

**ForBio annual meeting 1 – 2 February 2011**

***New Perspectives in Biological Systematics***

**Bergen Science Centre (VilVite)**



 **ForBio**  
Norsk-Svensk Forskerskole i Biosystematikk  
Norwegian-Swedish Research School in Biosystematics

## Welcome to Bergen! Welcome to the meeting!

**Venue:** Bergen Science Centre (Vitensenter): Thormøhlens gate 51, mezzanine, auditorium, conference room D (the latter for group discussions 2.2)  
<http://www.vilvite.no/>

**Conference dinner:** Bergen Aquarium (Akvariet i Bergen): Nordnesbakken 4  
<http://www.akvariet.no/>



### Venue and accommodation sites:

VilVite	Bergen Science Center – main conference site
AquB	Aquarium – conference dinner
YMCA	Bergen YMCA - hostel
MGj	Marken Gjestehus – hostel
HP	Hotel Park

Walking distance VilVite – Bergen Aquarium ca. 30 min, YMCA – VilVite ca. 15 min. For more detailed location and transportation info see conference info board.

## PROGRAM

### 1 February:

- 09:00 – 10:00 Welcome coffee
- 10:00 – 10:10 Welcome to the meeting  
(Christiane Todt and Endre Willassen, ForBio - Bergen Museum, University of Bergen)
- Session 1** Chair: Christiane Todt, Department of Biology / Bergen Museum, University of Bergen
- 10:10 – 10:30 **The Norwegian-Swedish research School in Biosystematics – Plans and Visions**  
(Christian Brochmann, ForBio - Natural History Museum, University of Oslo)
- 10:30 – 10:50 **Biosystematics in Natural History Collections**  
(Torbjørn Ekrem, Museum of Natural History and Archaeology, NTNU, Trondheim)
- 10:50 – 11:10 **Biodiversity in the cloud-forests of Costa Rica – a joined evolutionary biology project**  
(Livia Wanntorp, Swedish Museum of Natural History, Stockholm)
- 11:10 – 11:30 **Fisheries and biosystematics**  
(Geir Dahle, Institute of Marine Research, Bergen)
- 11:30 – 12:00 **Views from an outsider: Some personal comments on biological systematics, relating specifically to competitiveness and financing**  
(Ian Gjertz, The Research Council of Norway)
- 12:00 – 13:00 Lunch buffet at VilVite
- Session 2** Chair: Bjarte H. Jordal, Bergen Museum, University of Bergen
- 13:00 – 13:30 **Species trees and species delimitation when gene tree resolution is poor**  
(Bengt Oxelman, Department of Plant and Environmental Sciences, Gothenburg University)
- 13:30 – 14:00 **Evolution of development, new model systems and the necessity of biosystematics**  
(Maja Adamska, Sars International Centre for Marine Molecular Biology, Bergen)
- 14:00 – 14:30 **Progress in deep metazoan phylogenetics: past promises and future fantasies**  
(Ronald A. Jenner, Natural History Museum, London)
- 14:30 – 14:45 General discussion
- 14:45 – 15:20 Coffee break
- Session 3** Chair: Manuel Malaquias, Bergen Museum, University of Bergen
- 15:20 – 15:40 **The *Gyrodactylus* fauna of the 19th century – Museomics for ectoparasites recovered from historical fish collections**  
(Christoph Hahn, PhD candidate, Natural History Museum, University of Oslo)
- 15:40 – 16:00 **The Norwegian Taxonomy Initiative**  
(Ingrid Salvesen, Norwegian Biodiversity Information Centre, Trondheim)
- 16:00 – 16:20 **The Swedish Taxonomy Initiative – exploring Sweden's species**  
(Anna Karlsson, Swedish Species Information Centre, Uppsala)
- 16:20 – 16:30 General discussion
- 16:30 – 18:00 **Poster session** (PhD candidate posters)



19:00 Conference dinner at Bergen Aquarium

## 2 February:

- Session 4** Chair: Hans K. Stenøien, Museum of Natural History and Archaeology, NTNU, Trondheim
- 09:00 – 09:30 **Biosystematics in a post-molecular perspective – benefits with an integrative perspective to plant evolution**  
(Catarina Rydin, Evolutionary Biology Center, Uppsala University)
- 09:30 – 09:50 **The evolutionary history of some eastern African giant lobelias inferred from amplified fragment length polymorphism (AFLP) analysis**  
(Catherine Aloyce Masao, PhD candidate, Natural History Museum, University of Oslo)
- 09:50 – 10:10 **Phylogeography of the threatened peat moss *Sphagnum wulfianum* Girg. with emphasis on northern Europe**  
(Magni Olsen Kyrkjeeide, PhD candidate, Museum of Natural History and Archaeology, NTNU, Trondheim)
- 10:10 – 10:40 Coffee break
- Session 5** Chair: Heidi Solstad, Museum of Natural History and Archaeology, NTNU, Trondheim
- 10:40 – 11:00 **Cryptic speciation in arctic plants**  
(Lovisa Gustafsson, PhD candidate, Natural History Museum, University of Oslo)
- 11:00 – 11:20 **Cryptic diversity in the diatom *Chaetoceros socialis* Lauder**  
(Maria Degerlund & Siv Huseby, PhD candidates, Department of Arctic and Marine Biology, University of Tromsø)
- 11:20 – 11:50 **Molecular biology, ecology, taxonomy and phylogeny - A molecular approach of invertebrate diet analysis**  
(Bernt Rydland Olsen, PhD candidate, Centre for Geobiology, University of Bergen)
- 11:50 – 12:00 Introduction to group discussions (Jarle Werner Bjerke, Tromsø Museum, University of Tromsø)
- 12:00 – 13:00 Lunch buffet at VilVite
- Session 6** Chair: Jarle Werner Bjerke, Tromsø Museum, University of Tromsø
- 13:00 – 14:00 Group discussions
- 14:00 – 15:00 **General discussion with presentation of group discussion results**
- 15:00 – 17:00 Guided tours in Bergen Museum and Department of Biology

**Main organizing committee:** Christiane Todt, Endre Willassen, Heidi Solstad  
Thanks to all the helpers!



## Speakers' abstracts in presentation order

**1 February**

### **Biosystematics in Natural History Collections**

Torbjørn Ekrem

Museum of Natural History and Archaeology, NTNU, Trondheim, Norway

Although many natural history collections started as assemblages of curious objects meant to startle both the educated and common people, a taxonomic research aspect was present at an early stage. What has become of taxonomy and systematics in natural history collections? In this presentation I will attempt to give a museum perspective to biosystematics and particularly focus on the role natural history collections play in biosystematics research today.

### **Biodiversity in the cloud-forests of Costa Rica – a joined evolutionary biology project**

Livia Wanntorp<sup>1</sup>, Pelayo Roncero-Secado<sup>2</sup>, Lawrence Kirkendall<sup>2</sup>

<sup>1</sup>Swedish Museum of Natural History, Department of Phanerogamic Botany, Stockholm, Sweden

<sup>2</sup>University of Bergen, Norway

The Costa Rican species of *Gunnera* are generally known as “poor man’s umbrellas”-- their round, entire leaves can reach a diameter of over 2 m! While the more abundant and well-known *G. insignis* occurs from Nicaragua to Panama, *G. talamancana* is so far known only from the Talamanca mountain chain in southern Costa Rica. *Gunnera insignis* and *G. talamancana* form a well-established hybrid, which is common along the Pan-American Highway in the Talamancas. These two species and their hybrid are all clearly dependent upon disturbance, and are especially abundant on recent landslides and along highway borders which are continually disturbed by clearing and other roadside maintenance activities. In addition, we recorded an unknown fourth form or ecotype during fieldwork. Relationships between this ecotype and the other taxa are unknown. Intriguingly enough, a species of bark beetle, *Scolytodes gunnerae* Wood, has been shown to breed in live leaf petioles of both species of *Gunnera* and the hybrid. Breeding in live non-woody plant material is extraordinary in bark beetles, and seems to have selected for a suite of unusual life history traits (including extremely low brood size and lack of paternal care coupled with long maternal care). We here present the results of a joint evolutionary project aimed at confirming and more precisely documenting the delimitation of *G. talamancana* and *G. insignis* as well as to clarify the nature of the hybrid between these two species. We also present what is currently known about the interaction between species of *Gunnera* and *Scolytodes gunnerae* and mention possible future studies aiming to investigate the consequences for insect and plant of co-evolution between the beetle and *Gunnera*.

## **Fisheries and biosystematics**

Geir Dahle

Institute of Marine Research, Bergen, Norway

Stock assessment and quota recommendations to the annual fisheries as well as aquaculture management advice are key tasks for the Institute of Marine Research. Biosystematics includes identification and spatial and geographic distribution of the different species, all vital information for any assessments or management advice. Managers have mainly been concerned with the immediate resources of interest like the abundance and size of fish available for harvesting, but reduction in the genetic resources of natural fish populations has become an important fisheries management problem.

In the marine environment several species are characterized by extended pelagic larval stages and/or high migratory capabilities, reducing the potential for geographic differentiation between them. Although most of the marine environment lacks obvious barriers to migration and dispersal, circulation patterns, sea bed topography and other geographic features provide possibilities for isolation and differentiation. Although protein electrophoresis was the method of choice in the first decades of genetic studies, various DNA markers are now dominating in the chase for information about genetic differentiation, geographic distribution and other parameters that are crucial in population biology. Here I will present and discuss some of the methods available for species identification, differentiation and functional genetics, and how this information is used by management today, and could be used in the future.

## **Species trees and species delimitation when gene tree resolution is poor**

Bengt Oxelman, Bernard Pfeil

Department of Plant and Environmental Sciences, University of Gothenburg, Sweden

Recent developments and implementations of the multispecies coalescent to infer species trees from multiple gene trees offer exciting possibilities to identify species classifications that are optimal with respect to the model used. A possible advantage with these models is that uncertainties in for example gene tree estimation can be accounted for. On the other hand, it is not clear how such uncertainties affect the accuracy of species tree estimates. Here, we present results from simulations and from empirical data, which highlight this problem.

## Evolution of development, new model systems and the necessity of biosystematics

Maja Adamska

Sars International Centre for Marine Molecular Biology, Bergen, Norway

To understand evolutionary history of developmental mechanisms, evo-devo scientists compare developmental mechanisms – both in terms of cell and tissue movements and genes used to control them – utilized by modern organisms. For the comparisons to be meaningful, the model systems selected for such studies must be carefully selected. Phylogeny – “the branching order” of the clades represented by model organisms is crucial for correct interpretations of similarities and differences seen, and for deciphering the ancestral states. Somewhat surprisingly, deep animal phylogeny still remains an unresolved and hotly disputed issue. One of the key discrepancies in phylogenetic trees recovered by recent analyses is the phylogeny of sponges, which were most likely the first multicellular animals to evolve. Sponges are either argued to be a monophyletic group, whose peculiar body plan evolved after they split off the rest of multicellular animals, or paraphyletic, with an implication that the sponge body plan might be ancestral for all multicellular animals. Until recently, the great majority of developmental studies has been done using siliceous sponges, especially *Amphimedon queenslandica*, the only sponge for which complete genome sequence is available, and *Ephydatia* species, which are easily accessible freshwater organisms. We have generated a large genomic and transcriptomic dataset for a calcareous sponge, *Sycon ciliatum*, which is currently developed as a development model system by my group at the Sars Centre in Bergen. In my talk, I will describe similarities and differences in developmental processes, and the genetic toolkit likely to control them, between the siliceous and the calcareous sponges. Comparisons between the representatives of these two divergent sponge lineages, as well as the “higher” animals demonstrate fantastic evolutionary plasticity of the developmental mechanisms. A solid phylogenetic framework is now necessary for the final interpretation of the results.

## Progress in deep metazoan phylogenetics: past promises and future fantasies

Ronald A. Jenner

Department of Zoology, The Natural History Museum, London, UK

“A revolution in understanding animal evolution is upon us.” Thus ends Professor Peter Holland his preface for the 2009 book *Animal evolution. Genomes, fossils, and trees*. Holland’s statement captures the sense of excitement and imminent progress in the field of higher-level animal evolution, a sentiment certainly shared by many other workers. Yet, such a sense of heightened optimism, or perhaps hyperbole, is certainly not new, as other times in the recent past were equally labelled “revolutionary,” for example when explicit cladistic methods became available to analyze morphological data, when molecular phylogenetics came largely to replace morphological cladistics, and when phylogenomics came to replace molecular phylogenetics based on limited numbers of loci. I will chronicle recent developments in the field of deep metazoan phylogenetics in an attempt to distinguish genuine arrows of progress from mere cyclical change of opinions. I will identify remaining challenges, and explore how close we are to reaching the limits of what we can realistically hope to learn about the evolution of animal body plans.



## The *Gyrodactylus* fauna of the 19th century –Museomics for ectoparasites recovered from historical fish collections

Christoph Hahn<sup>1</sup>, Tor A. Bakke<sup>1</sup>, Philip D. Harris<sup>1</sup>, Steven Weiss<sup>2</sup>, Lutz Bachmann<sup>1</sup>

<sup>1</sup>National Centre for Biosystematics, Natural History Museum, University of Oslo, Norway

<sup>2</sup>Institute for Zoology, Karl-Franzens University Graz, Austria

*Gyrodactylus* v. Nordmann, 1832 (Platyhelminthes; Monogenea; Gyrodactylidae) is a genus of viviparous ectoparasites infecting teleost fish species throughout the world. The 400 described species are thought to represent only about 2% of the worldwide diversity. The genus displays a unique assemblage of biological features including (hyper-)viviparity, progenesis and different reproductive modes (parthenogenesis vs. sexual reproduction) during ontogeny. Host switching rather than co-evolution is thought to be the main mechanism for speciation in *Gyrodactylus*. In order to revise the controversial taxonomy also the role of hybridization and polyploidisation is assessed critically. The great potential of *Gyrodactylus* for exploring speciation in real time is unquestionable. *Gyrodactylus salaris* is known as a major pathogen of salmon in Norway which, apart from its economic importance, has imposed significant ecological burdens upon freshwater ecosystems, associated with the regimes of chemical eradication which have been applied. *G. salaris* is thought to have evolved by a host shift from a related, benign species, *G. thymalli* on grayling. This has been the focus of extensive research in previous years but neither morphological nor molecular analyses have been sufficiently powerful to identify the origin of the host shift. Salmonids are, due to the nature of their habitats, highly affected by geographical fragmentation, causing isolation and rather complex phylogenetic patterns. To reconcile these host patterns with the complex *Gyrodactylus* phylogenies and to disentangle host-switches from co-evolutionary events is an ambitious task, particularly as human impacts such as e.g., water pollution, overfishing and use of hydropower frequently caused regional extinction of former abundant freshwater fish species. The impact of stocking on autochthonous fish populations is also an important issue in conservation biology and there are numerous examples for human-induced ecosystem alterations by accidentally introducing non-native species into previously balanced systems. Historical changes in fish diversity are well documented in ichthyological collections, but so far no attempts have been made to explore the ectoparasites unwittingly collected together with their hosts. We screened selected salmonids deposited in NHM Vienna, Austria and found *Gyrodactylus* specimens on salmon (collected in 1876) and grayling (1880). Using hook morphology, the parasites were identified as *G. derjavinoidea* and *G. thymalli* respectively. To utilize molecular data we have successfully overcome the particularly challenging levels of DNA-degradation in this material and we are currently analysing the COI sequence of the latter specimen. We are the first to apply museomics approaches to *Gyrodactylus* diversity and we intend to add a temporal dimension to the understanding of the current distribution in European watercourses. The potential of the approach has already been recognised by two grants based on the pilot study. Systematic screenings of the fish collections of NHM Vienna, Austria and MNHN Paris, France, as well as Norwegian collections, will start in 2011 and the utilisation of Next Generation Sequencing approaches in the study will be assessed carefully as soon as more historical parasite material has been detected.

### **The Norwegian Taxonomy Initiative**

Ingrid Salvesen

The Norwegian Biodiversity Information Centre, Trondheim, Norway

There are assumed to be around 53 000 species in Norway. So far, rather more than 39 000 of these are known. However, basic knowledge about very many of the species is poor and there is a great need to improve scientific expertise associated with our knowledge of species (biosystematics). The Norwegian Taxonomy Initiative (NTI) has been set up to try to fill these gaps in our knowledge and to help to improve expertise and recruitment in the field of biosystematics. A large number of species not previously recognised in Norway will probably be discovered through this initiative, doubtless also species that are new to science.

NTI was established in 2009 by a grant from the Norwegian Government. The Norwegian Biodiversity Information Centre (Artsdatabanken) is responsible for coordinating the taxonomy initiative. It is organised by a steering committee appointed by the Ministry of the Environment and a project coordinator employed at the Centre. NTI will be run in close cooperation with the Swedish Taxonomy Initiative. A bilateral collaboration agreement between the two initiatives was signed on 09.09.09 at the ministerial level. Good coordination with other mapping activities in Norway is also regarded as being of great importance.

Key tasks in the initial phase of the initiative has been to establish an efficient organisation and a scientific base, begin the species diversity mapping, and organise a good infrastructure for data flow and communication of results. Several mapping projects have now been initiated which will contribute to improve our knowledge of poorly known species of algae, fungi, lichens, mosses, insects and other invertebrates.

### **The Swedish Taxonomy Initiative - exploring Sweden's species**

Anna Karlsson

Swedish Species Information Centre, Uppsala, Sweden

In 2002 the Swedish Species Information Centre (SSIC) was commissioned by the Swedish Parliament to identify all species of plants, fungi and multicellular animals in the country. The Swedish Taxonomy Initiative was born! The aim of the project is to make knowledge about all Swedish species readily available to scientists, conservationists and the public. The project includes taxonomic research and inventories of poorly known groups of organisms and species. The knowledge gained is presented in a popular Encyclopedia of the Swedish Flora and Fauna. The first volume was published in 2005 and there will be about 100 volumes in all. The Swedish Taxonomy Initiative supports research and inventories through yearly advertised grants. The taxonomic work is performed by both Swedish and international researchers. The two largest inventory projects so far within the STI are a Marine Inventory and the Swedish Malaise Trap Project. The research and inventories supported by the Swedish Taxonomy Initiative have so far resulted in the discovery of around 2,300 species new to the country, of which 1,000 are new to science. Not surprisingly, most new findings are made among insects, fungi (incl. lichens) and marine invertebrates.

There are large collections of animals, plants and fungi at the natural history museums in Sweden. They constitute an essential resource for nature conservation. Thus, the STI offers grants for curating the collections of poorly known groups of organisms and making them available to the public.

Since 2007 the Swedish Taxonomy Initiative runs a postgraduate school, offering courses about biodiversity. The courses are mostly on taxonomic methodology or about taxonomically poorly known groups, and are organized in cooperation with Swedish universities and natural history museums. A Norwegian-Swedish joint research school in biosystematics started in 2010.

## 2 February

### **Biosystematics in a post-molecular perspective – benefits with an integrative perspective to plant evolution**

Catarina Rydin

Department of Systematic Biology, Evolutionary Biology Centre, University, Sweden

Molecular data was nothing less than a revolution for systematics; a completely new source of information became available and could be used to test hypotheses. We are now approaching a time when many or even most phylogenetic questions have been addressed using molecular data. A large proportion of them have been resolved and the results provide important bases for further studies in evolutionary biology and ecology. Other phylogenetic questions have proven difficult to resolve, even using the wealth of information provided by whole genome sequencing. Relationships among the six extant clades of seed plants is an example of the latter. Incompatible, yet seemingly well-supported hypotheses continue to be proposed and the phylogeny as well as origin and evolution of key innovations, such as the angiosperm carpel, are unknown. It is of course possible to use yet more molecular data in the search for ways to choose among alternative hypotheses, but another option is to (in addition) utilize other sources of data.

The vast majority of seed plant diversity is extinct and fossils may be crucial to bridge the gaps between the sparse remnants of the historical diversity. A question, consistently in focus, is to find the sister group of the Gnetales. As in all major seed plant clades except angiosperms, extant gnetalean diversity is small compared to the historical diversity and further studies on relationships among living and extinct members of the Gnetales might provide important clues to finding its sister group. Several fossils document a substantial diversity in the *Welwitschia* clade in the Early Cretaceous and there are a few potential relatives of *Gnetum*. However, interrelationships among plants in the *Gnetum-Welwitschia* clade and its stem lineage are so far poorly understood. Ephedroids are common in the Early Cretaceous and a few of them share uniquely derived features with extant *Ephedra*. It has typically not been possible to assign them to any particular subclade within *Ephedra*, but in some cases, it has also not been possible to separate them from the extant genus by any character. Are these fossils members of the extant clade or do they represent extinct stem lineages? The answer has profound consequences for trait evolution and the timing of evolutionary events in the clade. Using a case study of *Ephedra*, I exemplify how an integrative approach based on molecular data, morphology, micromorphology, anatomy and histology can clarify placement of fossils and corroborate hypotheses on plant evolution.



### The evolutionary history of some eastern African giant lobelias inferred from AFLP analysis

Catherine Aloyce Masao<sup>1,2</sup>, Pantaleo Munishi<sup>3</sup>, Rosalía Piñeiro<sup>2</sup>, Magnus Popp<sup>2</sup>, Virginia Mirré<sup>2</sup>,  
Eric Knox<sup>4</sup>, Sileshi Nemomissa<sup>5</sup>, Christian Brochmann<sup>2</sup>

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<sup>3</sup>Sokoine University of Agriculture, Department of Forest Biology, Morogoro, Tanzania

<sup>4</sup>Department of Biology, Indiana University, Bloomington, USA

<sup>5</sup>National Herbarium of Ethiopia, University of Addis Ababa, Ethiopia

Giant lobelias and giant senecios are emblematic of the afro-alpine flora in the high mountains of eastern Africa, and have high ecological and touristic value. Previous morphological and chloroplast DNA studies of the giant lobelias gave partly contradictory results for the *Giberroa* and *Deckenii* species groups. Here we use AFLP analysis to assess genetic diversity and evolutionary history of six species. In particular, we test the hypotheses that the Great Rift Valley is a major barrier and that *Lobelia bequaertii* is of hybrid origin. We are currently analyzing the AFLP data and only preliminary conclusions are presented here. The main division in the dataset was as expected observed along the Rift Valley. *Lobelia bequaertii* was placed in the *Giberroa* group, not in the *Deckenii* group, consistent with the previous chloroplast DNA study but contradictory to the traditional morphology-based classification. *Lobelia bequaertii* does not appear to be of recent hybrid origin, but may represent a good example of parallel evolution of morphological traits.

### Phylogeography of the threatened peat moss *Sphagnum wulfianum* Girg. with emphasis on northern Europe

Magni Olsen Kyrkjeeide, Hans K. Stenøien, Kristian Hassel, Kjell Ivar Flatberg  
Museum of Natural History and Archaeology, NTNU, Trondheim, Norway

An increasing number of phylogeographic studies reveal possible glacial refugia during the last glacial maximum (ca. 20,000 years ago) and post-glacial colonization patterns for several species, but little is known of migration routes of mosses. The hypothesis of *in situ* glacial survival states that species survived in ice free areas within the ice sheets in the northern hemisphere. The climate in these ice free areas was probably too harsh and dry for most species, i.e. unsuitable for species like peat mosses which grows in moist habitats. However, two peat mosses only found in Scandinavia in Europe today most likely originated in Europe 40,000 years ago, before the last glacial maximum. Here, the phylogeography of another peat moss, *Sphagnum wulfianum*, which is mainly found in areas previously covered by ice in Europe, have been studied to find how genetic variation is distributed in Northern Europe and the possible immigrations routes into Scandinavia after the last glaciation. 11 microsatellite markers were amplified from 43 populations (717 shoots) distributed in nine countries, including two populations from North America. The data were analyzed using genetic diversity statistics, Bayesian clustering methods (Structure), and coalescence theory (IM and Migrate). Genetic diversity statistics show that genetic variation in microsatellite loci is extremely low (mean  $H_e=0.01\pm0.03$ ) in this species and that populations are highly differentiated ( $F_{ST}=0.79$ ). Most populations are monomorphic and only 22 haplotypes are recognized, with one of them found in 23 populations. Two main genetic clusters are recognized in the dataset and they diverged recently, most likely after the last glacial maximum, hence, Scandinavia was probably colonized after the last glacial maximum. The low genetic variation found may be due to

bottlenecks in the past and/or colonization by repeated founder events. In Europe, The Baltics is the region with the highest genetic variation and the estimated migration rate is higher from The Baltics to Scandinavia than the other direction. The most common haplotype is not found in The Baltics, only in Scandinavia, Finland and Russia, meaning there have probably been two colonization routes into Scandinavia, one south-east from the Baltic States and one from Eastern Europe through Finland. Thus, Scandinavia acts as a contact zone. North America seems to have higher genetic diversity than Europe and even though no haplotypes are shared between these two regions, many alleles are shared, i.e. migration from west may be possible. However, more samples from North America are needed to conclude if there has been migration from North America into Europe.

### Cryptic Speciation in Arctic Plant

Lovisa Gustafsson<sup>1</sup>, Christian Parisod<sup>2</sup>, Eric Schranz<sup>3</sup>, Liv Borgen<sup>1</sup>,  
Galina Gusarova<sup>1</sup>, Christian Brochmann<sup>1</sup>

<sup>1</sup>National Centre for Biosystematics, Natural History Museum, University of Oslo, Norway

<sup>2</sup>Evolutionary Botany, University of Neuchatel, Switzerland

<sup>3</sup>University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, the Netherlands

The arctic flora has long been considered depauperate as compared to other regions of the world. However, estimates of species diversity are based on morphological differentiation (taxonomic species) and may not provide accurate numbers of biological species. In recent experiments, crosses within each of three diploid, circumpolar species of *Draba* (Brassicaceae) resulted in mostly sterile hybrids, suggesting that formation of cryptic biological species may be common in arctic plants (Grundt et al. 2006, PNAS). The aim of the present study is to provide further insights into patterns and processes underlying speciation in the Arctic.

We currently perform intraspecific crosses within several diploid species sampled in Alaska, Canada and arctic Norway. The fertility of hybrids will enable us to draw conclusions about the generality of sibling species formation in the Arctic. We compare selfers vs. outcrossers to address the underlying evolutionary forces (drift vs. selection), expecting selfing to facilitate the accumulation of hybrid incompatibilities through genetic drift. We also aim at unravelling more precise molecular mechanisms underlying reproductive barriers in *Draba nivalis*, as a follow-up of Skrede et al. 2008 (Evolution). QTL analyses are made on F2 hybrids from reciprocal crosses by associating seed set and pollen fertility with a range of molecular markers ("Brassicaceae Building Block" markers, microsatellites, AFLPs and SSAPs). We ask to what extent chromosomal rearrangements and nuclear-nuclear and cytonuclear incompatibilities contribute to intrinsic reproductive barriers and aim to characterize putative speciation loci.

Brassicaceae Building Block markers can offer great comparative strength. These 24 conserved genomic blocks can give additional QTL markers, and also enable us to reconstruct the *Draba* genome evolution by investigating the reshuffling of these blocks from the ancestral n=8 karyotype. The Brassicaceae Building Block markers also show great potential as universal markers for the entire Brassicaceae family.

**Cryptic diversity in the diatom *Chaetoceros socialis* Lauder**Maria Degerlund<sup>1</sup>, Siv Huseby<sup>1</sup>, Adriana Zingone<sup>2</sup>, Bjarne Landfald<sup>3</sup><sup>1</sup>Department of Arctic and Marine Biology, University of Tromsø, Norway<sup>2</sup>Laboratory of Ecology and Evolution of Plankton, Stazione Zoologica Anton Dohrn, Napoli, Italy<sup>3</sup>Norwegian College of Fishery Science, University of Tromsø, Norway

*Chaetoceros socialis* is among the most important spring bloom species in North Atlantic and Arctic waters. In addition to being characteristic of cold waters, *C. socialis* is also prominent in much warmer waters, such as the Gulf of California or the Gulf of Naples. Such wide ecological plasticity may indicate a high phenotypic variability, but may also relate to cryptic diversity within the species. Monocultures of *C. socialis* isolated from NE Atlantic waters (4 strains) and from the Gulf of Naples (5 autumn + 3 spring strains) were cultivated at 2.5, 8 and 13°C (12 h day-length and scalar irradiance 20  $\mu\text{mol quanta m}^{-2} \text{s}^{-1}$ ), and analysed for morphology, physiology (growth, photosynthetic yield) and biochemistry (UPLC metabolomic profiles). In addition, sequence analysis of LSU rRNA was performed for phylogenetic confirmation of the species. The northern strains had significantly higher growth at low temperatures than the southern ones, and vice versa. Also, there was no significant difference in growth between the spring and autumn strains from the Gulf of Naples, indicating that they originated from the same population despite being subject to temporal segregation during the annual cycle. Maximum observed growth rates were achieved at 13°C for both groups of strains. This is interesting since northern strains of *C. socialis* reach their maximum abundances at sea surface temperatures of 2-6°C. The variations observed in growth of *C. socialis* and the differences observed between groups of strains were also reflected in photosynthetic yield, confirming the ecological plasticity of the species. General morphological characters (observed in light microscope) did not reveal any differentiation between southern and northern strains, but these should be further examined in EM. The ribosomal RNA gene analyses indicated a divergence between the southern and the northern strains of *C. socialis*, pointing towards cryptic diversity within the species. The sequence data of the strains from the Gulf of Naples were in accordance with the phenotypic similarity observed between spring and autumn strains.



**Molecular biology, ecology, taxonomy and phylogeny –  
A molecular approach of invertebrate diet analysis**

Bernt Rydland Olsen<sup>1</sup>, Kristin Dahlgren<sup>2</sup>, Christoffer Schander<sup>1,3</sup>, Ulf Båmstedt<sup>2</sup>,  
Hans Tore Rapp<sup>1</sup>, Christofer Troedsson<sup>3</sup>

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Within all ecosystems, organisms interact with each other in various ways, as for example through predator-prey relationships or through competition. Predator prey relationships can be essential information for ecologists, and there is awareness among management stakeholders that feeding behaviour need to be part of their knowledge when management plans is prepared. Unfortunately, stomach analyses have often been limited to tedious dissections and microscopy that can lead to a bias towards food with hard and less digestible parts. Molecular methods contribute to improve gut content analysis, but a magic formula to describe the diet of small marine invertebrates is yet to be discovered. Complete ecosystem description depends also on taxonomy and phylogeny, and interdisciplinary collaboration between phylogeny, taxonomy, ecology and molecular biology are required. The copepod *Limnocalanus macrurus* is an important predator in the Baltic Sea and has biomasses measured to constitute close to 50% of the northern Baltic Sea mesozooplankton. Consequently in order to describe their role in this community one has to describe what they feed on. Our hypothesis was that *L. macrurus* is an omnivorous with strong herbivorous tendencies during spring and summer based on e.g. wax ester content. The aim of this study was to test this by a new PCR-based method with eukaryotic universal 18S rRNA gene-targeted primers 1131F and 1629R, a conserved region of the 18S rRNA gene. Universal primers target a vast range of organisms but the predator DNA will dominate since amplification goes in favour of the amplicon that has the highest concentration present. However, when this problem is solved the universal primers can describe the diversity among the prey and possibly reveal unknown prey. Denaturing High-Performance Liquid Chromatography (DHPLC) makes it possible to exploit these advantages of the universal primers. DNA extracts from *L. macrurus* was as expected, dominated by predator DNA, and with the DHPLC we shifted the ratio “predator:prey” DNA down to a level that made it possible to amplify prey DNA. Thus, we were able to use universal primers and conduct virtually unbiased screening of large amount of specimens and search for unknown prey. Crustacean sequences extracted from our samples were tested with maximum parsimony, using the phylogenetic software PAUP 4.08b, together with a set of other crustacean sequences extracted from GenBank. We found that our hypothesis of strong herbivore tendencies was not true; *L. macrurus* fed mainly on other Crustaceans. *L. macrurus* feeding behaviour is still omnivorous but not with strong carnivore tendencies as first hypothesized. Universal primers and the DHPLC worked well, but to be able to process the molecular information one need interdisciplinary collaboration with taxonomy and phylogenetics.

## Poster abstracts in alphabetical order

### Poster 1: **Discovery of *Pseudocalanus moultoni* in East Atlantic waters based on mitochondrial COI sequence variation**

Ole Nicolai Staurland Aarbakke

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Marine copepods of the genus *Pseudocalanus* Boeck 1872 are common and abundant throughout the northern hemisphere where they constitute an important link between primary production and higher trophic levels. They are a major food source for larval cod, *Gadus morhua* and adult planktivorous fish (e.g. sprat, *Sprattus sprattus*). The seven described species all co-occur with at least two and often several sibling species. Species level identification of members of the *Pseudocalanus* genus is difficult due to extraordinarily weak interspecific divergence of morphologic and morphometric traits. Because growth tends to be influenced by temperature, size is no good criterion either. Due to their difficult identification, these species are often pooled together and treated as *Pseudocalanus spp.* When species level identification through microscopy is applied, the confusing taxonomy of *Pseudocalanus* is evident. Studies in the Baltic Sea traditionally identified members of the genus as *P. elongatus*. Following Bucklin et al. 2003 molecular assessment, *Pseudocalanus* in the Baltic has been named either *P. acuspes* or *Pseudocalanus sp.* Scientists focusing on the White Sea usually name their species *P. minutus*, while investigations in the North Sea report *P. elongatus*. In the western Pacific the genus is represented by two members, *P. minutus* and *P. newmani* and in the eastern Pacific, *P. mimus*, *P. moultoni* and *P. newmani* are reported. In an effort to resolve the taxonomy of *Pseudocalanus* in coastal Norwegian and Svalbard waters, mitochondrial cytochrome oxidase I (mtCOI) genes were sequenced from individuals in samples from several fjords. This work resulted in the finding of a species previously not reported from Norwegian waters, namely *Pseudocalanus moultoni*, which is considered coastal and normally occurs on the east and west coasts of North America. Through comparison of mtCOI gene sequences and reconstructed phylogenies, we present the relationship between the two native, and the newly discovered Norwegian, populations. Zooplankton have been put forward as “beacons of climate change” because through rapid response to slight temperature changes, they weak environmental signals. Recent publications investigating the response of pelagic zooplankton amplify communities to climate warming have revealed a northward movement of many species. With its numerous species, if accurately identified, *Pseudocalanus* could prove to be an excellent genus with respect to ecosystem monitoring.

### Poster 2: **Molecular and Morphological Taxonomy of North American *Micropsectra* (Diptera: Chironomidae)**

Alyssa Anderson<sup>1,2</sup>, Torbjørn Ekrem<sup>2</sup>, Elisabeth Stur<sup>2</sup>

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*Micropsectra* (Diptera: Chironomidae) is a particularly species-rich genus within the aquatic fly family Chironomidae and can be quite useful in biological monitoring studies when examined at the species level. Species within this genus are found in a variety of freshwater habitats and have a wide distribution throughout the Nearctic and Palaearctic regions; however, comparatively few systematic and taxonomic studies have focused on the differentiation and description of Nearctic species. Species within the *Micropsectra* are often quite similar morphologically and can be difficult to differentiate and the lack of comprehensive taxonomic keys, particularly for the Nearctic region, makes species-level identification

nearly impossible in many cases. Furthermore, while many *Micropsectra* species are thought to be Holarctic in distribution, there may be situations where the Palearctic and Nearctic counterparts are morphologically similar but actually two distinct species. Thus, the intent of this research is to use molecular-based tools to help resolve these taxonomic problems and provide the framework for better elucidation of North American *Micropsectra* species. Larval specimens of *Micropsectra* were collected from six groundwater dominated streams throughout Minnesota, USA during late winter/early spring of 2010 and reared through to adulthood, resulting in a total of 104 adult specimens, all associated with pupal exuviae. The head, wings, hypopygium, and exuviae of all specimens were slide mounted, while the thorax and abdomen were stored in ethanol for molecular procedures. Specimens were identified and separated into one of four species groups. A subset of 48 specimens, chosen as representatives of each species, were selected for DNA extraction, PCR amplification, and sequencing of the mitochondrial cytochrome oxidase I (COI) gene. Sequences from our specimens will be compared to sequences of *Micropsectra* species that have previously been published. Preliminary results indicate that from the specimens in this study, we have found one species new to science, one species new to North America, and at least two other species that are new to Minnesota and the north central United States. Results of this study will help to enhance the efficiency, effectiveness, and reliability of species identification of *Micropsectra* by providing a useful contribution to the development of taxonomic keys for Nearctic *Micropsectra* and an analysis of genetic and morphological variation between populations of species with a transatlantic distribution.

### Poster 3: Phylogeny and generic delimitation of the *Metalasia* clade

Annika Bengtson, Per Ola Karis

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*Metalasia* is a South African genus of ericoid shrublets in the paper daisy tribe Gnaphalieae (Asteraceae) currently consisting of 53 species with its main distribution in the Cape Floristic Region. Earlier studies have grouped *Metalasia* with a number of the closely related genera in a “*Metalasia* clade” varying somewhat in its content, but the current study includes *Atrichantha*, *Hydroidea*, *Dolichothrix*, *Calotesta*, *Lachnospermum*, *Planea* and *Phaenocoma*. This is a diverse group with a large variation in many characters and there was a possibility that some of the smaller genera could have their closest relatives within *Metalasia*. A few morphological studies have tried to resolve the relationships within the clade but this has proved difficult and as little molecular work has been done the relationships within the clade have until now remained unresolved. The aim of the current study was to resolve the phylogenetic relationships of the *Metalasia* clade using plastid (trnL-trnF and psbA-trnH) and nuclear (ETS and ITS) sequence data. The *Metalasia* clade is here shown to be a monophyletic group, and its position within Gnaphalieae is confirmed. The phylogenetic positions of the smaller genera in relation to *Metalasia* are determined and one of them shown to belong within *Metalasia*. The genus *Metalasia* itself appears monophyletic but with the species divided into two well supported sister groups. A phylogeny of the clade will be presented.



**Poster 4: Intra-specific variation in west-Palaeartic aquatic insects, with emphasis on loss of flight ability in craneflies and stoneflies**

Louis Boumans

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In 2010 the Museum of Natural History in Oslo launched a project to investigate the diversity of aquatic insects with an emphasis on Nordic stoneflies (Plecoptera) and craneflies (Diptera, Tipulidae). The project consists of two parts: A DNA barcoding library representing the mitochondrial diversity of the 35 stonefly species known from Norway, and a PhD research project addressing within-species diversity and (incipient) speciation in a selected number of stoneflies and other aquatic insects using molecular markers. Several species of stoneflies and craneflies display local loss of flight ability in one or both sexes. Stonefly nymphs are mostly found in running water. Loss of flight occurs in males before females, in many species at a small geographic scale. In contrast, the craneflies *Tipula gimmerthali* and *T. luteipennis* have larvae inhabiting marshes. In these species, the females are flightless over a large part of their distribution range, but flying populations occur locally. In various insects, loss of flight is associated with high altitudes and latitudes, and climatic conditions like cold and windiness. However, these associations are impressionistic, and strong statistical evidence is lacking.

Molecular and morphological characters are used to address the following questions:

Is loss of flight entirely genetically determined?

How often did loss of flight happen, under what environmental circumstances?

Has loss of flight affected past vicariance and dispersal events?

‘This will be done in a phylogeographic framework that includes samples covering as much as possible of the species’ distribution area. In addition to this central theme, the same data will be used to address a number of currently unresolved taxonomic issues. Despite the fact that the stonefly populations in Scandinavia cannot be older than the Holocene, some species display considerable variation in morphology or acoustic (drumming) signals even within Norway. Special attention is given to species like *Leuctra hippopus* and *Capnia bifrons* that display local variation in flight ability.

**Poster 5: The phylogenetics and dynamic expression patterns of Sox genes in the calcareous sponge *Sycon ciliatum***

Sofia Fortunato, Sven Leininger, Marcin Adamski, Christin Zwafink,

Brith Bergum, Maja Adamska

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Sox genes encode transcription factors involved in development of animals, playing a variety of functions ranging from sex determination to cell differentiation. However, only recently have studies demonstrated that Sox genes are present in sponges, the most basal metazoans. In the fully sequenced genome of the demosponge *Amphimedon queenslandica*, four Sox genes were found that belonged to three of the five major invertebrate Sox classes: *SoxB*, *SoxC* and *SoxF*. To gain insight into evolution of the Sox family of genes, we are investigating these genes in the calcareous sponge, *Sycon ciliatum*. This sponge is commonly found in Norwegian fjords and has been chosen as a new model system by our research group for developmental biology studies. To date, we have identified five Sox genes within an EST dataset generated from adult, larval and juvenile samples. The phylogenetic analysis, based on the HMG domain sequences, suggests that (i) two of the identified Sox genes are putative *SoxB*, (ii) two belong to *SoxEF* and (iii) one belongs to *SoxC*. To better understand the role of Sox genes in sponge development, we are currently studying the expression patterns of the identified genes using *in situ* hybridization. *SoxB* is dynamically expressed during Sycon development, beginning in early embryonic stages and continuing in

differentiating cells in the juvenile stages. While *SoxEf* is not expressed in oocytes, embryos, larvae or young post-larvae, its expression becomes detectable in the inner cells of stage three juveniles, likely coinciding with cell differentiation. The three identified Sox genes are expressed during embryogenesis and metamorphosis as well as in adult cells of *S. ciliatum* in dynamically changing and unique patterns. Overall, this study is the first to show the expression patterns of Sox genes throughout embryogenesis and metamorphosis in a sponge. Determining the developmental expression patterns of *S. ciliatum* Sox genes and the phylogenetic relationships with their sponge and basal metazoan homologues will provide insights into evolution and function of these important developmental regulators.

**Poster 6. Occurrence and phylogenetic implications of microRNAs in the fish parasite  
*Gyrodactylus salaris* and related species**

Bastian Fromm

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*Gyrodactylus* is an extremely diverse and widely distributed genus of monogenean flatworms (Platyhelminthes) and currently includes 400 described small ecto-parasitic species of poorly understood phylogeny (500µm size in average). They cause serious diseases to teleost fish and are therefore of a high level of economic interest: *Gyrodactylus salaris* causes severe damage to the Salmon (*Salmo salar*) stocks in Norway. As they are platyhelminths, they might also play an important role to our understanding of early metazoan evolution. Finally *Gyrodactylus* has a unique reproductive mode with (hyper-)viviparity and progenesis, making it also very interesting from a developmental point of view. To unravel several issues on genetics, systematics and development of this very interesting and important group of parasites, the project focuses on the miRNA inventory of the genus *Gyrodactylus*. MiRNAs are single-stranded, 22 nucleotide long, noncoding transcripts derived from different genome encoded hairpin precursors and regulate gene expression by a number of different mechanisms. First described from the nematode *Caenorhabditis elegans*, they represent the most recently discovered gene regulators. They are involved in a broad variety of biological processes. In evolutionary terms miRNAs are quite unusual in that they are continuously added, highly conserved, and rarely lost from metazoan genomes. Obviously, they are under massive selection, and may, accordingly, represent suitable phylogenetic markers which even allow the reconstruction of the miRNA complement of the most recent common ancestor of all Metazoa. The miRNA inventory of *Gyrodactylus salaris* will be tested (1) as a character for delimiting these cryptic species (2) as a phylogenetic marker for *Gyrodactylus* and other representatives of Platyhelminthes and (3) as a marker for developmental traits in *Gyrodactylus*. To get sequence information of the miRNAs of *Gyrodactylus salaris* I follow a straight forward next-generation sequencing strategy: sequencing and assembling the *Gyrodactylus salaris* genome as a part of Lutz Bachmanns *Gyrodactylus* genome-sequencing project and sequencing and assembling miRNAs from totalRNA extracts. For the quiet challenging task of extracting high quality RNA containing miRNAs from these small animals several commercially available RNA extractions methods were compared for their respective performance by meanings of micro-fluidics electrophoresis (manuscript in work). Eventually miRNA-containing totalRNA in the necessary concentration and purity for a next-generation sequencing run was extracted from only 150 individuals. The sample has already been delivered to the Norwegian High-Throughput Sequencing Centre (NSC) where it was approved and processed for sequencing: the miRNA-library is prepared and will be sequenced in the end of 2010. Another very promising result of the extraction methods-comparison was that the preparation of detectable amounts of RNA was possible from even single *Gyrodactylus* specimen, which will later allow investigating different levels of miRNAs between single specimens. The *Gyrodactylus salaris* genome-sequencing project has reached its final sequencing step and will be ready as reference in 2011. Together with already published miRNA data from e.g. *Schistosoma* sp. - closely related parasites - I look forward to get aligned miRNA-sequences in the first months of 2011.

**Poster 7: Timing of colonization and divergence of the African *Lychnis* L. (Caryophyllaceae)**Abel Gizaw<sup>1,2</sup>, Sileshi Nemomissa<sup>1</sup>, Christian Brochmann<sup>2</sup>, Magnus Popp<sup>2</sup><sup>1</sup>Department of Biology, Addis Ababa University, Addis Ababa, Ethiopia<sup>2</sup>National Centre for Biosystematics, Natural History Museum, University of Oslo, Norway

The African representatives of *Lychnis* (Caryophyllaceae) comprise five species and two non-autonomous subspecies which are distributed in the Ethiopian highlands and in the mountains of East Africa (Kenya, Tanzania, and Uganda), Central Africa (Rwanda, Burundi, and the Democratic Republic of Congo), and West Africa (Cameroon and Nigeria). A recent biogeographical study based on chloroplast (*rps16* intron and *psbE-petL*) and nuclear (ITS and the low copy-*RPB2*) DNA sequences showed that the ancestor of the African *Lychnis* immigrated from Eurasia to the Ethiopian highlands and diverged into different lineages. However, the absolute time of colonization and divergence in the African mountains is still not known. Here we use a fossil-calibrated relaxed molecular clock to model sequence evolution of the cpDNA regions *rps16* and *psbE-petL*. The chloroplast region *matK* and one fossil calibration point will be used to infer the age of the African *Lychnis*. More specifically, we ask: (1) when did the African *Lychnis* diverge from Eurasian *Lychnis*? And (2) when and where did subsequent divergence within the African *Lychnis* lineage occur?

**Poster 8: Promiscuity and genomic diversity**

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Extra pair fertilization (EPF) is related to high levels of genetic diversity in birds (Petrie et al. 1998) and produces more heterozygous offspring (Foerster et al. 2003; Stapleton et al. 2007; Fossøy et al. 2008). We have examined whether EPF affects genetic diversity differently on sex chromosomes and autosomal markers.

Because the genes on the Z chromosome has a smaller effective population size compared to the autosomal genes, specifically  $\frac{3}{4}$ , the expected ratio, or null hypothesis, between Z chromosome- and autosome SNPs is  $Z/A = \frac{3}{4}$  for all species. However, if EPF has a larger effect on the occurrence of SNPs on either chromosome, the ratio  $Z/A$  will exhibit a positive or negative correlation to EPF.

We quantified the levels of genetic diversity (single nucleotide polymorphisms (SNP)) on 20 passerine species, and performed a comparative analysis (controlling for phylogeny). 10 introns, 5 on the Z-chromosome and 5 on autosomes were sequenced (totalling ~ 5 Kbp, and 9 males per species). The tissue samples were collected from specific populations where the EPY rate was known (there are sometimes differences in the amounts of EPF between populations of the same species).

Our preliminary analysis revealed no differential effects of EPY on sex chromosomes and autosomal chromosomes (i.e. no correlation). The autosomal markers showed a positive correlation to EPY on their own, thus confirming the findings of Petrie et al. (1998). There was however no significant effect of EPY on the Z-linked markers.

**Poster 9: Genetic differentiation and reproductive isolation in the redstart, *Phoenicurus phoenicurus***

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Oddmund Kleven, Jiri Porkert, Arild Johnsen  
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Sequencing of the mitochondrial COI and 16S regions in the common redstart (*Phoenicurus phoenicurus*) has revealed two very different haplotypes, which cluster into two distinct clades. The magnitude of the intraspecific divergence suggests that these lineages separated more than 2 million years ago, yet both haplotypes currently co-exist and interbreed in Europe. In order to determine if the two haplotypes can be attributed to different geographical origins, we sequenced a number of individuals across a wide geographic area. Additionally, to increase our sample size, we sequenced a number of museum specimens using newly developed primers that amplify a short, variable region (approximately 100bp) of the COI gene. These primers are particularly suited for use in museum specimens because they allow easy haplotype determination of old degraded DNA. In the future, several nuclear introns (both sex-linked and autosomal) will also be sequenced in order to assess whether mtDNA and nuclear DNA show similar haplotype structure. With the genetic mtDNA structure resolved, we investigated both sperm morphometry and assortative mating as likely mechanisms maintaining the divergence. We tested for assortative mating in 60 pairs of redstarts from Norway and Czech Republic, but found no support for assortative mating as a general mechanism in this species. However, when we examined pairs ( $n=36$ ) from a single Norwegian population (Trysil), we found a trend for assortative mating (Fischer exact test,  $P = 0.18$ ). Sperm morphometry was measured for 77 males from populations across Norway and the Czech Republic; sperm morphometry encompasses several sperm size components (e.g. head and midpiece length, etc). All sperm samples were measured before the haplotype was determined. As before, we found no support for sperm morphometry as a mechanism of reproductive isolation. However, we did find a trend towards increased midpiece length for haplotype 1 (T-test  $t_{73} = 1.7$ ,  $p = 0.099$ ). Additionally, in a comparison of head size between the different populations, we found that birds from Norway (Valdres) had significantly shorter heads relative to the two remaining Norwegian populations and the population from the Czech Republic. And that one population, Trysil, also had significantly shorter heads than the population from Czech Republic.

**Poster 10: Searching for the roots of the arctic flora: biogeographic connections to the Himalayas**

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Two main hypotheses have been suggested for the origin of the arctic flora: (i) *in situ* persistence/adaptation of a local Tertiary forest element, consisting of species which occurred in open patches in the forest, and/or (ii) immigration from southern alpine regions, consisting of species preadapted to cold and open habitats. Hultén hypothesized that many contemporary arctic plant species descend from alpine ancestors, which occurred further south in Asia and migrated northwards to Beringia in the late Tertiary or early Quaternary, from where they radiated east- and westwards and reached circumpolar distributions before the onset of the Pleistocene glaciations.

To test these hypotheses we will conduct a comparative phylogenetic and phylogeographic analysis of several plant groups comprising both arctic species and species occurring further south in Asia, with particular emphasis on the Hengduan Mountains in the Himalayas (e.g. the genera *Cassiope*, *Diapensia*,

and *Braya*). The Hengduan Mountains, which are situated in the southeast Qinghai-Tibetan Plateau, constitute the major part of the so-called south-central biodiversity hotspot in the Himalayas. This region has been inferred as an important refugium throughout the Pleistocene climatic cycles, as well as a centre of plant diversification during the uplift of the Qinghai-Tibetan Plateau and the Pleistocene interglacials. It may therefore have served a source for many arctic plant species.

By using state-of-the-art molecular phylogenetic/phylogeographic methods and dating tools, we will (i) investigate the connection and the direction of migration between the Hengduan Mountains and the Arctic (which not necessarily was from the south to the north), and (ii) estimate the timing of migrations to distinguish between the hypotheses of *in situ* survival of old Tertiary elements in the Arctic versus late Tertiary/early Quaternary (or even later) origin of the arctic lineages.

We currently search for appropriate low-copy nuclear DNA genes, such as RNA polymerase genes. Field sampling in the Hengduan Mountains is carried out in 2010 and 2011.

#### Poster 11: **Tough, tiny and terrific Caryophyllaceae, their phylogeny and biogeography**

Anneleen Kool, Mats Thulin

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Caryophyllaceae is a nearly cosmopolitan family in Caryophyllales and consists of about 86 genera and 2200 species. The Paronychioideae subfamily often includes those members of Caryophyllaceae that have stipules and consists of approximately 33 genera and 500 species. Its circumscription has been notoriously difficult and part of Paronychioideae is sometimes treated as a separate family, Illecebraceae. Currently what used to be Paronychioideae is considered a basal paraphyletic grade within Caryophyllaceae. The three biggest paronychioid genera are *Paronychia* (approx. 110 species), *Herniaria* (approx. 45 species) and *Polycarpaea* (approx. 50 species). Paronychioid Caryophyllaceae is often well adapted to drought or occur in mountainous regions. In addition the majority of the species in this group are narrow endemics that occur only in very limited areas.

A molecular phylogenetic study based on four plastid markers (*rps16*, *ndhF*, *trnL-F* and *rbcL*) as well as ITS obtained from more than 150 paronychioid taxa was made. It shows that *Paronychia* currently consists of two distantly related groups. *Paronychia* s.s. includes a large group of poorly delimited South American endemics that are sister to the North American *Paronychia* plus *P. canariensis* (a Macaronesian endemic). The African *Paronychia* is sister to the New World taxa and sister to all of these are the *Paronychia* species from Europe. *Polycarpaea* consists of at least three different groups; one endemic to the Canary Islands (including the type species), one with its centre of diversity in the Horn of Africa and one including the widespread *P. corymbosa* and its relatives as well as the endemics of Australia. This last clade has evolved C4-photosynthesis. The group closest related to the Horn of Africa *Polycarpaea* consists of two species of *Polycarpon* that occur in South America. *Herniaria* is monophyletic but will most probably come to include the remaining *Paronychia*, which includes a large group of Turkish endemics.



**Poster 12: Position and intratribal relationships in the tribe Danaideae (Rubiaceae)**Åsa Krüger<sup>1,2</sup>, Sylvain G. Razafimandimbison<sup>2</sup>, Birgitta Bremer<sup>2</sup><sup>1</sup>Department of Botany, Stockholm University, Sweden<sup>2</sup>Bergius Foundation and Royal Swedish Academy of Sciences, Stockholm, Sweden

The Madagascar-centered tribe Danaideae of the subfamily Rubioideae (Rubiaceae) consists of approximately 55 species distributed in three genera; the lianescent *Danais* and the arborescent *Schismatoclada* and *Payera*. So far the main part of the conducted research on the tribe has been based on morphological characters but no potential synapomorphy has been mentioned. The tribe is considered to be monophyletic based on molecular data, although *Payera* has never before been included. However, the phylogenetic placement of Danaideae has been debated. This study focuses entirely on Danaideae, including all three genera. Nuclear and chloroplast data has been analyzed by Bayesian and parsimony approaches to reconstruct a robust phylogeny of the tribe. The resulting phylogeny is used to address questions regarding both position of the tribe and also the intratribal relationships. Of the three genera only *Danais* show good support to be a monophyletic genus according to present classification.

**Poster 13: Molecular insight in the systematics of Chaetodermatidae (Caudofoveata, Mollusca)**

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The worm-shaped aplacophoran molluscs (Caudofoveata and Solenogastres) are generally considered basal among Mollusca but their relative position other molluscs is debated. It is paramount to unravel these relationships in order to understand the evolution of the phylum Mollusca. The main objective of this project is to construct a solid hypothesis for the phylogeny of Caudofoveata (=Chaetodermomorpha). Thereby, both the placement of the taxon relative to other molluscs and the phylogenetic relationships within Caudofoveata are investigated.

The systematics of the largest family within the Caudofoveates, the Chaetodermatidae, is still a matter of discussion, and the relationships within this family are currently unresolved. The relationships have never been tested in a molecular phylogeny. Presented here are the results of the first molecular analysis of the family Chaetodermatidae, providing new insight to the systematics of this family. The molecular data is not supporting the current hypotheses based on morphological characters, but suggesting that different characters are needed to resolve the phylogenetic relationships within this family.

**Poster 14: Phylogeny of parasitic barnacles (Rhizocephala)**

Christoph Noever

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Rhizocephalans are a crustaceans that are closely related to the sessile barnacles (Thoracica) and together with the burrowing barnacles (Acrothoracica) forming the Cirripedia. It is an exclusively parasitic taxon, infesting various other crustaceans. Due to their lifestyle they have evolved a highly modified morphology compared to other crustaceans, lacking almost all arthropod features like segmentation, a centralized nervous system, any alimentary tract or appendages. Their adult morphology consists of a root-like structure inside their host by which they absorb nutrients and a sac like external part containing the reproductive organs. The affiliation to the Cirripedia could be early recognized by a special larval form which they share with the Thoracica and Acrothoracica, the cypris larva. Due to the only very few morphological features of the adult parasites, the internal phylogeny of the Rhizocephala is still ambiguous and molecular methods are promising to solve evolutionary questions of this highly diverged group of crustaceans.

In the present study, various ribosomal and mitochondrial genes (16S, 18S, 28S, COI) were used to construct a comprehensive phylogeny of parasitic barnacles, giving new insights to the evolution of these highly specialized parasites and the co-evolutionary relationships with their hosts.

**Poster 15: What's on your boots? An investigation into the role humans play in protist dispersal**

Allison L. Perrigo, Maria Romeralo, Sandra L. Baldauf

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The biogeography of protists is an emerging topic that has been strongly debated over the last decades. Dictyostelids, or cellular slime molds, are a ubiquitous group of protists that spend most of their life cycle as single-cell amoebae feeding on bacteria in the soil. When starved, the amoebae aggregate to form a multi-cellular fruiting body with spores in a mass at the terminus that are later dispersed through passive attachment to soil-arthropods, small vertebrates and birds. There is no evidence for wind dispersal in this group and little is known about the mechanisms that drive their worldwide distribution. Here we consider the potential role humans play in dictyostelid dispersal. To do this, soil samples were collected from the underside of boots from scientists after their summer field seasons in various localities around the world. Samples were analyzed using a soil dilution plating technique. The samples yielded dictyostelid spores and amoebae capable of producing viable fruiting bodies. This demonstrates that humans could potentially be responsible for dispersing protists over long distances, a finding that corroborates earlier studies performed on testate amoeba. These findings have implications regarding how naturally occurring protistan faunas are surveyed and understood. As such, these issues should be taken into account when considering the biogeography and natural distribution of protists.

Poster 16: **Molecular Phylogeny and micromorphology of *Acanthophyllum* C. A. Mey (Caryophyllaceae)**

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*Acanthophyllum* C. A. Mey. (Caryophyllaceae, Caryophylloideae, Caryophylleae) with some 60 species worldwide, is a mainly Irano-Turanian genus with its center of diversification in NE Iran and adjacent areas in Turkmenistan and Afghanistan. Comprising one of the steppe and meadow vegetation elements of the country, the species of the genus are considered as one of the important members of Caryophyllaceae in Iran. Delimitation of *Acanthophyllum* has been subjected to some controversies and modifications. The closest genera to it are: *Allochrysa*, *Diaphanoptera*, *Gypsophila*, *Ochtonophila* and *Saponaria*. However, *Acanthophyllum* is among the poorly studied genera of the tribe from molecular aspects. Furthermore, the monophyly of the genus has not yet been investigated based on molecular markers. Aims of present study are summarized below: Molecular systematic study using selected chloroplast and nuclear DNA markers. Molecular phylogenetic study including representatives of all sections of *Acanthophyllum*, beside the selected species from its allied genera would help to evaluate the infrageneric classifications within *Acanthophyllum* itself on one hand, and to investigate its relationship with allied genera on the other hand.

Stem and leaf anatomical studies on *Acanthophyllum* species. Cross sections from middle part of current year mature leaves and stems will be subjected to comprehensive light microscopic studies to evaluate systematic application of anatomical characters within *Acanthophyllum*. Seed coat micromorphological studies of *Acanthophyllum* using SEM. Seed coat features have been used in taxonomy of several genera of Caryophyllaceae at different taxonomic levels. It seems that seed coat features could provide valuable source of data in evaluating and revision of infrageneric taxa within *Acanthophyllum*. Review of subgeneric classification of *Acanthophyllum* based on all sources of data obtained, as well revising the borders between it and its allies are the final aims of the present project.

Poster 17: **Polymastiidae (Porifera: Demospongiae: Hadromerida) with ornamented exotyles: morphology, taxonomy, description of new species**

Alexander Plotkin, Elena Gerasimova, Hans Tore Rapp

Department of Biology / Centre for Geobiology, University of Bergen, Norway

The world-wide distributed sponge family Polymastiidae is characterized by extremely simple and uniform spicules, the smooth monactines. However, several polymastiid species have evolved surface protective monactines with peculiar ornamented distal extremities, the exotyles. Most of these species were allocated to *Sphaerotylus*, *Proteleia* and *Tylexocladus*, and the shape of the exotyle extremities was regarded as the main character discriminating these three genera. We have revised all species with ornamented exotyles based on the type and not type material, and found that they should be re-arranged if taking account of other characters. Morphological evidence clearly divides the studied taxonomic space into two distinct groups of species, *capitatus*-group and *borealis*-group. The *capitatus*-group is characterized by the velvet surface, the principal monactines and exotyles shorter than 2 mm, and the regular spherical knobs on the extremities of the exotyles. It is composed by at least four *Sphaerotylus* spp. *S. sceptrum* also comes closer to this group but differs by the heterogeneity of its cortex and the reduction of the distal knobs. *Proteleia sollasi*, *Polymastia tapetum* and *Polymastia umbraculum* share most of features with the *capitatus*-group but are distinguished by the umbrelliform extremities of the exotyles. Additionally *P. sollasi* differs from others by the supplementary cortical palisade. The *borealis*-group is characterized by a shaggy surface, the principal monactines exceeding 2 mm in length, and the

exotyles exceeding 5 mm and bearing irregular distal knobs varying from spherical to umbrelliform. This group includes at least two species of *Sphaerotylus*. *Proteleia burtoni* and *Tylexocladus hispidus* also come close to these, although the former is distinguished by the grapnel-like exotyles and the latter differs by the denticulate exotyles. We have also found striking similarities between the *borealis*-group and some polymastiids with non-ornamented exotyles, *Suberitechinus hispidus* and *Polymastia invaginata*. Finally, we have discovered a new species of *Sphaerotylus* from Western Greenland, which combines the features of both the *borealis*- and *capitatus*-groups. Our study has made us suggest the polyphyly of *Sphaerotylus* and calls for a thorough phylogenetic analysis of all polymastiid taxa characterized by exotyles.

**Poster 18: Windfelled Norway spruce plantations: Regrowth and soil development following one generation of planted *Picea abies* forests**

Heidi Iren Saure

Department of Biology, University of Bergen, Norway

Densely planted *Picea abies* forests are criticised for giving low plant diversity and acidified soils. Little is known of the long term effects on plant diversity and soil conditions, following removal of the forests. Vegetation and soil conditions were investigated on 4 years old windfelled clear-cuts of first generation spruce plantations (40-60 years old). Similar investigations were carried out in the remnant spruce forests. The investigation was situated in Western Norway. Field- and ground vegetation on the clear-cuts was very different from understory vegetation in the spruce plantations. 216 species were registered on the windfelled sites and 50 percent of the species were newcomers. The increase was greatest within the plant groups of mosses, herbs and graminoids, whereas the number of liverworts was reduced. A constant shrub layer was developed, consisting of e.g. *Rubus idaeus* and *Betula pubescens*. The field-vegetation had reached a high cover, being dominated by e.g. *Avenella flexuosa*, *Deschampsia cespitosa*, *Anthoxanthum odoratum*, *Agrostis* species, *Carex* species, *Veronica officinalis* and small ferns. The good vegetation cover of the bottom layer was maintained after clearing, and was dominated by e.g. *Hylocomium splendens*, *Rhytidiadelphus loreus*, *R. triquetrus*, *Polytrichastrum formosum*, *Dicranum* species and *Thuidium tamariscinum*. Soil conditions were improved by a distinct increase in pH, nitrogen, and calcium in the humus layer, whereas the amounts of potassium decreased after removal of the tree layer. Classification (TWINSPAN) and ordination (PCA and RA) of the species display that there are distinct and site-dependent differences in the understory vegetation within both clear-cuts and spruce plantations. Ordinations show that improved light and temperature conditions after removal of the tree layer, disturbances from windthrow, forestry-machines-, and grazing animals, and the increase in nitrogen, pH and cations have been important for the good regeneration of vegetation. Partial RDA demonstrated that site-dependent factors not measured in field, decisively influenced regrowth. It is suggested that some of these factors may be soil seed banks, adjacent vegetation, the size of the windfelled clear-cuts and different utilisation history prior to planting. The understory vegetation in the spruce plantations is distinctly oceanic and relatively species-rich, and the forests were classified as small fern forests (Eu-Piceetum dryopteridetosum). Vegetation on the windfelled clear-cuts is associated with richer soil than vegetation in adjacent plantations. It is concluded that neither potential vegetation nor soil conditions are permanently depauperated after one generation of planted spruce forests at Sunnmøre, Western Norway.

**Poster 19: Gastrulation and germ layer specification in rotifers**

Sabrina Schiemann

Sars International Centre for Marine Molecular Biology, Bergen, Norway

The high level of metazoan biodiversity seen today has arisen through evolutionary processes. However, the exact relationships between the broad range of metazoan phyla and the events that led to the complexity of body plans are not widely known. The study of embryonic development is one of the major keys to understand the evolution of animal body plans.

Presently rotifers have been poorly investigated in this field of research. To shed light on rotifer development, my project focuses on the bdelloid species *Adineta vaga*. I use time-lapse (4D) microscopy to investigate the cell lineage within this species and document every cellular event during embryogenesis. Furthermore, I complement these studies with research at the molecular level by identifying conserved gene regulatory networks, which may be of great importance for organogenesis in rotifers.

Here, I present the cell lineage of *Adineta vaga* up to the 400-cell stage and compare these results with that of other closely related taxa such as spiralian and lophophorates. Despite evolutionary divergences, I found strong similarities between the rotifer cell lineage and that of other spiralian.

**Poster 20: Intraspecific phylogeny of *Silene acaulis* (L.) Jacq. (Caryophyllaceae)**

Marian Schubert

National Centre for Biosystematics, Natural History Museum, University of Oslo, Norway

The arctic-alpine *Silene acaulis* is a wide spread species occurring in the holarctic belt, with a distribution reaching southern USA in North America and Mediterranean mountain ranges in Europe. Recently even a population in East Anatolia, Turkey was described. *S. acaulis* is obviously a heterogeneous species with at least 7 described subspecies (The International Plant Names Index). At least three of them seem to be synonymous to each other. The description of these subspecies is mainly based on morphological data, mostly regarding continuous characters. In our study we would like to test the genetic support for at least one (perhaps more) of the described subspecies, appearing to be the most accepted one - *S. acaulis* subsp. *subacaulescens* (F.N. Williams) Hultén. This subspecies occurs not in arctic habitats, but populates mainly alpine habitats extending from Alaska till New Mexico and Arizona.

As molecular markers we use a group of nuclear ribosomal (nr)DNA genes encoding holozymes of the RNA polymerase (RNAP) family. We combine 2 to 7 introns of genes encoding the second largest subunit of the RNA polymerase. So far we have genetic material of 30 individuals originating from habitats covering nearly the whole distribution of *S. acaulis*. Beside the intraspecific phylogeny of *S. acaulis*, we are also trying to elucidate possible geographical patterns hidden in our data, e.g. is there a correlation of geographical origin with genetic similarity? The analyses will be carried out by a combination of phylogenetic and phylogeographical inference, such as maximum likelihood estimations and bayesian statistics.



**Poster 21: Cryptic species in Basidiomycota: Patterns & processes**Kristian Skaven Seierstad<sup>1</sup>, Karl-Henrik Larsson<sup>1</sup>, Håvard Kauserud<sup>2</sup><sup>1</sup> National Centre for Biosystematics, Natural History Museum, University of Oslo, Norway<sup>2</sup> Microbial Evolution Research Group, Department of Biology, University of Oslo, Norway

Despite the sparse amount of phylogeographic studies conducted among fungi, the results of these show that fungal morphospecies often consist of several cryptic species or independent evolutionary lineages that only can be differentiated based on molecular data, habitat or ecology. The evolutionary lineages often occur in sympatry, but intrinsic mechanisms can restrain gene flow among them and their adaption to different hosts and substrates can differ. My PhD thesis will focus on the patterns and processes that leads to such differentiating in some designated saprotrophic and symbiotic species complexes of the Basidiomycota with regard to substrate/host affinity. Starting by describing the biogeographic pattern of a morphospecies on a broad scale by using Sanger sequencing, then try to point out which evolutionary processes that lead to the patterns observed by extending the amount of genetic markers and use more species specific markers (e.g. microsatellites). It is further planned to use ecological niche modeling to resolve which ecological factors (e.g. temperature, precipitation) that limit distribution of fungal species.

**Poster 22: The amazing world of microsculpture - cuticular structures as an informative source for the taxonomy of Entiinae (Hymenoptera: Eulophidae)**Josef Straka  
Lund University, Sweden

The Entiinae (formerly known as Euderinae) are a relatively small subfamily of Eulophidae (Hymenoptera parasitica: Chalcidoidea) with 17 valid genera worldwide, including several parasitoids of major agricultural pests. Our knowledge of this subfamily is still fragmentary. The number of critically examined morphological characters has hitherto been relatively low: Most descriptions of species and genera have mainly focused on setal line patterns and pigmentation of the wings, the shape of the antennomeres in males, and the length of the terminal metasomal tergite in females. Details in microsculpture of the exoskeleton were often too small to be seen in light microscopes and consequently got only marginal attention in earlier publications about this subfamily. Scanning electron microscopy is a powerful modern tool for the discovery of details in microsculpture of the exoskeleton: These can be used to delimit genera and species groups by morphological examination.

**Poster 23: Phylogeny, historical biogeography and phylogeography of *Selaginella***

Stina Weststrand, Petra Korall

Department of Systematic Biology, Evolutionary Biology Centre, Uppsala University, Sweden

Studying biogeography in a broad range of lineages is needed to pose general biogeographical hypotheses. However, plant biogeography studies have so far mainly focused on seed plants, and few have targeted plants that are dispersed by spores. In my PhD project I use the lycophyte family Selaginellaceae (spikemosses) as the study organism. The family has an origin in the Late Carboniferous, and it comprises the single genus *Selaginella* with approximately 700 species. The main species distribution is throughout subtropical and tropical areas, even though some ten percent of the species diversity is found in temperate regions. In contrast to most other spore dispersed plants, *Selaginella* is heterosporous meaning that two kinds of spores are produced, mega- and microspores. The spores give rise to a female and male gametophyte, respectively, implying that intragametophytic selfing is not possible. How does this affect the plants' ability to disperse?

The main focus of my studies lies on the occurrence of long-distance dispersal on different temporal, spatial, and phylogenetic scales in *Selaginella*. The first part of the project addresses the question if the disjunct distributions seen in *Selaginella* are due to long-distance dispersal or historical vicariance events. To start with, I will focus on historical biogeography in the family Selaginellaceae as a whole, and evaluate possible vicariance scenarios as a response to the breakup of Gondwana. Subsequently, studies on a more regional scale will be conducted by investigating biogeographical patterns in a well-supported group of taxa in Southeast Asia/Australasia. This is a region with extensive land mass changes due to, among other events, the collision between India and Asia in the Eocene, and sea level fluctuations. The second part of the project will be conducted at the intraspecific level. I will test if any phylogeographical patterns are discernable in *Selaginella*, and the main study object will be the single Swedish species, *Selaginella selaginoides*. Overall my PhD project aims to give us new insights into which impact long-distance dispersal has in shaping the biogeography of spore dispersed plants.

**Poster 24: Phylogeny and biogeography of African *Swertia* L. (Gentianaceae)  
inferred from chloroplast DNA sequences**

Tigist Wondimu<sup>1,2</sup>, Christian Brochmann<sup>2</sup>, Magnus Popp<sup>2</sup>, Mulugeta Kebede<sup>3</sup>,  
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*Swertia* is a large genus in the *Gentianella* lineage (subtribe *Swertiinae*) and includes more than 130 species. It is a cosmopolitan genus originated in the Himalayas (Yuan and Küpfer, 1993). A phylogenetic study by Chassot, *et al.*, 2001, including four species of African *Swertia* has shown the existence of two distantly related clades, suggesting at least two migration events from Asia to Africa. However, only 17% of the species occurring in Africa were included in the phylogenetic study. Hence, more data is required to infer the phylogeny of the genus. The present study aims at inferring the phylogeny and biogeography of African *Swertia* based on molecular data. Sixteen species were collected in the field in 12 mountain systems of East Africa, Ethiopia and Madagascar. Two non-coding cpDNA regions, *trnL-F* (both the intron and the intergenic spacer) and *trnS-fm* intergenic spacer, were sequenced. Phylogenetic trees were constructed by maximum likelihood and non-parametric bootstrap analysis. The result of this analysis confirmed that *Swertia* is a paraphyletic genus and introduce in to Africa twice.

**Poster 25: An evolutionary study of Fuscideaceae (Umbilicariales, Pezizomycotina, Ascomyceta)**

Martina Zahradnikova  
Natural History Collections, Bergen Museum, University of Bergen, Norway

This PhD project concentrates on understanding the evolution of the lichen family Fuscideaceae. It provides an overview of the systematic placement in Ascomycota, and clarifies the relationships of its anticipated genera. The lichen family Fuscideaceae with the two seemingly unrelated crustose lichen genera *Fuscidea* V.Wirth & Vězda, and *Maronea* A.Massal was described by Hafellner (1984) and assigned to the suborder Teloschistinea, Lecanorales, based on the *Teloschistes*-type asci. The contemporary placement of the Fuscideaceae is as a group *incertae sedis* within the Lecanoromycetidae, Lecanoromycetes, Pezizomycotina (Hofstetter *et al.* 2007; Lumbsch *et al.* 2007). It currently accommodates these genera: *Fuscidea*, *Maronea*, *Ropalospora*, *Hueidea*, *Lettauia*, *Orphniospora*, and *Sarrameana* according to Eriksson (2006). Lumbsch *et al.* (2007) excluded *Sarrameana* from the family sensu Eriksson (2006). Bylin *et al.* (2007) showed that *Fuscidea* and *Maronea* formed a monophyletic group defined as the Fuscideaceae. The genus *Ropalospora* was tentatively placed in the Umbilicariales as a sister group of the Ophioparmaceae. This genus is not very closely related to *Fuscidea* and *Maronea* and should be excluded from the Fuscideaceae. Investigation of phylogenetic relationships of taxa within *Fuscidea* will elucidate which species should be assigned to the genus, and which should not. Moreover, it will give insight concerning the circumscription of *Fuscidea*, and the morphological characters that will characterize this genus. It is also important to clarify taxonomic problems at species and subspecific levels, e.g., for *Fuscidea cyathoides* (with 3 infraspecific taxa), *Fuscidea pusilla*/*F. lightfootii* (possibly conspecific), perhaps also *Ropalospora viridis*/*R. chlorantha* (possibly conspecific). Besides a few corticolous species of the Fuscideaceae, almost all species are exclusively saxicolous. One of several exceptions is *Fuscidea cyathoides* s.l. which occurs both on rock and bark. How did substrate-specificity in *Fuscidea* develop? An approach to answer this could be to study the photobionts. For example, do saxicolous and corticolous specimens have different photobionts? The most recent methods will be used for reconstructing the phylogenetic trees and answering all questions. Of course, the commonly used sequences of the mitochondrial small ribosomal DNA (mtSSU), and the nuclear large and small ribosomal DNA (nuLSU and nuSSU) will also be used. Sequences will be analysed separately and in combination. Usage of statistic methods will be necessary for overcoming conflicts between datasets from different genes. This will be an important part of analytical procedures. Morphologic and anatomic investigations can be necessary to correlate the phylogenetic tree with morphological features.

**Poster 26: Phylogeny of the family Aglajidae (Gastropoda: Cephalaspidea) and systematic revision of the genus *Chelidonura*: preliminary results**

Andrea Zamora, Manuel Malaquias  
Bergen Museum, Natural History Collections, University of Bergen, Norway

Aglajidae is a family of marine opisthobranchs occurring worldwide in tropical and temperate habitats, inhabiting coral reefs, rocky shores, and soft bottoms. Systematic work has been based mostly on the description of the external morphology whereas data on the anatomy and internal shells remain poorly known for most species. Description of species based on juvenile forms and chromatic variations have been common and this lead to a confusing taxonomy with high numbers of synonym names. The genus *Chelidonura* is the most diverse of the family, with over fifteen species worldwide. A multilocus coalescent Bayesian framework (based on mitochondrial COI, 12SrRNA, and 16SrRNA genes and nuclear 28SrRNA and Histone-3 genes) will be used to infer species trees. This will be combined with morphological, and anatomical information in order to discriminate between species and generate species-

level phylogenies to hypothesize on the origin, diversification patterns, and biogeography of the Aglajidae. Here, we present a preliminary molecular phylogeny obtained from COI sequence data largely gathered from Genbank. Characters of the external morphology and new anatomical data of *Chelidonura* species are discussed and a summary on the present knowledge of Aglajidae systematics is given. This project is funded through a doctoral grant to the first author by the Consejo Nacional de Ciencia y Tecnología (CONACYT- México), fellowship BAZS/188890/2010.

**Poster 27: Climate change, genetic diversity and ecological resilience – studies in the Baltic Sea littoral**

Jenny Zie

Department of Systems Ecology, Stockholm University, Sweden

The potential consequences of global warming on the biota in aquatic ecosystems represent one major question in contemporary ecological research. Observed and predicted future increases in global surface temperature (IPCC, 2007) make it crucial to know how temperature affects ecosystem processes (Raich et al. 2006) and community structure (Schiel et al., 2004). Global warming might reduce compositional stability and increase temporal species turnover by causing future species extinctions and diversity loss (Millenium Ecosystem Assessment, 2005), since it is uncertain whether species adaptation can keep up with the high rates of ecosystems change. On the other hand, more diverse communities are expected to show faster recovery due to higher response diversity (Elmqvist et al., 2003), as diversity might alter the response of a community to warming and provide an insurance against changing conditions. The link between global change and biodiversity is therefore important from two perspectives: how does global change drive diversity and how does diversity affect ecosystem responses to global change. The biota in an ecosystem is made up by separate species or functional groups, and the viability of the different populations depends on its genetic diversity. Low genetic diversity may be the result of local adaptation and desired in that particular environment, but it also makes the population more susceptible towards environmental changes. It has been shown that populations of a wide range of species in the Baltic Sea have relatively low genetic diversity (Johannesson & André, 2006), which makes the ecosystem very vulnerable to climate changes. An alarming fact considering that the annual average water temperature in the Baltic Sea has already increased by 1.4°C during the last 100 years (MacKenzie & Schiedek, 2007). It is therefore essential to study how warming affects populations of different species (through studying their genetic diversity) and ecosystem functioning. In this project, specimens will be collected from the thermal flumes of a Swedish nuclear power plant, which temporal flume comprises the entire range of future temperature predictions for the next century (IPCC, 2007). This has already been done during the 1980s, making it possible to compare the genetic diversity of past populations, before the increased water temperature, with the genetic diversity of contemporary populations. I plan to 1) Examine the genetic diversity within selected species belonging to different functional groups, in samples collected 1982-2012. Has the genetic diversity changed with time? Is there a difference in the genetic diversity between warm- and coldwater populations? 2) Collect detailed data on the reproductional traits and life cycles of selected species, i.e. data on diatom life cycles, seasonal occurrence of algal gametophytes and sporophytes, algal release of zoospores, seasonal occurrence of snail eggs and developmental stages of insect larvae. 3) If possible, subject selected species to a temperature treatment in an experimental set up. Thereafter investigate if there is a connection between survival and the degree of genetic diversity.

## Participants

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**Maja Adamska**, Sars International Centre for Marine Molecular Biology, Bergen (*talk 1 Feb*)

**Inger Greve Alsos**, Tromsø museum, Universitetet i Tromsø (*ForBio*)

**Heidi Lie Andersen**, Bergen museum, Universitetet i Bergen

**Alyssa Anderson**, NTNU Vitenskapsmuseet, Trondheim (*poster 2*)

**Sandra L. Baldauf**, Evolutionsbiologiskt centrum, Uppsala universitet

**Annika Bengtson**, Botaniska institutionen, Stockholms universitet (*poster 3*)

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**Christian Brochmann**, Naturhistorisk museum, Universitetet i Oslo (*talk 1 Feb, ForBio*)

**Geir Dahle**, Havforskningsinstituttet, Bergen (*talk 1 Feb*)

**Thomas Dahlgren**, Uni Miljø, Bergen

**Maria Degerlund**, Institutt for arktisk og marin biologi, Universitetet i Tromsø (*talk 2 Feb*)

**Torbjørn Ekrem**, NTNU Vitenskapsmuseet, Trondheim (*talk 1 Feb*)

**Sofia Fortunato**, Sars International Centre for Marine Molecular Biology, Bergen (*poster 5*)

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**Abel Gizaw**, Naturhistorisk museum, Universitetet i Oslo (*poster 7*)

**Ian Gjertz**, Forskningsrådet, Oslo (*talk 1 Feb*)

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**Siv Huseby**, Institutt for arktisk og marin biologi, Universitetet i Tromsø (*talk 2 Feb*)

**Ronald A. Jenner**, Natural History Museum, London (*talk 1 Feb*)

**Arild Johnsen**, Naturhistorisk museum, Universitetet i Oslo

**Anna Karlsson**, ArtDatabanken, Stockholm (*talk 1 Feb*)

**Lawrence Kirkendall**, Institutt for biologi, Universitetet i Bergen

**Anneleen Kool**, Evolutionsbiologiskt centrum, Uppsala universitet (*poster 11*)

**Åsa Krüger**, Botaniska institutionen, Stockholms universitet (*poster 12*)

**Magni Olsen Kyrkjeide**, NTNU Vitenskapsmuseet, Trondheim (*talk 2 Feb*)

**Karl-Henrik Larsson**, Naturhistorisk museum, Universitetet i Oslo

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**Manuel Malaquias**, Bergen museum, Universitetet i Bergen  
**Catherine Aloyce Masao**, Naturhistorisk museum, Universitetet i Oslo (*talk 2 Feb*)  
**Kenneth Meland**, Institutt for biologi, Universitetet i Bergen  
**Nina Therese Mikkelsen**, Bergen museum, Universitetet i Bergen (*poster 13*)  
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**Bengt Oxelman**, Institutionen för växt- och miljövetenskaper, Göteborgs universitet (*talk 1 Feb*)  
**Allison L. Perrigo**, Evolutionsbiologiskt centrum, Uppsala universitet (*poster 15*)  
**Atefeh Pirani Osguei**, Institutionen för växt- och miljövetenskaper, Göteborgs universitet/University of Tehran (*poster 16*)  
**Alexander Plotkin**, Institutt for biologi, Universitetet i Bergen (*poster 17*)  
**Hans Tore Rapp**, Institutt for biologi/Senter for geobiologi, Universitetet i Bergen  
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**Per Salvesen**, Bergen museum, Universitetet i Bergen  
**Ingrid Salvesen**, Artsdatabanken, Trondheim (*talk 1 Feb*)  
**Heidi Iren Saure**, Institutt for biologi, Universitetet i Bergen (*poster 18*)  
**Sabrina Schiemann**, Sars International Centre for Marine Molecular Biology, Bergen (*poster 19*)  
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**Marian Schubert**, Naturhistorisk museum, Universitetet i Oslo (*poster 20*)  
**Kristian Skaven Seierstad**, Naturhistorisk museum, Universitetet i Oslo (*poster 21*)  
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**Livia Wanntorp**, Naturhistoriska riksmuseet, Stockholm (*talk 1 Feb*)  
**Stina Weststrand**, Evolutionsbiologiskt centrum, Uppsala universitet (*poster 23*)  
**Rupert Wienerroither**, Havforskningsinstituttet Bergen  
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**Tigist Wondimu**, Naturhistorisk museum, Universitetet i Oslo (*poster 24*)  
**Martina Zahradnikova**, Bergen museum, Universitetet i Bergen (*poster 25*)  
**Andrea Zamora Silva**, Bergen museum, Universitetet i Bergen (*poster 26*)  
**Jenny Zie**, Systemekologiska institutionen, Stockholm universitet (*poster 27*)  
**Lise Øvreås**, Institutt for biologi, Universitetet i Bergen

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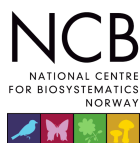
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