A revised molecular phylogeny of the subclass Calcaronea

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Calcereous sponges are acknowledged to be taxonomically challenging and molecular data does not support the current morphology-based classification. We sequenced a short fragment (C-region) of the 28S gene, which was recently proposed as the most phylogenetically informative marker to be used as a DNA-barcode for calcareous sponges. Our analyses, that combine newly generated sequences with those from previous studies, include a total of 125 sequences representing ca. 71 taxa across 23 (out of 56) genera and all 14 families of Calcaronea. Our results are congruent with previous studies in that the current ordinal classification within Calcaronea is artificial, and most families and genera are non-monophyletic. Our study also supports the basal position of Leucosolenia, however, the increased taxon sampling reveals this genus to also be polyphyletic. We further recovered a well-supported monophyletic clade that includes Sycon-like species with a stem collected in both shallow- and deep-water. This study highlights the need for a thorough revision of the class Calcaronea and provides a molecular framework for future studies.

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POSTER

Unraveling the coevolutionary history of the mutualistic interaction between *Piper* plants and *Carollia* bats in the Neotropics

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*Piper* is one of the most diverse plant genera of all angiosperms and it dominates the understory of most Neotropical forest. *Piper* seeds are primarily dispersed by a small clade of frugivorous bats the genus *Carollia* (short-tailed bats), which are evoked as *Piper*-specialized seed dispersers for their reliability and effectiveness. The mutualistic interaction between *Carollia* and *Piper* extends through the geographic distribution of the Neotropics and is crucial for natural forest regeneration, as *Piper* is one of the first colonizers. Reciprocal dependence between *Carollia* and *Piper* and similar diversification times suggest that this ecological interaction underlines a shared evolutionary history. Here, we study the *Piper-Carollia* coevolutionary patterns over a large scale in the Neotropics using a novel cophylogenetic approach that integrates network analysis. We also investigate biogeographical patterns of this mutualistic interaction and compare shifts in speciation rates under different diversification scenarios aiming to reconstruct the shared evolutionary history of *Piper* and *Carollia*. The results of this study highlight the role of seed dispersal ecology and asymmetric interactions on shaping the evolutionary history of Neotropical taxa.
POSTER

Historical biogeography of amphibians and reptiles of the Cerrado savannas of the Neotropics

Josué Anderson Rêgo Azevedo¹, Cristiano de Campos Nogueira², Alexandre Antonelli¹

Identifying the mechanisms and process that generate endemism patterns is a major step in understanding the evolution of biotas. Therefore, such knowledge is essential for conservation efforts aiming to protect biogeographical processes at continental scales. From the delimitation of different biogeographic units, it is possible to verify if such endemism pattern corresponds to a general process, which can be caused, for example, by the appearance of a geographical barrier that isolates many elements of an ancestral biota. Common distributional patterns could also be generated by many unrelated events among distinct groups, generating coincident ranges. Therefore, only with the aid of phylogenetic information it is possible to infer if regionalization patterns were generated by a general historical processes, like vicariance, providing clues on the history of the formation of biotas. Many biogeographical units coincident between species of amphibians and reptiles were found over the Cerrado region, the biggest block of Neotropical savannas. Located in the central portion of South America, Cerrado is surrounded by megadiverse biomes, like Atlantic Forest and Amazon rainforest, that influences its species composition. The aims of this study are to: (1) to investigate historical relationships between the lineages within the biogeographical units of the Cerrado and among the Cerrado and surrounding biomes; (2) to distinguish between congruent and unique events between both herpetofaunal groups; (3) to verify if the coincidence of distributions between anurans and squamates in the Cerrado are related to the same historical process and; (4) to interpret these results in the light of available information on the geological history of central Brazil and the Neotropics. Herein we used historical biogeographical analyses and temporal information derived from molecular dating to identify coincident and unique biogeographical events between anurans and squamates of the Cerrado, uncovering and describing patterns of historical relationships among biogeographical units.
POSTER

The Swedish Taxonomy Initiative, progress report.

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Sweden’s biodiversity is much richer than previously thought. More than 3 000 new species, of which 1 000 are new to science, have been discovered since the Swedish Taxonomy Initiative (STI) was established in 2002.

The aims of STI are to chart and describe all multicellular species of plants, fungi and animals in Sweden. This is achieved by funding taxonomic research and inventories of poorly known organismal groups, and by grants to digitization and curation of biological collections at the Swedish natural history museums.

In order to make facts and data available to scientists, professionals in nature conservation and interested members of the public, some important tools and systems are developed: Artfakta (facts on species- digital information), Nationalnyckeln (reference books), Dyntaxa (taxonomic database), Species Observation System (=Artportalen), and a digital tool for identification keys.
POSTER

Using historical herbarium specimens to investigate plant genome evolution during parallel invasions (Ambrosia artemisiifolia L.)

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Common ragweed (Ambrosia artemisiifolia L.) is an annual weed native to North America that became invasive upon introduction to Europe and is now established on all continents except Antarctica. The study of invasive plants offers an excellent opportunity to answer fundamental evolutionary questions. Does parallel adaptation to similar environments affect the same genes? What types of mutations (de novo vs. standing variation) contribute most to adaptation in the introduced range? We will use genomic data derived from a large number of historic (from herbarium sheets) and modern common ragweed samples from North America, Europe and Australia to infer post-introduction changes in population structure, identify selected alleles in the different ranges and track changes in allele frequencies over time. Low-depth shotgun sequencing data will be mapped against a draft reference genome, genotype-likelihoods will be inferred using ANGSD, and population genetic structure will be estimated. To identify genomic regions putatively under selection, an outlier analysis based on the genomic distribution of Wright’s fixation index $F_{ST}$ will be performed along with environment-allele associations. We expect to find repeated patterns of local adaptation and a higher frequency of adaptation from standing variation compared to de novo mutations in the introduced range. Moreover, we expect to find that large-effect alleles will contribute more to adaptation in the introduced range, as they are less prone to loss by drift and should respond more quickly to selection.
ORAL

Beware, Norway is being invaded by the Europeans right now!

Ursula Brandes, Siri Fjellheim
Norwegian University of Life Sciences

It is easy to notice if you are overrun by foreign soldiers, which threaten your life. It is harder to notice some harmless and beautiful looking plant to quietly appear and slowly replace the native vegetation. And, without a passport, how can you know its citizenship?

I reconstructed the expansion history of *Cytisus scoparius* in Europe and Norway based on genetic analyses. Results show a strong influence from human dispersal, which would have facilitated the species invasiveness in Norway. Distinguishing native from introduced plants is the basis of management decisions, while understanding the introduction history is important to restrict further plant invasion and to understand the processes driving it.
ORAL

A whole lot of Biodiversity; assessing benthic marine communities through metagenomics

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Marine mud is a habitat that dominates the ocean floor; a wonderful world of diverse marine species, but we lack in the capabilities to rapidly and accurately characterise the whole community living there. Quantifying the biodiversity of marine mud communities not only gives us insights into ecology, but this habitat is heavily impacted by two major industries; fisheries and petroleum, and can help us to understand human impact on the marine environment. Biodiversity quantification techniques have evolved rapidly over the last decade, and it is now possible to identify whole communities of organisms simultaneously using DNA. However, many of the current genetic methods commonly produce biased datasets. In our study, we further developed metabarcoding methods to enable accurate extraction and quantification of eukaryotic DNA from bulk sediment samples. We conducted experiments on mock marine benthic communities in order to remove two current limitations of metabarcoding techniques, bias from PCR steps and false positives from extracellular DNA (eDNA) contamination. Our experiments showed that eDNA contamination can be reduced significantly, with two different treatment methods: phosphate buffer washing and enzymatic degradation. Also by removing PCR from the metabarcoding pipeline, and implementing shotgun sequencing and bioinformatic sorting, bias is potentially reduced and accuracy of biodiversity estimates increased. Further developments of metabarcoding techniques along these lines should enable accurate quantification of genetic biodiversity of the whole living marine benthic community. This will be of high relevance for future approaches in environmental monitoring as well as for fundamental community ecology.
KEYNOTE

Paedomorphic evolution in the deep-sea fauna

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The deep-sea environment (deeper 200 m) covers nearly two-thirds of the Earth surface mostly constituting of soft-sediment habitats and harbouring largely unknown fauna. A number of recent studies have uncovered the great biodiversity and high level of endemism in many groups of invertebrates in the deep ocean. Nevertheless, there is still insufficient understanding of evolutionary processes such as natural selection, adaptation, gene flow or mutation that could underlie the pathways of the deep-sea colonization events. Paedomorphosis (i.e. retention by an organism of juvenile or even larval traits into later life) has been reported as a common feature among a great variety of deep-sea taxa. In this talk we will show an example of paedomorphic deep-sea annelids, so-called quill worms, from the subfamily Hyalinoeciinae. Quill worms comprise three genera showing lack or underdevelopment of several morphological characters present in other adult onuphids. We will review the current status of knowledge in diversity of the deep-sea quill worms, present the first DNA-sequence-based phylogeny of this group, and trace the evolution of paedomorphic characters within Hyalinoeciinae. We will also discuss the problems related to assessing the phylogenetic position of paedomorphic taxa based only on morphological characters, such as difficulties in distinguishing between primary absence and secondary loss of characters. Sequence data of genes are the most reliable source of information to use in phylogeny reconstructions involving paedomorphic taxa because they are not affected by the phenotypic variability of life history stages and remain constant markers of evolutionary descent.
Sampling paradoxes in marine invertebrate genetic connectivity: 
The case study of the ‘meiofauna paradox’

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Marine populations were historically perceived as ‘open’ due to the lack of obvious barriers in the sea. Water column and marine currents were thus discussed as dispersal highways for pelagic larvae (e.g., larvae released to the water column), ultimately guaranteeing high genetic connectivity levels among extremely distant populations. In contrast species without pelagic stages were expected to have restricted distributions. Recent biogeographic evidence has challenged these ideas, uncovering several cases of genetic heterogeneity for pelagic dispersed species and several cases of haplotype homogeneity for non-pelagic dispersed species. Along this line, the ‘meiofauna paradox’ was defined: the seemingly cosmopolitan distributions of meiofauna taxa despite absence of pelagic stage.

These long-lasting ideas have remained and influenced scientific thinking, but only recently they have been thoroughly tested. We challenge these ideas by exploring several hypotheses:

1. Historically ‘intuitive expectations’ lacked hypothesis testing and, based on modern evidence, are likely incorrect;

2. The distribution range and the dispersal abilities of a given species are affected by several factors such as life cycle, life history, presence of competitors or predators, former geological and climatological events and are not exclusively explained by its dispersal abilities alone (i.e. simply the presence/absence of pelagic larvae).

3. Integrating biogeographical evidence from different species and studying these systems will allow generating a more complete picture of marine connectivity dynamics.
ORAL

The enigmatic case of morphological stasis in the marine annelid *Stygocapitella subterranea*: biogeographical and morphological evidence

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The presence of cryptic species in some organismal groups is not by any means surprising. Interstitial taxa (i.e. organisms living between sand grains in marine sediments) are characterized by their small size, paucity of distinguishing characters and a high degree of convergence. As a result, many interstitial species have been regarded as cosmopolitan. Recent studies have unveiled a high prevalence of cryptic species in these species, yet the evolutionary history of these species remains unknown.

In this work we investigate the genetic and morphological differentiation of the interstitial annelid *Stygocapitella subterranea* - a recognised cryptic species’ complex. Specifically, we explored population connectivity at intercontinental, continental, and regional scales (North American Atlantic and Pacific coastlines and North European coastline) using four marker genes (CO1, 16S, ITS1 and ITS2) and further examined specimens using light and scanning electron microscopy. We discovered that albeit significant genetic differentiation among populations, no diagnosable morphological differences was found suggesting a case of morphological stasis (i.e. high genetic differentiation despite no morphological differences). Furthermore, some species (formally, OTUs) occur in sympatry. Our results are discussed in the light of theoretical predictions of genetic and morphological differentiation, marine population connectivity, population migration dynamics in response to past environmental changes (e.g. Quaternary Glacial Periods), ecological niche occupation and taxonomic implications of morphological stasis (i.e. high genetic divergence despite no morphological differences).
ORAL

Phylogeny and habitat use of Ampharetidae in chemosynthesis-based ecosystems

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Deep-sea chemosynthesis-based ecosystems (CBEs) - hydrothermal vents, cold seeps and organic falls - share many environmental characteristics and several families and genera of organisms, emphasizing the evolutionary link between them. The description of intermediate ecosystems, such as hydrothermal seeps and sedimented vents, has lead to the belief that CBEs should be considered a continuum rather than discrete ecosystems. However, on a global scale the proportion of species shared between CBEs is very low, and in light of the ecosystem continuum hypothesis there is a lot of interest in determining how environmental and biogeographical factors are shaping these differences. Polychaetes in the family Ampharetidae are tube-dwelling deposit feeders and almost ubiquitous in CBEs, but most species are restricted to one type of CBE. Here we present a multigene phylogeny of Ampharetidae with an emphasis on species from CBEs and also include a review of their microhabitat. The phylogeny revealed that ampharetids have adapted into CBEs at least five times independently, with subsequent diversification, and shifts between ecosystems have happened within at least three of the clades. Although the amount of data available on the microhabitat of each species varies, our review showed that ampharetids at hydrothermal vents can have a very wide niche in terms of substratum and temperature. The effect of niche width on habitat specificity and the distribution of species will be discussed.
The Norwegian Barcode of Life Network (NorBOL)

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NorBOL (www.norbol.org) was formed in 2007 as a national network to 1) advance barcoding of Norwegian and Arctic biodiversity, 2) raise funding, 3) curate barcode reference material, 4) coordinate and initiate new barcoding projects, and 5) increase public awareness of DNA barcoding and barcoding results in Norway. NorBOL is a regional node within iBOL, with a particular responsibility for Polar Regions. NorBOL is coordinated by the NTNU University Museum in Trondheim and connects 17 institutions, including all four major natural history museums as well as all major biological research institutes in Norway. Despite strong support among research institutions, substantial external funding was only first achieved in 2012 through a grant from the Norwegian Biodiversity Information Centre. Further funding was obtained in 2014 from both the Research Council of Norway and the Norwegian Biodiversity Information Centre. Since then, barcoding progress of the Norwegian fauna, flora and fungi has increased and the Barcode of Life Data Systems database currently holds more than 60 000 published sequence records (36 000 DNA barcodes) of more than 12 400 species from Norway and polar regions. The goal for NorBOL is to barcode 20,000 species by the end of 2018. NorBOL currently targets barcoding of terrestrial arthropods, plants, lichens, fungi, marine invertebrates, fish, and material from bioinventory projects supported by the Norwegian Taxonomy Initiative. We collaborate with Swedish and Danish institutions on sampling of marine invertebrates, earthworms and insects. As the standard barcodes have limited taxonomic resolution in many vascular plant groups, we are engaged in testing if low coverage shotgun sequencing of herbarium material is useful to obtain the full plant plastid genomes.
Moss mites (Acari: Oribatida) are abundant and species rich soil-dwelling arthropods (200,000 specimens and 50 species m⁻²). Approximately 10,000 species are known worldwide and altogether 330 from Finland. The fossil record of oribatids spans to the Devonian Period, approximately 400 m years. Due to their vast abundance, minute size (0.1-1 mm) and lack of taxonomic experts only few studies concerning the oribatid diversity in phylogenetic framework has been conducted.

We investigate the phylogeny and species delineation of oribatids using as model group the genus *Carabodes* Koch 1835, that is represented in Finland by 10 morphologically well-defined and widely distributed species. We study the evolutionary affinities of populations including geographical, habitat-related and morphological variation with multi loci sequence data (nuclear 28S rRNA and non-coding ITS in addition to mitochondrial COI and 16S rRNA). It is of particular interest to examine whether the commonly used COI barcodes are suitable for species identification. Preliminary results from the analysis of COI sequences for five species show that the barcoding gap in *Carabodes* species is wide with the distance of 10% between species. Moreover, the results from the GMYC and ABGD delineations verified the presence of five species within the material. The results indicate that for this particular genus the one loci method in species identification may be usable, but preliminary results for other less-known genera however indicate that additional molecular markers would be beneficial in the assessments of inter- and intra-specific variation.
RICH NATURAL RESOURCES VS POOR FUNDING?
Can the sequencing of amphibians and reptiles be a solution for conservation in a developing country with a great biodiversity?

Harith Farooq, Simon Loader, Alexandre Antonelli and Amadeu Soares

Identifying areas where biodiversity is concentrated and understanding why they exist are issues concerning both conservation planning and evolutionary biology.

This project aims to enhance conservation on two biodiversity hotspots in Mozambique: the Eastern Afromontane and the Coastal Forests of East Africa, through the integration of phylogenetic, spatial data and distribution modeling.

The integration of phylogenetic, spatial data and distribution modeling can include cryptic diversity and may be useful to confirm known areas of endemism as well as finding new biodiversity hotspots. We plan to use new and existing spatial and phylogenetic data to map the Phylogenetic Endemism (PE) of the amphibians and reptiles’ intraspecific lineages from several species and complexes showing high phylogeographic structure. Using spatial and non-spatial regressive models we will test whether PE can be predicted by measures of Quaternary climate change, forest stability, topographic heterogeneity, and current climate.

Finally we will intersect the Phylogenetic Endemism results with the protected areas in Mozambique in order to evaluate the current conservation effectiveness in the country.

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Using Microbiomic Signatures to Investigate the Diet of Hymenopteran Larvae

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Cynipids are a family of gall-associated hymenopterans commonly known as gall wasps. The study of cynipid biology is often complicated by the presence of parasitoid species that attack them, and sometimes by the alternation of sexual and asexual generations. Most cynipids are gall-inducers, usually with a very narrow host specificity, but some of them, known as inquilines, are unable to initialize the gall and must take over galls made by other insects, usually killing them in the process. Cynipids likely evolved from a parasitoid ancestor, but how this happened, and how many times the evolutionary transition between different life styles occurred, is open to debate. It has even been suggested that some cynipids might actually be true parasitoids. Currently, methods to study the biology of gall-associated hymenopteran larvae rely mostly on morphology and direct observation, but these are time consuming and not entirely reliable. Another possible method of characterizing insects with a different diet could rely on the molecular analysis of their associated gut bacteria.

In order to address the question of whether hymenopteran larvae with different life styles have distinct microbiomic signatures, we have sequenced larvae of the gall-inducer cynipid Diplolepis rosea, as well as those of three of its associated species: the inquiline cynipid Periclistus brandtii, and the parasitoids Torymus bedeguaris (Chalcidoidea) and Orthopelma mediator (Icneumonoidea). We aim to identify the bacterial species associated with a carnivorous and phytophagus diet, and possibly with inquiline.

Knowledge of the composition of the gut microbiome associated with different life histories has interesting application in the study of other cynipid groups and may be used for the development of a PCR-based diet assay.
A central task of speciation genetics is to investigate the onset and timing of reproductive barriers in order to distinguish between causes and consequences of speciation. This project will look at the ‘speciation continuum’ in the brown algal genus, *Fucus* and will identify molecular mechanisms of speciation in two sister species. Hybrid zones between the two species *Fucus distichus* and *Fucus serratus* provide a unique situation to examine mechanisms of reinforcement, adaptation and speciation at a molecular level, in a non-model marine algal species. I will use Next-generation sequencing of transcriptome libraries to better understand the molecular basis of speciation in these ecologically important marine macroalgae. By studying speciation in *Fucus* we can better understand the influence of speciation on both the patterns of biodiversity and species adaptation.
ORAL

Mammal extinctions of the recent past

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University of Gothenburg

In the recent years we have been witnessing well-recorded, dramatic declines in population numbers of several mammal species and several instances of extinction, which can be attributed to large extent to the impact of our own species. These negative trends raise concerns and worries about human impact on the natural world and about the future of biodiversity. However, in order to properly assess the magnitude and severity of the current rate of species loss, we need to understand, how many extinctions we would expect under natural conditions, including fluctuations in climate. Such information is available in the fossil record, which provides a direct evidence, though incomplete, of past biodiversity. Here we use a well-curated fossil data set of the past 130,000 years to reconstruct the loss of mammal species through time and estimate extinction rates and their temporal variation. The observed time period encompasses the last glacial maximum and the preceding warm period (last interglacial), which was similar to today's climate (Holocene). We observe a dramatic increase of extinction rates toward the present, particularly within the last 500 years, which coincides with the accelerated population growth and expansion of humans. Further we use all available current IUCN assessments of mammal species, in order to model the expected extinction of mammal species in the future. The results are alarming and show that we are entering an unprecedented extinction of mammal species, which may lead to a loss of more than 1000 species by the year 2100, if conservation efforts remain unchanged. Our results also show that an effective conservation of the current mammal diversity (maintaining all species at their current protection status), can significantly buffer the steep extinction curve, potentially preventing around 500 species from extinction before the year 2100.
ORAL

Understanding the History of Life Using Morphology and Fossils: New Computational Approaches and Probabilistic Models

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Morphological data is necessary for inferring phylogenetic trees that include fossils, which represent the only source of data that allows us a glimpse into true evolutionary history. However, molecular sequence data are more widely used for phylogenetic analyses. This is due to the relative ease of generating large amounts of genetic data, concerns about subjectivity in the acquisition of morphological data, and the relative lack of models of morphological evolution. As a result, when phylogenetic incongruence arises between morphological/paleontological and molecular datasets, the latter is often viewed as more robust, even when the divergences in question occurred in deep time. Molecular data, however, are not infallible, and the meaningful influence of fossil data in phylogeny estimation and comparative analyses is well established. Therefore, efforts towards improving the methodological process of generating and analyzing morphological data in a phylogenetic context are a priority.

Here, I discuss computational approaches illustrating that: 1) systematic biases and misleading signal may have a profound effect on molecular phylogenetic analyses; 2) the inclusion of phenomic-scale datasets in combined analyses can affect phylogenetic inference and comparative methods, even when morphological characters are vastly outnumbered; and 3) morphological data extraction can potentially be automated and scaled up effectively and efficiently. To demonstrate these points, I use three case studies, respectively: 1) the position of turtles within the amniote tree of life; 2) the evolutionary history and origin of snakes; and 3) the evolution of shape across North Atlantic communities in planktonic foraminifera. These studies set the groundwork for future work aiming to improve computational methods for analyzing morphological and paleontological data, both in terms of data extraction and data interpretation/analysis.

Further, I discuss my current work on developing probabilistic models of morphological evolution. Probabilistic models are necessary for the use of modern statistical phylogenetic inference machinery using Bayesian and maximum likelihood frameworks. This project will focus on: (1) Expanding probabilistic models of morphological evolution beyond the standard Mk(v) model (Lewis 2001) by improving the modelling of rate variation and trait correlation; and (2) Implementing these improved models in user-friendly software packages.
ORAL

High-throughput molecular methods for studying trophic interactions

Kamenova, S. & G. Gussarova
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Quantitative food webs provide a powerful framework for understanding and sustainably managing fundamental ecological functions. However, drawing a comprehensive picture of trophic interactions in real food webs is challenging because of (i) their inherent complexity; (ii) our limited capacity to empirically quantify trophic interactions. DNA-based species identification methods such as DNA barcoding and metabarcoding are already revolutionizing our capacity to deal with biological complexity and offer a promising and powerful framework for studying complex species interactions. Using various organisms - from insects to reindeer - as a model, I will present the set of molecular methods I developed during the last three years. I will discuss their usefulness for quantifying direct trophic interactions and impacts on ecosystem services as well as their potential as diagnostic tool for informed, data-driven ecosystem management. Furthermore, I will discuss the relative advantages and pitfalls associated with molecular diet analysis and will provide practical guidelines and perspectives for future developments.
KEYNOTE

Transforming subjective knowledge into insights through objective model-based analyses

Lacey Knowles
University of Michigan

Shifts in the scale of data collection today have driven major changes in scientific endeavors, but how we approach our questions – that is the framework that is applied – is arguably key to the insights our investigations might provide. In particular, model-based analyses bring powerful methods for testing hypotheses and estimating parameters. However, the true transformative potential of this objective machinery rests on how we communicate our expert knowledge and understanding to the statistical apparatus. By reference to specific examples, I show that (i) model formulation deserves not only more attention to increase the insights gained through model-based analyses, but also that (ii) the subjectivity of model formulation itself should not be overlooked when making model-based inferences. These lessons are highlighted with three applications of models-based analyses: species delimitation, phylogenetic discord, and phylogeographic study.
Species delimitation and phylogenetic relationships in *Limnodrilus* (Annelida: Clitellata: Naididae)

Yingkui Liu

University of Gothenburg

The freshwater *Limnodrilus* worms (Clitellata: Naididae: Tubificinae) are segmented hermaphroditic annelids, bearing a unique clitellum (“girdle”) during sexual maturity. *Limnodrilus* species are abundant, and ecologically and economically important in many respects, but taxonomic controversy, especially regarding the diagnosis of the cosmopolitan *Limnodrilus hoffmeisteri* Claparède, 1862 (the type species of the genus), has lasted for more than a century. In addition, the phylogenetic position of *Limnodrilus* within the subfamily Tubificinae has been uncertain. Taxonomic studies based on molecular data, e.g., using DNA-barcoding (for animals, the mitochondrial marker COI), have revealed several examples of cryptic speciation among widely distributed clitellate morphospecies. In this thesis, I used both mitochondrial COI barcodes and nuclear ITS data to explore primary species hypotheses from a sample of the morphologically defined *L. hoffmeisteri* collected in the northern hemisphere, and a final conclusion about species boundaries was based on the congruence of the mitochondrial and nuclear phylogenies. Furthermore, the phylogeny of *Limnodrilus* was estimated based on multiple-loci data of several *Limnodrilus* species and other naidid taxa.

The molecular study showed that the well-known taxon “*L. hoffmeisteri*” actually represents a species complex (with at least ten species) rather than a single, cosmopolitan, species with great morphological variation. This work also showed that DNA barcoding, without using additional nuclear data, is likely to overestimate the number of species. In addition, by combining morphological and genetic information, a neotype of *L. hoffmeisteri sensu stricto* was designated. The neotype of *L. hoffmeisteri* is a baseline for future taxonomic work on the many cryptic species.

*Limnodrilus sensu stricto* is a well-demarcated, monophyletic genus of the naidid subfamily Tubificinae, containing at least three main evolutionary lineages (i.e., three species groups). The sister lineage of *Limnodrilus* in our taxon sample is a group of three genera, *Baltidrilus*, *Lophochaeta* and *Varichaetadrilus*. However, *Limnodrilus rubripenis* Loden, 1977 is phylogenetically closer to *Varichaetadrilus* than to other *Limnodrilus* species.
KEYNOTE

Linking ecology and macroevolution in replicated radiations of island lizards

D. Luke Mahler

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The central aim of my research is to understand how ecological and evolutionary factors combine to generate biodiversity over large spatial and temporal scales. In this seminar, I will describe how I use radiations of Anolis lizards on Caribbean islands as a natural evolutionary experiment to test hypotheses about macroevolution and biogeography. First, I will examine independent radiations of island anoles to ask whether macroevolution in ecologically similar settings can produce repeatable outcomes. I will provide evidence for exceptional phenotypic similarity among entire island anole faunas, and will show how such large-scale deterministic convergence can be explained by G.G. Simpson’s model of the macroevolutionary adaptive landscape. Second, I will use distributions of both native and exotic species of Anolis on Caribbean islands to test key predictions from island biogeography theory at a large spatial scale. I will show that while anole island biogeography in the past was determined by geographic area and isolation, in the Anthropocene — an epoch proposed for the present time interval — it is increasingly dominated by patterns of trade among human populations.
POSTER

Ctenophores – native aliens in Norwegian waters

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Ctenophores are known to play important roles in the world’s ocean ecosystems and share physiological attributes that allow them to better exploit the changing environmental conditions than many other zooplankton groups. Yet, they remain neglected in most zooplankton studies and monitoring programs, and are considered one of the most difficult groups of pelagic animals to study; they are fragile and require special sampling and preservation. At the same time, our taxonomical knowledge of ctenophores remains rudimentary at best. Consequently, their diversity and ecological role are grossly oversimplified and misunderstood, leading to biased views of ecosystem functioning. Here, we present preliminary results of an ongoing project with the primary goal of describing and documenting the diversity of ctenophores in Norwegian waters, from the North Sea to the high Arctic. Combining morphological and molecular methods, the project will increase taxonomic knowledge, which is a valuable first step towards establishing a baseline for future ecological studies, monitoring of climate impacts, and assessing the threat of introduced species. By engaging the public audience in collecting samples, the project increases the geographical area coverage and, in return, the laymen involved will come to appreciate completely new aspects of their own environment.
ORAL

Dating grasses

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The Poaceae comprise 12,000 species worldwide, and are also the most economically important plant family. The phylogenetic history of the family is well understood, but a limited fossil record has hampered our understanding of its history of diversification. Age estimates for the crown node are still controversial and generally vary between 55 and 130 Ma.

Here we present a new fossil-calibrated phylogeny for Poaceae, with special emphasis of the north-temperate Pooideae subfamily (4200 spp.). Our analysis incorporates novel fossil evidence and applies calibration priors obtained by novel methodology (PyRate) that estimates speciation times while taking fossilisation probability into account.

Our results unambiguously favour an old age for crown Poaceae (>100 Ma) as well as for crown Pooideae (59–72 Ma). However, the onset of diversification for the major pooid tribes (Aveneae, Poeae, Stipeae, Triticeae) happened at a much later time, and coincided with the abrupt climate cooling at the Eocene/Oligocene boundary (~34 Ma ago).

These findings have wide implications on how to interpret adaptations to the temperate climate in grasses.
ORAL

Invasion of a novel adaptive zone facilitated build-up of morphological and species diversity in an avian radiation

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Much of our current knowledge about the diversity of life comes from studies of adaptive radiations. Classic examples of such radiations are the result of colonization of isolated and depauperate areas, such as islands and lakes, where radiation has occurred in the absence of competitors and close relatives. Here, we explore the radiation of a large passerine bird clade, the honeyeaters (Family Meliphagidae) that has diversified throughout both the Australian continent and a multitude of Indo-Pacific islands. Honeyeaters possess unique adaptations for nectarivory and it has been hypothesized that a shift to a sugar-rich diet represented a key innovation that allowed them to access previously unused ecological space where they could diversify against the background diversity of their relatives. Integrating analyses of functional trait diversity and evolution with geographic information for the honeyeaters and related clades, we find strong support for this hypothesis. We show that following an ancestral shift in diet, honeyeaters experienced shifts to substantially higher rates of body size evolution and expansion in size morphospace. Furthermore, our results show that honeyeaters and their relatives commonly locally coexist and have produced mutually independent and geographically congruent gradients of regional diversity. Unlike their relatives, however, honeyeaters sustain much higher richness at smaller spatial scales, likely because significant and rapid ecological divergence among species has allowed higher levels of coexistence. Together, these results afford a prime example of radiation against the background diversity of related and potentially competing species, thus fulfilling core predictions of adaptive radiation following the evolution of novel traits.
The roles of abiotic factors and biotic interactions in the diversification of *Odontomachus* trap-jaw ants

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The Indo-Pacific is one of the most diverse insular landscapes around the world. The evolution and distribution of life forms on such islands have inspired the most influential ecological and evolutionary theories, from Island Biogeography to the Taxon Cycles of geographical expansions and contractions. However, testing such evolutionary models using integrative approaches (e.g., phylogenetics, paleogeography, ecology) and hyperdiverse organisms (e.g., insects) remains largely unexplored. The focus of this study is on the trap-jaw ant genus *Odontomachus* as a model organism to elucidate the roles of paleogeography and ecology for the evolutionary success of insects in tropical and subtropical environments. At the genus level, there exists three main global lineages with disjunct geographical distributions, namely the Old World clade (Afrotropics, Palearctic and Oriental regions), the New World clade, and the Indo-Pacific clade (Malay Archipelago and Oceania). The origin of *Odontomachus* trap-jaw ants (39–45 Ma) coincides with the warm climate associated with the early Cenozoic. The ants’ ancestral widespread distribution together in the Oriental and New World regions is in line with the Boreotropical para-tropical rain forests dominating the Northern Hemisphere. A mid-Miocene long-distance dispersal from the New World, along the Equatorial Pacific, is the most likely biogeographical scenario for the origin of the Indo-Pacific ant clade. Biotic interactions and shifts in habitat preferences might have facilitated further geographical range expansion across distinct Melanesian ant lineages over the past 10 Ma, in line with the Taxon Cycle hypothesis. Evidence of habitat preference shifts to marginal environments (e.g., coastal habitats) in New Guinea followed by geographical expansion, are recovered in the Australo-Papuan *ruficeps* group and in the Indo-Malayan *infandus* group. Coincidently, such groups rapidly radiated to become the most species-rich *Odontomachus* lineages in the Indo-Pacific. Overall, the link between ecological expansion and geographic range expansion might have ultimately enhanced local speciation in Indo-Pacific insect communities.
Metabarcoding emerged as a high-throughput solution for DNA barcoding of samples containing large number of individuals (e.g., Malaise trap or pitfall trap samples) or environmental DNA samples in which the organisms are not physically present. For animals, metabarcoding has been based mainly on sequencing short fragments within the ‘barcoding region’ of the mitochondrial gene cytochrome oxidase I (COI). Nevertheless, several problems with PCR primers, resulting from the hypervariability of the third position of each codon of the gene, have been documented; these problems are potentially confounding and may introduce bias during the amplification step. These errors can cause less reliable results to be generated or impede the detection of species that are indeed present in the sample and the habitat.

Using the most comprehensive dataset of mitochondrial genomes belonging to Hexapoda to date (1600 mitogenomes corresponding to 1115 species), we have developed and evaluated new primers for several markers, as well as evaluated previously published primers, and tested two different primer design software. Three properties of the primers and the barcodes were analysed using in silico PCR: taxonomic coverage, exclusive taxonomic resolution, and total taxonomic resolution. Our results highlight the importance of degeneracy in the primers (i.e., wobble bases) for matching a high percentage of the target sequences, in contrast to widely used ‘universal’ primers lacking degeneracies that showed a much lower taxonomic coverage. Also, the results indicate that the genes for the ribosomal subunits (12S, 16S) are very good candidates for metabarcoding, sometimes surpassing COI. Finally, we propose the combined use of the 16S and COI barcodes amplified with the primers presented here for metabarcoding of bulk samples of insects. We also encourage the construction of local mitochondrial reference databases: while other markers showed high potential for DNA barcoding (e.g., Cytochrome b, NADH dehydrogenase 5), the lack of reference data and the low taxonomic coverage of the primers impedes their use.
Challenges and opportunities in Norwegian hydrozoan taxonomy: Lessons from project HYPNO

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Artsdatabanken’s project HYPNO (Hydrozoan Pelagic Diversity of Norway) has been successfully charting hydrozoan diversity in Norway for the last couple of years. During this time, several challenges for the taxonomy of the group have been identified, many of them related to the insufficiently documented morphological and genetic variation in Norwegian hydrozoans. Some specific examples of these challenges, and of the opportunities they offer for the development of hydrozoan taxonomy, will be presented, through the discussion of selected study cases. Previously undocumented morphological variation, cryptic versus unrecognizable species, taxa in need of redefinition, and missing planktonic or benthic stages in the life cycle of several meroplanktonic hydrozoans are only some of the issues that can be illustrated with examples extracted from genera such as Plotocnide, Nanomia, Clytia, Euphysa, Catablema, Lizzia, and Halopsis in the Norwegian fauna. The athecate family Pandeidae and the thecate families Laodiceidae, Mitrocomidae, and Campanulinidae offer particularly interesting opportunities for the assessment of species-boundaries and life cycle studies in the area. Taxa that establish highly specific associations with other invertebrates (such as members of Proboscidactyla and Bythotiar) may represent potential candidates for high genetic differentiation and/or cryptic speciation. The benefits of careful sampling and handling of specimens is stressed and illustrated through the general results of the project and by new records of the occurrence of Tesserogastria musculosa in the Norwegian fjords. It is argued that the results and experiences of HYPNO demonstrate that supraspecific and species level taxonomy in Norwegian Hydrozoa is still rewarding and that many interesting findings can be expected in the future.
ORAL

A RAD-seq study of the Norwegian red-listed sister-species
*Carex jemtlandica* and *C. lepidocarpa* (sect. Ceratocystis, Cyperaceae)

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Hybridization is common in sedges, and particularly so in *Carex* L. section *Ceratocystis* Dumort.; a small, presumably young, and monophyletic group of the sedge family (*Cyperaceae* Juss.). Within this section, the taxonomic treatment of the members is highly disputed. Least agreement concerns the distinction and taxonomy of the two closely related species *C. jemtlandica* (Palmgren) Palmgren and *C. lepidocarpa* Tausch. Using restriction site associated DNA sequencing (RAD-seq), we studied population genetic structure in, and hybridization and introgression between, these two species in Norway. Our results show that despite ongoing hybridization and introgression, *C. jemtlandica* and *C. lepidocarpa* remain genetically distinct also in sympatric populations, most likely due to reduced fertility in hybrids. A lower genetic diversity within *C. jemtlandica* compared to *C. lepidocarpa* lend support for the origin of *C. jemtlandica* from *C. lepidocarpa* (or a near ancestor). The presence of two distinct gene pools in the dataset, largely in agreement with our morphological assignment, indicates that *C. jemtlandica* and *C. lepidocarpa* should be regarded as evolutionary distinct entities. This has implications for conservation management strategies for these two red-listed species in Norway.
ORAL

Diversity and Systematics of the Indo-West Pacific genus *Haloa* (Euopisthobranchia, Cephalaspidea)

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The traditional genus *Haminoea* occurs exclusively in shallow habitats associated with sea grass, algae, mangroves or coral reefs. Preliminary molecular analysis of the family Haminoeidae (presented at the 5th International Workshop on Opisthobranchs – Porto, Portugal) showed that contrary to traditional view the genus is apparently not monophyletic, with Atlantic/East Pacific (AEP) and Indo-West Pacific (IWP) species forming two distinct groups, the true *Haminoea* (type species *H. hydatis*) and "*Haloa*". The IWP clade "*Haloa*" is more closely related to the intertidal IWP rocky-shore genus *Smaragdinella* rather than to the highly similar AEP *Haminoea*. Additionally, further molecular analyses of the IWP clade "*Haloa*" have uncovered four distinct subclades that may be distinct genera. Preliminary work recognized over 100 worldwide nominal species names of traditional *Haminoea*; however, the majority of these (ca. 65) refer to IWP species. The majority of these species were described based exclusively on shells which are highly similar and thus raising doubts about the exact number of valid species.

Morpho-anatomical characters together with multi-locus molecular phylogenetics based on mitochondrial (COI, 12S rRNA, 16S rRNA) and nuclear genes (Histone-3, 18S rRNA, 28S rRNA), will be used to discriminate between subclades, species and infer relationships. Here we present an overview of the diversity of the IWP clades and a preliminary molecular phylogeny including samples from several regions of IWP: East Africa, Indo-Malaya, West Pacific, Central Pacific and Oceania.

Keywords: Cephalaspidea, Haminoeidae, *Haminoea, Haloa*, Indo-West Pacific
The cinquefoils (genus *Potentilla*) of the Rose family (Rosaceae) is a large genus of approximately 300 species which are found almost exclusively on the northern hemisphere, and circa 20 of them are part of the Norwegian flora. Its circumscription has changed drastically over the years from Linnaeus' *Systema Naturae* to the molecular phylogenetic studies conducted today. Some 20 years ago, the first thorough molecular phylogenetic investigation of the genus and its putatively closest relatives discovered that the then circumscription was polyphyletic. Subsequent articles, using both nuclear and chloroplast DNA regions, showed that some species were more related to the mantles (*Alchemilla*) and to the strawberries (*Fragaria*). However, most of the species formed a large clade close to the North American genera *Horkelia* and *Ivesia*. This so called *Potentilla* 'core group', or the Argentea clade as it has also been named, thus contains a majority of the species of the potentillas. Relationships within the core group have however been difficult to resolve based on data traditionally used in systematic research, like morphology and Sanger sequencing data. This has been hypothesised to be due to widespread hybridisation, chromosome doubling and apomixis. High throughput sequencing methods, such as targeted capture, will be used to resolve phylogenetic relationships and to track the biological mechanisms behind the large species diversity in the group. The project will contribute new knowledge about this group of common, but incompletely known, flowering plants and improve our understanding of evolutionary relationships, speciation processes, species delimitations and geographic origin of the species in the group. It will also develop methods and molecular markers that can be used in other evolutionary studies in the economically important Rose family.
ORAL

Validation of metabarcoding approaches targeting soil microarthropod in field study

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Soil mites, together with collembolans are the most abundant and diverse arthropods in the soil. There is an urgent need for an alternative technique to improve the field survey efficiency, which has so far relied heavily on morphological identification. Soil core sampling and DNA extraction methods for the purpose of assessment of the soil mesofauna diversity by metabarcoding have not yet been fully assessed. We therefore undertook a comparison of the morphospecies approach with three molecular approaches, differing in the types of DNA extracted from soil samples: total soil environmental DNA, extracellular DNA and DNA obtained from animals collected from the soil (DNA soup). By validating the metabarcoding approach with a morphospecies list and comparing the different metabarcoding approaches, we showed that it could recover all collembolan morphospecies. Besides collembolan morphospecies, the metabarcoding approach revealed more species than provided by the morphospecies identification. Moreover, those additional species were difficult to identify morphologically. Due to lack of references, recovering mite species from field samplings need further investigation. The metabarcoding approach with different DNA extraction methods, (i) total soil environmental DNA, (ii) extracellular DNA, and (iii) DNA soup, provided similar alpha diversity and rarefaction curves. However, the DNA soup revealed significantly different beta diversity compared with total environmental DNA and extracellular DNA. We present a protocol on how to employ the metabarcoding approach for investigation of soil microarthropod diversity in field studies. We propose that DNA soup should be used if taking the beta diversity into account is the aim. Phosphate buffer extraction is a good choice to recover the rare species, but the sampling procedure needs to be done carefully and a reasonable replication should be involved.

Key words: metabarcoding, Collembola, mite, soil mesofauna, COI barcode, DNA soup, extracellular DNA, total soil DNA
Molecular authentication of *Hypericum perforatum* (St. John's wort) herbal products

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Many herbal products have a long history of use, but there are rising concerns over product efficacy, safety and quality in the wake of recent cases exposing discrepancies between labeling and constituents. Monitoring and authentication of herbal food supplements is complicated as products often contain highly processed and biologically degraded ingredients.

The aim of this study was to evaluate the efficacy and efficiency of amplicon metabarcoding (AMB) to detect substitution in single and multi-ingredient *Hypericum perforatum* (St. John’s wort) herbal products and to test its ability to be used as novel authentication methods of herbal products.

We used a wide range of herbal products that included *H. perforatum* according to the label. The samples were purchased in European countries from pharmacies, herbal shops, and supermarkets or via e-commerce, and were sold as herbal teas, capsules, tablets and extracts.

The fidelity for *H. perforatum* in single ingredient was 76% and 62% for multi-ingredient herbal products.

AMB shows a good resolution in testing herbal products, and can be used in the future as a complementary approach to standard authentication methods, such as macroscopic and microscopic characterization and phytochemical analysis of target compounds.
ORAL

Amazon biodiversity patterns: can we predict the diversity?

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The quantification of biological diversity is fundamental for many biological and societal applications, including conservation, understanding biological interactions, and for designing management strategies. However, virtually all we know about biodiversity derives from the study of aboveground macro-organisms. Soil biodiversity, by comparison, is overwhelmingly richer but consists mostly of lesser-known micro-organisms. In this study we use metabarcoding techniques to sequence 16S and 18S markers from environmental samples (soils and litter) in 39 Brazilian Amazon plots. We test the OTUS richness and composition against physical-chemical soil characteristics, geographical locality and kind of environment. Although several soils variables had significant effect in OTUs richness and composition no general pattern of soils kind was found. The patterns of diversity and distribution of 16S and 18S OTUs do not following the well knowledge vertebrate and plants biogeography, showing that despite centuries of research we still know very little about how the great majority of the world’s biodiversity is distributed. However, even without richness gradient of diversity we could observe composition difference among localities and environments. The use of marker with better taxonomic resolution and use of other diversity indices, such phylogenetic diversity can help to understand the distribution of the most terrestrial diversity.
KEYNOTE

Phylogenetic exploration of medicinal plant diversity

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The use of plants for medicine is closely associated with human culture and has provided both local healthcare and new leads. Through evolution plants have developed sophisticated chemical defenses, which may explain their bioactivity in humans. Intuitively, the evolutionary history of plants may enable predictive approaches allowing systematic evaluation of current and potential medicinal value as well as help guide safety, conservation policies and agriculture. A series of case studies have highlighted that medicinal use, plant defensive compounds and bioactivity are correlated with phylogeny to some extent and suggested methods for identifying the potentially most useful species. Developing new systematic and integrative approaches and tools to synthesize and take advantage of systematics, phylogeny, bioinformatics, ethnobotany, natural products, chemistry and bioactivity studies could supplement traditional selection approaches with the ultimate aim of providing better healthcare. Museum and botanical garden collections provide easy access to expertise and biodiversity for improving selection and focusing drug lead discovery efforts and avoid destructive collection of rare and threatened species. At the same time, engaging in addressing societal challenges provides added value and great potential for increasing public awareness and appreciation of the collections. This presentation will summarize recent studies, current efforts, and future directions as well as introducing the work of the MedPlant International Training Network (www.MedPlant.eu) educating 15 young scientists in phylogenetic exploration of medicinal plant diversity. Examples are provided of phylogenetic exploration and selection of drug lead candidates in central nervous system disorders (Amaryllidaceae), immunological disorders (Aloe L.), cancer research (Euphorbia L. and Thapsia L.), and malaria (Cinchona L.) as well as for authentication of horsetail (Equisetum L.) herbal products. We conclude that in the era of big data and genomics, botanists of the 21st century, can set the agenda by taking advantage of collections, collaboration, and an interdisciplinary approach to help develop new understanding, tools, better medicines and policies for sustainable and ethically responsible biodiversity use and agriculture.
ORAL

Publishing and using biodiversity data in research

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The Global Biodiversity Information Facility (GBIF) is an open-data research infrastructure funded by the world’s governments and aimed at providing anyone, anywhere access to data about life on Earth. Participating countries and organizations use standards and open-source tools to share information about where and when species have been found. This knowledge derives from many sources, ranging from museum specimens to geotagged smartphone photos. GBIF provides a central access point and index of the global biodiversity data. Most of biodiversity data is evidence that a verified source found a specific organism at a specific time and place. This open-access data provides research materials for hundreds of peer-reviewed publications each year, supporting analyses not possible before. GBIF-enabled science topics range from the impacts of climate change and the spread of invasive and alien species to priorities for conservation and protected areas. The complex data on the world’s biodiversity is a result of centuries of studying the natural world. This wealth of information from public and private institutions, once digitized and published, is openly available through GBIF.org. Scientists can contribute to this aggregated scientific evidence, and at the same time, gain additional visibility of their efforts and collections through data publishing. One of the GBIF’s missions is to promote publishing of open-access biodiversity data. By making your data discoverable and accessible through GBIF, you contribute to open availability to global knowledge about biodiversity, and thus to the solutions that not only promote its conservation and sustainable use, but also impact global biodiversity policy - therefore bridging the gap between basic science and decision-making. Data publishing enables integration of datasets and new opportunities for collaboration among data originators and data analysts. Data published as datasets at GBIF.org or as peer-reviewed data papers enables clear crediting of individuals and institutions for their work of creating and curating biodiversity data, achieved though persistent DOIs and bibliographic citations. Using those, collection managers can trace usage and citations of digitized data. GBIF provides a full set of technical solutions to fulfil the open data requirements from funding agencies.
POSTER

Ethnopharmacological investigation and documentation of traditional knowledge about dioecious plants in South India

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Though, for decades the documentation of traditional uses of plants are carried out and enormous literature is available on ethnopharmacological study dealing with traditional uses of plants. Yet, considering dioecy as phenomenon in plant kingdom and documenting the traditional uses of plants based on their gender is lacking. It is known that in angiosperms, 6% of flowering plant species would be dioecious (i.e., having separate sexes contains either only male or female flowers in a plant) and it is evident that based on resource allocation principle in plants, trade-offs between allocation of resource various between genders of dioecious plants. Studies also show that differences in reproductive demands between the sexes of dioecious plants could cause divergence in physiology between the sexes which in turn affects the production and concentration of secondary metabolites. Therefore the present study aims to document the traditional knowledge of folk healers in order document their perception on dioecious plants, awareness about dioecious plants, and if aware, their preference on usage over the gender of dioecious plants. The study was conducted among Malayali communities in parts of Eastern Ghats in Tamil Nadu. Total 40 traditional healers aged 45 to 85 were interviewed and documented their knowledge on dioecious plants. The results were the awareness about dioecious plants among people depends on the habit of the plant (i.e., 100% awareness on tree species, however for herb and shrubs people are unsure about dioecious species). People preference over genders of plant is that they prefer male plant timber over female (For example; Borassus species). And also people cut down male plants at their garden considering it has no values (For example; Carica papaya L.) and selectively cut male plant for fire wood in forest (For example; Myristic species).
Systematics and evolution of clam shrimps (Crustacea, Branchiopoda) with focus on morphology and functionality of (clasper) limbs

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Clam shrimps, consisting of the three orders Spinicaudata, Laevicaudata, and Cyclestherida, are carapace-bearing crustaceans belonging to the class Branchiopoda. Together with Notostraca (tadpole shrimps) and Anostraca (fairy shrimps), they make up the “large branchiopods”, which all inhabit seasonally astatic freshwater pools. The “large branchiopods” are ancient-looking crustaceans going around 500 million years back in the fossil record, with a high degree of morphological stasis seen in several of the groups. Most branchiopods have very characteristic foliaceous and lobed trunk limbs, showing serial similarity from anterior to posterior. The male clam shrimps hold some evolutionary and morphologically informative secondary sexual organs in form of their first (and sometimes second) pair of trunk limbs, which have been modified into gripping structures called claspers. During mating and mate guarding the male uses its claspers to grasp around the female’s carapace margin, giving the male a firm grip of the female. External limb morphology, including that of male claspers, has for a long time played important roles in species descriptions and classification of Branchiopoda. However claspers also present problems phylogenetically and questions about homology of various structures have long been discussed. In order to solve some of these problems a clasper-based phylogeny has been made (based primarily on scanning electron microscopy, SEM) and functionality in relation to mating behavior been studied (based on close-up video recordings). The clam shrimp order Laevicaudata, consisting of around 40 species, is in need of a larger revision to reflect the group’s systematics and evolution and to establish a comprehensive phylogeny of the group. This work will be based on morphological data including clasper limbs and other characters as well as molecular data.
POSTER

Genetic study reveals recent isolation of Sundarbans Tigers from mainland Bengal tiger (*Panthers tigris tigris*) population, India

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Morphological differences of tigers of Sundarbans Islands, mainly body weight and skull size and shape make them unique compared to Bengal tigers from the mainland. Thus, this raised a question of their possible ecological and genetic distinctiveness from mainland populations. By using nine microsatellites markers and 3 kb of four mitochondrial DNA (mtDNA) genes, we evaluated genetic variation, population structure and demographic history of Sundarbans tiger. We also visualize historical and contemporary connectivity among tiger populations from Sundarbans and mainland India. Genetic variation in Sundarbans tigers (He=0.58) is lower in comparison to mainland tiger populations, such as Peninsular and northern (He is 0.70 and 0.67 respectively). Molecular data supports migration between mainland and Sundarbans populations until very recent times (FST=0.06). Demographic analyses done by using both markers (mtDNA and Microsatellite) suggest that Sundarbans tigers have diverged recently from mainland tiger population within last 2000 years. Recent migration and divergence within last 2000 years from mainland tiger population might be due to anthropogenic activities and change in geography and vegetation in many parts of Sundarbans due to series of climatic changes. Biogeographical changes are thought to have had a profound impact on the geographic distribution of the Sundarbans fauna, including tigers. The anthropogenic activities in the late 17th century, such as conversion of forest areas to cultivated land, the establishment of historical trading places, and extension of agriculture due to development of irrigation canal in the Ganges basin. It has resulted in increased human population density (1437.4 persons /km\(^2\)), and settlement of people in and around Sundarbans. Severe habitat fragmentation and habitat loss caused complete isolation of tigers in Sundarbans because they are very sensitive to human disturbance. Conclusively, because of morphological differences and recent divergence from mainland tiger population Sundarbans tiger should be treated as different conservation unit.
ORAL

Population genetic structure of Bengal tiger (*Panthera tigris tigris*) in human dominated Terai Arc Landscape (TAL), India

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Since the last two centuries, Tiger (*Panthera tigris*) have faced a serious threat of decline in population sizes due to the massive shrinkage in their geographical ranges, fragmentation of their habitats owing to human activity, declining populations of major prey species and poaching pressure. These factors are known to affect the genetic characteristics of populations and decrease local effective population sizes. The Terai Arc Landscape (TAL) at the foothills of the Himalaya is one of the 42 source sites of tigers around the globe. Therefore, information on how landscape features and anthropogenic factors affect the genetic structure and variation is desirable to improve appropriate management strategies for accomplishing long-term conservation goals. We document, for the first time, the genetic characteristics of this tiger population by genotyping 71 tiger samples using 13 microsatellite markers from the western region of TAL (WTAL). Specifically, we aimed to estimate the genetic variability, population structure, and gene flow. The microsatellite markers indicate that the levels of allelic diversity (\(MNA = 6.6\)) and genetic variation (\(H_o =0.50, H_e = 0.64\)) were slightly lower than those reported previously in other Bengal tiger populations. We observed moderate gene flow and significant genetic differentiation (\(F_{ST} = 0.060\)), and identified the presence of cryptic genetic structure using Bayesian and non-Bayesian approaches. There was low and significantly asymmetric migration between the two main subpopulations of the Rajaji Tiger Reserve and the Corbett Tiger Reserve in WTAL. Sibship relationships indicate that the functionality of the corridor between these subpopulations may be retained if the quality of the habitat does not deteriorate. However, we found that gene flow is not adequate in view of changing land use matrices. We discuss the need to maintain connectivity by implementing the measures that have been suggested previously to minimize the level of human disturbance, including relocation of villages and industries, prevention of encroachment, and banning sand and boulder mining in the corridors.
The project “Norwegian Marine Amphipoda” funded by the Norwegian Species Initiative is an introductory examination of the amphipod fauna of Norway using both morphologic and molecular species delimitation.

Since the first systematic mappings by G.O. Sars in the late 1890s of Norwegian amphipods, the number of taxa registered has approximately doubled. This is partly due to an increase of the area, and partly a reflection of the general amphipod taxonomy, where 50% of the present valid names have been assigned the last 50 years.

Providing a “DNA-barcode” (COI) to as many as possible of the amphipod-taxa from Norwegian marine waters will help in the validation of how many taxa we have in the geographic area, as well as being a tool for coordinating the taxon-name usage in monitoring and mapping in the future.
A Phylogeny of the Tribe Anthospermeae (Rubiaceae) Based on Molecular Data

Olle Thureborn 1, Sylvain G. Razafimandimbison 2, Niklas Wikström 1, Catarina Rydin 1

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The pantropical tribe Anthospermeae belongs to the species-rich and mostly herbaceous Spermacoceae alliance in the subfamily Rubioideae (Rubiaceae), with no less than 200 species currently classified in 11 genera. Anthospermeae is currently divided into three subtribes: Anthosperminae, Coprosminae and Operculariinae. Members of Anthosperminae occur in Africa, Madagascar, Macaronesia, Yemen and Saudi Arabia; Coprosminae has a wide amphi-transpacific distribution and Operculariinae is restricted to Australia and Tasmania. Most species are small trees or shrubs, with only few species that are perennial herbs. Flowers of the tribe are either unisexual or hermaphroditic and their fruits are either fleshy or dry. Anthospermeae are unusual in that the species of this tribe have anemophilous flowers in a family otherwise characterized by having predominately zoophilous flowers. Apart from anemophilous flowers other characters such as non-heterostylous flowers, filaments being inserted below the middle of the corolla tube and pollen morphology have been used for delimiting the tribe.

The aim of the present project is to reveal new insights into the generic limits and evolutionary relationships within the tribe, and provide a basis for further studies of morphological evolution and diversification dynamics in the group. Previous molecular phylogenetic studies of Anthospermeae were based on limited sampling of taxa and data. We reconstruct the phylogeny of Anthospermeae using standard nrDNA and cpDNA sequencing data and increased taxon sampling. Phylogenetic analyses of the datasets will be performed using Bayesian inference and maximum likelihood (ML).
POSTER

Systematic and taxonomic revision of Empidoidea (Insecta: Diptera), with emphasis on Empididae and Hybotidae

Emma Wahlberg

Swedish Museum of Natural History / University of Stockholm

Previous studies on the classification and phylogeny of the Empidoidea have been based on morphological characters, several taxa have been placed incertae sedis and many evolutionary questions remain unanswered. Established molecular methods are now used to test the support for the monophyly of families and subgroups, and characters in previously published hypotheses will be re-evaluated. There are several thousand specimens from the Swedish Malaise Trap Project from nearly 50 localities in Sweden. The availability of material is extremely high, additional sampling is restricted to uncovered habitats and taxa. A minimum of four genes will be used in the analysis, and the COI gene is used for DNA barcoding. Bayesian and maximum likelihood analyses are used to infer evolutionary models. The revision of the systematics of the Empidoidea will provide a fundament to further taxonomic studies and production of updated determination keys.
KEYNOTE

DNA barcoding marine life underscores the needs for taxonomists

Endre Willassen

Department of Natural History, University Museum of Bergen

Taxonomy is underpinning all major subjects of biology and the biodiversity disciplines in particular. It is sometimes stated that “the species name is the key to the knowledge about it”, implicitly emphasizing that correctly identified species are the access points to accumulated data and knowledge about the units of biological diversity. In the age of web-based biodiversity informatics, DNA-barcodes have become an increasingly important linked element in the nexus of different biodiversity databases. The University Museum of Bergen has been engaged in DNA-barcoding of marine animals with the BOLD-system since 2006, first with fish species from the Mid-Atlantic ridge, later with invertebrates under the auspice of the NorBOL consortium, and additionally as part of an inventory of West African continental shelf fauna. In this talk I will present some insights from these activities and show how “DNA-barcoding” plays a dual role in species identification and species discovery. One of the lessons is that “DNA-barcodes” have great potential in mediating a better global understanding of units of biodiversity. This apparently requires stronger efforts in the field of taxonomic revisions because genetic databases have a high proportion of taxonomic discordance. Some of the conflicts stem from simple misidentifications, cross-contaminated DNA, and others from different taxonomic cultures in different parts of the world. In many less well studied groups it is also clear that the established taxonomy is not accounting for the large divergence among genetic clusters of “morphospecies”. Implications of such observations should be a renaissance for voucher-based revisionary taxonomy.
A chemo-systematic and phylogenetic revisit to the lichen *Cetraria islandica* species complex in Iceland

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The lichen *Cetraria islandica*, or Iceland moss, is a symbiotic association including but not limited to green algae, fungi (Parmeliaceae, Ascomycota) and bacteria. It has been used in traditional medicine to treat bronchial and inflammatory conditions, gastritis and ulcers. However, the taxonomy of Iceland moss is still controversial due to the ambiguous species boundaries between *C. islandica* chemotypes and its sibling species *C. ericetorum*. Furthermore, their chemical profiles have not been thoroughly investigated for food safety and pharmacovigilance, which would trigger problems in the authentication and standardization of herbal products. Thus, we aimed to assess the species boundaries between members in *Cetraria islandica* species complex using UPLS-MS metabolite profiling and molecular phylogenetics. In total 141 lichen specimens have been collected around Iceland from 2012 to 2016. Three chemotypes of the species complex were identified by metabolite profiling and chemometrics, which differed in the presence of fumarprotocetraric acid (FA) and composition of protolichesterinic acid analogues. Phylogenetic analysis based on 6 fungal genetic markers (i.e. nrITS, TSR, MCM7, GPD, RPB1 and RPB2) recognized two species in the complex, and supported the presence of two races of *Cetraria islandica* in Iceland: one is FA-containing and distributed in oceanic area, while the other is chemical variable (both FA-containing and FA-deficient) and mostly located in central and northern Iceland. The current research could contribute to the taxonomy and herbal standardization of Iceland moss products.
ORAL

Life across the Mid-Atlantic Ridge: Unique fungal-algal association pattern of the lichen *Cetrariella delisei* in Iceland

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Lichens, as a symbiotic association of fungal and photosynthetic partners, are ecologically and evolutionarily highly successful, covering 8% of global land surface. The high dispersal power of lichen seems to be associated with high fungal selectivity for locally-adapted photobionts. In this study, we aimed to investigate fungal-algal association pattern of the lichen *Cetrariella delisei* within the context of Icelandic cetrarioid lichens, to understand how species association patterns correlate with the habitat, phylogeography and secondary metabolite profile. *Cetrariella delisei* stands out from other cetrarioid lichens dwelling in wet bogs and fens. Multilocus phylogenies of fungal and algal partners were generated using 88 specimens, including 13 cetrarioid lichen species of 7 genera. Phylogenetic analysis as well as morphological observations suggested the presence of a new *Trebouxia* algal lineage associating with *C. delisei*. Two strongly supported sub-clades of the photobionts were recognized, which are geographically separated by the Mid-Atlantic Ridge. All the closely-related cetrarioid lichens, however, associate with photobionts (e.g. *Trebouxia jamesii* or *T. simplex*) with no such geographic correlation. *C. delisei* also has a unique chemical profile, which is mainly composed of depsides, especially gyrophoric and hiascic acids, while the sibling species are characteristic of depsidones and aliphatic lactones. Our results suggested that geography and ecology might shape the genetic difference of photobionts associated with *C. delisei*, and such association might facilitate the dispersal of *C. delisei* through Iceland. Differences in chemical profiles of cetrarioid lichens may be driven by both ecology and the identity of algal photobionts.
Genome-wide association mapping and factors associated with carbon sequestration in common peatmoss *Sphagnum magellanicum* Brid.

Narjes Yousefi¹, Péter Szövényi², Kristian Hassel¹, Kjell Ivar Flatberg¹, Gustaf Granath³, Håkan Rydin⁴ and Hans K. Stenøien¹

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Approximately one-third of world’s terrestrial carbon along with enormous amounts of methane is stored in Northern hemisphere peatlands. Peat mosses (genus *Sphagnum*) are the main constituents of peatlands, and few if any other plant genera are more important contributors to global climate regulation. It is of interest to understand what genetic and environmental factors are associated with carbon sequestration in peat mosses. *Sphagnum magellanicum* is a common and widespread species with pronounced spatial genetic structure throughout its distribution range. In order to determine genetic factors associated with carbon sequestration in peat mosses, we performed genome-wide association mapping of plants from 62 sites worldwide, covering a wide range of microhabitats. We generated over 30 000 high quality SNPs using RAD-sequencing and related these SNPs to 19 environment and eight vegetation variables estimated over two growing seasons for each site. Our preliminary results show that despite strong genetic clustering within the species, the mixed-linear models robustly control for these effects and we are able to detect multiple significant associations. We investigate the importance of environment factors driving vegetation traits, as well as the potential association of environmental factors and spatial genetic structure. We present the final results from our association mapping analyses.

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Since the family Fuscideaceae was introduced in 1984, its taxonomic position and the genera assigned to it have been a matter of debate. Currently, its photobiont remains unknown. We aimed to 1) assess and clarify the taxonomy and evolution of the Fuscideaceae sensu Eriksson & al., (2006), and 2) identify the photobiont in Fuscidea. Four genes from two genomes: mitochondrial (mtSSU), nuclear (ITS, SSU and LSU) of ribosomal DNA, was analyzed by the Bayesian inference and the maximum likelihood method. Our results showed that the Fuscideaceae comprised of Fuscidea, Maronea, Printzeniella gen. nov., and Ropalospora. The family was assigned in the Umbilicariales, in addition to the Umbilicariaceae, Elixiaceae, and Ophioparmaceae. The genus Fuscidea was split in six larger monophyletic clades, including Maronea. The photobiont was identified as Apatococcus known only as free-living algae, including two lichenized species from which one was circumscribed as A. fuscidea sp. nov. To conclude, Fuscidea, Maronea, Printzeniella, and Ropalospora were assigned with certainty in the Fuscideacea, and Hueidea with a question mark in the Umbilicariales. The genus Fuscidea is in association with the lichenized Apatococcus species and appeared to be paraphyletic as Maronea was securely nested within this genus.
Evolution of stomach botflies (Oestridae: Gasterophilus): a phylogenetic perspective

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Larvae of the Gasterophilus (Diptera: Oestridae) are obligate endoparasites to equids and live on the mucosa of the equid gastrointestinal tract, inducing horse gastrointestinal myiasis. Amount to six Gasterophilus species have been found in China, while eight species exist worldwide. They occupy almost the same niche by parasitizing same/similar hosts of Equus spp., sharing almost identical life cycles. However, they exhibit abundant biological and morphological variation, e.g., egg production, oviposition sites, conditions for egg hatching, and development locations of each larval stage. To trace the evolution of Gasterophilus, we sequenced mitochondrial genomes of those widely distributed horse botflies, and reconstructed the phylogeny of Gasterophilus using mitogenomic data.

Our results reveal that the mitochondrial genomes of Gasterophilus spp. are circular molecules containing all 37 genes usually present in bilaterians: 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, and 22 transfer RNA (tRNA) genes, with identical gene order and orientation as other known calyptrates. We investigated the evolution of different life cycle strategies and selected morphological characters based on the resultant trees and discussed how the biological variation among species of Gasterophilus may have evolved.
ORAL

Extinct lineage of Paederinae rove beetles from the Cretaceous Burmese amber

Dagmara Żyła, Josh Jenkins Shaw, Alexey Solodovnikov

Natural History Museum of Denmark, Biosystematics Section, Zoological Museum, Universitetsparken 15, DK-2100 Copenhagen, Denmark

With more than 61,000 described living species (Parker, 2016) Staphylinidae (rove beetles) is the most speciose family of Coleoptera, currently divided into 32 subfamilies (Thayer, 2016). Among them, the subfamily Paederinae is one of the most diverse, with more than 220 genera and about 6300 species described and is distributed worldwide (Schomann & Solodovnikov, 2016). Paederinae are proved to be monophyletic, however a group sister to this subfamily is not clear yet, with either subfamily Staphylininae, or one of the Staphylininae lineages being suggested (e.g. Solodovnikov et al., 2013, Brunke et al., 2016). For a long time, the subfamily had been divided into two tribes, Pinophilini and Paederini, and 13 subtribes (two in Pinophilini, 11 in Paederini) (Newton & Thayer, 2005). However, the recent first molecular-based phylogeny (Schomann & Solodovnikov, 2016) suggested a division of Paederinae into four tribes, Pinophilini, Cylindroxystini, Lathrobiini and Paederini. As the taxon sampling in that study was rather limited, more effort to explore Paederinae phylogeny is obviously needed. One source of phylogenetically useful information is the fossil record and recently, we are witnessing an increased appreciation for the importance of fossils in building a phylogeny, and testing various evolutionary hypotheses. However, this approach brings many challenges, especially for such a complex group as rove beetles and requires a thorough morphological analysis of both extinct and extant groups.

So far, the described fossil record of Paederinae includes 6 genera and 27 species (EDNA database; Solodovnikov et al., 2013) and the age of these fossils ranges between Early Cretaceous to Miocene. Here, we describe a new, extinct lineage of Paederinae from the Cretaceous Burmese amber and confirm its relationships by phylogenetic analysis using Bayesian Inference and Maximum Parsimony methods. We contribute to the understanding of early stages of Paederinae evolution and call for further investigation.
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Raclariu, Ancuta Cristina  
Ritter, Camila  
Rønsted, Nina  
Salvesen, Ingrid  
Schigel, Dmitry  
Seethapathy, GS  
Sigvardt, Zandra Maria Skandrup  
Singh, Sujeet  
Smedmark, Jenny  
Tandberg, Anne Helene  
Thureborn, Olle  
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Cover: Sebastian Münster, _Meerwunder vnd seltzame Thier / wie die in den Mitnächtigen Ländern / im Meer vnd auff dem Landt gefunden werden_ (taken from the vignettes on Olaus Magnus’s _Carta marina_), Basel c. 1544