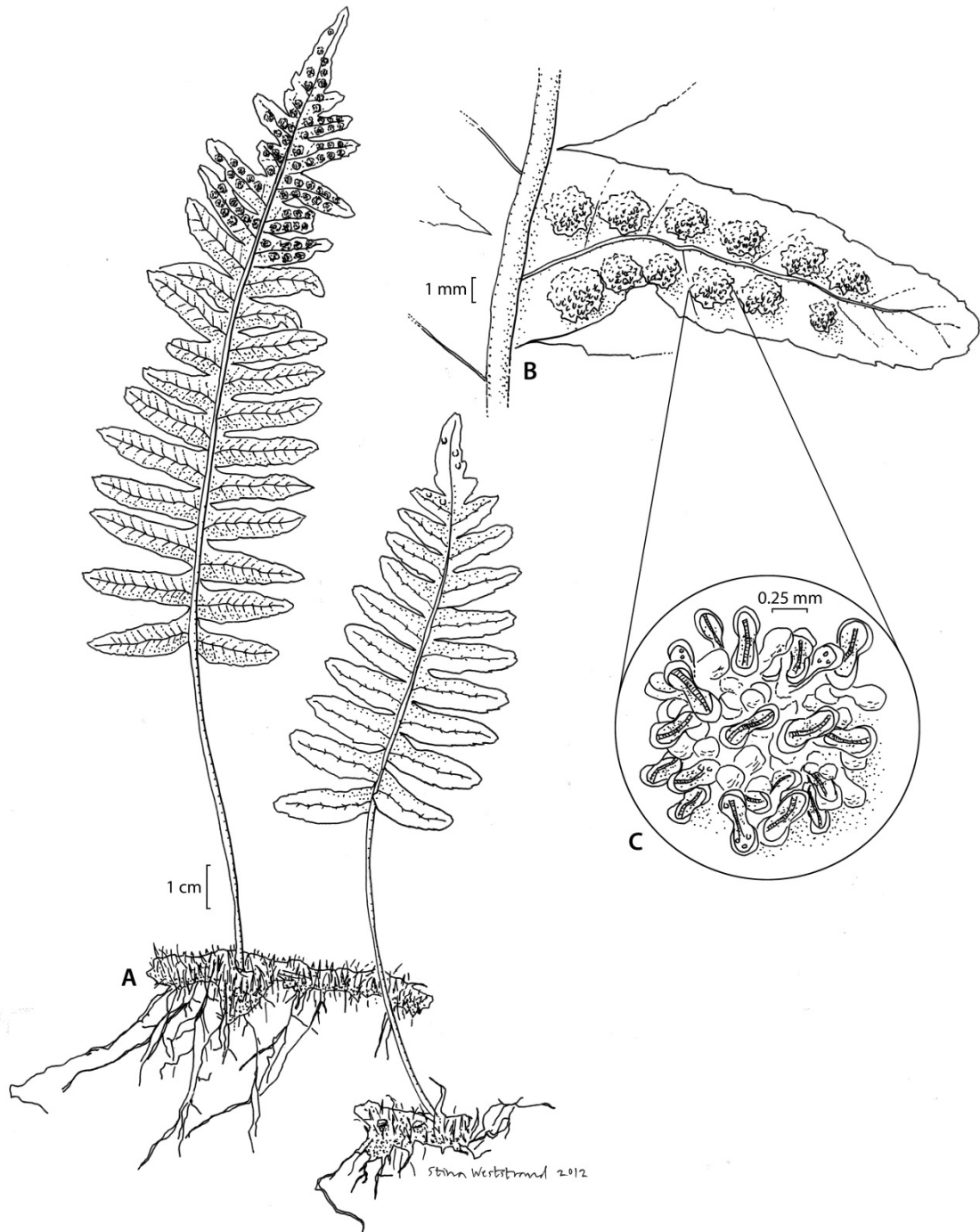


FORBIO ANNUAL MEETING

4 – 6 MARCH 2013



UiO  **Natural History Museum**
University of Oslo



NTNU – Trondheim
Norwegian University of
Science and Technology



**NORWEGIAN BIODIVERSITY
INFORMATION CENTRE**



**The Research Council
of Norway**

Illustration front page: *Polypodium vulgare* by Stina Weststrand. In the autumn of 2012 Stina participated in a ForBio & STIRS course in scientific illustration techniques given by Emma Hultén. Her project during the course was to draw an illustration of the fern *Polypodium vulgare*.

Welcome to Oslo!

Conference venue and accommodation: Quality Hotel 33, Østre Aker Vei 33, 0581 Oslo.

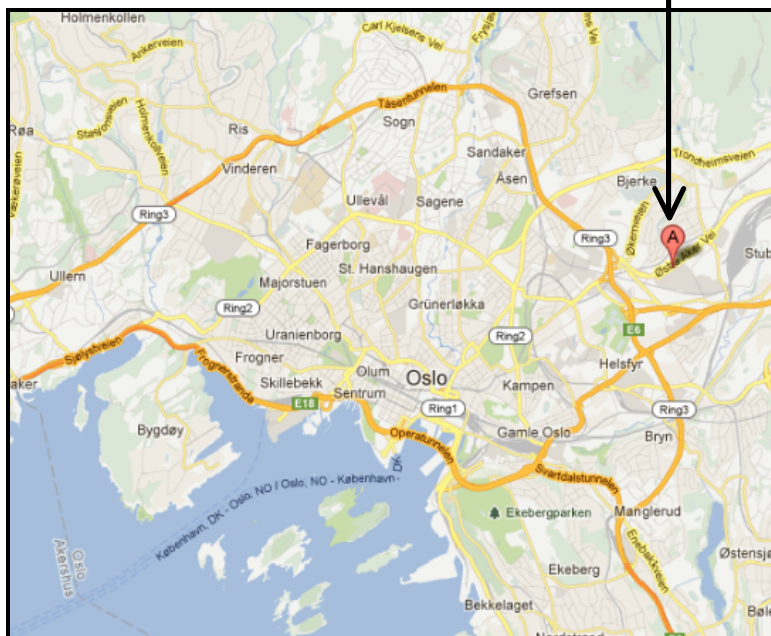
How to get there?

Bus from Gardermoen Airport every 10-20 minutes just outside the terminal:

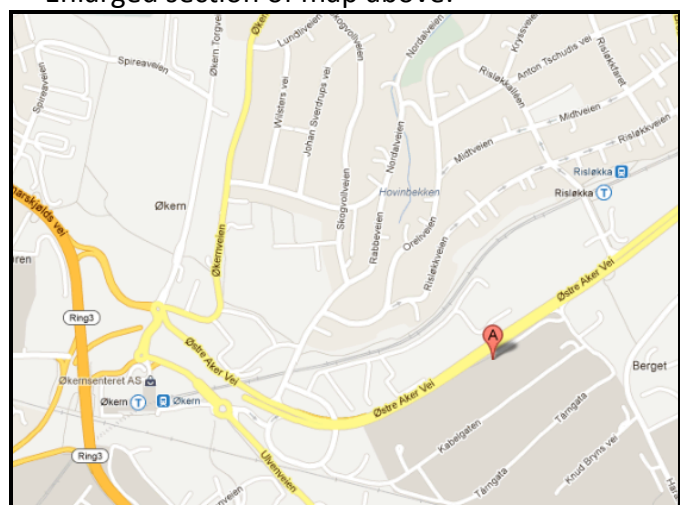
F3 Flybussekspressen Bekkestua: Quality Hotel 33 is a five minutes walk from the bus stop in Risløkkalléen.

From Oslo centre: Underground 5 (Vestli) going east to Risløkka. Quality Hotel 33 is a five minutes walk from Risløkka underground station.

Quality Hotel 33



Enlarged section of map above:



Program: ForBio Annual Meeting 2013, Oslo

MONDAY 4 MARCH

09:00 – 10:00 REGISTRATION AND COFFEE

Session 1:

10:00 – 10:15 **Welcome**

Magnus Popp, Natural History Museum, University of Oslo

10:15 – 11:00 **The evolution of communication systems in tiger moths (Lepidoptera: Erebidae: Arctiinae)**

Susan Weller, University of Minnesota

COFFEE

11:30 – 12:00 Presentations of posters (1 slide, 2 min each)

LUNCH

Session 2:

13:00 – 13:20 **The mysterious case of the golden-branched netted column: Unimaginable diversity of unimagined creatures in our Nordic soils**

Allison Perrigo, Uppsala University

13:20 – 13:40 **What have the spikemosses been up to during the last 350 million years?**

Stina Weststrand, Uppsala University

13:40 – 14:00 **A phylogenomic approach to understand the diversification of bark beetles and associated microbes**

Dario Pistone, University Museum of Bergen

COFFEE

Session 3:

14:30 – 15:00 **Chinese whispers... Identification literature and species distribution**

Malin Strand, Swedish Species Information Centre and Swedish University of Agricultural Sciences

15:00 – 15:20 **Investigating the origin of incongruence between gene trees of the mushroom-forming fungi**

Elisabet Sjökvist, Gothenburg University

15:20 – 15:40 **Sampling in scientific collections: Is good faith enough?**

Magni Olsen Kyrkjeeide, Museum of Natural History and Archaeology, Norwegian University of Science and Technology, Trondheim

16:00 – 18:00 POSTER SESSION AND COFFEE

19:30 MEET AND GREET including dinner (Quality Hotel 33, Oslo)

TUESDAY 5 MARCH

Session 1:

- 09:00 – 09:45 **Integrated methods for biodiversity research**
Sarah Bourlat, Gothenburg University
- 09:45 – 10:05 **Using DNA barcoding to evaluate bioinvasion risks associated with ballast water transport of zooplankton to the Arctic**
Christopher Ware, Tromsø University Museum
- 10:05 – 10:25 **Carnivorous sponges of the deep Atlantic: Investigating the emergence of a unique feeding strategy within phylum Porifera**
Jon Thomassen Hestetun, University of Bergen

COFFEE

Session 2:

- 11:00 – 11:20 **Phylogeny and biogeography of *Diapensia* (Diapensiaceae)**
Yan Hou, Natural History Museum, University of Oslo
- 11:20 – 11:40 **Evolution and biogeography of *Baccharis* (Asteraceae): A megadiverse neotropical genus**
Gustavo Heiden, Gothenburg University
- 11:40 – 12:00 **Cryptic diversity, delimitation and phylogeny of Nordic species of *Cognettia* (Clitellata: Enchytraeidae)**
Svante Martinsson, Gothenburg University

LUNCH

Session 3:

- 13:00 – 13:30 **Including the uncertainty in topology and divergence times in historical biogeography reconstruction — Two examples from the coffee family**
Jenny Smedmark, University Museum of Bergen
- 13:30 – 13:50 **A coalescent-based test to distinguish between paralogy, hybridisation and lineage sorting**
Filipe de Sousa, Gothenburg University
- 13:50 – 14:10 **Cryptic speciation in Basidiomycota**
Kristian Skaven Seierstad, Natural History Museum, University of Oslo

COFFEE

Session 4:

- 14:40 – 15:00 **Exploring species diversity and phylogeny of some obscure, pantropical rainforest lichens — DNA-barcoding, phylogenetics and taxonomy**
Mika Bendiksby, Natural History Museum, University of Oslo
- 15:00 – 15:20 **Substantial loss and gain of microRNA families in flatworms**
Bastian Fromm, Natural History Museum, University of Oslo

Workshop:

- 15:30 – 18:30 **Workflows for data refinement and ecological niche modeling**
Mattias Obst, Gothenburg University, Sweden
See <http://www.forbio.uio.no/events/meeting/2013/biovel.pdf> for more information.
- 15:30 – 16:30 Meeting for supervisors of ForBio members
- 19:00 CONFERENCE DINNER (Quality Hotel 33, Oslo)

WEDNESDAY 6 MARCH

Session 1:

09:00 – 09:45 **Consensus and confusion in molluscan phylogeny**

Julia Sigwart, Queens University Belfast

09:45 – 10:05 **New methods answer old questions — Phylogeny and systematics of the Chaetodermatidae (Caudofoveata, Mollusca)**

Nina Therese Mikkelsen, University Museum of Bergen

COFFEE

Session 2:

10:30 – 11:15 **Millions of characters: The potentials and pitfalls of applying next generation sequencing technologies to biosystematic research**

Marie Louise Davey, The University Centre in Svalbard, Longyearbyen

11:15 – 12:00 **RADseq data: the next workhorse in phylogeography and population genetics?**

Emiliano Trucchi, University of Oslo

LUNCH

Session 3:

13:00 – 13:20 **Unraveling the maze: Orb-weavers evolution, current knowledge and future perspectives**

Dimitar Dimitrov, Natural History Museum, University of Oslo

13:20 – 13:40 **Molecular phylogeny of the family Aglajidae (Gastropoda: Cephalaspidea)**

Andrea Zamora, University Museum of Bergen

13:40 – 14:00 **Parasitic barnacles and their coevolution with the king crabs**

Christoph Noever, University of Bergen

COFFEE

14:30 – 15:30 **Plenary discussion and awards**

Speakers' abstracts in presentation order

4 March

The evolution of communication systems in tiger moths (Lepidoptera: Erebidae: Arctiinae)

Susan Weller

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Tiger moths (Arctiinae) possess a combination of traits that make them ideal for examining the evolution of insect signals. Phylogenetic studies show that interspecific defense signals (visual, acoustic) evolved first and were then co-opted for intraspecific courtship signals. These signal systems are imperfectly correlated with larval hosts and acquired secondary metabolites. Many tiger moth larvae acquire secondary metabolites from plant or fungal hosts, often transferring them to the adult stage. Coloration can be an honest aposematic signal, however, brightly colored Batesian mimics co-occur with Müllerian. In addition to coloration, tiger moths deter night predators by producing bursts of ultrasonic clicks. Three classes of ultrasonic signals exist: 1. Complex signals that disorient bats ("jamming"), 2. Simple signals that bats learn and associate with poisonous moths (aposematic), 3. Simple signals emitted by palatable moths which bats avoid (Batesian). Acoustic mimics (both Batesian and Müllerian) co-occur with the aposematic species. Thus, like coloration, ultrasonic clicks can be aposematic or mimetic. These interspecific signals have been co-opted for use in intraspecific communication. One class of plant metabolites, pyrrolizidine alkaloids (PAs), are incorporated into male courtship pheromones or transferred as a nuptial gift to the female. In some non-PA defended species, simple acoustic signals are incorporated into courtship displays where males "sing" to females to gain copulation. The evolution of inter- and intraspecific signal systems are intertwined with the evolution of larval diet. My plenary talk will focus on our emerging consensus on the origins and evolution of defense and mating signal evolution in tiger moths.

The mysterious case of the golden-branched netted column: Unimaginable diversity of unimagined creatures in our Nordic soils

Allison Perrigo, Maria Romeralo & Sandra Baldauf
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Estimating the diversity of terrestrial protists is difficult due to the large amount of molecular diversity in relation to morphological variation that is often encountered. Some well-recognized species are in fact made up of many cryptic and pseudo-cryptic species. In this study we looked at sixty isolates of the cellular slime mold *Dictyostelium aureostipes* (Amoebozoa) and assessed them in the context of a molecular phylogeny using two previously established molecular regions, the nuclear SSU and ITS, as well as a novel mitochondrial marker, a section of the ATPase 1 coding region (atp1). Both the combined nuclear and the mitochondrial phylogenies indicated five well-supported clades within this species complex. In addition, several 'rogue' isolates appeared to belong within the *D. aureostipes* complex, but were molecularly distinct and did not group with any of the five major clades that were observed. The clades tended to show biogeographic patterns, including circumpolar specificity in one of the five groups. Furthermore, different isolates from the same country or region often belonged to different clades, indicating sympatry while maintaining lack of genetic exchange among the clades. The genetic diversity of this group highlights the unseen diversity of the dictyostelids, a factor that has often resulted in both taxonomic confusion and underestimates of diversity in these, and other, terrestrial protists.

What have the spikemosses been up to during the last 350 million years?

Stina Weststrand & Petra Korall
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The spikemosses, or the lycophyte family Selaginellaceae, have been around for about 350 million years and today they have a worldwide distribution. They are dispersed by spores and little is known about their dispersal and distribution patterns. As an example of a heterosporous plant, where two different kinds of spores are needed for reproduction, the spikemosses make up an interesting study system for plant dispersal biology. Is long distance dispersal common in the group, or are disjunct distributions mainly a result of historical vicariance events? What can a large-scale phylogeny and biogeographical analyses tell us?

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

Dario Pistone & Bjarte Jordal
University Museum of Bergen
Dario.Pistone@um.uib.no

Bark and ambrosia beetles in the weevil subfamily Scolytinae present high species diversity and remarkably varied ecological adaptations to several habitats. So far, using DNA sequences from a limited number of nuclear and mitochondrial genes, and morphological characters, the phylogenetic relationships among different tribes were partially reconstructed, but resolution is still limited. Bark and ambrosia beetles exhibit complex models of host-plant coevolution, fungus farming, sub-sociality and inbreeding. A large scale phylogeny of Scolytinae will illuminate many aspects of key evolutionary traits within this group. We aim at establishing a robust phylogenetic hypothesis for bark and ambrosia beetles based on morphological data and DNA sequences from 15-20 protein encoding nuclear genes. Considering limitations of next-generation sequencing, we decided to use different approaches focusing directly on specific genes. Hence, we will apply selective methods to investigate a total of 60-70 nuclear genes, in order to obtain, at least, 10-15 informative markers. So far, one of the most successful strategy was based on NCBI database collection of long (~1000bp) uncharacterized mRNAs obtained from the bark beetle *Dendroctonus ponderosae*; alignments with sequences of insects and other arthropods allowed to characterize these genes and select conserved regions useful for primer design. Hitherto, we exhaustively investigated eleven genes, in terms of PCR and sequencing success, and phylogenetic signal, selecting six of them to be used in phylogeny reconstruction: elongation factorII, heat-shock protein70, eukaryotic release-factor1, cyclinC, glycoside-idrolase family31, muscular protein20. Here we present preliminary data and results on the development of these new molecular markers.

Chinese whispers... Identification literature and species distribution

Malin Strand^{1,2}
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²Swedish University of Agricultural Sciences
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We are all human and we all prefer an easy road. I can see no other explanation than this to the high number of flaws I have observed and handled during my timely proofreading of species lists. In my work with writing and editing the Encyclopedia of the Swedish Fauna and Flora I have collected examples of where things can, and often do, go wrong over time and also found just how often it is related to the identification literature. I will give you some brief examples of this and show how false positives often, through a pattern much resembling "Chinese whispers", get circulated and forwarded until they become true. I will also show what this can do to research results in biology/ecology, and mention some possibilities to correct data.

Investigating the origin of incongruence between gene trees of the mushroom-forming fungi

Elisabet Sjökvist¹, Bernard Pfeil¹, Yann Bertrand¹ & Mats Töpel²

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The Agaricomycetes - mushroom forming fungi - are currently divided into 12 major well established lineages, whose relationships relative to one another are still unresolved. Using multi labeled trees of gene families from 54 Basidiomycete genomes we aim to map the processes leading to the different phylogenetic signals for different genes. This includes hybridization, genome duplication, rapid radiations, heterotachy, positive selection and paralogy. The main goal is not to get a fully resolved tree, but to know to what extent different evolutionary processes are involved in the formation of the Agaricomycete diversity.

Sampling in scientific collections: Is good faith enough?

Magni Olsen Kyrkjeeide, Kjell Ivar Flatberg, Kristian Hassel, Heidi Solstad & Hans K. Stenøien

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Genetic studies of plants often rely on sampling of specimens from herbaria. Sampling from herbaria saves time and field work expenses. Usually it also increases the sample sizes as material collected over several years can be used, and makes it easier to access samples from areas which are difficult to visit. Apparently as herbaria samples are already identified anyone can sample from specimens even if they have no knowledge about the morphology of the targeted taxa. But what if the samples are misidentified? And what could be the consequences if you draw conclusion from data of misidentified specimens?

5 March

Integrated methods for biodiversity research

Sarah Bourlat

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In the last two decades the relationship between biodiversity and ecosystem function has become a central issue, while biodiversity loss has been identified as a major driver of ecosystem change. As a result, ecological research transforms into a species-rich scientific discipline with increased focus on the ability to document, study, and predict the biodiversity composition in ecosystems. However, the analysis of patterns of biodiversity over large temporal and spatial scales is still very difficult to achieve as it requires biologists and environmental scientists to integrate their expertise, data, and methodologies across the traditional biological disciplines. The Biodiversity Virtual e-Laboratory, BioVeL, addresses this challenge (for details, see www.biovel.eu<<http://www.biovel.eu>>). In BioVeL, scientists and computer engineers are working together to develop tools for pipelining data and analysis into efficient analytical pipelines, called workflows. Workflows are complex digital data manipulations and modeling tasks that execute sequences of web services. BioVeL designs and deploys such workflows for a selected number of important areas in ecological and conservation research, e.g. for the analysis of data sets with ecological, taxonomic, phylogenetic, and environmental information. The workflows allow the researcher to (i) explore, access, refine, and format large data sets from major data providers, (ii) combine disparate data sets with the researchers' individual data, and (iii) run complex and computationally intense analytical cycles. The workshop (Workflows for data refinement and ecological niche modeling) will demonstrate newly released workflows and present scientific showcases based on these workflows.

Using DNA barcoding to evaluate bioinvasion risks associated with ballast water transport of zooplankton to the Arctic

Christopher Ware¹, Jørgen Berge², Jan Sundet³, Jamie Kirkpatrick⁴ & Inger Greve Alsos¹

¹Tromsø University Museum

² Department of Arctic and Marine Biology, University of Tromsø

³Institute of Marine Research, Tromsø

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Reducing or preventing the release of invasive species into new habitats is a primary goal of environmental management. In the Arctic there is a need to better characterise marine bioinvasion risks. We sampled the ballast water tanks of ships discharging ballast water in the high-Arctic archipelago Svalbard, to evaluate the potential for ship-mediated species introductions to occur. Previous taxonomic studies of ballast water have shown that high densities of viable zooplankton can be transferred to new habitats in ballast water, but have typically failed to identify a large proportion of these organisms. To improve our ability to accurately evaluate risk associated with species introduction, we used DNA barcoding to help identify larval forms within our samples, and taxonomic groups difficult to identify based on morphological characters. By sequencing the standard barcoding region for animals, the mitochondrial cytochrome c oxidase subunit 1(COI), we have been able to identify a higher percentage of sampled organisms than would have been possible using traditional techniques. Sample enumeration is ongoing, however preliminary results reveal that ballast water transfer to Svalbard can mediate the introduction of a number of non-native organisms. Current management requires the mid-ocean exchange of ballast water prior to final discharge in Svalbard waters, yet our data indicate that this process is limited in efficacy. Accordingly, there is a need to further consider the way marine bioinvasion risks are managed in Svalbard and the wider Arctic. The methods employed in this study present an efficient means with which to do this.

Carnivorous sponges of the deep Atlantic: Investigating the emergence of a unique feeding strategy within phylum Porifera

Jon Thomassen Hestetun

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Sponges are generally known as filter-feeding aquatic animals possessing an aquiferous system for filtering nutrients from surrounding water. Diverging sharply from this traditional view, it has comparatively recently been discovered that sponges in the deep-sea demosponge family Cladorhizidae depend instead on passively trapping and feeding on small crustaceans and other animals, and for species in the family, the aquiferous system is lacking or severely modified. Cladorhizids are typically erect, with adhesive branches, filaments or inflatable spheres, adapted to entangle prey, which become enveloped by amoeboid cells migrating to the area of contact. The carnivorous feeding habit is now considered general for all cladorhizid species, as well as for several members of related families. The evolutionary history for the group is largely unknown, with no molecular data, and it is suspected that the current systematics do not reflect evolutionary relationships within the Cladorhizidae and allied groups. New species of Cladorhizidae are still regularly described. In this presentation, I will introduce this unique group of sponges, talk about newly described cladorhizid material collected mostly in the bathyal and abyssal parts of Atlantic Ocean (2000–5000 m), give a biogeographic overview based on current data, as well as present work on a tentative molecular phylogeny on the family.

Phylogeny and Biogeography of the *Diapensia* (Diapensiaceae)

Yan Hou

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The evolutionary relationship between the Arctic-boreal and southern alpine Asian plants is poorly understood. Here we study that relationship using the small plant genus *Diapensia* L. (Diapensiaceae). The genus consists of five taxa and has a disjunct distribution in the Arctic-boreal region and alpine regions in southern Asia. *Diapensia lapponica* has an Arctic-boreal distribution and consists of two subspecies, *D. lapponica* subsp. *lapponica* and *D. lapponica* subsp. *obovata*. The two subspecies are given species rank by some taxonomist. The remaining three species, *D. himalaica*, *D. purpurea*, and *D. wardii* are distributed in the Himalayas and Hengduan Mountains in China. We aim to infer the phylogeny of *Diapensia* to test if 1) the two subspecies of *D. lapponica* form monophyletic groups, and 2) if a single dispersal between the Arctic-boreal region and the south Asian alpine region is enough to explain the current distribution pattern, and 3) if we can deduce the direction of the migration. We will also attempt to date the split(s) between the Arctic-boreal species and the southern Asian species occurred. So far, our study included 33 individuals of *D. lapponica*, representing the majority of its distribution area, five individuals of *D. himalaica* and six individuals of *D. purpurea* from Asia. No material from *D. wardii* has been studied due to lack of material. We have sequenced five plastid DNA regions: petL-psbE, psbJ-petA, psbA-trnH, rpl16 and matK gene. Data analysis is currently in progress.

Evolution and biogeography of *Baccharis* (Asteraceae): a megadiverse neotropical genus

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Neotropical grasslands (campos de altitude, campos rupestres, pampas, paramos), savannas (cerrado, chaco, espinhal) and upper montane forests (*Araucaria* forests, cloud forests, etc.) harbor unique floras with high levels of endemism. Due to the complex taxonomy and wide distribution in the Neotropics, megadiverse genera as *Baccharis* L. (Asteraceae) are being neglected in systematic research, lacking phylogenies which would allow testing hypotheses on their evolution and biogeography. *Baccharis* comprises about 400 mostly dioecious species, with higher diversity in grasslands, savannas and montane vegetation, and has been target of proposals of segregation in smaller taxa or of the lumping of not strictly dioecious taxa. Some morphologically well circumscribed infrageneric taxa of *Baccharis* are potential candidates to be applied as proxies to help assess the diversification and biogeographic history of some Neotropical biomes. Taxonomic and phylogenetic studies on *Baccharis* are now underway by the authors, based on morphological and molecular data, along with a biogeographical approach. This study aims to test the monophyly of the genus and its infrageneric groups, and may provide evidence on the evolution of dioecy, on the wide spectrum of life forms and morphological diversity within the genus, and on the infrageneric and specific relationships of *Baccharis*. The data are also likely to help understanding the historical assembly of open and montane vegetation in the Americas.

**Cryptic diversity, delimitation and phylogeny of Nordic species of *Cognettia*
(Clitellata: Enchytraeidae)**

Svante Martinsson & Christer Ers us

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Cognettia is an enchytraeid genus commonly found in acidic terrestrial habitats, such as coniferous forest and bogs. In particular *Cognettia sphagnetorum* has been used as a model in several studies focusing on e.g. climate change, forest and soil ecology, and it has been shown to play a key role in the decomposition of organic matters and nutrient cycling. The diversity of the genus in northern Europe is here assessed using four molecular markers, COI, 16S, H3 and ITS. The COI dataset was used for preliminary identification and delimitation of specimen clusters and for testing the existence of a barcoding-gap. Single gene-trees were estimated for all genes using Bayesian Inference, and multi-locus species-trees were estimated using both multi-species coalescent and concatenated Bayesian inference. Eight species were found, *Cognettia cognettii*, *C. lapponica*, four species within the morphotaxon *C. sphagnetorum* and two within *C. glandulosa*. *C. sphagnetorum* s.l. is not found monophyletic whereas *C. glandulosa* s.l. seems to be. In the multi-locus species trees two main clades are recovered, one consisting of *C. lapponica* and two species of *C. sphagnetorum*, the second consisting of the two other species of *C. sphagnetorum* and the two species of *C. glandulosa*. *Cognettia cognettii* is found as sister group to either clade, with non to moderate support, depending on analysis. As cryptic species are found in this genus we recommend that material of *Cognettia* used in future studies should be identified using a molecular barcode.

**Including the uncertainty in topology and divergence times in historical biogeography
reconstruction — Two examples from the coffee family**

Jenny Smedmark

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When hypotheses of historical biogeography are evaluated, both the resolution of phylogenetic relationships and age estimates of individual nodes often have a direct impact on what explanation is concluded to be most likely. There is, however, usually some uncertainty associated with the topology, and confidence intervals of estimated divergence times are often large, something that is rarely incorporated in biogeographical analyses. We used two groups in the coffee family, both with disjunct pantropical geographic distributions, to explore how the uncertainty in topology and estimated divergence times affect conclusions in biogeographical analysis. Results from both groups using a single phylogenetic tree, such as the maximum likelihood tree with mean estimates of divergence times, provided clear support for one specific interpretation. Analyses of a large sample of dated phylogenies did, however, show that these results were not consistent, emphasizing the importance of using methods that account for the uncertainty in topology, branch lengths, and estimated divergence times in historical biogeographic inference.

A coalescent-based test to distinguish between paralogy, hybridisation and lineage sorting

Filipe de Sousa, Yann Bertrand, Bengt Oxelman & Bernard Pfeil
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Phylogenetic inference from multiple gene sequences has become a standard approach in Systematics. However, various natural processes may lead to incongruence among gene trees. These include: lineage sorting, when two gene lineages do not follow the speciation pattern, sharing instead a common ancestral copy deeper in the species tree; hybridisation, which may occur through introgression or through an ancient hybrid speciation event; paralogy, when there is gene duplication in one species and subsequent loss of copies in descendant species. The phylogenetic effect of each of these processes has been widely debated but no current methods deal with all processes simultaneously. Here, we present a method to distinguish between these three processes using gene linkage information and coalescent simulations. Closely linked genes, i.e. genes that occur in physically close loci, are expected to show phylogenetic variation caused by lineage sorting or possibly due to paralogy caused by tandem duplication. However, incongruence due to hybridisation is mostly expected among distantly linked or unlinked genes, as the fixation of large chromosomal blocks after hybridisation is presumed to be faster than the generation and fixation of new alleles through mutation and recombination, which may in turn lead to lineage sorting differences among closely linked genes. Using a simulation approach, we show that it is possible to identify genes affected by paralogy and hybridisation, even at small tree depths. Paralogous genes can thus be excluded from further analysis, whereas genes that share the same evolutionary history, i.e., those only affected by lineage sorting, can be pooled for phylogenetic reconstruction.

Cryptic speciation in Basidiomycota

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Although fungi are less studied than other organism groups, phylogeographic studies of fungal morphospecies often reveal structured genetic diversity, i.e. cryptic species. Cryptic species are the result of diversification without alteration in morphology. Two of my PhD-projects focus on (I) *Hygrophorus piceae* s.l. and (II) *Trichaptum abietinum* and the closely related *T. fuscoviolaceum*. *Hygrophorus piceae* is an ectomycorrhizal basidiomycete restricted to *Picea abies*. Analysis of multi-locus sequence, nuclear and mitochondrial, data reveals at least five well separated lineages with no conflict among genes. All five lineages exist in Fennoscandia and some places also in sympatry. Geographical and ecological differences between them are not obvious. A more complex genetic pattern is apparent in the *T. abietinum*/*T. fuscoviolaceum* aggregate. They differ in morphology and ecology, but intermediate forms have been proposed. Both are basidiomycete saprobes on conifers. A global sample of the two species, using multi-locus data, indicates that they are well separated. Geographical groups within the species can be identified, despite conflict among genes.

Exploring species diversity and phylogeny of some obscure, pantropical rainforest lichens — DNA-barcoding, phylogenetics and taxonomy

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Lichens occurring in the Tropics are generally poorly known, and crustose lichens in particular. We use DNA sequencing to test hypotheses about species delimitation and phylogeny of three obscure pantropical lichen genera, *Eschatogonia*, *Krogia*, and *Phyllopsora*. Although common epiphytes on rainforest trees, species delimitation and phylogeny of these genera are poorly understood; even their family affiliation remain unsettled. Einar Timdal is one of very few people with expert knowledge on these genera. He has published several revisions based on morphological and TLC studies of their secondary metabolites, but is still not able to determine more than about 90 % of the material and suspects there are much undiscovered and 'hidden' diversity. Only a single DNA sequence of *Phyllopsora* exists in GenBank (with obscure determination), and so far none of *Eschatogonia* and *Krogia*. An 'NHM-Småforsk' grant has funded our molecular phylogenetic investigation of the smaller genera *Eschatogonia* and *Krogia*, as well as preliminary data for a *Phyllopsora* revision. About 70 *Phyllopsora* species are recognized today, of which 30 are described since the year 2000. Our molecular phylogenetic results and taxonomic conclusions on *Eschatogonia* and *Krogia* will be presented, as well as preliminary results on *Phyllopsora*.

Substantial loss of conserved and gain of novel microRNA families in flatworms

Bastian Fromm¹, Merete Molton Worren², Christoph Hahn¹, Eivind Hovig^{2,3} & Lutz Bachmann¹

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²Department of Informatics, University of Oslo,

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Platyhelminthes are basal lophothrochozoans consisting of the mostly free-living and polyphyletic Turbellaria and the parasitic and monophyletic Neodermata, which include economically important monogenean flatworms (Monogenea), the human-health related flukes (Trematoda), and tapeworms (Cestoda). Using the newly designed bioinformatics pipeline MiRCandRef the microRNA complement of the monogenean flatworm *Gyrodactylus salaris* was disentangled. It consists of 40 microRNA hairpin loci with known seeds, and 34 with yet undescribed seeds. A comparison of the microRNA complement of *G. salaris* with the previously published ones of *Schmidtea mediterranea* (Turbellaria), *Schistosoma japonicum* (Trematoda), and *Echinococcus granulosus* (Cestoda) reveals a substantial loss of conserved bilaterian, protostomian and lophotrochozoan microRNAs in flatworms and especially within the parasitic Neodermata that to such an extent has never been reported from any other group. At the same time, many novel microRNAs with yet unknown function evolved in each flatworm lineage individually. The presence and absence of conserved microRNAs support the monophyly of Platyhelminthes and the phylogenetic relationship of Turbellaria (Monogenea (Trematoda+Cestoda)) within.

WORKSHOP 1

Workflows for data refinement and ecological niche modeling

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Requirements: Bring your own laptop. All workflows offered will be browser-based and don't need any desktop installations. A sample data set will be provided with each workflow.

Background: In the last two decades the relationship between biodiversity and ecosystem function has become a central issue in ecology, while biodiversity loss has been identified as a major driver of ecosystem change. As a result, ecological research transforms into a species-rich scientific discipline with increased focus on the ability to document, study, and predict the biodiversity composition in ecosystems. However, the analysis of patterns of biodiversity over large temporal and spatial scales is still very difficult to achieve as it requires biologists and environmental scientists to integrate their expertise, data, and methodologies across the traditional biological disciplines. The Biodiversity Virtual e-Laboratory, BioVeL, addresses this challenge (for details, see www.biovel.eu). In the BioVeL, scientists and computer engineers are working together to develop tools for pipelining data and analysis into efficient analytical pipelines, called workflows. Workflows are complex digital data manipulations and modelling tasks that execute sequences of web services. BioVeL designs and deploys such workflows for a selected number of important areas in systematic, ecological, and conservation research, e.g. for the analysis of data sets with ecological, taxonomic, phylogenetic, and environmental information. The workflows allow the researcher to (i) explore, access, refine, and format large data sets from major data providers, (ii) combine disparate data sets with the researchers' individual data, and (iii) run complex and computationally intense analytical cycles. The workshop is a collaboration between SwedishLifeWatch (<http://www.slu.se/lifewatch>), NordicLifeWatch (http://www.lifewatch.eu/en_GB/joint-nordic), and BioVeL (www.biovel.eu).

In session 1 we will give an overview over SwedishLifeWatch (<http://www.slu.se/lifewatch>), NordicLifeWatch, and BioVeL, and demonstrate newly released workflows for taxonomic data refinement, ecological niche modeling (and possibly phylogenetic inference), together with the presentation of scientific showcases based on these workflows.

In session 2 we will offer a hand on training where participants will learn to use these workflows and run scientific analysis on their own laptops.

In session 3 we will discuss possibilities for individual research projects by the students and how they can be supported.

6 March

Consensus and confusion in molluscan phylogeny

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Molluscs are the second largest and morphologically most disparate animal phylum, they are ubiquitous, and have a formidable fossil record. Monophyly of the eight Recent molluscan classes is undisputed, but relationships between these groups and patterns of early molluscan radiation have remained elusive. Molecular, fossil and anatomical data show apparently contradictory evidence for branching patterns within Mollusca. The traditional reductionist model of the 'hypothetical molluscan ancestor' has hampered the resolution of molluscan topology; some hypotheses rejected as artifacts (e.g. *Serialia*) continue to find additional support and cannot be dismissed conclusively. Derived conditions in major body plan modifications, such as shell-loss, have occurred repeatedly in most groups. Rather than interesting sidelines, these anomalies, and evidence for rampant reversals, apparently represent the true norm of molluscan evolution. Based on new molecular clock results – the first to include multiple exemplars of all 8 classes – diversification of molluscs started immediately in the early Cambrian and was far more rapid and more complex than previously appreciated. Extensive evolutionary plasticity by heterochronic shifts in development and multiple convergent adaptations, as demonstrated in extant molluscs, were already within the evolutionary potential of their Cambrian forebears, and continue today.

New methods answer old questions — Phylogeny and systematics of the Chaetodermatidae (Caudofoveata, Mollusca)

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The shell-less, worm-shaped Caudofoveata is by far the least known group of molluscs. These small, benthic marine animals can be difficult to sample, and possess few defining characters. The internal relationships of the taxon are unclear, and the relationships between and within the genera of Chaetodermatidae have been continuously debated since the description of the very first species of Caudofoveata. Up until now the evolutionary relationships of the group have never been investigated in a modern phylogenetic analysis, neither based on morphological nor molecular data. We here use molecular phylogenetics to resolve the relationships of the largest family within the caudofoveates, the Chaetodermatidae, in the North Atlantic. Phylogenetic analyses were performed using mitochondrial (COI, 16S) and nuclear genes (18S, 28S and H3) from 40 specimens from 8 species belonging to the two major genera within the family, *Falcidens* and *Chaetoderma*. Our molecular data do not agree with the current classification based on morphological characters. In our analyses, *Falcidens* and *Chaetoderma* are not recovered as monophyletic. The only character distinguishing the currently recognized genera is the morphology of the radula. Comparative examination of radula morphology revealed that the 'generic' differences may in fact be related to ontogeny: in *Chaetoderma nitidulum*, the nominal species for the family Chaetodermatidae, the radula changes gradually from a *Falcidens*-type radula in small specimens to a *Chaetoderma*-type radula in larger specimens. We thus conclude that the currently recognized genera within Chaetodermatidae are in need of revision, and other characters than radula morphology need to be used for genus delimitation.

Millions of characters: The potentials and pitfalls of applying next generation sequencing technologies to biosystematic research

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The development of 'Next Generation' sequencing (NGS) over the course of the past 10 years has revolutionized molecular biology. It can be used to sequence millions of base pairs at a fraction of the per-base cost of traditional Sanger sequencing. This has created substantial possibilities in biosystematics research, and has many applications within the field. It is now possible to quickly and affordably sequence multiple genomes, multiplex large numbers of markers and individuals, develop species specific microsatellite markers, and to SNP genotype hundreds of individuals. As will be demonstrated in the presentation of several case studies, these data can readily be applied to questions in biosystematics related to phylogeny, phylogeography, and evolutionary processes. While the potential for NGS in biosystematic applications is high, the approach carries with it additional new challenges. Robust methods for addressing sequencing errors, quality filtering, and assembly of large NGS datasets are still under development. The bottleneck in sequence-based research has now shifted from one of sequencing cost to that of data analysis, and both software and bioinformatics expertise is often lacking, slowing the effective analysis of large datasets.

RADseq data: the next workhorse in phylogeography and population genetics?

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Next-generation sequencing (NGS) methods that allow for genome scan in multiple individuals are expected to trigger a new golden age in phylogeography, phylogenetics and population genetics likely merging these fields with ecological genomics. Neutral and adaptive processes are now likely to be addressed with the same toolkit of molecular markers. However, the implementation of whole-genome data in ecological adaptations studies is far advanced than in the investigation of neutral evolutionary dynamics. This is mainly due to the most common output data type of most NGS methods (e.g. unlinked SNPs) in contrast with the historical importance of using gene trees, mainly through coalescent-based analytical approaches, in phylogeography and phylogenetics. Nevertheless, solutions that can make the set of excellent statistical tools for DNA sequences analysis, employed in phylogeography and phylogenetics so far, available to deal with NGS data are of the utmost importance. Here we will show how RAD sequencing data can be used to address classical questions in phylogeography and we will also propose a novel method to use this kind data to infer past demography. This approach is here employed in (i) the analysis the past population history of a king penguin (*Aptenodytes patagonicus*) colony breeding on Crozet archipelago and (ii) to describe the past evolutionary dynamics of two populations of African porcupines (*Hystrix cristata* and *H. africaeaustralis*).

Unraveling the maze: orb weavers evolution, current knowledge and future perspectives

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We present the first dated spider phylogeny that includes substantial representation of orbweavers diversity. In the light of these new evidences, we revisit alternative hypothesis that aim to explain diversification in spiders. The present study is based on a combination of newly collected sequence data and information already available in public data bases for six loci for close to three hundred taxa.

Molecular phylogeny of the family Aglajidae (Gastropoda: Cephalaspidea)

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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 molecular data remains 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. A multilocus coalescent Bayesian framework, based on mitochondrial (COI, 16SrRNA) and nuclear (28SrRNA, Histone-3) genes was used to infer species trees. At the moment, this is the most comprehensive molecular phylogeny of the family. The sequences in this phylogeny were obtained from our own DNA extractions, but some sequences from Genbank were also included. This project is funded through a doctoral grant to the first author by the Consejo Nacional de Ciencia y Tecnologia (CONACYT-Mèxico), fellowship BAZS/188890/2010.

Parasitic barnacles and their coevolution with the king crabs

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Parasitic barnacles (Rhizocephala) are highly adapted parasites that are closely related to the sessile rock barnacles. Having a highly modified morphology, they lack most traits normally found in arthropods. Their body consists of a branched root system inside their host, by which they take up nutrients, and an external sac containing the reproductive organs. Despite their crab-like appearance, molecular data revealed that king crabs are in fact heavily modified, giant hermit crabs. They must therefore have evolved from an hermit crab morphology due to strong selection pressure for a large body size. Based on molecular methods, we show the co-evolutionary relationship of the king crabs and their rhizocephalan parasites.

Poster abstracts in alphabetical order of first author

The serotonergic nervous system of the kinorhynch *Pycnophyes kielensis*

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We investigated the nervous system of the homalorhagid kinorhynch species *Pycnophyes kielensis*. Specimens were stained with primary antibodies binding on 5-hydroxytryptamine (5-HT, Serotonin), α - and β -Tubulin, and DAPI. The 3D structure of nerve cells was visualized by use of confocal laser scanning microscopy and 3D reconstruction software. The serotonergic nervous system comprises a brain that is arranged in a perikarya – neuropil – perikarya ring around the pharyngeal bulb, behind the introvert. Associated to this rings are somata that extend anteriorly and posteriorly. Ventrally from the brain, runs a nerve cord posteriorly with associated somata. The stained nervous system conforms to the typical cycloneuralian brain that is characterized by an equally thick circumpharyngeal nerve ring and found in kinorhynchs, nematodes, nematomorphs, priapulids, and loriciferans. These data are the first step in our quest to investigate the evolution and development of Kinorhyncha, in order to get new data about the ancestry of segmentation within Ecdysozoa

Phylogenetic footprinting of microRNAs in *Gyrodactylus*

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MicroRNAs (miRNAs) are a recently discovered class of RNAs that regulate gene expression. They are highly conserved and it has been shown that they are continuously added to metazoan genomes through evolutionary time, but only rarely lost. Presence/absence patterns of conserved miRNAs have been forwarded in previous studies on a variety of taxa as supporting evidence for inferred phylogenetic relationships. Recently, the miRNA complement of *Gyrodactylus salaris* (Platyhelminthes, Monogenea), an important ectoparasite on Norwegian stocks of Atlantic Salmon (*Salmo salar*), has been described. The present project addressed the conservation of miRNA loci and their suitability as phylogenetic markers in *Gyrodactylus*. PCR primer pairs targeting flanking regions of 62 miRNA hairpin loci were designed to amplify and sequence the respective loci from *G. salaris* Lier strain, *G. salaris* Pålbu strain, *G. thymalli*, *G. derjavinoidea*, *G. teuchis*, *G. truttae*, and *G. birmani*, all members of the taxonomically complex wagneri group. All loci could be amplified from the *G. salaris* strains and the sibling species *G. thymalli*. However, only 40% of the loci could be confirmed from the more distantly related species, which points at substantial sequence variation in the targeted flanking regions. Sequences of 25 miRNA hairpin loci could be obtained for all 7 taxa, which resulted in a concatenated alignment of 2812bp. A genetic distance based Neighbor joining analysis confirmed a close relationship of *G. thymalli* and *G. salaris*. There was as much sequence variation within *G. salaris* as between *G. thymalli* and *G. salaris*. The data support earlier suggestions of synonymizing both species. Accordingly, pathogenicity and host specificity can only be seen as strain rather than species characteristics.

NorBOL: Norwegian Barcode of Life Network

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The Norwegian barcode of Life Network was formed after the Inaugural Workshop in Canada in June, 2007. Our aims were to establish a national network for barcoding national as well as Arctic biodiversity, to raise funding in support of barcoding and curation of barcoded material, to co-ordinate and initiate new barcoding projects, and to raise public awareness about the barcoding and barcoding results in Norway. NorBOL is a regional node within iBOL, with a particular responsibility for polar barcoding. NorBOL was led by the Natural History Museum, University of Oslo until 2011, when leadership was taken over by the NTNU Museum of Natural History and Archaeology in Trondheim. At present, the network comprises 16 institutions, including all four major natural history museums as well as all major research institutes. In spite of strong support among research institutions, national fund-raising has had limited success, and only from 2012 we were successful in establishing a substantial economic basis for the network's activities 2012-2015 through a grant from the Norwegian Biodiversity Information Centre. Since then, barcoding progress of the Norwegian fauna, flora and funga has increased and the Barcode of Life Data Systems database currently holds close to 7000 DNA barcodes of 2100 BINs from Norway. The target for NorBOL is set to 20,000 species barcoded over 6 years. At present, NorBOL primarily targets barcoding of museum collections, vascular plants of the north, coastal marine invertebrates, and inventory projects supported by the Norwegian Taxonomy Initiative that focus on various little known organism groups.

DNA barcoding of bark and ambrosia beetles reveals excessive NUMTs and consistent east-west divergence across the Palearctic

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In view of the increased rate of introduced species, a DNA barcoding library is very useful for rapid identification and detection of potential pest species. We tested the performance of species identification in the most dominating group of wood boring insects – the bark and ambrosia beetles – with particular focus on broad geographical sampling across the boreal Palearctic forests. Neighbour-joining analyses of Cytochrome Oxidase I sequences from 151 species in 40 genera revealed very low levels of identification errors, but included the discovery of a likely cryptic Nearctic species of *Dryocoetes autographus*, a paraphyletic *Xyleborinus saxeseni*, the presence of *Orthotomicus suturalis* in North America, and the likely hybrid origin of shared mitochondrial haplotypes in *Pityophthorus micrographus* and *P. pityographus*. The mitochondrial data also revealed consistent divergence across the Palearctic or Holarctic, confirmed by data from the large ribosomal subunit (28S). Some populations had considerable variation at the mitochondrial barcoding marker, but were invariant at the nuclear ribosomal marker. This must be viewed in light of the high number NUMTs detected in eight bark beetle species, suggesting the likely presence of additional cryptic NUMTs. The occurrence of paralogous COI copies, hybridisation or cryptic speciation in these beetles, as seen in many other insect groups, demands a stronger focus on data quality assessment in the construction of DNA barcoding databases.

Extensive polyploid hybridization within the fern genus *Woodsia*

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In the process of resolving the phylogeny of the cosmopolitan *Woodsia* ferns we have conducted the most comprehensive nuclear phylogeny of ferns. We have sequenced two nuclear regions (pgiC and RPA2) on up to 175 different specimens corresponding to some 30 species. In addition to the nuclear markers we have also sequenced 5 chloroplast regions (matK, rbcL, atpA, atpB and trnGR). The results show an extensive hybridization and chromosome doubling within the genus *Woodsia*. As many as 19 out of the 32 species we identify in the phylogeny are polyploids. The Scandinavian species *Woodsia alpina* is the allopolyploid hybrid of *Woodsia ilvensis* × *Woodsia glabella*. In this study we show that the hybrid has originated multiple times, and also that both parents have, at least once each, acted as the donor of the maternally inherited chloroplast genome. An extreme hybrid is *Woodsia* × *abbeae*. It is a hybrid between the two species *Woodsia ilvensis* and *Woodsia oregana* subsp. *oregana* separated by as much as 30–50 million years.

Delimitation of *Puccinellia svalbardensis* — Molecular and morphological evidence call for a new species description

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Grasses of genus *Puccinellia* are ecologically important to arctic land ecosystems and supports for example large numbers of nesting goose in high arctic. As the speciation might be very recent by polyploidization or hybridization, the species status of rare species has to be well evaluated. *Puccinellia svalbardensis* has been considered as an endemic and rare species and is found exclusively on Spitsbergen, Svalbard. It has been definitely overlooked as many more locations have been found in the past ten years. Other *Puccinellia* species present in Spitsbergen are *P. angustata*, *P. vahliana*, *P. palibinii*, *P. phryganodes*, and subspecies of these. However, a recent study showed that the populations described as *P. palibinii* were not differentiated from *P. svalbardensis*. In this study, we collected samples of *P. svalbardensis* and co-occurring *Puccinellia* species in all areas where *P. svalbardensis* have been reported in Spitsbergen. Samples were analyzed by AFLP fingerprinting, morphology, and estimation of ploidy level. Ecological preferences were examined by vegetation analysis. AFLP results and selected morphological traits clearly supported an entity of *P. svalbardensis*. The data further indicated some possible hybridization most likely with the putative closest relative *P. angustata*. *Puccinellia svalbardensis*, including variants former assigned to *P. angustata* and *P. palibinii*, represent a separate species in Spitsbergen. Thus, the current description of *P. svalbardensis* does not seem to cover the variation belonging to this taxon. The history of speciation is still unclear. Preliminary sequencing results do not give the necessary resolution, but newly developed microsatellites may bring us closer to a solution.

Cryptic diversity in Nemertodermatida (Acoelomorpha)

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Nemertodermatida is a small taxon of marine worms with low dispersal capabilities. Two filiform species, *Sterreria psammicola* and *Nemertinoides elongatus* are mainly distinguished by the position and orientation of their sexual organs, leaving immature specimens difficult to identify. Both species have a wide distribution, ranging from the Mediterranean to the Western Atlantic, the North Sea and the Swedish West coast, *Sterreria* has even been reported from the Southwest and middle Pacific and the Western Indian Ocean. Cryptic species complexes appear to be likely. Three molecular markers in overall 100 specimens from 17 locations were analysed using Maximum likelihood and Bayesian frameworks. Morphological characters were supported by the molecular analyses were assigned. Species delimitation was tested with the program BP&P. This first study combining morphological and genetic data in Nemertodermatida shows that diversity in this taxon is much greater than accounted for so far. Both nominal species studied are in fact cryptic species complexes. Two new species, one in each genus, will be described. All specimens from the Mediterranean, the North Sea and the Swedish West coast belong to either genus whereas specimens from more distant localities cluster together in three main clades. These possibly constitute new species and possibly genera as well, but will not be described here. However, it is clearly shown that no species has a truly cosmopolitan distribution but that there are several very similar species present.

Phylogeny of Willughbeieae tribe and Biogeography of the Tabernaemontaneae – Vinceae – Willughbeieae clade (Apocynaceae, Rauvolfioideae)

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Willughbeieae is the second largest tribe Rauvolfioideae subfamily with 18 genera and 150 species and has pantropical distribution. The tribe has economic and ecological importance due to its edible fruit, medicinal properties and latex (e.g., *Parahancornia amapa*, *Hancornia speciosa* and *Landolphia senegalensis*). The taxonomic knowledge of genera and species of Willughbeieae is incomplete and largely outdated, and so far only ten species of the tribe were sampled in phylogenetic studies. In order to test the phylogenetic relationships of inter and infrageneric Willughbeieae, phylogenetic analyzes were performed using Bayesian inference based on markers in five regions of the chloroplast: the rpl16 and rps16 introns, spacer gene trns-G and the locus formed by the trnK intron and matK gene. Results support the monophyly of Willughbeieae and the current existence of three major lineages, two of these exclusively neotropical and a third with a mixture of four genera paleotropicalis (*Landolphia*, *Leuconotis*, *Saba*, *Willughbeia*) and one Neotropical (*Pacouria*). The positioning *Pacouria* is one of the most interesting results of this study, suggesting a dispersal event of transoceanic Paleotropics to the Neotropics after the disconnection of the main lineages of the tribe. Tabernaemontaneae, Vinceae and Willughbeieae, as currently circumscribed, comprise 42 genera and about 300 species that form a strongly supported clade (TVW clade). An overall correspondence between clade composition and geographic areas suggests simultaneous events of basal splits between paleotropical and neotropical lineages in all three tribes and subsequent splits within paleotropical and neotropical areas.

Mechanisms and patterns for putative hybridogenous speciation in *Carex* (Cyperaceae)

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The genus *Carex* (Cyperaceae) is, with its many species, among the quantitatively most important plant genera in northern alpine, boreal and arctic zones. In the northern hemisphere, we find between 120 and 160 species of *Carex*; around 100 of these species are found in mainland Norway. The majority of the species are distinct and relatively easy to distinguish from each other; however, there are four big species complexes within Northern European *Carex* species where frequent hybridization has been observed and where hybridogenous speciation is thought to occur. Normally, hybridogenous speciation takes place through hybridization followed by a doubling in chromosome number (allopolyploidy). In *Carex*, however, there are no distinct ploidy levels within the plants. Thus, it would seem like hybridogenous speciation in *Carex* occurs within the same ploidy level. In my PhD project, the aim is to study mechanisms and patterns for such putative hybridogenous speciation within two sections of *Carex*; namely sections *Vesicariae* and *Phacocystis*. I wish to conduct both morphological as well as molecular studies in this work. My goal is then to be able to learn more about the phylogeny and taxonomy of these two sections, in addition to getting a better understanding of how hybridogenous speciation within the same ploidy level might occur in plants.

Impact of invasive species on biodiversity: are they always harmful?

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Invasive hogweeds are infamous for negative ecological and socio-economic impact in Europe. *Heracleum persicum* (Norwegian name: 'tromsøpalme') is one of the noxious invasive species growing in Scandinavia. It is highly invasive in Norway, especially northern Norway, and is blacklisted in Norwegian blacklist. The impact of *H. persicum* on biodiversity has not been quantitatively studied yet in Norway. Thus, we aim to quantify the impact of *H. persicum* and its hybrids on biodiversity and explore habitat preference based on invaded vegetation characteristics and soil properties. We sampled 188 plots of 2 × 2 m² within Norway. Out of the 188 plots studied, 94 were in *Heracleum* and hybrids invaded area and rest in the adjacent non-invaded area (control). We estimated coverage of each species present in the plot. Soil samples were collected from each plot. Soil samples have not been analyzed yet. We compared species richness between invaded and control plots for the whole data and found a statistically significant difference in species number (t-test: $t = -2.2$, $df = 181$, $p = 0.029$). Abundance (% cover) of *H. persicum* is negatively correlated with species number for the whole data (Pearson product moment correlation = -0.30 , $df = 92$, $p = 0.0032$). However, when *H. persicum* and hybrids were separately analyzed, we found no statistically significant difference in species richness between invaded and control plots. Preliminary analysis shows that invaded plots are highly homogenous and control plots probably contain more unique species.

Comparative genomics, transcriptomics and evolution of response to cold hardening and vernalization in Pooideae

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The ability to tolerate the cool conditions of northern environments is one of the key features contributing to the ecological success of the grass subfamily Pooideae (Poaceae), and species of this subfamily constitute more than 90% of grass species in Northern parts of Europe, Asia and America. The occurrence of specific mechanisms for cold adaptation in the Pooideae's core group (tribes Aveneae, Triticeae, Bromeae and Poeae) is thought to coincide with the group's taxonomic diversification and a major cooling of the global climate during the transition from Eocene to Oligocene (~33.5 – 26 Ma). Even though the molecular mechanisms underlying those adaptations are mainly unknown, the recent availability of comprehensive genomic data for wheat (*Triticum aestivum*), perennial ryegrass (*Lolium perenne*) and the model grass (*Brachypodium distachyon*) enables comparative studies of genomic regions essential for cold stress response, i.e. cold hardening and vernalization. In the presented study we aim to compare genes of the core Pooideae members wheat and perennial ryegrass with homologous genes from *B. distachyon*, a sister of the core Pooideae. A study of the RNA expression during cold stress will also include basal Pooideae species represented by *Nardus stricta*, *Melica nutans*, *Stipa pennata* and *Stipa lagascae*. Our broad taxonomic sampling and the structural and functional comparison of the homologs will help to understand the evolution of cold response in the Pooideae on a genomic level. An extensive geographic sampling of *N. stricta*, *M. nutans* and the *Stipa* species will also allow us to elucidate patterns of differential gene expression in regard to major climatic regimes. Finally, reconstructing the evolution of cold response genes in the Pooideae subfamily will contribute to a better understanding of the processes involved in gene evolution across long phylogenetic distances.

Purple Polysphondyliids — same same or different?

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The dictyostelids are a group of about 150 species of solitary living soil amoebae that aggregate and form a multicellular organism under starvation conditions. The dictyostelid phylogeny is well-resolved into eight major groups, but within these groups many of the species relationships remain unclear. Molecular work with morphologically similar isolates provided evidence of cryptic species complexes, for instance in the morphospecies *Polysphondylium violaceum*. We developed a protocol to amplify the mitochondrial gene Atp1, and added it to two other nuclear regions (ITS1-5.8-S-ITS2 and 18S rDNA), to produce a phylogeny of eight isolates in the *P. violaceum* species complex using maximum likelihood and Bayesian methods to test the monophyly of the species complex, and to look for cryptic species within the group. In addition to six described species we assessed two putative isolates of *P. violaceum* to see if they were molecularly and morphologically consistent with the type. Atp1, when combined with ITS and SSU, provides strong evidence for the existence of a monophyletic *violaceum*-complex. In this group, the two isolates NZ16B and B10B are morphologically (e.g. aggregation size and pattern) and molecularly (Atp1 sequence similarity <97%) distinct from *P. violaceum*, and we propose that they should be described as new species. However, there is strong evidence that they are closely related as they share key features such the rare purple coloration and the typical polar granules. However, the multi-region phylogeny shows poor resolution among species in the *violaceum*-complex, and we propose more sampling to increase support for internal nodes.

WORKSHOP 2

Bioinformatics — make your own tools

Time and place: Mar 7, 2013 09:00 — Mar 8, 2013 16:00, Natural History Museum, Oslo

This workshop will give you an opportunity to work with your programming problems in an inspiring group where you will be able to get help from more experienced programmers as well as give help to other less experienced participants. This is a great opportunity for those of you who already participated in our “Introduction to Bioinformatics for Biosystematics” courses (see www.forbio.uio.no for more info) to keep up the work and learn more.

Note that this is not a course, and that you in order to find it useful will need some programming background in, for example Bash, Perl, Python, R and/or SQL. There is no schedule or program but we may agree to focus on one or a few problems we solve together while some may choose to work on their own problem.

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NEWS: ForBio collaborate with DEST (Distributed European School of Taxonomy):

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

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