the genus *Viles* de Laubenfels, 1934, and its establishment as the type genus of Vilesidae fam. nov., the sole family within Vilesida ord. nov. The genus *Viles* was previously synonymized with *Topsentia* Berg, 1899, but after re-examining the type species *Topsentia glabra*, we conclude that *T. glabra* belongs to Suberitida, thereby justifying the revalidation of *Viles*. We also propose the transfer of the genera *Petromica* and *Axinyssa* to Vilesida ord. nov., and we describe *Murus* gen. nov. within Vilesidae fam. nov. The type species of *Murus*, *Murus hirondellei* (Topsent, 1890) comb. nov., is a common mesophotic species. It was formerly assigned to *Phakellia* (Bubarida), but re-examination of the type material, together with new molecular data from the Northeast Atlantic and the Mediterranean, supports its inclusion in the new order. Additionally, we describe two new species of *Murus*: *Murus profunda* sp. nov. and *Murus sinenotis* sp. nov.

# Poster presentations

## Annuality and C4 photosynthesis co-occur but evolved independently in warm, dry environments

**Laura Schat**
*Department of Ecology, Environment and Plant Sciences, Stockholm University, Sweden*
**(Student)**

Warm and dry environments are characterised by low, unpredictable precipitation and high temperatures, creating conditions that challenge plant growth, reproduction and survival. Plants in these environments have evolved adaptive strategies to enhance water use efficiency and ensure reproductive success, two of which are annuality and C4 photosynthesis. It has previously been thought that these traits may represent a joint strategy for maximizing fitness in hot and dry environments. However, the extent to which they co-evolve or are selected for together remains unexplored. To address this, we used Pagel's models of independent and correlated evolution for over 4000 species of grasses (Poaceae). To account for rate heterogeneity and potential type 1 statistical errors, we used models that allow transition rates to vary in different parts of the tree. We found that there are more C4 than C3 annual grasses, that C4 origins predate evolution of annuality, perennial-to-annual transition rates are higher in C4 clades but no statistical support for correlated evolution between the two traits. Our results indicate that any habitat or trait similarities between annuals and C4 species (e.g. small seeds, fast growth) likely reflect independent adaptations to similar environmental conditions, or are contingent on (consequences of) the two traits, rather than a genetic or physiological links between them.

## Enamel microstructure in Eocene Sparnotheriodontidae (Litopterna, Mammalia) from Antarctica and southern South America

**Daniela C. Kalthoff**, Javier Gelfo & Thomas Mörs
*Enheten för Paleobiologi, Swedish Museum of Natural History, Sweden*

Among the few terrestrial mammals known from the Paleogene of Antarctica, the largest are South American native ungulates (SANUs), including Astrapotheria and the litoptern Sparnotheriodontidae. This study examines the enamel microstructure of postcanine teeth in three sparnotheriodontids: *Notiolofos arquinotiensis* and an indeterminate form from the Eocene of Antarctica, and *Phoradiadus divortiensis* from the Andes. All exhibit a three-zoned schmelzmuster: inner and outer radial enamel surrounding a thick zone of exclusively vertical Hunter-Schreger bands (HSB), with broad transition zones. This is a derived condition compared to the narrow transitions seen in most other SANUs with vertical HSB, except Astrapotherium._ Despite their classification within Litopterna based on gross dental traits, sparnotheriodontids show no clear enamel microstructure affinities with other litopterns described so far. Still, their schmelzmuster does not contradict a position as specialized clade within the order. Sparnotheriodontidae thus represents one of the earliest SANU lineages to evolve a schmelzmuster with exclusively vertical HSB.

## Going beyond macroevolutionary associations: testing gene-trait associations in Noctuidae (Insecta: Lepidoptera) using genome modifications

**Zachary J Nolen**, Jadranka Rota, Christopher Wheat & Niklas Wahlberg
*Department of Biology, Lund University, Sweden*

Reference genomes are being produced at an unprecedented rate, enabling both robust inference of phylogenetic relationships in challenging groups as well as investigations into the drivers behind diversification. We utilize more than 200 reference genomes to infer a phylogenetic tree for the moth family Noctuidae, one of the largest families in Lepidoptera, and investigate patterns of genome evolution across this tree. Robust inference of the evolutionary relationships for this group then forms the basis for future investigations into the genomic underpinnings of migratory behavior and host plant use, traits hypothesized to be drivers of diversification. Using comparative genomic methods, we will identify gene families whose rates of evolution shift in correlation with convergently evolved traits. Then, we will validate the functional relationship between these genes and the traits of interest using CRISPR knock outs. By identifying and functionally verifying genes associated with these traits, we can provide a better understanding to the processes by which convergent evolution of novel traits occurs and drives diversification.

## Grass snake systematics (*Natrix natrix*, Colubridea: Natricinae) in the light of whole-genome data: Emphasis on the Gotland population and possible taxonomic implications

**Patric Falck**
*Department of Bioinformatics and Genetics, Swedish Museum of Natural History, Sweden*
**(Student)**

Grass snakes, *Natrix natrix* (L.) have been extensively studied from a taxonomic and systematic perspective. Despite considerable research, the phylogenetic relationships and genetic history of certain regional populations remain unclear. This study investigates the genetic composition of grass snakes around the Baltic Sea with a particular focus on the Gotland population, previously recognized as *Natrix natrix gotlandica* Nilson & Andrén 1981. Using whole-genome sequencing from individuals around the Baltic Sea region we reconstructed phylogenomic hypotheses based on both mitochondrial (mtDNA) and nuclear (nDNA) data. Our results revealed an incongruent pattern between the mitochondrial and nuclear phylogenies, with the mitochondrial data placing the Gotland snakes nested within the eastern *N. n. scutata* lineage, indicating an eastern mitochondrial origin on Gotland, whereas the nuclear data identified a well-supported, diverged Gotland lineage within the *N. n. natrix* group. Additional nuclear data analyses indicated that Gotland individuals form a distinct and genetically isolated cluster, clearly separated from continental populations. Together, these findings indicate that the Gotland grass snakes constitute a genetically distinct population originating from multiple regions. The observed nuclear divergence and pronounced genetic isolation highlight the population as a subject for a taxonomic re-evaluation.

## Insect collection and identification in mosquito control

**Yayuan Chen**, Marie Langbak & Sandra Holmgren-Molin
*Biologisk myggkontroll, Nedre Dalälvens Utveckling AB, Sweden*

Biologisk Myggkontroll (Biological Mosquito Control) aims to reduce the abundance of floodwater mosquitoes to acceptable levels so that people can enjoy living in and visiting the Nedre Dalälven and Klarälven region. We conduct two large insect surveillance programs from May to September annually. Female blood-seeking mosquitoes (Culicidae) are collected with CDC miniature light traps baited with dry ice to monitor mosquito development, abundance, and species composition. Our follow-up surveillance program with emergence traps focuses on non-biting midges (Chironomidae) and evaluates potential effects of mosquito control on non-target insects. Collected samples are morphologically identified in our entomological lab: female mosquitoes to species; non-target insects to order or family (Nematocera to family, Chironomidae to subfamily). Additionally, we collect mosquito larvae before control treatments during spring. When morphological identification is impossible for early instar larvae, we use qPCR to identify the target species *Aedes sticticus*.

## *Nigritella* or *Gymnadenia*? A phylogeny of a controversial clade

**Jöran Klink**, Niklas Wahlberg & Mikael Hedrén
*Department of Biology, Lund University, Sweden* **(Student)**

Traditionally, *Nigritella* was treated as the sister genus to *Gymnadenia* (Orchidaceae). With its dense, almost globous inflorescence and non-resupinate flowers, *Nigritella*'s morphology contrasts strongly with *Gymnadenia*'s. However, since the rise of molecular methods, multiple studies have questioned the validity of *Nigritella* as a genus and rather positioned it within Gymnadenia. Similarly, studies supporting the sister relation between the two genera exist. Here we used the Angiosperm353 probe kit to once again reconstruct the phylogeny of this orchid clade, aiming to resolve the discussion once and for all.

## Predation and nutrients moderate insect emergence in long-term evaluation of Bti-based mosquito control in wet meadows in Sweden

**Sandra Holmgren-Molin**, Martina L. Schäfer, Christian Blue & Jan O. Lundström
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Mosquito control using *Bacillus thuringiensis israelensis* (Bti) is considered by Sweden and the EU to be sufficiently effective and ecologically safe in wetlands. However, mosquito control in environmentally protected wetlands demands increased understanding on non-target organisms with focus on the family Chironomidae (non-biting midges) and its subfamilies. We studied insect emergence and collected environmental variables from 12 wet meadows, six reference- and six experiment areas, in the River Dalälven floodplains of central Sweden 2012-2017. We found that while the target nuisance mosquitoes were significantly reduced by the Bti-treatment, neither non-biting midges nor the other Nematocera families showed any treatment effect. The emergence of Chironominae, a subfamily of non-biting midges did however show a treatment effect. Interestingly, further analysis showed that the emergence of Chironominae also was moderated by dissolved nitrogen and by predation from another subfamily of non-biting midges, Tanypodinae. With all factors in the analysis, the significant effect of Bti on Chironominae disappeared.

## Scientific illustration in the digital age - illustrating new species in Sapotaceae

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Scientific illustrations remain an essential and valuable part of systematics, even in the digital age. They provide information not easily captured through photography and allow for clarification of the type material chosen and are especially of use when working with herbarium materials. During 2024-2025, I illustrated several taxa within the plant family Sapotaceae new to science from Oceania under the supervision of Ulf Swenson and with the help of Jennifer Kearey (both NRM). I described and illustrated one new species of *Planchonella* for my bachelor's thesis and further worked on another species in the same genus before working on New Guinean species of the genus Pleioluma at Commonwealth Scientific and Industrial Research Organisation (CSIRO) in Canberra. In total, 12 new species have been illustrated and will in the future be published along with descriptions and updated knowledge of the phylogeny of the two genera

## Seed shape evolution of *Trichosanthes pilosa*

**Akari Bergquist**
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*Trichosanthes pilosa* (Japanese snake gourd) is a climbing plant in tropical and subtropical Asia and northern Australia, with uniquely croissant-shaped seeds bearing protruding lateral chambers. These seeds likely aid water absorption and retention, potentially facilitating adaptation to climates with strong precipitation seasonality. To explore adaptive evolution of seed morphology, climatic niches of *Trichosanthes* species were quantified and compared phylogenetically. Results indicate that while *T. pilosa* originated under monsoonal climates, it later expanded into broader niches, showing evidence of niche shift, whereas closely related species *T. cucumerina* exhibit niche conservatism. Comparative seed-shape analysis with *T. beccariana*, which has flatter dog-nose shaped seeds, highlights divergent adaptation of lateral chambers to distinct climatic regimes. Overall, croissant-shaped seeds may have facilitated ecological diversification by supporting water management under variable moisture conditions.

## The southwestern Baltic Sea–Kattegat area: a hotspot for the lichen genus *Xanthoria* s.l.

**Serhii Y. Kondratyuk**, Ulf Schiefelbein, Ingvar Kärnefelt, Mats Hansson & Arne Thell
*M.H. Kholodny Institute of Botany, Ukraine & Unit of Molecular Biosciences, Lund University, Sweden*

More than 3500 samples of lichen genus *Xanthoria* s.l. were collected at 135 localities in the Baltic Sea–Kattegat area during 2022–2025. Of these, 177 were selected for phylogenetic analyses using ITS and mt-sequences. The phylogenetic tree of *Xanthoria* s.str. reveals 24 clades possibly corresponding to species, six of which are described, i. e. *X. calcicola*, *X. coomae*, *X. ectaneoides*, *X. pedersenii*, *X. pylyporlykii* and *X. wennergrenii*. The studied area is undoubtedly a hotspot for the genus *Xanthoria* s.l. and the number of species is much higher than expected. *Rusavskia drevlyanica* and *Xanthoria coomae* are confirmed for the first time from the studied area. A close relationship between *Rusavskia drevlyanica* and *Zeroviella esfahanensis* is revealed.

## Tracing the origin of *Betonica officinalis* in Sweden: RADseq suggests long-term persistence in southern (Scanian) populations

**Tabea Dittmar**
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The biogeographical origin of *Betonica officinalis* L. in Sweden has long been debated as to whether its populations represent natural postglacial relicts or human introductions. Using RADseq data from 42 individuals across 35 sites in 14 European countries, we analysed 9,598 SNPs to map genetic structure and infer relationships among regions. We found strong differentiation between western and central Europe. Southern Swedish samples formed a distinct, well-supported clade closely related to central European populations, with isolation by distance and reduced diversity suggesting long-term persistence. However, two Scanian localities fell outside this core group and showed clear signatures of human introduction, and another population near Stockholm was found to be genetically distinct and may represent a separate Baltic-related or introduced lineage. These results highlight complex colonization histories and the importance of understanding genetic structure for conservation.

## Unravelling host-pathogen interactions: a transcriptomic approach using dual RNA-seq in the Tremella mesenterica and *Peniophora* association

**Elena Verdugo Torres**, Raquel Pino Bodas, Ana García Muñoz, Juan Periáñez, et al.
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Host-parasite systems provide a valuable opportunity to study coupled evolution since there is a strong connection between their interacting bionts. Here, we focus on the mycoparasite *Tremella mesenterica* (Tremellales, Agaricomycotina, Basidiomycota, Fungi), which grows associated with *Peniophora* spp., a corticioid fungus.

*Tremella mesenterica* exhibits a dimorphic life cycle, alternating between a yeast and a filamentous phase. Interestingly, the transition to the filamentous phase is unequivocally dependent on the presence of its fungal host. While this dynamic has been well documented, little is known about the underlying molecular mechanisms related to recognition and specificity between the two fungi. One way to address this knowledge-gap is by using transcriptomics. Using cultures of the two species, we obtained 1) three replicates of the transcriptome of each species growing separately and 2) three replicates of the dual transcriptome of the two species growing mixed in close contact. We conducted RNAseq analyses to identify differentially expressed genes (DEGs) in each species when they grow isolated or together. Our analyses will provide further insights into the expression of genes – and the metabolic pathways in which they could be involved – during the early stages of this biological association and will help us elucidate the first biochemical responses in this interaction.

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**Total registered: 125**
**Presentations and posters: 34**
**Registered students: 30**
**Presenting students: 12**