



Every even year, ForBio organizes a field course at the Skibotn field station of the University of Tromsø. These animals and plants are among those that can be met during these courses.

Welcome to Tromsø!

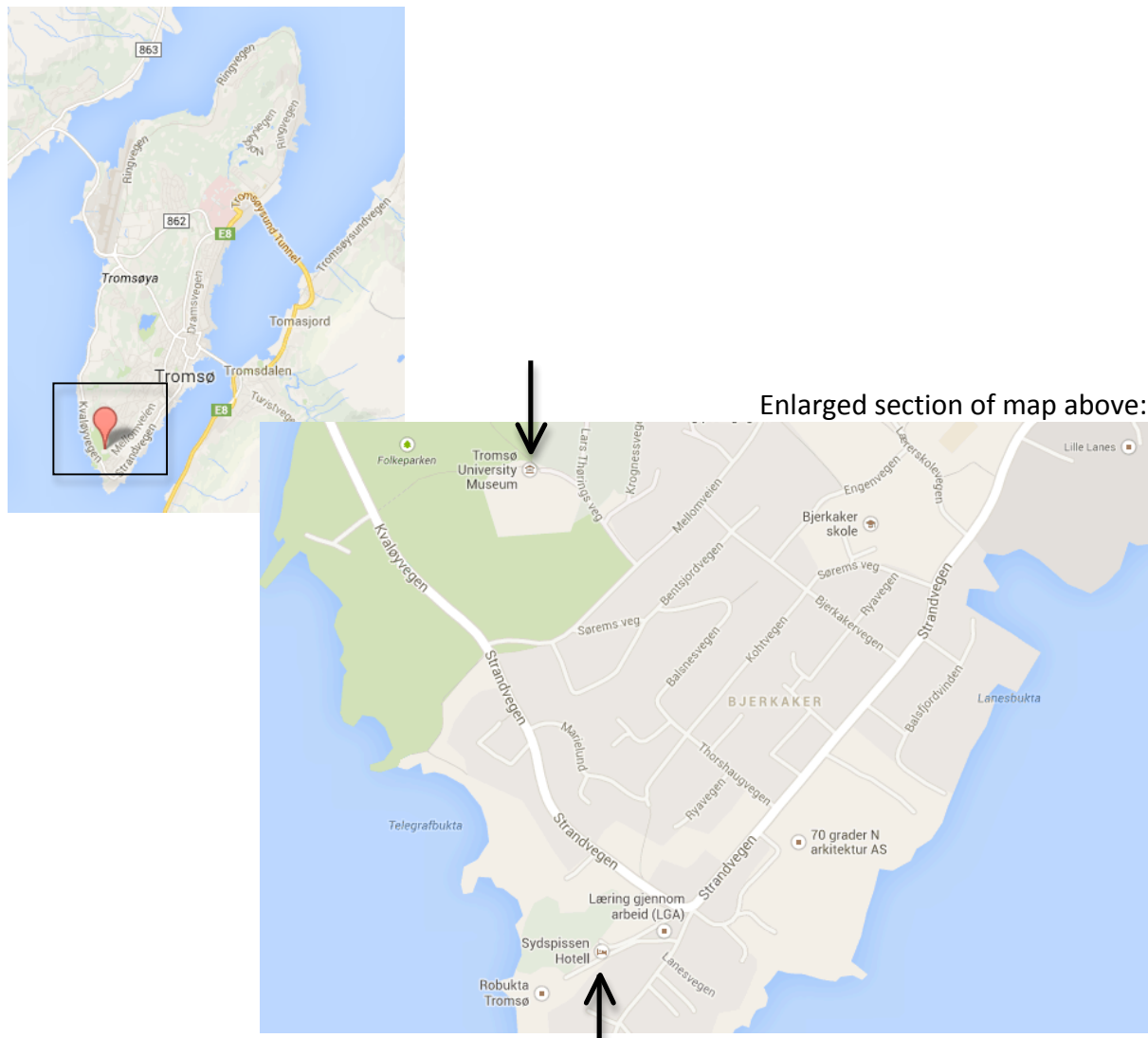
Meeting venue: Tromsø University Museum

Accommodation: Sydspissen hotel

How to get there?

Although there are public buses available in Tromsø, 3 people sharing a taxi will save money and a lot of time.

There are several ways to get from Tromsø airport to Sydspissen hotel using buses. Unfortunately, none of these are straight forward. One way is to take a flybussen (airport bus) to Tromsø center (Saturday and Sunday) or Polaria (Monday-Friday) and then take bus 34 to Sydspissen hotel in the direction of University of Tromsø. Alternatively, it is possible to take bus 40 or 42 (the bus stop is located behind the parking lot/garage which you can see when exiting the airport building) to Giæverbukta shopping mall and change to bus 34 in the direction of the city center. Detailed map with the bus stops and schedules for each bus are provided on this map (<https://mapsengine.google.com/map/edit?mid=zMbKa9qdOCu4.kn5nTQttbB7Q>). The flybussen costs 70 NOK and city buses cost 42 NOK (cash only!).



Program: ForBio Annual Meeting 2014, Tromsø

Monday, February 24, 2014

9:00 - 11:00 Registration and coffee

- 11:00 - 11:20 Magnus Popp, Natural History Museum, University of Oslo: *Welcome*
11:20 - 11:40 Aino Hosia, University Museum of Bergen: *Norwegian ctenophore diversity - new acquaintances*
11:40 - 12:00 Teppo Rämä, Tromsø University Museum: *Diversity of marine wood-inhabiting fungi in North Norway*
12:00 - 12:20 Mari Heggernes Eilertsen, Department of Biology, University of Bergen: *Phylogeography of Sycon abyssale (Porifera, Calcarea)*

12:20 - 13:20 Lunch

- 13:20 - 14:05 Barbara Gravendeel, Naturalis Biodiversity Center, University of Applied Science Leiden: *Next generation sequencing of fossil and extant arctic dung reveals a shift in fungal niche diversity at the end of the last Ice Age*
14:05 - 14:25 Ragnhildur Gudmundsdottir, Faculty of Life and Environmental Sciences, University of Iceland: *Ciliate epibionts on the groundwater amphipod Crangonyx islandicus*
14:25 - 14:45 Richard Mally, University Museum of Bergen: *Testing monophyly of megadiverse Spilomelinae (Insecta: Lepidoptera: Pyraloidea)*
14:45 Inga Meyer-Wachsmuth, Swedish Museum of Natural History: *Species discovery and delimitation in a complex of cryptic species*

15:05 - 15:40 Coffee

- 15:40 - 16:25 Jon Fjeldså, Natural History Museum of Denmark: *Museum collections in the age of genomics.*
16:25 - 16:45 Ursula Brandes, Department of Plant and Environmental Sciences, Norwegian University of Life Sciences: *Cytisus scoparius invasion in Norway – is it native, introduced or both?*
16:45 - 17:05 Narjes Yousefi, Museum of Natural History and Archaeology, Norwegian University of Science and Technology: *Factors responsible for high phenotypic diversity in northern peat mosses (Sphagnum)*
17:05 - 17:25 Sergei Tarasov, Natural History Museum, University of Oslo: *Large-scale morphological investigation provides new evidence for the phylogeny of dung beetles (Coleoptera, Scarabaeidae, Scarabaeinae): insight from parsimony and Bayesian partitioning analyses*

17:25 - 18:55 Poster Session and coffee

19:00 Dinner at Arctandria restaurant

Tuesday, February 25, 2014

- 9:00 - 9:45 Christiane Todt, University Museum of Bergen: *Aplacophoran mollusks in Norway – unexpected diversity of a minor marine invertebrate taxon*
- 9:45 - 10:05 Josef Berger, Department of Biology, Lund University: *Food web structure of parasitoid communities in the agricultural landscape of Skåne, Southern Sweden*
- 10:05 - 10:25 Martina Zahradníková, University Museum of Bergen, University of Bergen: *An evolutionary study of Fuscideaceae - (Umbilicariales, Pezizomycotina, Ascomyceta)*
- 10:25 - 11:00 Coffee**
- 11:00 - 11:20 Seppo Huhtinen, Herbarium, University of Turku: *Big small stuff - how to get thrilled using small epibryophytic ascomycetes*
- 11:20 - 11:40 Per Sjögren, Tromsø University Museum: *The use of sedimentary ancient DNA to reveal responses to climate change in NW Europe*
- 11:40 - 12:00 Marina Chelak, Department of Biosciences and Aquaculture, University of Nordland: *Calanus spp. abundance variability and environmental factors in the Iceland and Norwegian Seas over last decades*
- 12:00 - 12:20 Mari Kekkonen, Finnish Museum of Natural History: *A comparison of four DNA barcode-based species delineation methods – a story by gelechioid moths*
- 12:20 - 13:20 Lunch**
- 13:20 - 14:05 Thomas Pape, Natural History Museum of Denmark: *e-Nomenclature, e-Taxonomy, and e-Collections*
- 14:05 - 14:25 Raul Ramirez, Natural History Museum, University of Oslo: *Same barcode, different biology: a tale of two almost identical parasite strains*
- 14:25 - 14:45 Julien Amouret, Faculty of Life and Environmental Sciences, University of Iceland: *Evolutionary status of the redpoll subspecies Carduelis flammea islandica (Aves: Passeriformes: Fringillidae)*
- 14:45 - 15:05 Sarina Veldman, Evolutionary Biology Centre, Uppsala University: *Using DNA barcoding to trace trade in Tanzanian orchids*
- 15:05 - 15:40 Coffee**
- 15:40 - 16:25 Petra Korall, Evolutionary Biology Center, Uppsala University: *Fern biogeography: The challenge of understanding fern specific processes*
- 16:25 - 16:45 Sabrina Mazzoni, Natural History Museum, University of Oslo: *Modular R-wrappers for flexible implementation of MaxEnt Distribution Modelling*
- 16:45 - 17:05 Alexander Zizka, Department of Biological and Environmental Sciences, University of Gothenburg: *Contrasting African vs South American biodiversity: An eco-evolutionary approach*
- 17:05 - 17:25 Kristian Skaven Seierstad, Natural History Museum, University of Oslo: *Multi-locus sequencing indicates a complex phylogeographic pattern among two closely related saprobic fungi*

17:25 Poster Session and coffee

19:00 Dinner at Sydspissen hotel

Wednesday, February 26, 2014

- 9:00 - 9:45 Snæbjörn Pálsson, Faculty of Life and Environmental Sciences, University of Iceland: *On the origin of species in Iceland - few examples*
- 9:45 - 10:05 Dario Pistone, University Museum of Bergen: *A phylogenomic approach to understand the diversification of bark and ambrosia beetles and associated microbes*
- 10:05 - 10:25 Dilli Prasad Rijal, Tromsø University Museum: Next generation sequencing, universal tails and microsatellite marker development: a cost-benefit analysis for non-model organisms

10:25 Coffee

- 11:00 - 11:40 Gary Voelker, Biodiversity and Research Teaching Collection, Texas A&M University: *Old stuff in cases and new stuff in freezers: The importance of building and maximizing the use of museum collections in systematics-based research.*
- 11:40 - 12:00 Lísá Anne Libungan, Faculty of Life and Environmental Sciences, University of Iceland: *Otolith shape reveals the identity of Atlantic herring populations*
- 12:00 - 12:20 Nataliya Budaeva, University Museum of Bergen: *Systematics and diversity of quill worms, a group of the deep-sea epibenthic polychaetes*

12:20 Lunch

- 13:20 - 14:05 Dmitry Schigel, Department of Biosciences, University of Helsinki: *Field and not-so-field courses: Finland as a ForBio member*
- 14:05 - 14:25 Óskar Sindri Gíslason, Faculty of Life and Environmental Sciences, University of Iceland: *The Atlantic rock crab (*Cancer irroratus*) in Iceland*

14:25 - 15:25 Plenary discussion and awards

Speakers' abstracts in presentation order

Monday, 24 February 2014

Norwegian ctenophore diversity - new acquaintances

Aino Hosia¹ & Sanna Majaneva²

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Ctenophora is a relatively small monophyletic phylum with an estimated 100-150 valid species described. Despite the low number of species, ctenophore taxonomy is complicated by scarcity of taxonomic experts, lack of comprehensive keys or accounts on diversity, plethora of redundant species descriptions, and the existence of at least a few dozen known but currently undescribed species. The fragile ctenophores are often damaged beyond recognition during traditional net sampling, and some developmental stages, particularly the ubiquitous cydippid stage, are difficult to identify morphologically. In addition, ctenophores don't preserve well, presenting challenges for storing voucher or type specimens. Molecular methods are partly hampered by the extremely conservative 18S sequences, as well as the low number of available genetic sequences with reliable morphological identification. Artsdatabanken currently lists 8 ctenophore species as occurring in Norway, but recent research suggests the presence of several additional species, many of these lacking a formal description: An unidentified Mertensiid has been sequenced from the Arctic, an undescribed midwater Pleurobrachiid is distributed in West-Norwegian fjords, possibly wider, and a probably undescribed tentaculate ctenophore occurs in the deep waters off Jan Mayen. In addition, *Beroë abyssicola* is regularly observed, although whether this is a valid species remains an open question. The species identity of the Norwegian *Euplokamis* sp. also remains questionable. Ctenophores remain an understudied group, and dedicated sampling could reveal the presence of further species.

Diversity of marine wood-inhabiting fungi in North Norway.

Teppo Rämä

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Marine fungi are an ecological group of fungi that is poorly studied in northern waters. Their diversity in Norway was assessed for the first time focusing on the wood-inhabiting species, and using different study methods: high throughput amplicon sequencing of environmental samples, culturing combined with Sanger sequencing and α -taxonomy.

Phylogeography of *Sycon abyssale* (Porifera, Calcarea)

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Sycon Risso, 1827 is a worldwide genus of calcareous sponges found in various habitats from the littoral zone down to the abyssal areas. Over 100 species have been described, but how many of these are valid is unknown as the genus is in need of thorough revision. Recent studies have shown a

wide discrepancy between molecular phylogenetic results and traditionally recognized taxa in *Calcarea*, and *Sycon* has been shown polyphyletic. *Sycon abyssale* Borojevic & Graat-Kleeton, 1965 is quite abundant between 3000-4000 m depth in the North Atlantic and Nordic Seas, but has also been found in shallow hydrothermal vent fields near Jan Mayen (~600 m) along the Norwegian coast and in Norwegian fjord systems (100 m). This project aims to test the conspecificity of these populations by molecular methods (sequencing of 28S rRNA, ITS, ALG11) and to assess the genetic connectivity between them. It is of particular interest to examine the gene flow across the Greenland-Iceland-Faroes Ridge, which is hypothesised to be a major barrier to dispersal between the North Atlantic and the Nordic Seas. Preliminary results from analysis of 28S sequences, including several outgroups, confirm the polyphyly of the genus *Sycon* and show that specimens from the Norwegian Coast (265 m depth) and the Norwegian Channel (650 m depth) are not conspecific to the deeper populations (1700-2500 m; *Sycon abyssale sensu stricto*). Additional preliminary results will be presented.

Next generation sequencing of fossil and extant arctic dung reveals a shift in fungal niche diversity at the end of the last Ice Age

Barbara Gravendeel

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Host-fungal interactions are thought to define both modern and past ecosystems. Although faunal and floral composition of the Mammoth Steppe is well studied, little is known yet about the associated fungal diversity of this now extinct Arctic biome. Roche 454 and Ion Torrent sequencing of fungal Internal Transcribed Spacer rDNA from permafrost preserved mammoth and ground squirrel coprolites from Siberia and Alaska (ranging from 18,560 ± 50 BP to 12,200 ± 70 BP) and extant arctic hare, barnacle goose, lemming, tundra vole and muskox dung resulted in over 200 unique fungal hits encompassing dung fungi, lichens, mammal pathogens, mycorrhizal fungi, insect pathogens, obligate cellulose-degrading fungi, plant pathogens, and protist parasites. Especially the coprophilous fungal diversity in fossil arctic dung is surprisingly high when compared to modern arctic dung. The high diversity found seems correlated with the presence of large megafauna herds. These must have created - in their interaction with the vegetation - many niches for coprophilous fungi that disappeared together with their hosts at the end of the last Ice Age, suggesting that climate change played a much greater role in species extinction in the Arctic than previously assumed.

Ciliate epibionts on the groundwater amphipod *Crangonyx islandicus*

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Two subterranean freshwater amphipod species were recently discovered in Iceland, *Crangonyx islandicus* and *Crymostygious thingvallensis* (Kristjánsson and Svavarsson 2004). These species are found within the volcanic active zone in the groundwater system and genetic patterns within *C. islandicus* have shown that it has survived repeated glaciations in Iceland. Nothing is known of the ecosystem these amphipods inhabit but presence of ciliate epibionts in different stages as phoronts and adults were observed on specimens from Þingvallavatn, Svartárvatn, Lakagígur, Klapparós in Melrakkaslétta and at Sandur in Aðaldal. Analysis of the 18S ribosomal DNA marker suggest that the

sequences belong to a previously unsequenced species, most related to members of the genus *Gymnodinioides*, group Apostomatida. *Gymnodinioides* spp. are well known to be exuviotrophic crustacean parasites but the phoront stage is a nonfeeding stage which were found almost exclusively ventrally in sheltered locations on the amphipods; the most common location being the first and second joints on pereopod 3-5 and pleopod 1-3. This indicates a preference for location sheltered from possible grooming activity of the amphipods. A further study of ciliate variation living as epibionts or parasites from groundwater amphipods from N-America and Slovenia revealed distinct groups of ciliates on the different species.

Testing monophyly of megadiverse Spilomelinae (Insecta: Lepidoptera: Pyraloidea)

Richard Mally

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Spilomelinae are the most speciose subgroup of Pyraloidea and contain many species of economic importance, including invasive pests. Yet, the group as such is still in doubt, since Spilomelinae are exclusively defined by typological means and have repeatedly been claimed to be polyphyletic. As an initial step towards a stable, phylogenetically justified nomenclature, we present molecular results of our test on the monophyly of Spilomelinae. Our taxon sampling comprises representatives of most of the 15 Neotropical genus groups treated by Munroe (1995), 26 of the 30 spilomeline genera occurring in Europe and representatives from the Afrotropical and Oriental regions as well as 15 Pyraustinae taxa. We compiled molecular data of mitochondrial COI gene and nuclear genes CAD, EF1a, GAPDH, IDH and RpS5 and analyzed them phylogenetically using Maximum Likelihood and Bayesian Inference. Our results indicate a sister-group relationship of Spilomelinae and Pyraustinae. Spilomelinae only form a natural group with the inclusion of Wurthiinae, confirming the results of Mitter et al. (2012). None of the investigated genus groups turn out to be monophyletic. The Udea group sensu Mally & Nuss (2011) appears to be a key group at the base of the Spilomelinae-Pyraustinae clade. An analysis of morphological characters will follow and help to redefine Spilomelinae in a phylogenetic context.

Species discovery and delimitation in a complex of cryptic species

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Flagellophora apelti is a unique species of Nemertodermatida, a small marine taxon of mainly interstitial worm-like animals. Individuals of this species have a bursa, a characteristic shared with two other little known species and a unique broom organ. The broom is made of elongated glands and can be everted at the anterior tip; the frontal glands lie around it. It was thought to be associated with feeding behaviour, also because in no studied specimen a mouth could be identified. However, the broom organ is not connected to the gut. *Flagellophora apelti* has little potential of dispersal due to lack of dormant eggs, a larval stage and its interstitial life style. However, the species has been reported from as distant localities as e.g. the Mediterranean, Bermuda and Hawaii. Different methods for species "discovery", percentage of genetic divergence, parsimony networks, gene tree, were used to identify potential species. These findings were compared with results of a

GMYC analyses. The preliminary dataset, consisting of only the small ribosomal subunit gene (18S) supports the view that this species is in fact a complex of cryptic species; it may contain as many as seven species.

Museum collections in the age of genomics

Jon Fjeldsaa

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Because of new techniques, old museum specimens are now used to answer new scientific questions. However, there is also a need for renewed collecting efforts, and new preparation methods. It is now feasible to sequence whole genomes for large numbers of species, and making these enormous amounts of data available as an open research resource. This opens new perspectives for understanding how traits and genetic complexity evolves, but it also requires new standards for collecting well documented voucher specimens, and for obtaining new kinds of preparations that will allow high quality descriptions of traits. This will be a challenge for museum curators but may also represent an opportunity for boosting the development of museum collections. This talk will present some of the challenges and opportunities associated with the ongoing b10k project to sequence whole genomes of all bird species of the world.

***Cytisus scoparius* invasion in Norway – is it native, introduced or both?**

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The shrub *Cytisus scoparius* is native to the British Isles, central and southern Europe. It has been introduced to many countries around the world and is considered invasive in most of those and even in parts of its native range. In Norway it was first recorded in 1869, limited to the southernmost coast. In the last 50 years it has expanded northwards along the coast, and has also increased in abundance at old locations, including protected heathland. It is unknown if *C. scoparius* is native to Norway. Its recent invasive behaviour could have been caused by land-use change or introduction of European invasive genotypes. Knowledge of the origin of *C. scoparius*, causes and impact of the invasion are fundamental for making decisions on its future management in Norway. Fresh plant material of *C. scoparius* and herbarium specimens from locations in Norway and Europe are analysed for chloroplast SNP variation to reveal if Norwegian populations are native or were introduced. In addition, variation of the European samples from different time periods will reveal the extent of human mediated gene flow within the native range during the last century. Further, I will use next generation sequencing (ddRAD) to gain insights into the genetic population structure and genetic diversity within and between populations in Norway. Preliminary results indicate high level of chloroplast SNP variation in the Norwegian populations and relationships with different European samples indicating multiple introduction events to Norway.

Factors responsible for high phenotypic diversity in northern peat mosses (*Sphagnum*)

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Central Norway is an area with particular high diversity of peat mosses, almost all European peat moss species are found in this area. Understanding factors contributing to evolutionary (phylogenetic) diversity, species diversity and functional diversity is important for understanding the functional role of these organisms. Aim of this study is to understand the basis of the high diversity observed in complex traits in *Sphagnum* by using cultivation experiments, transplantation experiments and novel genome wide markers (RADseq). This will contribute to understanding principles of genome divergence during speciation. Different phenotypic morphs of *Sphagnum magellanicum*, “green morph” in mire margin and “red morph” in bog center are collected. Transplantation experiment and cultivation experiments to quantify the genetic and environmental factors contributing to quantitative variability in various characters separating the morphs and RAD sequencing to study genetic variability between morphs will be done.

Large-scale morphological investigation provides new evidence for the phylogeny of dung beetles (Coleoptera, Scarabaeidae, Scarabaeinae): insight from parsimony and Bayesian partitioning analyses

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Dung beetles form the subfamily Scarabaeinae have been a focus of 12 major morphological and molecular phylogenetic studies over last 20 years. Despite the phylogeny of dung beetles has been a hot topic of research, the consensus on their evolutionary phylogenetic pattern is still missing. In the frame of current project, I attempted to improve the morphological phylogeny for dung beetles by performing hitherto unprecedented phylogenetic analysis in terms of taxon sample and character coverage. A special emphasis was made on the phylogenetic analysis of data. I tried both parsimony and Bayesian analysis to morphology. To account for different evolutionary rates of characters in Bayesian framework, the data was partitioned using anatomy ontology. The network structure of anatomy ontology allows partitioning of data in many alternative ways. The alternative partitioning schemes of morphological data matrix were tested using Bayes factor.

Tuesday, 25 February 2014

Aplacophoran mollusks in Norway – unexpected diversity of a minor marine invertebrate taxon

Christiane Todt

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The aplacophoran mollusks (Solenogastres and Caudofoveata) are two of the so-called minor mollusk taxa, pointing to their relatively low species diversity (about 350 and 250 validly described species, respectively). These animals have recently been in the focus of a number of molecular and morphological studies elucidating mollusk evolution, but they are still seen by most as a rare and “difficult” group. A current project funded by the Norwegian Taxonomy Initiative (Artsprosjektet)

investigates the diversity and distribution of aplacophoran species in Norwegian waters. In the first two years, we have sorted and identified 1200 lots of aplacophorans. In addition to the eight species of Caudofoveata and 16 species of Solenogastres that previously had been known, we could add seven species of solenogasters new to Norway and more than 18 species new to science. The new findings largely increase the known diversity, spanning a wide range of families and genera. The new species come from both the relatively well-known coastal areas as well as the deep Norwegian Sea. Amongst the goals of the project is to build up a reference collection of Scandinavian aplacophoran mollusks at the University Museum of Bergen (Norway), including type material for the new species and voucher material for all others, and to produce a monography of Norwegian solenogasters. In my talk I will give an overview over current knowledge on this elusive animal group and present selected results from the ongoing biodiversity project.

Food web structure of parasitoid communities in the agricultural landscape of Skåne, Southern Sweden

Josef Berger

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Studies of trophic interactions in agricultural landscapes often focus on "major pest" species and their associates, whereas "minor pests" and non-specific polyphagous herbivores are rarely considered to be interesting. This study looks into the structure of parasitoid communities and their hosts from a biodiversity perspective. Parasitoid Hymenoptera and herbivorous Coleoptera were sampled quantitatively at 27 sites in the agricultural landscape of Skåne, Southern Sweden. The aim was to examine food web structure, identify determinants of local and regional species richness, assess the effect of landscape parameters on the spatio-temporal distribution of parasitoids and herbivorous beetles, and draw conclusions about their dispersal abilities. As a side effect, new associations of parasitoid species with the oilseed rape habitat were found.

An evolutionary study of Fuscideaceae - (Umbilicariales, Pezizomycotina, Ascomyceta)

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The evolution of the family Fuscideaceae and phylogenetic relationships of its anticipated genera were examined using mitochondrial small subunit (SSU) rDNA, nuclear large subunit (nuLSU) rDNA, and internal transcribed spacer (ITS). This lichen family with the two seemingly unrelated crustose lichen genera *Fuscidea*, and *Maronea* was described by Hafellner (1984) and assigned to the suborder Teloschistinea, Lecanorales, based on the Teloschistes-type asci. Investigation of phylogenetic relationships of taxa within Fuscidea elucidates which species should be assigned to the genus. Moreover, it gives insight concerning the circumscription of Fuscidea, and the morphological characters that will characterize this genus. The contemporary placement of the Fuscideaceae is as a group incertae sedis within the Lecanoromycetidae, Lecanoromycetes, Pezizomycotina. The family currently accommodates these genera: *Fuscidea*, *Maronea*, *Ropalospora*, *Hueidea*, *Lettauia*, *Orphniospora*, and *Sarrameana* (Eriksson 2006). Bylin et al. (2007) showed that *Fuscidea* and *Maronea* formed a monophyletic group based on SSU rDNA defined as the Fuscideaceae and that *Ropalospora* is not closely related to this group. Used specimens, collected from the different continents, were aligned with the extra sequences of ascomycetes obtained from GenBank for clarifying the systematic placement of Fuscideaceae in Ascomycota. Sequences will be analysed separately and in combination. Usage of statistic methods is necessary for overcoming

conflicts between datasets from different genes. Morphologic and anatomic investigations can be necessary to correlate the phylogenetic tree with morphological features. The preliminary results will be presented during the conference.

Big small stuff - how to get thrilled using small epibryophytic ascomycetes

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The miniature world of ascomycetous fungi on mosses has been systematically studied by very few, even though these fungi show highly specialized life strategies. These laborious studies have been carried out based on morphology alone. In Finland, a research program on deficiently known forest species concentrated on these fungi for five years, resulting in the very first, broad, species-based isolations and growth experiments. Based on sequencing these cultures, the first ever, five-gene phylogenetic tree embracing these fungi was constructed. It revealed many surprises, such as a basal clade exhibiting a tripartite association with cyanobacteria and sphagna; hence a new genus *Trizodia*. It was also shown that even ultimate nutritional microniche utilization can be adopted multiple times during the evolution. At least in five Ascomycete classes, a shift to the mostly undesirable substrate of mosses and liverworts has occurred multiple times during evolution.

The use of sedimentary ancient DNA to reveal responses to climate change in NW Europe

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By analysing ancient DNA from lake sediment cores from Spitsbergen, Bjørnøya and Andøya (N. Norway) we hope to detect the presence of more warmth demanding plant species during warmer phases of the Holocene and Late-Glacial periods. This is of relevance for plant distribution, - establishment and -migration under changing climatic conditions. In addition we study surface samples from northern Norway and short lake sediment cores from Scotland in order to assess how sedimentary environmental DNA reflect the surrounding vegetation and evaluate the use of it as a proxy for past vegetation and biodiversity.

***Calanus* spp. abundance, variability and environmental factors in the Iceland and Norwegian Seas over last decades**

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Calanus spp. are key elements of the arctic marine ecosystems. They are main mediators between primary producers and pelagic fishes in marine food webs. Convincing evidence suggest a change in *Calanus* congeners abundance and distribution in the North Atlantic as a response to fluctuations of the marine environment. The role of environmental factors in *Calanus* population dynamics can be understood though the comparison of the long-term data-series from different locations. In this project, we analyse data-series on *Calanus* complex (*C. finmarchicus*, *C. glacialis* and *C. hyperboreus*) from the northern Norwegian Sea, Svalbard and the Iceland Sea spanning from 15 to 25 years. We are exploring the variability of *Calanus* spp. abundance in respect to location, ambient sea surface

temperature, salinity, NAO index and the time of the phytoplankton spring bloom by implementing multivariate statistical methods and possibly a modelling approach. Initial results appear to show significant differences in *Calanus* abundance between sampling years in selected locations. We aim to identify the main environmental factors affecting the abundance of *Calanus spp.*, and describe the patterns of *Calanus* population dynamics in the Norwegian and Iceland Seas.

A comparison of four DNA barcode-based species delineation methods – a story by gelechioid moths

Mari Kekkonen

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The great number of undescribed species strongly calls for efficient means to enhance taxonomic workflow. DNA barcode-based species delineation is a promising option, providing putative species (operational taxonomic units, OTUs) to be used in further studies such as phylogenetic analyses and taxonomic revisions with additional data. The benefits of DNA-based delimitation are convincing as it offers increased speed, repeatability, and taxonomic accuracy by aiding the recognition of most cryptic species from the beginning. In this study, I compare four methods, Barcode Index Number (BIN), parsimony networks, Automatic Barcode Gap Discovery (ABGD), and General Mixed Yule-coalescent (GMYC), using two data sets of fairly well-known gelechioid moths. The two groups are different, because most Finnish gelechiine species are genetically distinct, while Australian elachistine species show much lower divergences making them a challenging group. This study aims (i) to test the congruence of OTU counts between the methods and previous taxonomic works and (ii) to compare the content of OTUs and described species

e-Nomenclature, e-Taxonomy, and e-Collections

Thomas Pape

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The world of informatics has gone electronic and the Taxasphere is no exception. While there is no replacement for neither real specimens nor genuine observations, the way we deal with the data is increasingly by means of digital tools. The ever increasing number of scientific names, not to forget the formal nomenclatural acts that in various ways govern their usage, and the documentation of the species that carry these names, represent a vast amount of data that can only be properly managed and mined in a digital format. Zoological nomenclature came second to botany in allowing for electronic publications, but the zoological Code has made the bold requirement that all e-works must be registered in the online ZooBank. Can we go further? Yes, absolutely, and we will. Taxonomy at the species-level remains a challenge, and in spite of hopes and promises that the new tools will bring us up to 'warp speed', the rate of description probably barely exceeds the rate of extinction. Is taxonomy destined to be a slow enterprise because species are hypotheses that must be processed by the human mind? Or is the Taxasphere simply an inert body that takes time to react? Or both? The immense amount of primary data tied up in preserved specimens deposited in our scientific collections can be made available – at least in part – electronically. Much can be done by adapting our workflow and re-setting priorities.

Same barcode, different biology: a tale of two almost identical parasite strains

Raul Ramirez

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Under most interpretations of the barcoding concept, taxa with the same mitochondrial barcode would normally be assigned to the same biological entity. Here we present evidence for highly divergent biological and behavioural properties in two Norwegian isolates of the monogenean parasite *Gyrodactylus salaris*, from different hosts, with identical CO1 barcode. The salmon-infecting Lierelva strain grew exponentially on salmon, but the charr-infecting Pålbufjorden strain showed low infectivity for this host and is entirely non-pathogenic to Atlantic salmon. On Arctic charr, both parasite strains successfully reproduced, but the salmon strain grew fastest on both hosts. Experiments revealed differences in reproductive rate which may account for the observed population differences, as salmon parasites gave birth at an earlier age than the charr parasites. Charr-infecting parasites were more active on salmon than salmon parasites on charr, possibly leading to enhanced mortality. Sequencing of 10 kb of nuclear genomic markers revealed only 4 SNPs, confirming that isolates of *G. salaris* with differences in fitness traits influencing establishment, fecundity and behaviour, may be remarkably similar at a molecular level and that in some cases, mitochondrial haplotype may not necessarily be a good proxy for biological identity. The framework for reporting and for control of *G. salaris* requires re-appraisal in the light of the discovery of such innocuous and non-pathogenic forms of the parasite.

Evolutionary status of the redpoll subspecies *Carduelis flammea islandica* (Aves: Passeriformes: Fringillidae)

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The Icelandic redpoll *Carduelis flammea islandica* is one of three subspecies of *Carduelis flammea*. The other two are *C. f. rostrata*, breeding in Greenland, and *C. f. flammea*, widely distributed at high latitudes in both N-America and Eurasia. Recent studies on variation of the mtDNA control region and in microsatellites among *C. f. rostrata* and *C. f. flammea* mainly from Scandinavia and related species (*C. hornemanni*, *C. cabaret*) didn't reveal clear genetic differentiation among the species. The lack of differentiation could result from introgression (hybridization has been supported by direct observations) and/or incomplete lineage assortment following recent diversification. Here we add result of the Icelandic subspecies *C. f. islandica* to previous analysis of the species complex to evaluate its reproductive isolation. The Icelandic subspecies is particularly interesting because of its intermediate size and colour between the two extreme forms; *C. cabaret* and *C. hornemanni*. This study includes in addition a comparison of different and highly variable genetic markers: mitochondrial (control region and COI) and nuclear introns (TGF β 2, Fib7, Brm-13, Rho, Ghr and Alas). Significant differences in haplotype frequencies of the mtDNA control region are observed between the Icelandic subspecies and the common redpoll (*C. f. flammea*). Variation in the COI reflects a geographical barrier, which describes two clades: one "mainland" and the other "arctic". This main finding supports a previous hypothesis describing two allopatric refugia during the last glaciation period.

Using DNA barcoding to trace trade in Tanzanian orchids

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Chikanda is a traditional Zambian snack mainly consisting of boiled orchid tubers (genera *Disa*, *Habenaria* and *Satyrium*) and peanuts. Due to increased demand, tubers are becoming more and more scarce in Zambia and are now also imported from surrounding countries such as Tanzania. Part of the tubers are poached from protected areas and unsustainable harvesting might put as many as 85 of the 157 *Disa*, *Habenaria* and *Satyrium* species at risk of overharvesting. The aim of our project is to identify both unprocessed orchid tubers and prepared chikanda sold at local markets by means of DNA barcoding and to map harvesting and trade in Tanzanian orchids. Market surveys have been conducted in Tanzania and Zambia to collect unprocessed orchid tubers and prepared chikanda. Informants were interviewed to obtain information on collection sites, harvesting times and harvesting methods. Several orchids were collected for DNA barcoding reference collections. DNA barcoding was used to identify tubers traded on the markets and Next Generation Sequencing (NGS) was used to identify species present in chikanda. Orchid tubers were commonly sold on Tanzanian and Zambian markets (Tunduma, Sumbawanga, Nakonde), and were impossible to identify by their morphological characters alone. Illegal orchid collection in protected areas and their surroundings was observed, and reported to have increased recently. NGS of the chikanda samples revealed presence of several orchid species (*Disa spp.*) and peanut (*Arachis hypogaea*). Next step will be to trace species back to their local collection sites.

Fern biogeography: The challenge of understanding fern specific processes

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Are ferns easily dispersed? Ferns differ in several aspects from seed plants, their sister group, in their life history. Ferns disperse by minute, haploid spores as compared to the diploid seeds in seed plants, a feature that should facilitate long distance dispersal. Counteracting is however that ferns need water for fertilization (not pollinated by wind or animals). These differences indicate that diversity and distribution patterns in ferns are complex and partly stem from processes other than the ones shaping the diversity of seed plants. My research focuses on the evolution and biogeography on ferns (and lycopods) at different temporal and spatial scales and addresses the question "What is the impact of long-distance dispersal in shaping the biogeography of ferns and lycopods?" In this framework I will talk about questions one can ask, what we need to address them, and how we can address them.

Contrasting African vs South American biodiversity: An eco-evolutionary approach

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Biodiversity in plants and animals is not equally distributed on the globe. The vast majority of species occurs in the tropic regions of the world. However, within these species rich regions the Africa is often considered as the "odd man" due to their outstandingly low species richness in many

groups. This pattern is especially evident in comparison to South America, which comprises about three times as many vascular plant species as Africa, with similar patterns observed for amphibians, birds, reptiles and other groups. These differences are surprising given these landmasses' similar areas, latitudinal position, Gondwanan geology, ancestral biota and current ecosystems. Potential explanations for this discrepancy in biodiversity could come from the different geo-tectonic histories or differences in present climate conditions. While it is generally accepted that present patterns of biodiversity have been shaped by a combination of current conditions and evolutionary history, the underlying causes and the importance of the individual factors remain unclear. In this project we are conducting a cross-taxonomic comparison of biodiversity patterns between the two continents to better quantify the influence of current climatic conditions on species richness. Here I present first results from continent –scale analyses of species diversity patterns in plants and different animal groups. Additionally I will outline integrative approaches to combine species diversity data with phylogenetic information in order to assess when and how the biodiversity dichotomy between Africa and South America evolved.

Multi-locus sequencing indicates a complex phylogeographic pattern among two closely related saprobic fungi

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Nuclear and mitochondrial sequences from worldwide samples of *Trichaptum abietinum* and *T. fuscoviolaceum* separate the two species and reveal a complex phylogenetic pattern both in regards to geography and host-reoccurrence. *T. abietinum* was divided into three main clades: A mainly North-American, a mainly European and a widespread group. *T. fuscoviolaceum* comprised two clades: A mainly European and a widespread group. *Trichaptum* is a cosmopolitan genus of saprobic basidiomycetes that causes white rot in both conifers and hardwood. The closely related *T. abietinum* and *T. fuscoviolaceum* are widely distributed pioneer saprobes of conifers. These have been subject to several mating studies which have indicated that *T. abietinum* consists of intersterility groups whereas no intersterility groups have been observed in *T. fuscoviolaceum*. The aim of this work was to explore the relation of these two species and their respective phylogeographic patterns.

Modular R-wrappers for flexible implementation of MaxEnt Distribution Modelling

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Current Maximum Entropy (MaxEnt) Distribution Modelling is largely fixed to the methodological approach and the functionalities of the popular but “inflexible” maxent.jar software. Halvorsen et al. (2014), propose a decoupling of the variable transformation, model selection and model assessment phases of modelling by MaxEnt, and encourage full explorations of parameters options and settings. This requires a more flexible, practical, interpretable, traceable methodology. Here, we present a new conceptual framework for practical distribution modelling by MaxEnt: the “Modular and Functionally Integrated Component-based Approach” (MFICA) – by which the core components are decoupled then wrapped together more flexibly into component-based functional modules. Computational object-oriented and systems approaches are integrated with ecological, statistical and modelling theory and practices to handle the complexity associated with the process. Objects (variables, results etc.) are defined according to specific modelling parameters. Properties (e.g.,

content) are inherited to each object and new objects are created in a flexible and automated way. The MFICA is operationalized through modular R-scripts wrapped around maxent.jar, and the full modelling process. A trail of models of increasing complexity is built (traceability and interpretability), to suit different modelling purposes. The MFICA scripts produce a diverse range of outputs that integrate and guide the process.

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On the origin of species in Iceland - few examples

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The Icelandic biota is characterized with low species diversity, which can be explained by the short period since the island was covered by glaciers and its geographic isolation. Molecular variation is expected to be small within species in Iceland due to recolonization from southern refugia and bottlenecks in population size. Studies on genetic variation in three freshwater invertebrate species show distinct patterns. Sequence variation in the caddisfly *Potamophylax cingulatus* shows patterns of distinct clades within Europe, common to several species in Europe. Variation in the circumpolar caddisfly *Apatania zonella* and one of the recently discovered groundwater amphipods in Iceland *Crangonyx islandicus*, both bad dispersers, show however large variation. The phylogeny of *Apatania* points to a paraphyly of *Apatania zonella*, with distinct lineages in North America and Eurasia, both co-occurring in Iceland. Genetic variation in the endemic *Crangonyx islandicus* is large with a common ancestor predating the onset of Ice age, 4-5 Myr ago, even presenting cryptic species. Geographic patterns provide evidence of several subglacial refugia along the tectonic plate boundary in Iceland

A phylogenomic approach to understand the diversification of bark and ambrosia beetles and associated microbes

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Phylogeny of bark and ambrosia beetles in the weevil subfamily Scolytinae is currently based either on a few ad hoc selected morphological characters, or relatively few nuclear and mitochondrial genes. At present, all strongly supported nodes occur at tribal and generic levels, and deeper relationships between tribes remains unclear due to lack of resolution in the molecular data. The genome of the bark beetle *Dendroctonus ponderosae* was recently sequenced and it represents the second beetle genome to be published after *Tribolium castaneum*. We applied a combined strategy based on genomic/transcriptomic data from Coleoptera and other insect species to select novel single-copy protein coding genes for phylogenetic analyses. At present, we have screened 70 different genes for a group of 48 beetle species, with the intent to solve relationships within Scolytinae and assess their closest weevil relatives. Sequenced regions of screened genes were aligned and their structure was exhaustively investigated, particularly for the presence of introns and potential paralogous copies. Our aim is to establish a robust phylogenetic hypothesis for bark and ambrosia beetles by means of reliable DNA sequence data from 15-20 nuclear genes. A comprehensive phylogeny for bark and ambrosia beetles will enable detailed studies on key ecological traits, such as host-plant coevolution, fungus farming, and sub-social family structures

with regular inbreeding. Here, we present preliminary data and results on the development of these new molecular markers and the utility of these genes in beetles' phylogeny.

Next generation sequencing, universal tails and microsatellite marker development: a cost-benefit analysis for non-model organisms

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Biological invasion is one of the prevalent threats to global biodiversity. Ecological and economic impacts of invasion have been globally reported. However, genetics of invasive species have still not received ample consideration. Species of *Heracleum* have received considerable attention in Europe due to their large size and rapid colonization. We used next generation sequencing to develop microsatellite library for *Heracleum persicum*, one of the problematic invasive species widespread in Scandinavia. A cost-effective three primers PCR approach with modified forward primer, reverse primer, and fluorescently labelled universal tail were used to test the functionality of each marker. Thirty new and 10 microsatellite markers previously reported for *H. mantegazzianum* were screened for eight individuals of *H. persicum* from different populations covering its entire range. Out of the 40 markers tested, 27 markers were successfully amplified in single reaction. All 27 markers were accommodated in three multiplexes with similar PCR conditions. One of the markers failed to amplify in multiplex. Microsatellite markers for *H. persicum* have not been reported so far. We have tested and reported 24 novel nuclear microsatellite markers which could be instrumental in understanding population genetics of *H. persicum*. In addition, 18 novel markers were cross-amplified with *H. mantegazzianum*, *H. sphondylium*, and putative hybrid *H. persicum* × *H. sphondylium*. Thus, these markers can serve as important genetic resources for understanding population genetics of *Heracleum* species and their hybrids. We conclude that microsatellite development project becomes three times cheaper if universal tails are used instead of directly labelled primers.

Old stuff in cases and new stuff in freezers: The importance of building and maximizing the use of museum collections in systematics-based research.

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Museum collections have a centuries-long history of being valuable to systematic and taxonomic research. Collections usage over most of that time has been limited to traditional specimens. However, with the advent of molecular techniques, researchers from a variety of disciplines have been able access newer material, namely frozen tissue or blood samples that have been available since the early 1990's. Despite the increased user-base, the growth of avian (and other) collections have suffered greatly due to lack of funding, the lack of experienced collectors, and in some cases an outright disdain for sacrificing birds for scientific endeavors. At a time when new disciplines (e.g., macro-ecology) are making broad general statements about biodiversity patterns, distributions, and conservation goals, continued collections growth and increasingly fine sampling efforts seem especially critical. I will use examples from my research to show that continued collecting is imperative to understanding and documenting biodiversity, and that referencing old stuff in cases (voucher specimens) and adding new voucher material still has a place in biodiversity-related disciplines. Specifically, I will focus on the description of a new Forest Robin (*Stiphornis*) species, and the systematics of an African mouse genus (*Dendromus*), and will discuss biogeographic patterns in each.

Otolith shape reveals the identity of Atlantic herring populations

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Otolith shape is thought to be affected by genetic and environmental factors. By analysing otolith shape of herring in the NE Atlantic we found clear differences among populations on a large geographical scale which spawned in different time of the year. Here, we study otolith shape variation among local herring populations found on a small geographical scale in southern Norway. Three local herring populations are thought to exist in the Landvik area based on differences in life history characteristics such as length at age, maturity of ogives, spawning time, migration and vertebral count. To test if otolith shape differed among these populations, herring were sampled during spawning in 2012 in the newly brackish Lake Landvik connected to the ocean by Reddal canal and two adjacent fjords, Bufjord and Strandfjord. Results indicate shape differences among the populations which suggests otolith shape analyses might be powerful enough to detect differences between herring populations at small and large geographical scales.

Systematics and diversity of quill worms, a group of the deep-sea epibenthic polychaetes

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The quill worms represent a monophyletic group of marine bristle worms with worldwide distribution in the deep sea. The group comprises four genera of the family Onuphidae having unique quill-like organic tubes secreted by their inhabitants. Quill worms are believed to be specialized motile omnivores or scavengers. One of the apparent adaptations in this group to the deep-sea environment is the ability for epibenthic crawling in search for scattered food sources on the seafloor. Quill worms are known to breed their young inside the parental tubes or even to be viviparous which presumably limits the ability of species to disperse widely. Despite this fact, some morphological species of quill worms are known to have very wide geographical and vertical ranges. Although the quill worms are very abundant in many deep-sea benthic communities, their taxonomy and systematics remain poorly developed due to extreme degree of intraspecific morphological variation. In my talk I will present the current state of knowledge in the diversity of quill worms and will revise their system based on morphological and molecular data. The analyses of five genetic markers support the monophyly of the whole group and two genera, *Hyalinoecia* and *Leptoecia*. We recognize 14 species within *Hyalinoecia* including two cryptic species formerly belonging to a cosmopolitan quill worm *H. tubicola* and a new species from the slope depths off Chile. We suggest synonymization of *Neonuphis* with *Leptoecia* and recognize nine species in the latter including two new species from Australian slope and abyssal South Atlantic.

Field and not-so-field courses: Finland as a ForBio member

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Taxonomy expertise and species knowledge are in danger of disappearance: gurus are aging, funding is shrinking, and students are either interested in school teaching or "something molecular". At the

same time, species expertise is fundamental for biodiversity research and related fields. To some extent, molecular barcoding, museum collections, books and journal publications, and biodiversity databases freeze the present-day species knowledge. Shrinking university budgets put additional risks of cancellation of summer and field courses, and taxonomic expertise is often transferred in a medieval way through individual teaching from a supervisor to a postgraduate student. E-tools for preservation, mobilizing and availability of taxonomic knowledge can't fully compensate for lack of new generation of well-educated species experts. Text is gradually losing its role as a key way of information transfer and education tool, but contact teaching, field workshops, group work remain efficient in educating new experts. Modern ecological and analytical methods are essential components for success: methods and best practices courses such as sample collection and preparation courses for molecular ecology, molecular barcoding courses, and biodiversity informatics courses would be a welcome addition to the "green coat" biologists' portfolio. In Finland, national taxonomic expertise and network of great field stations such as Lammi and Konnevesi (forests and lakes), Oulanka (forests and river), Tvärminne (Baltic sea), Nåtö (Åland archipelago) and Kilpisjärvi (tundra) set the excellent stage for preserving and developing field courses.

The Atlantic rock crab (*Cancer irroratus*) in Iceland

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The Atlantic rock crab (*Cancer irroratus*) was first recorded in Iceland in 2006 and has since rapidly spread throughout the country's southwestern and western coastal waters. The transport of larvae in ballast water is regarded as the most probable means by which introduction into Iceland occurred. As this species is commercially valuable, it may be possible to establish a viable industry harvesting rock crabs in Iceland, however to do this more information on species wide genetic diversity and demography is required. In this study genetic variation at seven microsatellite markers was analysed in samples from Iceland and five sites in North America, capturing most of the known range of this species. Our results divided samples from the native range into two groups, divided by a previously proposed barrier to gene flow, compatible with local hydrographic factors restricting larval-mediated gene flow. The Icelandic population was markedly differentiated from all other samples, but exhibited comparable levels of genetic diversity with no evidence of small population effects or genetic bottlenecks. No single population could be identified as a source for the Icelandic population. Genetic data indicate that the number of founders of the Icelandic population was sufficient to retain genetic variation. As the Icelandic population shows evidence of self-recruitment and population expansion it may represent a potential harvestable resource in Iceland.

Poster abstracts in alphabetical order of first author

A new reptile fossil reset the lizard molecular clock - but how precise are divergence date estimates?

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For molecular divergences to be useful it is essential to know the extent to which the results are influenced by the method and fossils used, as well as the chosen input parameters. The choice of prior for age distribution in molecular clock analyses is known to affect divergence result estimates but to what extent remains unclear. To examine this problem we used a RAG-1 DNA data set of amniotes comprising mainly lepidosaurs (lizards, snakes, and the New Zealand tuatara). Divergence analyses constrained by a range of well dated fossils that include a new record for the oldest lepidosaur (Middle Triassic, Germany) were carried out multiple times using different priors (e.g. exponential, lognormal, uniform). Results show that the effect of using different types of priors is comparable to that of using different fossil constraints. Such differences can have a radical effect on divergence date estimates and thus also interpretations of evolutionary history.

The *Cochlearia officinalis* complex

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In Norway we recognize three subspecies of the *Cochlearia officinalis* based on ecological and morphological differentiation. In this project these subspecies are investigated by using microsatellite markers and RADsequencing, to see how different they are genetically. *Cochlearia officinalis* is a tetraploid and a part of a polyploid complex. Closely related *Cochlearia* individuals of other ploidal levels; diploid and octoploid, are included in the analyses to investigate the origin of the tetraploid subspecies.

Using Genomic Tools to Explore South Australian Biodiversity

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The modern herbarium has many tools to study the local flora, but also many challenges. With shrinking budgets and rising temperatures there is a need to develop cost effective approaches to study and conserve species diversity in dynamic ecosystems. At the State Herbarium of South Australia, we developed Next Generation sequencing methods on several research projects of importance to the state flora. The research ranged from population genetic to phylogenetic and ecological questions, including the evaluation of taxonomic and conservation status of narrowly endemic Eucalyptus and Acacia species, to the effect of invasive species on native flora and fauna. The tools we developed to address these studies varied as well: we utilised amplicon deep sequencing of genes for species identification and diversity as well as metabarcoding. We also developed a low cost and efficient complexity reduction method for marker discovery and screening. The combination of approaches enabled us to undertake a genomic survey of the state flora. The

techniques we developed has given the State Herbarium the tools to rapidly respond to new biodiversity challenges.

NCBIminer: Supermatrices made easy

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NCBIminer is highly efficient and flexible open source software for data mining sequence data from Gene Bank and provides a user-friendly platform that enables users to download high quality sequences with desired attributes. It is specifically designed for easy of use and does not require knowledge of programming or relational databases. However, users with more advanced programming skills also get the possibility to interact with the software in an unrestricted way. NCBIminer deals with feature types, such as gene, CDS, rRNA, and other Gene Bank defined feature type. It uses one or more reference sequence as primer, and can download sequences for distantly related taxonomic groups with high accuracy. It can also filter sequences by sequence length or similarities with the reference sequence using user defined parameters.

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 16 institutions, including all four major natural history museums as well as all major 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 (2012-2015). 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 11500 DNA barcodes of more than 3800 species from Norway. From 2014 to 2018 NorBOL will also be funded by the Research Council of Norway through a 25.6 mill NOK grant to develop a full-scale national research infrastructure on DNA barcoding. The main target for production of DNA barcodes in this period is set to 100,000 specimens from 20,000 species, roughly 1/3 of the estimated species diversity in Norway.

Evolutionary diversity of *Santalum* spp in Australia

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Species of Australian native sandalwoods are widely distributed along the southern dry regions of Australia. Two of these economically relevant hemiparasitic trees (*Santalum spicatum* and *Santalum acuminatum*) are at present, facing increasing threats from wild harvesting; browsing by feral animals; and habitat fragmentation. Studies aiming at understanding their genetic diversity to help us to predict responses to climatic changes, and other stressors, are lacking. Our project studies the remnant populations in South Australia, to reconstruct the historical processes underlying their geographic distributions; to reveal their current genetic structure; and to determine which of the external stresses have had the greatest impact. We collected leaf samples from extant populations of *Santalum* spp. across South Australia and from the state herbarium. These samples have been genotyped using classic approaches (ITS region and chloroplast microsatellites markers) and we also applied NGS techniques (Ion Torrent sequencer). Preliminary results of the DNA sequences from the nrDNA marker ITS and chloroplast microsatellites, indicate a high degree of genetic variation both, between and within populations of South Australia, we then collate these results with our most recent NGS data.

Molecular identification of endangered species in trade: the case of Salep (orchid tubers)

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DNA barcoding is a powerful tool for species identification from cryptic substrates such as processed herbal products, powdered medicinal plants, wild harvested roots and tubers. Multiple molecular markers can be used for barcoding, but group-specific tailored combinations of several markers are most reliable for unambiguous species identification. Identification of species of recent allopolyploid origin poses an additional challenge for barcoding as selective amplification of alleles from either parent species can distort the accuracy of the identification. Orchid tubers are internationally traded for their use in traditional medicine, food and beverage production. All orchids are CITES listed and their international trade is regulated. However, in many parts of the world orchid tubers are illegally traded in large volumes. In this study, 46 identified orchid taxa from Iran were sequenced for nrITS1, nrITS2, matK, and trnL to produce a reference sequence library. Reference libraries were augmented by integration of available sequences data of related taxa from NCBI GenBank. Orchid tubers samples of 40 purchased accessions from different markets in Iran were sequenced to test the efficacy and accuracy of the reference library. A maximum likelihood phylogenetic approach was used to create a phylogram of reference and query sequences. The majority of samples were identifiable with bootstrap support of 80 or higher. However, expanding the reference library with multiple accessions from Iran and surrounding areas would increase identification, especially for the genera *Ophrys* and *Dactylorhiza*. Molecular identification of Iranian orchids shows good promise as a method to identify and monitor orchid tuber trade.

Systematic position and origins of the Scandinavian endemics *Nigritella nigra* ssp. *nigra* and *Gymnigritella runei* (Orchidaceae)

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The Scandinavian endemic *Nigritella nigra* ssp. *nigra* is a triploid orchid, reproducing asexually by seed (agamospermy/adventitious embryony). The closest extant relative, *N. nigra* ssp. *austriaca* is a tetraploid confined to the mountains of Continental Europe and cannot be the direct ancestor of the Scandinavian subspecies. Accordingly, ssp. *nigra* may be a remnant of an old polyploid complex that survived the last ice close to the Weichselian ice sheet and that subsequently became extinct from its refugial areas outside Scandinavia. The neoendemic *Gymnigritella runei* has evolved by a rare hybridization event between *Nigritella nigra* and *Gymnadenia conopsea*, possibly in southern Lapland where it is found at a handful of localities today. Apparently, it arose from an unreduced egg cell in *Nigritella nigra* that was fertilized by a normal, haploid gamete from *G. conopsea*. Interestingly, some genetic differentiation, probably arising from accumulation of somatic mutations, has been observed in both *N. nigra* ssp. *nigra* and in *Gymnigritella runei*.

Integrative taxonomy and phylogeny of family Cladorhizidae

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The deep-sea demosponge family Cladorhizidae is known for its carnivorous feeding-mode, found to be ubiquitous within the family. This feature is generally regarded as an adaptation to the nutrient-poor conditions of the deep sea, where the cladorhizids constitute a large part of the sponge fauna, with a depth record of 8840 m. Increased sampling activity in the deep sea as well as in special habitats such as hydrothermal vents and cold seeps has contributed to the description of a number of new cladorhizid species in the most recent years, and more than 120 species are now registered in the World Porifera Database. Compared to species described earlier, several new species display unusual combinations of spicules, adding to the morphological diversity and the complexity of the systematics of the group. The evolutionary history for the group is largely unknown, with only fragmentary molecular data available, and it is suspected that the current spicule-based systematics does not in all cases accurately reflect evolutionary relationships within the Cladorhizidae and allied groups. We provide a review of the systematics of family Cladorhizidae based on currently available molecular and morphological data of a comprehensive set of species and genera of the group, using this integrative approach to present a phylogeny of the Cladorhizidae.

Ecotypic variation and phenotypic plasticity in the hemi-parasitic plant *Rhinanthus angustifolius*

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Many species adapt to local environmental conditions by forming distinct ecotypes. Ecotypes may evolve quickly, especially when selection is strong, as in hay meadows, where plants experience mowing in the midst of the growth season. Several plants, otherwise flowering late in the season, have adapted to this situation by evolving early-flowering meadow ecotypes that flower and set fruit before mowing. The annual hemi-parasitic plant *Rhinanthus angustifolius* is one example. The

species is commonly divided into a late flowering subspecies, *R. angustifolius ssp. angustifolius*, and an early flowering subspecies, *R. angustifolius ssp. grandiflorus*. However, *R. angustifolius* parasitizes on a broad range of host species, and studies on closely related hemi-parasitic species have showed that the host can induce phenotypic variation. Does *R. angustifolius* also show phenotypic plasticity in response to different host species? And are ecotypes consistent between different host environments?

Phylogeny and biogeography of the pantropical pinhole borers (Curculionidae: Platypodinae) reveal historically conserved endemism at the continental scale

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The first molecular phylogeny of Platypodinae is presented. This is a tropical group of weevils and found throughout the world's tropical forests. Distribution of genera is generally restricted to a single continent and biogeographical analyses show that geography is sometimes more representative for relationships than are morphological characters. The phylogenetic analyses also revealed a strongly polyphyletic *Platypus* which indicates that much work remains to obtain a reliable classification of the group.

Testing species boundaries in the staphylinid beetle genus *Mocyta*

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Species of the staphylinid genus *Mocyta* are difficult to identify based on their morphology, and variation between individuals within a species may be very large. In my study, I will test whether the species of *Mocyta* that can be recognized based on morphology differ genetically, and if genetic variation corresponds to morphological variation within species. I will also investigate if there is, in general, significant genetic variation among different Norwegian populations and among European populations of the most common and widespread species *Mocyta fungi*. Further, I will test if genetic variation within *Mocyta fungi* has a geographic structure and/or correlates with ecological parameters of the habitats where the specimens were collected. Finally, there are indications that at least some Norwegian populations of *M. fungi* are parthenogenetic, and questions regarding geographic boundaries, origins, and cause of the parthenogenesis will be considered.

Systematics and Evolutionary history of *Tanytarsus* van der Wulp, 1874 (Diptera: Chironomidae)

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In this project I will revise *Tanytarsus* species from the East Palaearctic and the Oriental Region, associate unknown and cryptic life stages delineate and describe species using molecular and morphological techniques in this taxonomically difficult genus. The evolutionary history of *Tanytarsus sensu lato* including the genera *Caladomyia*, *Corynocera*, *Nimbocera* and *Virgatanytarsus* will be inferred basing on morphological and molecular data. In doing so, I will also examine the utility of two mitochondrial (COI, COII) and five nuclear (CAD, EF-1 α , PGD, AATS1, TPI) protein coding markers for estimating lower-level phylogenetic relationships within the dipteran family Chironomidae. Finally, mitochondrial and nuclear markers will be used to analyse species boundaries

between genetically and geographically divergent populations of *Tanytarsus brundini* and its sister species in the chinyensis group.

Modular R-wrappers for flexible implementation of MaxEnt Distribution Modelling

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Current Maximum Entropy (MaxEnt) Distribution Modelling is largely fixed to the methodological approach and the functionalities of the popular but “inflexible” maxent.jar software. Halvorsen et al. (2014), propose a decoupling of the variable transformation, model selection and model assessment phases of modelling by MaxEnt, and encourage full explorations of parameters options and settings. This requires a more flexible, practical, interpretable, traceable methodology. Here, we present a new conceptual framework for practical distribution modelling by MaxEnt: the “Modular and Functionally Integrated Component-based Approach” (MFICA) – by which the core components are decoupled then wrapped together more flexibly into component-based functional modules. Computational object-oriented and systems approaches are integrated with ecological, statistical and modelling theory and practices to handle the complexity associated with the process. Objects (variables, results etc.) are defined according to specific modelling parameters. Properties (e.g., content) are inherited to each object and new objects are created in a flexible and automated way. The MFICA is operationalized through modular R-scripts wrapped around maxent.jar, and the full modelling process. A trail of models of increasing complexity is built (traceability and interpretability), to suit different modelling purposes. The MFICA scripts produce a diverse range of outputs that integrate and guide the process.

Seasonal dynamics of meroplankton and red king crab larvae (*Paralithodes camtschaticus*) in an arctic fjord

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Many benthic organisms produce pelagic larvae which spend anywhere from hours to months in the pelagic before settling on the sea floor. Such larvae are often referred to as meroplankton and despite being an important life stage for benthic organisms and being present in the pelagic they have not been given as much attention as other zooplankton. They can act as both grazers on phytoplankton and as prey for other organisms and can have an important role in the pelagic ecosystem. Currently, there is limited research on the timing, composition and ecological role of meroplankton in North-Norwegian fjords. Therefore, we investigated the taxonomic composition and annual dynamics of meroplankton abundance in the Porsanger Fjord, Norway. Gut fluorescence and feeding experiments on selected species of meroplankton caught in the field is also planned. One commercially and ecologically important species of meroplanktonic larvae is the red king crab (*Paralithodes camtschaticus*). This is an alien species in Norwegian waters and is under extensive investigation. To obtain the best management strategies of the species there is a need to understand all aspects of their life history. To help elucidate some of the questions surrounding larval drift, the timing, abundance and distribution of king crab larvae is being investigated in the Porsanger Fjord, Norway. In this fjord, the crab has been present since the early 2000 and is part of an extensive monitoring program looking at the population growth and ecological effects on benthic populations.

The ecology and biodiversity of wood-inhabiting Ascomycota

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Wood-inhabiting fungi are a highly diverse species group and inter alia key providers of ecosystem functions, yet majority of species still being ecologically and taxonomically poorly known. Recently, as the key importance of fungi is being increasingly acknowledged, the amount of ecological and biodiversity surveys considering fungi have increased. However, species producing small and poorly detectable fruit bodies, such as most wood-inhabiting Ascomycota species, remain still severely neglected in research and are thus poorly known or undiscovered. The aim of this study was to investigate habitat requirements and biodiversity of wood-inhabiting Ascomycota in boreal forests. This is accomplished by comparing fungal communities of Ascomycota species on large decaying logs in unmanaged and previously managed forests. We used especially accurate repeated survey method where the occurrences were recorded for all Ascomycota species that produced fruit bodies visible to the naked eye. The species were identified to species level in the field or sampled for microscopical identification. Since many Ascomycota species are very difficult or impossible to determine to species level using morphological characters, we will also utilize molecular methods aiding the determination work and try to classify each detected specimen as operational taxonomic units when species identities are not known. We expect to gain new information especially on ecology, distribution and causes for endangerment of poorly known wood-inhabiting Ascomycota species and discuss the usage of this information in the evaluation of their threat statuses.

Evolution of vernalization and daylength response in the grass subfamily Pooideae

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Members of the subfamily Pooideae (Poaceae) are the predominant grasses in northern, temperate climates and it is assumed that their ancestors were distributed in the tropics and subtropics. It is known that some temperate grasses have adapted to the cool conditions and long days by using these as environmental cues to time their flowering. Synchronising flowering with favourable conditions is essential to increase reproductive output and hence fitness. Flowering in response to vernalization (i.e. an extended period of cold temperature) and long days and their molecular background are well described in the Pooideae's crown group, the core Pooideae (including e.g. *Hordeum vulgare*). However, it is not known whether vernalization response and long day induction of flowering evolved at the basis of the subfamily or within. To pinpoint the evolutionary origin of those mechanisms and to reconstruct the history of key genes involved in vernalization response and long day induction are two of the aims in this project. We combine growth chamber experiments including several non-core Pooideae species with gene expression analyses and comparative genomics. A distribution-wide sampling of selected species will also give insights in intraspecific variation of vernalization response. Preliminary results hint towards an early evolution of vernalization response and long day induction, however after the divergence of the most basal Pooideae. There are also signs pointing towards a conserved molecular regulation.

***Sibbaldia* – a molecular phylogenetic study of a remarkably polyphyletic genus in Rosaceae**

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Using DNA sequence data from nuclear ribosomal ITS in combination with plastid trnLF spacer and trnL intron data we show that *Sibbaldia* is a polyphyletic assemblage. It falls into five separate clades of Potentilleae, three within Fragariinae, and two within Potentilla. Our results are largely congruent with a previous study based on anther structure. Four of the sampled *Sibbaldia* species remain in *Sibbaldia*, one [*adpressa*] is classified in *Sibbaldianthe*, one [*perpusilloides*] is found to represent an independent lineage in Fragariinae and is classified in the new genus *Chamaecallis*, one [*micropetala*] is nested within the *Potentilla anserina* clade, and four species belong in a basal clade within *Potentilla*. *Sibbaldiopsis* is found to be very close, if not congeneric with *Sibbaldia*.

Protist diversity along a pH gradient

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The impact of pH on microorganisms has been a difficult task to study that is being explored anew since the rise of culture-independent sequencing methods. In soil bacterial and fungal communities pH was found to have an effect on abundance and diversity. In marine environments, pH increase was reported to have negative effects on growth rate of certain protists killing the least tolerant ones within 24 hours. To address the effect of pH on soil protist community structure we sampled a unique location. The Hoosfield acid strip at Rothamsted Research, in Harpenden, UK has been part of a long-term liming experiment in which the soil pH has been modified by uneven chalk application. All other environmental factors along the site are constant. By assessing samples from this locality, we will be able to assess the effect of pH without disturbance by humidity, temperature or vegetation. Using next-generation sequencing technology (Illumina MiSeq), we amplified and sequenced a part of the protist 18S rRNA directly from soil samples from this pH gradient. We aim to assess soil protists diversity, compare the diversity of protist species along the pH gradient, evaluate the correlation between pH and community composition and put that into a context with previous cultivation-based studies in the field of protist ecology.

***Kinorhyncha* of Southern Norway**

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Kinorhyncha is a phylum of microscopic, benthic, free-living invertebrates with a cosmopolitan distribution. They are found at all depths. Interest in species taxonomy of *Kinorhyncha* has increased during the last two decades, and each year several new species are described. However, as single species are often described within patchy areas, the knowledge of each species' geographical distribution remains poor. At present, only three *Kinorhyncha* species are known to occur in Norwegian waters: *Echinoderes dujardini*, *E. setiger* and *Pycnophyes spitsbergensis* (Norwegian Species Database: Artsdatabanken). This might be due to a lack of surveys performed in Norwegian waters; species diversity reported from locations such as the Iberian Peninsula and Greenland - places where they have recently conducted extensive sediment sampling - suggest that the species diversity in Norway is largely underestimated. Molecular taxonomy has only rarely been the tool of choice for *Kinorhyncha* taxonomists. In my Master thesis, I use an extensive field survey combined

with morphology and molecular markers to infer the *Kinorhyncha* diversity and distribution. This should provide us with tools (such as COI barcoding) to accurately and rapidly identify previously and newly described species. This could also provide some more insight into sister taxa to the *Kinorhyncha* phylum, of which there has been some controversy.

Towards conservation genomics: studying 'migration of adaptation' in a threatened non-model plant species

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The application of genomics to species of conservation concern shows great promise, and will transform our understanding of the amount, distribution and functional significance of neutral and adaptive genetic diversity in natural populations. Understanding how northern species have responded to Quaternary environmental changes, either by surviving in extreme and unfavourable refugia over considerable time periods, or by escaping unfavourable conditions in more southern or eastern refugia is important to predict species' future responses to climate change. Furthermore, understanding the genetic basis of adaptation in response to environmental variation is fundamental, as adaptation plays a key role in the extension of the ecological niche to marginal habitats. The present project aims to use RADseq to identify SNPs in a first step towards investigating both neutral and adaptive genetic composition of a threatened, non-model plant species (*Carex scirpoidea*) in order to disentangle the effects of historical gene flow, genetic drift and selection, combining large-scale phylogeographic and outlier analyses coupled with local ecological data to find candidate loci for local adaptation. To test if the outlier loci actually are related to adaptations, we will test their selective advantage in selection experiments. Further, we will evaluate how the inclusion of data on adaptive divergence adds information on the species' evolutionary potential, and how this affects the delimitation of conservation units. The results of this study will be of profound interest, not least for understanding processes associated with the adaptive potential and persistence of populations during environmental changes, which will enable more empirically based and sustainable conservation strategies for threatened and fragmented populations.

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The Distributed European School of Taxonomy (DEST, www.taxonomytraining.eu) provides high-quality training to future taxonomists. Courses are open to participants from inside and outside of Europe. ForBio is now collaborating with DEST and fund participation in DEST courses. Contact Heidi Solstad heidi.solstad@ntnu.no for more information.

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