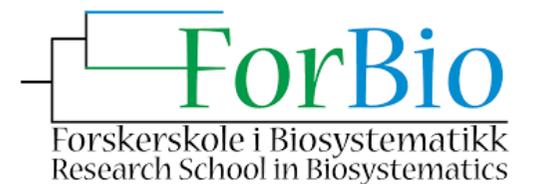


ForBio Annual Meeting 2018

Tromsø Museum
12-14th February



Welcome to the 7th Annual ForBio Meeting at Tromsø Museum

Organising Committee

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Inger Greve Alsos, Tromsø University Museum, University of Tromsø,
Galina Gusarova, Tromsø University Museum, University of Tromsø

Meeting Schedule

Feb 12

09:30 **Registration and coffee**

11:30 **WELCOME**

Lena Aarekol, Director of Tromsø University Museum

Hugo de Boer, Leader of ForBio, University of Oslo

12:00 **Aino Hosia**, Department of Natural History, University Museum of Bergen. *'Barcoding the hydrozoan diversity of Norway'*

12:40 **Jake Goodall**, Life and Environmental Sciences, University of Iceland: *'Phenotypic Plasticity and Regulatory Control of Shell Colour in the Common Whelk, Buccinum undatum'*

13:00 **Lunch**

14:00 **Oriol Canals**, Departament de Biologia Evolutiva, University of Barcelona: *'Feasibility of molecular and microscopic methods to assess microeucaryote diversity'*

14:20 **Camila Ritter**, University of Gothenburg: *'Assessing eukaryotic and prokaryote diversity from bulk insect samples'*

14:40 **Ragnhildur Guðmundsdóttir**, University of Iceland: *'Assessment of ciliates associated with the groundwater amphipod Crangonyx islandicus'*

15:00 **Coffee/ tea break**

Feb 12

15:30 Oral speed presentations

Tobias R. Vonnahme, Department of Arctic Marine Systems Ecology, University of Tromsø: *'Microbial communities and fluxes in the cryosphere'*

Isolde Callisto Puts, Ekologi, Miljö och Geovetenskap (EMG), Umeå University: *'The bacterial- and primary production in brownifying and warming Nordic lakes'*

Yennie K. Bredin, Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences: *'Assessing the importance of mycorrhizal diversity along a flooding gradient in Amazonian Várzea forests'*

Fernanda Miranda, Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, *'Algal biomass production in wastewater-flue gas system'*

16:00 Oral speed presentations

Baldur Kristjánsson, Department of Biology, University of Iceland: *'Compensating fitness reducing mutations in Drosophila melanogaster'*

Chao Song, NTNU University Museum, Trondheim: *'DNA barcoding revealing of a hyper diverse aquatic insect'*

Tea Huotari, Department of Agricultural Sciences, University of Helsinki: *'Exposing the long-term dynamics of arthropod communities at high Arctic using recent advances in metagenomics'*

Feb 12

Josué Anderson Rêgo Azevedo, Department of Biological and Environmental Sciences, University of Gothenburg: *'Population genetics and species delimitation of the Neotropical lizards of the genus Kentropyx (Squamata) in South America'*

16.30 Harith Omar Morgadinho Farooq, University of Aveiro, Portugal, and University of Gothenburg: *'Can the sequencing of amphibians and reptiles contribute to conservation in a developing country with a huge biodiversity'*

16:50 Poster session 1

Feb 13

09:00 **Inger Alsos**, Tromsø University Museum. **Keynote:**
'Environmental plant DNA from soil and sediments: where are we and where are we going'

09:40 **Vanessa Bieker**, NTNU University Museum, Trondheim:
'Using historical herbarium specimens of an invasive plant species (Ambrosia artemisiifolia L.) for evolutionary genomics'

10:00 **Brecht Verstraete**, Natural History Museum, University of Oslo: *'A new MSCA International Training Network: Plant.ID, molecular identification of plants for the world of tomorrow'*

10:20 **Ida M. Mienna**, NTNU University Museum, Trondheim:
'The spatial distribution of phylogenetic diversity and endemism in the Norwegian vascular flora'

10:40 **Coffee/ tea break**

11:10 **Methee Phumthum**, Department of Bioscience, Aarhus University: *'Important medicinal plant families in Thailand'*

11:30 **Olena Meleshko**, NTNU University Museum, Trondheim: *'Is interspecific gene flow in peatmosses (Sphagnum) constrained by phylogenetic relatedness and life-history traits?'*

11:50 **Narjes Yousefi**, NTNU University Museum, Trondheim:
'Genetic and morphological variation in the circumpolar distribution range of Sphagnum warnstorffii: indications of vicariant divergence within a common peatmoss'

12:10 **Sandra Garcés-Pastor**, Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona: *'Testing the suitability of two novel universal eukaryotic metabarcoding markers for diatom analysis of peat bog communities'*

Feb 13

12:30 **Lunch**

13:30 **Hans Tore Rapp**, Centre for Geobiology, University of Bergen. **Keynote:** *'Exploration of deep-water sponge ecosystems in the North Atlantic'*

14:10 **José Cerca**, Natural History Museum, University of Oslo:
'Four ways to become cryptic'

14:30 **Owen Wangensteen**, Norwegian College of Fishery Science, University of Tromsø: *'Mitochondrial metabarcoding of marine hard-bottom communities with applications to metapopulogeography'*

14:50 **Sébastien Matlosz**, Life and Environmental Sciences, University of Iceland: *'DNA methylation in Arctic charr: Epigenetics to help understand polymorphism'*

15:10 **Coffee/ tea break**

15:40 **Quentin Horta-Lacueva**, Life and Environmental Sciences, University of Iceland: *'Mechanisms of reproductive isolation in two sympatric morphs of Arctic charr from a subarctic lake, Thingvallavatn'*

16:00 **Kalina Hristova Kapralova**, Life and Environmental Sciences, University of Iceland: *'Romance under the waves: Documentary on mating behaviours of Large Benthivorous Charr in Lake Thingvallavatn, Iceland'*

Feb 13

16:20 Oral speed presentations

Kelsey Lorberau, Department of Arctic and Marine Biology, University of Tromsø: *'Bridging Paleoecology (aDNA) with Modern Ecological Understanding'*

Ardian Høgøy Abaz, The Arboretum and Botanical Gardens, University Museum, University of Bergen: *'Molecular phylogeny of Rubus and its relatives within the supertribe Rosodae'*

Ingrid Toresen, The Arboretum and Botanical Gardens, University Museum, University of Bergen: *'Molecular phylogeny and intra-generic classification of Potentilla L.'*

Nannie Persson, University Museum, University of Bergen: *'Untangling the origin of a polyploid: The evolutionary history of Potentilla norvegica (Rosaceae) using single-copy nuclear markers'*

Malene Nygård, NTNU University Museum, Trondheim: *'Conservation genomic studies of red-listed angiosperm species prevalent in Central Norway'*

16:50 Oral speed presentations

Eirin Bruholt, Natural History Museum, University of Oslo: *'The systematic relationships of the North Atlantic and arctic Cochlearia L. taxa'*

Beatriz Neves, Department of Botany, National Museum, Federal University of Rio de Janeiro: *'Evidencing Drivers of Spatial Trait Variation Across a Latitudinal Gradient in the Brazilian Atlantic Forest'*

William Hatchett, Faculty of biosciences and aquaculture, Nord University: *'Reinforcement in Fucus species'*

Feb 13

Anna Patova, Deep-sea biology research group, University of Bergen: *'Conservation genomics of North Atlantic sponge grounds: assessing diversity, connectivity and vulnerability of deep-sea habitat forming species'*

17:30 Poster session 2

18:00 **Guided tour with Per Helge Nylund**: Exhibitions of Tromsø University Museum: *biological and cultural diversity of the Northern Norway.*

19:00 **Dinner** (Rotunden, Tromsø University Museum)

Feb 14

09:30 **Miquel Arnedo**, Department of Biology, University of Barcelona. **Keynote:** Replaying life's tape: How species proliferate and diversify on islands.

10:10 **Sonja Kistenich**, Natural History Museum, University of Oslo: *'Molecular phylogenetics and taxonomy of the tropical lichen genus Phyllopsora'*

10:30 **Andreas Frisch**, NTNU University Museum, Trondheim: *'Mapping the diversity of crustose lichenized and lichenicolous fungi in Norwegian rainforests'*

10:50 **Coffee/ tea break**

11:20 **Michael Martin**, NTNU University Museum, Trondheim: *'Ancient DNA to reveal the genetic history of European reindeer'*

11:40 **Tobias Andermann**, Biological and Environmental Sciences, Gothenburg University: *'Current extinction of mammals more than 100 times higher than during Last Glacial Maximum'*

12:00 **Stefaniya Kamenova**, CEES, University of Oslo: *'REININ project: Reindeer interactions from plants and birds to humans: balancing the odds of climate change'*

12:20 **Lunch**

13:30 **Bernhard Eitzinger**, Department of Agricultural Sciences, University of Helsinki: *'Modelling trophic link distribution in a tundra arthropod community'*

13:50 **Trude Magnussen**, Natural History Museum, University of Oslo: *'Towards an integrative taxonomic revision of Allodia s. str. (Diptera, Mycetophilidae)'*

14:10 **Emma Wahlberg**, Department of Zoology, Swedish Museum of Natural History, Stockholm: *'Molecular phylogenetics reveals unknown relationships within Empidoidea (Diptera)'*

14:40 **Plenary discussions and awards**



ForBio is a teaching and research initiative funded by the Norwegian Taxonomy Initiative and the Research Council of Norway



Tromsø University Museum has kindly collaborated to make this meeting possible

Abstracts of oral and poster presentations

Feb 12

Barcoding the hydrozoan diversity of Norway

Aino Hosia, Luis Martell

Department of Natural History, University Museum of Bergen

There are over 100 species of pelagic Hydrozoa recorded from Norway, including both hydromedusae and siphonophores. As predators on other zooplankton they play an important role in the pelagic ecosystems. Unfortunately, pelagic Hydrozoa tend to be fragile and difficult to sample in good condition, and many of the fixatives normally used for zooplankton cause distortion and shrinkage rendering the animals difficult or impossible to identify morphologically. As a result, pelagic hydrozoans (and other gelatinous zooplankton) are often excluded from zooplankton surveys, and there is limited information on their diversity and distributions.

For the past three years, we have been working on a rewarding Norwegian Taxonomy Initiative project, HYPNO, charting the diversity of pelagic hydrozoans in Norwegian waters using integrative morphological and molecular taxonomy. We have so far documented and taken DNA samples from ca. 80 species of pelagic hydrozoans occurring in Norway. On the side, benthic stages for more than 50 species have been collected. Our success rate for sequencing barcodes at species level is currently 95% for 16S and 83% COI, with generally -but not always- good separation (barcode gap) at species level. HYPNO illustrates several of the benefits of straightforward DNA-barcoding, but also many of the pitfalls and challenges. The project has resulted in several new species records for Norway as well as the linkage of previously unassociated pelagic and benthic life stages for several species. The discovery of both cryptic species and species with plastic morphology necessitates the redescription of some species. Future applications of the accumulated data potentially include improved monitoring of gelatinous zooplankton distributions and trophic role through metabarcoding applications.

Phenotypic Plasticity and Regulatory Control of Shell Colour in the Common Whelk, *Buccinum undatum*

Jake Goodall 1, Hildur Magnúsdóttir 1, Kristen Westfall 2, Snæbjörn Pálsson 1, Erla Björk Örnólfsdóttir 3, Zophonías O. Jónsson 1
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2 Department of Fisheries and Oceans, Government of Canada, Canada
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All living organisms exhibit phenotypic trait variation that is essential to evolution by natural selection. Phenotypic plasticity has been studied extensively in aquatic gastropods, where the same genotype can exhibit a range of shell shapes and colours under different environmental conditions. Whilst much interest has been garnered towards the physical properties of gastropod shell shape and colour, the molecular processes underlying such plastic phenotypes remain poorly characterised. Within the Bay of Breiðafjörður (Iceland), the common whelk (*Buccinum undatum*; Gastropoda; Mollusca) exhibits extreme variation in shell colour, including dark to light shades of white, brown, blue, red, orange, yellow, green, purple and pink. Although the common whelk is widely distributed throughout the North-Atlantic, Breiðafjörður is the only known area to which the species exhibits such extreme shell colour plasticity across such small geographic distances.

Exploiting the high phenotypic variation within the Bay of Breiðafjörður's *B. undatum* population, RNA-Seq analyses were undertaken in relation to shell colour. The following presentation details emerging results from global transcriptional comparisons, with particular focus on the characterisation of key biomineralisation and pigmentation genes associated with the evolution, maintenance and regulation of shell colour plasticity in gastropod molluscs.

Feasibility of molecular and microscopic methods to assess microeucaryote diversity

Oriol Canals¹, Ramon Massana², Vanessa Balagué², Humbert Salvadó¹

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The microeukaryote community of a partial nitrification reactor prior to anammox (an innovative and cheaper wastewater treatment technology focused on nitrogen removal of high ammonium loaded wastewater) has been studied using both molecular and microscopic methods. The diversity and abundance data provided by both detection methods have been compared. Up to 12 microeukaryotic taxa were observed by microscope, from which six belonged to Alveolata (specifically Ciliophora), two to Excavata and one each to Amoebozoa, Archaeplastida, Opisthokonta and Stramenopiles.

On the other hand, the molecular survey (Illumina) on the V4 region in the 18S rDNA gene provided 16 main OTUs. From these, only 13 were comparable with microscopic results, since the remaining three OTUs belonged to Fungi, organisms that were not considered in the microscope analysis. Seven of the other 13 OTUs corresponded to Alveolata (specifically to Ciliophora), two to Archaeplastida and one each to Amoebozoa, Opisthokonta, Rhizaria and Stramenopiles. No Excavata sequences were obtained. Four results were consistent between microscopic and molecular methods: the green algae *Polytoma* sp. and the ciliates *Epistylis camprubii*, *Colpoda aspera* and *Cyclidium glaucoma*. Regarding the microscopic results, five taxa were not detected in the molecular survey: nucleariids < 20µm, the ciliates *Opercularia coarctata* and *Vorticellides microstoma*-complex, and the Excavata *Tetramitus rostratus* and kinetoplastids.

On the other hand, five of the 13 OTUs obtained were not detected by microscopy in the samples analysed, although four of these OTUs were observed in other samples throughout the study period, suggesting that these taxa were indeed present in the analysed samples, but at abundances lower than the detection limit of the counting methodology or as resting stages organisms have not been yet sequenced at the V4 18S rDNA region, cases that exemplify the need for comprehensive taxonomic studies in order to provide morphological and molecular data on more eukaryote species.

Assessing eukaryotic and prokaryote diversity from bulk insect samples

Camila D. Ritter^{1,2*}, Alexander Zizka^{1,2}, Alexandre Antonelli^{1,2,3}

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Insects make up a substantial portion of extant eukaryote diversity and interact with the majority of organisms in any given ecosystem. New techniques such as metabarcoding make it possible to quantify insect biodiversity as well as insect-ecosystem interactions through DNA sequencing. The goal of this study was to assess the diversity of eukaryotic 18S and prokaryotic 16S diversity when targeting bulk insect samples. We use DNA metabarcoding to estimate the total prokaryote and eukaryote diversity in insect samples from 39 survey plots in a longitudinal transect across Brazilian Amazonia. We use these data to characterize biodiversity and community composition based on operational taxonomic unit (OTUs). We use of non-destructive protocols to preserve the specimens for future morphological examination. We expect obtain a big fraction of terrestrial diversity which will provide a cost-effective way to assess diversity since the samples will contain all insect network interactions. We expect with this data be able to characterize patterns of biodiversity distribution across Amazonia.

Assessment of ciliates associated with the groundwater amphipod *Crangonyx islandicus*

Ragnhildur Guðmundsdóttir¹, Bjarni Kristófer Kristjánsson², Viggó Þór Marteinsson³ and Snæbjörn Pálsson¹

¹ University of Iceland

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The endemic groundwater amphipod, *Crangonyx islandicus*, lives in springs in lava fields of the volcanic zone in Iceland. Inspection of the amphipods and molecular analysis of the 18S RNA revealed ciliates associated with the amphipods. Five unknown sequences were revealed from the orders Apostomatida and Philasterida.

To explore the ecosystem of the springs we applied the eDNA methods by filtering water samples, and using artificial substrate to sample microbes. DNA was extracted from the water samples, the substrate and from the amphipods. Ciliate 18S RNA was targeted by specific primers and sequenced. Distinct microbial assemblages were found on each sample type with some overlapping, especially of the water samples and the artificial substrate.

The most common ciliates found in the amphipods (90%) are relatives of the genus *Fusiforma* (Apostomatida), known for being epibionts on crustaceans in the marine environment. Other common ciliate taxa are from the genera *Miamiensis* (6%) and *Trichodina* (1%), both known for parasitizing freshwater organisms. The rest is divided between 13 OTUs with total 2.5% of the total sequences. In both the water samples and on the artificial substrate, the most common group was from the subclass Hymenostomatia with 14% and 36% respectively.

The metabarcoding method confirms our previous findings on the species associated with *C. islandicus* and adds more taxa to otherwise poorly studied ciliate fauna of Iceland and to the ecology of its groundwater ecosystem.

Feb 12 Poster session 1

Microbial communities and fluxes in the cryosphere

Tobias R. Vonnahme¹, Christine Dybwad¹, Ulrike Dietrich¹, Katharina Bading², Fernanda Vasconcelos³, Marit Reigstad¹, Josef Elster⁴, Rolf Gradinger¹

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Microbial communities in high Arctic fjords can be affected by sea ice formation and glacial meltwater input. Both processes are changing drastically with a changing climate. Sea ice can act as a habitat for specific sea ice algae, adapted to low light but dependent on substrates. Glaciers are known to harbour a large variety of specific snow algae and cyanobacteria, as well as chemolithoautotrophic bacteria and archaea. These organisms have been shown to be important for supplying the glacial system with nutrients, such as reduced iron, and nitrogen. The importance of icebergs for iron inputs has been shown in Antarctica, but the direct effects on high Arctic fjords are, yet, hardly studied. The project and field work is organized by ForBIO PhD students and the background and study design will be presented on the poster. We will investigate microbial communities, their biomass and viability together with potential environmental controls, such as nutrient concentrations. We will study the role of microbial communities and physiology on downward export fluxes. Additionally, microalgae will be cultured and screened for their biotechnological potential. Microbial community structures will be studied in the field, using next-generation sequencing technologies for sequencing 16S and 18S genes and microscopy. Fluxes will be measured via short term sediment traps. Nutrient, POC, PON, and chlorophyll, will be sampled in the field and measured in Tromsø. Multivariate analyses will be used to investigate the connectivity and most important environmental controls on bacteria, archaea, microalgae, microzooplankton, and ichthyoplankton communities in the fjords. Sampling in the light winter and in early summer will help to differentiate sea ice ecosystems and the same system controlled by glacial meltwater input.

The bacterial- and primary production in brownifying and warming Nordic lakes

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Many of our Nordic lakes are turning brown by an increased inflow of colored organic material (here measured as dissolved organic carbon, DOC). This brownification is highly linked to climate change and is an essential process governing Nordic lake ecology. Colored DOC affects both light and nutrient conditions, hence also primary production (PP) at the base of the food web, and can therefore have far-reaching effects on whole-lake ecosystem production.

Recent research has shown that DOC additions enhance mobilization of basal energy through increased bacterial production (BP). In clear-water, low-DOC lakes (i.e. high-latitude lakes), DOC additions can also have an indirect positive effect on PP via nutrients associated with the dissolved organic material. Besides increased mobilization, the warming effect due to climate change is most prominent in high-latitude lakes. However, the effect of warming in addition to brownification is rarely investigated. We aim to predict the future PP and BP of high-latitude Nordic lakes that undergo climate-change induced brownification by understanding the performance of basal producers (BP and PP) under both browning and warming.

Using twelve mesocosms (EXEF, Röback) we exposed natural communities of bacteria, primary producers (both benthic and pelagic) and consumers (zooplankton and zoobenthos) to six different concentrations of DOC (ranging between 0-8 mg/L) at two different temperatures (ambient and 3 degrees warming). We measured pelagic PP and BP every other week for ten weeks (October to December, 2017). Results suggest that temperature affects BP as well as PP. Future PP in clear-water high-latitude Nordic lakes are suggested to initially increase by nutrients associated with DOC, but in more brownified lakes PP will decrease because of light limitation. This is in accordance with field observations.

Assessing the importance of mycorrhizal diversity along a flooding gradient in Amazonian Várzea forests

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Diverse mycorrhiza communities are considered important for tree growth and forest health. In the world's most species rich floodplain forests, the Amazonian Várzea, we might also expect a diverse mycorrhiza community to play an important role in forest structure and succession. Yet the monomodal annual floods, which deposit and erode tons of soil every year and leave the trees under several meters of water for months, strongly influenced the Várzea. Thus, only specialist tree species persist in this highly dynamic forest system, conditioned and shaped by the rivers, but how do the annual floods and high tree species turnover affect the presence of fungal diversity and mycorrhiza-tree interactions?

Using metabarcoding and DNA sequencing we assess the influence of flood height and duration along with tree species richness on mycorrhiza communities. To estimate total mycorrhiza diversity along a flooding gradient we use DNA metabarcoding to analyse soil samples from 20 inventory plots in the Juruá, Brazilian Amazonia. We use these data to characterize biodiversity and community composition based on operational taxonomic unit (OTUs). From our analysis, we expect to gain insights about the relative abundance and diversity of mycorrhiza communities along the flooding gradient in várzea forest. Insights, that may help us characterize distributional patterns of mycorrhiza-tree diversity and understand the importance of mycorrhiza biodiversity for the world's most productive floodplain forests.

Algal biomass production in wastewater-flue gas system

Fernanda Miranda

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Wastewater has been used as a source of nutrients for microalgae with the objective of promoting great algal biomass and lipid production. However, not necessarily wastewater contains all resources needed for algal production. Usually, wastewater contains large amount of organic nutrients, such as organic carbon, that are not readily available for algal uptake. This makes the use of an external source of carbon necessary.

Here, we used flue gas with the objective of supplying microalgae with the limiting resource carbon. We ran a 7 days long experiment where light was continuously supplied to the different treatments. We measured algal biomass production in three treatments: artificial medium, wastewater, and wastewater sterilized. To these treatments, we added flues gas and we did not add flue gas to having a control treatment. All treatments were replicated twice. We used the green algae *Coelastrella* sp., which is commonly found in Swedish wastewater and showed great results with this type of medium compared with other green algae strains. Algal biomass production was greatly triggered by the addition of flue gas. After 3 days of experiment, the differences could be seen with the naked eyes. Nitrogen and phosphorus concentrations dropped below the level of nutrients detection in the treatments with flue gas addition.

Our results support the hypothesis that algal production is limited by carbon in system where wastewater is used. The addition of an external source of carbon is needed and flue gas showed potential for that.

Compensating fitness reducing mutations in *Drosophila melanogaster*

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Evolution occurs by tinkering, whereby existing structures and genes are polished and/or reused for adaptation and evolutionary novelties. Novel features result from natural selection promoting and fixing in populations mutations that generate favorable phenotypes.

We study material from a major long-term artificial selection experiment. This experiment was done on populations of fruit flies (*Drosophila melanogaster*) first by altering their genetic make-up by introgression of 3 deleterious alleles (in *vestigial*, *rhomboid* and *net*) into wild type fly population. This led to severe changes in the wing. Next artificial selection was applied, that is propagation the individuals with the best wings, for 24 to 32 generations. This led to full compensation, the wings became wild-type, in 3 replicate populations. In contrast, control lineages whereas natural selection was free to act, showed no change in wing morphology. This shows that wild populations harbor cryptic genetic diversity, that selection can act on to adjust (or compensate for changes in) phenotypic traits. In this project we ask, how does the developmental regulatory system respond to such changes? Using Illumina whole transcriptome sequencing of wing discs from roaming third instar larvae, we seek to answer this question.

DNA barcoding revealing of a hyper diverse aquatic insect

Chao Song^{1,2}, Xiaolong Lin², Qian, Wang³, Xinhua Wang¹

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A dataset including 3671 COI barcodes representing 162 morphospecies was used to explore the utility of COI barcode in species differentiation of a super-diverse aquatic insect genus *Polypedilum* Kieffer. The genus is the largest chironomid genus with 520 currently known valid species worldwide, and are extremely difficult to be identified to species-level morphologically.

The BOLD system presented 286 BINs on January 13, 2017, among which 121 unique and 30 non-unique BINs (348 barcodes, 93 morphospecies) were uploaded by our lab. Molecular operational taxonomic units (OTUs) are ranged from 158 to 345, based on both distance-based (Automatic Barcoding Gap Discovery (ABGD), Barcode Index Numbers (BINs), j-Molecular Operational Taxonomic Unit, Neighbor joining ID-trees (NJ), Pre-Threshold Clustering) and phylogeny based approach (Generalized Mixed Yule Coalescent model (GMYC) and Poisson Tree Process (bPTP + mPTP)). In comparison, GMYC, bPTP, mPTP and BINs generate more taxonomic lineages than morphospecies numbers. While ABGD, j-MOTU, NJ, Pre-Threshold Clustering and ABGD yielded a conservative number of species when setting higher thresholds.

Moreover, nine species complexes with deep intraspecific divergences reveal 18 potential cryptic species, which needs further taxonomic research including complete life histories as well as nuclear genes even genomics studies. The discrimination of *Polypedilum* species by DNA barcodes was proved successful with 94.4% identification-success rate. Besides, we made possible taxonomic implications of some taxonomic anomalous records in the BOLD database. Overall consideration, a 5–8% threshold on average for COI barcodes is applicative in delimitating *Polypedilum* non-biting species.

Exposing the long-term dynamics of arthropod communities at high Arctic using recent advances in metagenomics

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The Arctic, as other parts of the globe, is dominated by arthropods, which sustain many ecological functions. The Arctic is also one of the fastest warming regions on the planet, but we still know little about how current change affects both arthropod communities, whole ecosystems, and their functioning. Despite the advantages of the Arctic for analyzing change at the community and ecosystem -level, longer records of species level information from high latitudes are still very few.

In this project we are analyzing the single most comprehensive time series of arthropod samples from high altitudes derived from the Zackenberg research station in Northeast Greenland, where arthropod samples have been collected over 18 years. Our objective is to use the collection, utilize recent advances in genomics and statistical modelling to come up with species-level correlates to climatic response, temporal patterns in community structure, and evidence of structural and functional tipping points during two decades of rapid climatic change. We use a PCR-free mitochondrial metagenomic approach to resolve the collection to the species level data and show that this method is valid for analyzing environmental monitoring data and revealing changes at community level.

Changes happening at the high Arctic can be seen as an indicator of changes about to happen in other parts of the world, and therefore our results provide crucial information when aiming to predict future change.

Population genetics and species delimitation of the Neotropical lizards of the genus *Kentropyx* (Squamata) in South America

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The Neotropics is the richest and most diverse of the Terrestrial Ecoregions of the World. Within its huge area, the two biggest biomes are highlighted due their differential biodiversity: The Amazon rainforest and the Cerrado savannas. These two biomes also share a huge contact/transition zone forming an ecotone with singular characteristics. The group of terrestrial lizards of the genus *Kentropyx* occurs over the mentioned areas and is an interesting model to study how species evolved over these different biomes and how they have adapted to the different climates of the whole region.

The goals of this study are to identify the species diversity of the genus *Kentropyx* (through a species delimitation analysis) and then reconstruct the biogeographical history of the group. From this information we hope to clarify if these lizards have originated in the forested biomes and colonized the savannas (or the contrary). Also, we hope to understand the role of the ecotone in the diversity of the group: Is the ecotone area a geographic barrier or is it permeable to the migration of the species. To achieve these goals, we will sequence 240 individuals of approximately 11 species using the Ultraconserved Elements of the vertebrate genome.

The second step will involve the sequencing of the genome of one of the species (*Kentropyx calcarata*) that occurs in the Amazon/Cerrado ecotone zone. For this phylogeographical study we will acquire the sequences using RAD-seq. We will then investigate if there are genomic regions under selective pressures due to landscape conditions (e.g., vegetation, climate) that could indicate differential adaptive potentials of these lizards to the effects of climate change. We expect to identify environmental and historical factors responsible for the evolution of diversity in the Amazon-Cerrado ecotone, aiming to support long-term strategies for biodiversity conservation.

Oral presentation

Can the sequencing of amphibians and reptiles contribute to conservation in a developing country with a huge biodiversity?

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

This project aims to enhance conservation by understanding how the inselberg's forests in Northern Mozambique are connected through the integration of phylogenetic, spatial data and distribution modeling.

The integration of phylogenetic, spatial data and distribution modeling can include cryptic diversity and may be useful to confirm known areas of endemism as well as finding new biodiversity hotspots.

We plan to use new and existing spatial and phylogenetic data to map the Phylogenetic Endemism (PE) of the amphibians and reptiles' intraspecific lineages from several species and complexes showing high phylogeographic structure. Using spatial and non-spatial regressive models we will test whether PE can be predicted by measures of Quaternary climate change, forest stability, topographic heterogeneity, and current climate.

Finally we will intersect the areas found to accumulate rare diversity with the protected areas in Mozambique in order to evaluate the current conservation effectiveness in the country and help redefine a new network area for protected areas.

Feb 13

Using historical herbarium specimens of an invasive plant species (*Ambrosia artemisiifolia* L.) for evolutionary genomics

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The study of invasive plants offers an excellent opportunity to answer fundamental evolutionary questions about whether parallel adaptation to similar introduced environments affects the same genomic regions.

Ambrosia artemisiifolia (common ragweed) is an annual weed that is native to North America. In Europe, it became invasive upon introduction during the late 19th century and is today established on all continents except Antarctica. Its highly allergic pollen is the main cause of hay fever and the plant produces high annual costs (control, health care, reduced crop production).

We combine genomic data from historic herbarium sheets with modern data from both the native (North America) and introduced (Europe) ranges to infer temporal changes in the population structure. Moreover, changes in allele frequency variation in genomic regions putatively under selection will be identified and tracked over time. To achieve this, low-depth shotgun sequencing data will be mapped against a reference genome and the genotype likelihoods will be inferred using ANGSD. The population genetic structure will be inferred using NGSAdmix. To identify genomic regions putatively under selection, an outlier analysis based on the genomic distribution of Wright's fixation index F_{ST} will be performed along with environment-allele associations. We expect to find repeated patterns of local adaptation and a higher frequency of adaptation from standing variation compared to de novo mutations in the introduced range. Moreover, we will test different introduction scenarios and try to identify the source population(s) of European common ragweed.

A new MSCA International Training Network: Plant.ID, molecular identification of plants for the world of tomorrow

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Many of the nearly 400,000 species of plants provide food, feed, medicines, and construction materials. Besides these positive impacts, plants also affect us negatively through pollen allergies, poisonous species, as invasive species, and as adulterants in herbal medicines.

Nevertheless, plants are the most promising biological resource for our future. Current extinction risks of global flora and vast decline in taxonomic expertise demand accurate and rapid identification approaches to understand and valorise botanical biodiversity. Advances in genomic data and DNA sequencing are revolutionizing plant systematics, and modern molecular identification methods make it possible to accurately determine plants in ways that were technically impossible only a decade ago. To efficiently harvest the potential of the opportunities provided by new genomic techniques, society today is in urgent need of trained biosystematists experienced in both taxonomy and in handling enormous amounts of genomic data.

Plant.ID, led by the Natural History Museum in Oslo, will be training a group of 15 PhD students working in different institutions in Europe to innovatively address these challenges by bringing together academic and non-academic partners including regulatory agencies, industry, SMEs and NGO stakeholders, with the aim of developing molecular identification of plants through tailored approaches to species delimitation, metabarcoding, gene capture, and genomic barcoding, in order to empower stakeholders with simplified molecular identification of plants. We will provide an overview of the planned projects and show how these are connected and address the challenges above.

The spatial distribution of phylogenetic diversity and endemism in the Norwegian vascular flora

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Biodiversity is commonly measured as the local abundance of discrete species. However, this approach fails to incorporate evolutionary relationships among species and thus gives an incomplete picture of the diversity in a given region. Recently developed methods for spatial phylogenetics combine species occurrence datasets with molecular phylogenetic data to recover information about the spatial distribution of phylogenetic diversity and endemism across a geographic region. Previous studies have applied these methods to regions with a long evolutionary history, e.g. Australia and California. Norway, however, has a relatively short evolutionary history as the region was covered by the Fennoscandian Ice Sheet between 22 and 9.7 cal kyr BP. By applying spatial phylogenetics to the about 1300 native vascular plants in Norway, we can explore spatial biodiversity patterns in a relatively young region.

Our primary aim is to test whether plant phylogenetic diversity is non-randomly distributed across Norway, and to seek causal mechanisms for the revealed patterns, e.g. anthropogenic effects, abiotic factors or a consequence of postglacial migration routes. We also aim to identify high-diversity regions of plants in Norway that are currently not within protected areas, and to use the data to objectively define Norwegian phytogeographic regions. We used GenBank resources and Sanger sequencing of herbarium specimens to complete a multiple sequence alignment (MSA) of one nuclear marker (ITS) and two plastid genes (*matK*, *rbcL*). We used a maximum likelihood approach to infer a phylogenetic hypothesis from the MSA and we verified congruence with the topology and ordinal classification currently accepted by the Angiosperm Phylogeny Group IV (APGIV). We analysed the phylogeny in combination with geo-referenced occurrence data from the GBIF using the software Biodiverse. We also performed pairwise linear correlation analyses in order to determine if phylogenetic diversity outlier regions are associated with various environmental explanatory variables (e.g. temperature, precipitation, soil pH, time since glacial ice cover, human population density). Preliminary results will be presented.

Important medicinal plant families in Thailand

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Many currently used medicines were developed from plant active compounds. However, searching medicinal properties from plants randomly needs a huge amount of time and economic resources. To follow ethnomedicinal uses is one of the good ways to reduce those costs.

The aim of our study is to identify important plant taxa based on ethnobotanical uses in Thailand. Over 16,000 use reports of medicinal plants from Thailand were collected from Books, Theses, scientific reports and journal articles which were published from 1990 to 2014. The proportion of the number of medicinal species and the total number of all species in a particular family was computed. The result showed that 22 out of 206 medicinal plant families in Thailand had a higher proportion of medicinal species than other families. Moreover, Fabaceae, Apocynaceae, Asteraceae, Lamiaceae, and Rubiaceae had very high proportions of medicinal plants. We suggest that plant species from these plant families should be good candidates for new pharmaceutical discoveries.

Is interspecific gene flow in peatmosses (*Sphagnum*) constrained by phylogenetic relatedness and life-history traits?

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Introgression and hybridization are important processes leading to speciation in plants. Peatmosses – *Sphagnum* (Bryophyta) – is a species-rich genus (ca. 300 species worldwide), which includes five morphologically diverse subgenera. There is numerous evidence of hybridization and allopolyploidization in *Sphagnum*, and the genus is considered to be taxonomically difficult.

We summarize current knowledge about occurrence of hybridization in *Sphagnum* and explore how it is associated with relatedness and seven life-history traits of parental species using the factorial analysis of mixed data. We demonstrate that up to 20% of all *Sphagnum* species potentially hybridize, mostly producing from one to four allopolyploid hybrids. There are many inter-subgeneric hybrids. Parents of admixed individuals (i.e. haploid individuals resulted from admixture between different species) are more related to each other than parents of allopolyploids (i.e. polyploid hybrids between different species). Hybridization tends to be more intensive in monoicous and polyicous species with high sporulation frequency and small spores. However, neither phylogenetic proximity nor life-history traits fully explain occurrence and incidence of hybridization in peatmosses. The implications of this are discussed.

Genetic and morphological variation in the circumpolar distribution range of *Sphagnum warnstorffii*: indications of vicariant divergence within a common peatmoss

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The Quaternary climatic oscillations caused pronounced changes in the distribution of the genetic variation among populations as well as phenotypic diversification worldwide. How important these processes have been in plants with high gene flow potential has been less studied. *Sphagnum warnstorffii* is a peatmoss species with a wide circumpolar distribution range exhibiting considerable morphological variation. In particular, many arctic plants differ morphologically from plants in the rest of its distribution range.

We used single nucleotide polymorphism (SNP) genotyping to investigate the patterns of genetic diversity in 112 plants from 105 localities sampled throughout the species distribution range, and explored how this was correlated with phenotypic variation. Genetic cluster analysis identified two main genetic lineages with average F_{ST} equal to 0.21 between them. The first cluster is restricted to the arctic region, while the second has a wider distribution range covering the arctic, boreal and boreo-nemoral regions of Eurasia and North America. We show that morphological variation is mostly concordant with patterns of genetic differentiation, and possibly representing adaptation to local environments. Based on approximate Bayesian computation simulations, we find that the two lineages likely diverged from each other before the Last Glacial Maximum (LGM). Our results show that vicariance due to glacial oscillations likely played a role for current patterns of diversification within a common peatmoss exhibiting a high gene flow potential.

Testing the suitability of two novel universal eukaryotic metabarcoding markers for diatom analysis of peat bog communities

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Diatoms are micro-algal freshwater indicators widely used to infer water quality in limnological and paleoecological studies. Traditional assessments based on microscopic morphological determinations are time-consuming and may lead to identification uncertainties. In contrast, metabarcoding techniques allow to perform fast, objective and simultaneous characterization of a wide array of taxa from environmental samples.

This study aims to contrast the information about diatom assemblages that can be provided by two novel eukaryotic universal metabarcoding markers (rRNA 18S-V7 region and Leray fragment of the mitochondrial cytochrome c oxidase, COI), comparing the results to those from morphological analyses. Diatom assemblages from four peat bog communities were analyzed using light microscopic morphology and both metabarcoding markers. Our results from biodiversity calculations and community dissimilarity analyses show that both metabarcoding markers can broadly recover the same information provided by morphological analysis, and can be useful to characterize and detect changes within these communities. COI is a promising marker for diatom metabarcoding, but the quality of the results is crucially dependent on the availability of a complete reference database, which is currently unavailable for this marker. The less variable 18S-V7 yielded more comparable results to morphological analyses, powered by the availability of a more exhaustive reference database, but it showed lower taxonomic resolution, since the sequences of some closely related species could not be distinguished by this marker. Future improvements in COI reference databases may contribute to boost the utility of this marker to obtain detailed, objective and reproducible diatom molecular biodiversity data from environmental samples.

Four ways to become cryptic

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The development and application of DNA sequencing in systematics uncovered unrecognized diversity within previously established species – i.e. 'cryptic species'. At first sight, the unveiling of cryptic species suggested the occurrence of taxonomic artefacts and generated a discussion focusing on revalidation of taxonomic practices.

Nevertheless, an overlooked angle is that cryptic species might result from evolutionary processes such as selection for a conserved morphology. In this communication I suggest that cryptic species can result from various evolutionary processes, including morphological stasis (i.e. conservation of a morphological plan), recent speciation, parallel and convergent evolution. I exemplify some of these ideas through analyzing recently published literature and recently obtained results in our laboratory. On a broader scope, I suggest that morphological stasis is an overlooked phenomenon and that it challenges classical ecological, paleobiological and evolutionary concepts.

Mitochondrial metabarcoding of marine hard-bottom communities with applications to metaphylogeography

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We present a novel eukaryotic metabarcoding procedure for biodiversity assessment of structurally complex marine hard-bottom ecosystems, introducing an enhanced universal primer set for mitochondrial cytochrome c oxidase I (COI), able to amplify a wide range of eukaryotic supergroups, including metazoans, rhodophytes and stramenopiles. This method was tested on eight different marine littoral benthic communities from two marine protected areas, one in the Balearic Islands (Western Mediterranean) and the other in the Spanish Atlantic Coast. We found unexpectedly high values for MOTU richness, suggesting that these communities host an astonishing amount of yet undescribed eukaryotic biodiversity. Despite the significant gaps currently found in sequence reference databases, we were able to successfully assign over 90% of the sequenced reads to phylum or lower taxonomical level. Our results show that COI metabarcoding can provide biodiversity data with very high resolution, even at intra-specific (haplotype) level.

The comparison of the sequences detected from both ocean basins allowed to assess intra-specific diversity, to recover haplotype networks and to get insights on phylogeographic structure for hundreds of MOTUs simultaneously. We also compared the haplotype networks inferred by metaphylogeography of those species for which classical mitochondrial phylogeography studies were available, and the results were reassuringly similar. This novel universal primer set for COI can potentially be used for biodiversity assessment for a wide range of taxa.

DNA methylation in Arctic charr: Epigenetics to help understand polymorphism

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Arctic charr (*Salvelinus alpinus*) is a polymorphic cold-water fish species belonging to the Salmonidæ family. In Iceland, *Salvelinus alpinus* is found in many places, but in Lake Þingvallavatn it displays remarkable morphological variation, in particular in terms of head and trophic apparatus development.

The research team led by Professor Sigurður S. Snorrason has been working on understanding the reasons for these morphological differences for years now, and some molecular pathways and gene expression differences have been highlighted recently. The main focus of this PhD project is to highlight DNA methylation differences during early development between those morphotypes. Differentially methylated regions will then allow to identify new candidate genes that might be responsible for the differences in craniofacial bone development in this species.

Mechanisms of reproductive isolation in two sympatric morphs of Arctic charr from a subarctic lake, Thingvallavatn

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With their recent natural history and large diversity of ecological niches offered to fish communities, postglacial lakes constitute unique systems for the study of the early stages of sympatric speciation (e.g. the formation of divergent species within a same home range). Lake Thingvallavatn, Iceland, is one such system, which presents fabulous opportunities to investigate this puzzling process. Four different morphs of Arctic charr (*Salvinellus alpinus*) coexist in this lake and are thought to originate from the same population that colonised the basin approximately 10,000 years ago. In this system, the two smallest morphs show different ecological specialisations (one is a limnetic planktivorous (PL), the other a small epi-benthic benthivorous (SB)) and form two distinct reproductive populations. However, their spawning time and location overlap to a large extent. The mechanisms explaining the development and the maintenance of such segregation are still unknown.

We hypothesise that reproductive barriers preventing gene flow between the two morphs act on pre-zygotic and/or postzygotic stages of reproduction. Thus, we expect the pre-zygotic barriers to be the product of mate choice divergences and/or small-scale differences in the spawning time and location. To tackle this we will develop assortative mating experiments in laboratory conditions and set observational field studies on fine scale habitat selection during reproduction. On a post-zygotic level, we predict that hybrids display lower fitness in particular traits conferring them selective disadvantages in comparison to pure-morph individuals. To test this prediction, we will develop laboratory experiments studying various life history traits (survival, growth rate), morphology (head shape), physiology (response to metabolic stressors) and behaviour (foraging ability and personality) in hybrid and pure-morph individuals.

Romance under the waves: Documentary on mating behaviours of Large Benthivorous Charr in Lake Thingvallavatn, Iceland

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Thingvallavatn harbors four morphs of Arctic charr that differ in body size, morphology, behavior and life history characteristics. Arctic charr in Thingvallavatn has been extensively studied for the last four decades. However, very little of the findings have been accessible to a wider public. The only documentary on one of the variants of Arctic charr in Thingvallavatn – the Large Benthivorous (LB) morph - was made in the 1980s in the biggest documented spawning grounds near Ólafsdráttur. Whilst it is innovative for its time and retains scientific relevance, the format and storage medium has aged and thus has become incompatible for current screening equipment.

We have produced footage of the mating behaviors of the LB morph following the previously-defined methods, but with new equipment, better resolution and more hours of filming. Taking into account that more research has been done since the initial filming took place, it was possible able to add more value to already existing material. The film offers a unique opportunity to present Icelandic nature and research findings to a broad local and international audience. The film portrays two viewpoints – that of a researcher and that of a fish. From researcher perspective, the film shows the human part of film creation. Whilst the part devoted to fish shows various mating tactics of the LB Arctic charr, the way in which the charr modify their environment during their spawning period and the environment which has contributed to the development of this morph.

Feb 13 Poster session 2

Bridging Paleoecology (aDNA) with Modern Ecological Understanding

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Our understanding of ecosystem structure and functioning is largely informed by studies on short temporal scales, and little is known about the extent in which processes of the past have shaped the landscapes we see today. Metabarcoding DNA from lake sediments is a powerful tool employed to elucidate past biodiversity and ecosystem state shifts. Information about the recent past can provide a framework for understanding the processes that formed modern ecosystems. Within the research fields of paleoecology and contemporary ecology, however, there is a considerable lack of congruency between study design and therefore a need to improve the integration of methods and analysis.

In order to bridge the gap, this project aims to address typical study design and analysis of both paleoecological and modern ecological research to better understand the the overlap in different spatial, temporal, and taxonomic resolutions. In particular, this study will use sites part of the long-term ecological project COAT (Climate ecological Observatory for Arctic Tundra) to assess the extent in which paleoecology can inform and improve the existing hypotheses for climatic and anthropogenic impacts on vegetation.

Molecular phylogeny of *Rubus* and its relatives within the supertribe Rosodae

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The genus *Rubus* plays important economic and ecological roles, in berry production, as ornamental plants and as invasives. *Rubus* belong to the Rose family, and is currently placed in the supertribe Rosodae, of the subfamily Rosoideae. Further systematic placement of *Rubus* has not yet been clarified, although several studies have tried. Morphology has been of limited phylogenetic use within this group. Eriksson *et al.* (2003) discussed *Rubus*' placement in Rosoidae as problematic, because different data sets based on chloroplast and nuclear genes were incongruent with respect to the placement of *Rubus*. In Potter *et al.* (2007), which is the last major study of the rose family, *Rubus* remains unresolved under the supertribe level due to low support. Overall, the small amounts of data in previous studies are not satisfactory to determine the location of *Rubus*.

The objective of this project is to clarify the uncertain relationship between the genus *Rubus* and other well defined genera within the supertribe Rosodae, based on a supported phylogenetic tree of several different genes.

Molecular phylogeny and intra-generic classification of *Potentilla* L.

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The phylogeny of the rose family is partly unresolved, and many clades show low support in the studies performed so far, or have not been studied in detail. The latter is especially true for the genus *Potentilla*. This genus was revised morphologically by Wolf in 1908. He identified 305 species arranged into six groups. Recent studies of *Potentilla* based on DNA sequence data have resulted in new systematics where a few genera have been discovered to be parts of *Potentilla*, while several taxa have been excluded from the genus. The relationships between the major *Potentilla* clades are still unclear. Eriksson et al. (2003) showed that the *Potentilla reptans*-clade has an unstable position in the phylogenetic tree. That study was based on few molecular data but Töpel et al. (2011) studied *Potentilla* with nuclear ITS and one chloroplast gene. They found six well supported clades within *Potentilla*, but the position of the *P. reptans* clade was equivocal when the chloroplast and the nuclear gene were compared. Incongruences between chloroplast and nuclear phylogenies have been attributed to allopolyploidy caused by hybridization events (Töpel et al. 2011, Smedmark et al. 2003).

The objective of this project is to clarify the relationships between well-supported major clades of *Potentilla* and determine the position of the *P. reptans* clade by using a supported phylogenetic tree of low copy genes, as well as to make inferences on proposed hybridization events.

Untangling the origin of a polyploid: The evolutionary history of *Potentilla norvegica* (Rosaceae) using single-copy nuclear markers

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The evolution of species is generally a slow process, working over thousands or even millions of years. However, sometimes new species evolve within a relatively short period of time through a mechanism known as polyploidisation, defined by a duplication of all the chromosomes in the genome. This can happen either within a species, or after two species have formed a hybrid. Previous molecular studies of the cinquefoils (*Potentilla*) of the Rose family have been unsuccessful in resolving a large part of the genus using morphology or traditional DNA regions used in systematic research. In fact, most of the species are polyploid (from four to twelve sets of chromosomes), in many cases most likely as a result from hybridisation in combination with polyploidisation. Since one extant species thus may have more than one parental lineage, we need to “molecularly dissect” them and perform phylogenetic analyses based on regions representing all their different sets of chromosomes, rather than on traditionally used regions that represent the genome as a whole.

To develop a method for this, we start by focusing on *Potentilla norvegica*, which has populations reported as octoploid (8x) and decaploid (10x). Initial cloning of the single-copy nuclear gene GAPCP1 from specimens representing its circumpolar distribution and the two subspecies suggests that the allele variation is high – an indication of multiple parental lineages. To extend the study we plan on performing Target Capture, a high-throughput sequencing method that can produce more than ten times more data than cloning. This project will contribute new knowledge about speciation through polyploidisation, and the evolutionary relationships and species delimitations of this group of common, but incompletely known, flowering plants in the Norwegian flora. In addition, it will develop methods and molecular markers that can be used in other evolutionary studies in the economically important Rose family.

Conservation genomic studies of red-listed angiosperm species prevalent in Central Norway

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Taxonomy does not always reflect underlying genetic diversity. Several species, as traditionally circumscribed, contain a considerable amount of cryptic diversity. Genetically distinct and more or less reproductively isolated lineages classified under one species name may have distinct potential in a changing environment. Thus, it is essential for long-term conservation to identify these evolutionary significant units (ESUs).

In this project, a target enrichment (capture) technique will be implemented on selected non-model red-listed angiosperm taxa: *Eurybia sibirica*, and the *Carex flava* complex. High-throughput sequencing (HTS) of genomes and transcriptomes from freshly collected material of a subset of the targeted taxa will be used for designing target capture probes. Genomic data will be produced from both herbarium- and field-collected specimens (throughout their distribution area). We aim to delimit ESUs, infer phylogeographic patterns, resolve phylogenetic relationships and assess the vulnerability of focal taxa. *Eurybia sibirica* have gone through a severe population reduction the last 100 years in Norway. We will combine genetic analyses with distribution modelling to study the population genomics and distribution of *E. sibirica* through time. The *Carex flava* complex contains several red-listed Norwegian taxa. Worldwide, there is little consensus regarding species delimitation within this complex. We will resolve the phylogenetic history of the *Carex flava* complex using genomic analyses. In addition, we want to test if the target capture technique can give a higher intraspecific resolution compared to RAD-seq using *C. jemtlandica* and *C. lepidocarpa* as model species.

The systematic relationships of the North Atlantic and arctic *Cochlearia* L. taxa

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The overall aim of the project is to provide a full overview of the systematic relationships of the North Atlantic and arctic *Cochlearia* taxa – as a resource for future studies, e.g. investigations of local adaptation and evolution of cold tolerance in response to climate change. The immediate goal of this master project is to provide a full overview of the systematic relationships of the North Atlantic and arctic *Cochlearia* taxa. The genus *Cochlearia* is common around most of Europe, and is abundantly found also in arctic areas. In mainland Norway, the common species is the tetraploid *Cochlearia officinalis*. The *Cochlearia officinalis* complex is an arctic-boreal polyploid complex which previously has been studied cytologically, morphologically and genetically. The arctic plant *Cochlearia groenlandica* differs in several ways from the usual biennial *C. officinalis* in mainland Norway by being diploid, perennial and having smaller flowers, as well as chemically and ecologically. The arctic and northwestern European plants seem to be reproductively isolated, and have traditionally been considered different species. In addition, the arctic plants might represent more than one species. *Cochlearia groenlandica* is mainly found in the high Arctic, whereas the more southern arctic plants in northern mainland Russia-Siberia, the Russian Far East and in Beringian Alaska differ morphologically and have traditionally been accepted as *Cochlearia arctica*.

Cochlearia samples have already been collected in western Greenland, including the type locality, in August 2017. Plants will be grown in the Phytotrone at The Department of Biosciences, UiO, and the material will be compared genetically and morphologically to *Cochlearia* plants from other arctic and North Atlantic localities. An optimized RAD-sequencing (RADseq) protocol for *Cochlearia*, which successfully has been used in two previous master projects addressing genetic variation in Northern Norway and Iceland, will be used to provide genomic single nucleotide polymorphism (SNP) data. The data will be analysed by appropriate analytic tools to detect genetic structure and unravel evolutionary and biogeographic relationships.

Evidencing Drivers of Spatial Trait Variation Across a Latitudinal Gradient in the Brazilian Atlantic Forest

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Within the Neotropics, Brazil has the highest level of species diversity in plants. As part of its landscape, the Atlantic Forest stands out as a biodiversity hotspot in which bromeliads undergone a significant rapid diversification.

We investigate size and shape variation of leaves and floral bracts across a latitudinal gradient in this biome through study of a species complex of the genus *Vriesea* (Bromeliaceae). To understand which forces can explain the morphological variation observed, we are testing the genetic structure using two chloroplast markers, and climate (temperature and precipitation) influence. Besides, we test the traditional taxonomic delimitation of the taxa, and historical biogeographic patterns that can predict the spatial distribution. A total of 211 individuals from 14 natural populations were sampled. Preliminary results show a gradual change from lanceolate to wide-elliptic bracts, as well from linear to narrow-obovate leaves, recognized between northern and southern populations. Leaves and floral bracts do not covary and were treated in different datasets. Trait variation is congruent with the genetic pattern, and with the theory of Late Quaternary stable areas within the forest. We will test statistically all those factors and provide new insights on the drivers of spatial trait variation in Neotropics.

Reinforcement in *Fucus* species

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The macroalgal genus *Fucus* (Phaeophyceae, Heterokonta) are ecosystem engineers that provide structure and complexity to otherwise inhospitable and barren rocky shorelines. *Fucus* populations also provide nutrients and shelter for many invertebrate and fish species and have an important ecological function in the littoral ecosystem. The genus originated in the North Pacific and after the opening of the Bering Strait (4.1–7.4 Myr BP), colonized the North Atlantic where it radiated into two distinct lineages that diverged 0.9–2.25 Myr BP: Lineage 1 including *F. distichus*, *F. serratus*; and Lineage 2 including *F. spiralis*, *F. vesiculosus*, and others. Although hybridization is not common between Lineage 1 and 2 species, hybridization within each lineage is prevalent. Lineage 1 consists of the dioecious *F. serratus* with a temperate east Atlantic distribution. The sister species *F. distichus* is a hermaphrodite and characterized by an Arctic distribution. Species form distinct patterns of zonation in the intertidal/subtidal, thereby producing a range of ecotypes to gradients in salinity, temperature, and desiccation. Furthermore, as the limited dispersal of *Fucus* gametes leads to significant genetic structure at a scale of kilometers, patterns of local adaptation can be significant, for example, evidence for strong local adaptation to salinity has been demonstrated for *F. serratus* at scales.

These factors make *Fucus* an ideal group in which to study mechanisms of speciation. The evolution of species is central to evolutionary biology and speciation is increasingly viewed as a continuum. Crucial processes include local adaptation on one end of the spectrum and reproductive isolation on the other. Three hybrid zones involving *F. distichus* and *F. serratus* have been identified in the Central/East Atlantic. The zones consisted of a natural zone in Northern Norway (ca. 10,000 yrs of sympatry), and two others resulting from the introduction of either species: Iceland (*F. serratus* introduced and 100 yrs of sympatry) and the Kattegatt (*F. distichus*, introduced and 100 yrs of sympatry). A recent study of the *F. distichus* and *F. serratus* contact zones has found strong evidence for reinforcement as hybridization and introgression significantly decreased with increasing duration of sympatry and F1 hybrids were absent from the oldest contact zone. I hope to understand how reproductive isolation mechanisms evolve in the *Fucus* speciation continuum, from local adaptation to complete reproductive isolation, by specifically targeting both end of the speciation continuum.

Conservation genomics of North Atlantic sponge grounds: assessing diversity, connectivity and vulnerability of deep-sea habitat forming species

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The deep sea is the largest ecosystems on Earth, and sponges have important biological functions in its benthic communities. They maintain biodiversity, create shelter, serve as a food source for other species, and influence the flow of essential nutrients. The future of the sponge grounds is uncertain due to an increasing human imprint in deep-sea ecosystems. These ecosystems are sensitive to oil and gas exploration, climate change, fisheries, radioactive and general waste disposal, and other anthropogenic impacts. Our knowledge on sponge grounds and their key species remains limited. Our project will focus on glass sponge aggregations of the temperate and boreal North Atlantic. Samples have been collected in the course of several oceanographic campaigns (e.g. Hudson 2016, Martha Black 2017, Angéles Alvariño 2017 and G.O. Sars 2016-2017), groundfish surveys (e.g. on the Scotian shelf) or through contact with other researchers and institutions, both from within and outside the SponGES project consortium. The main aim of the project is to investigate the genetic diversity, structure and connectivity of key habitat-forming sponge species of the North Atlantic. We will focus on three hexactinellid species – *Vazella pourtalesi*, *Pheronema carpenteri* and *Aphrocallistes beatrix* – known to form structurally complex habitats in different areas of the North Atlantic (and for which no information exists on their genetic diversity or connectivity. Specifically, we aim to i) understand the spatial patterns of genetic diversity across each species distribution range at various scales (within and across populations) ii) assess the impact that variable degrees of fishing pressure have on the genetic diversity and structure of the different populations iii) evaluate the contribution of sexual vs asexual reproduction on the structuring of the populations. To accomplish the goals, this up-to-date population genomics tools and methods using a RADseq approach will be employed. The generated data will deepen our understanding of the genetic patterns which occur at deep-sea sponge grounds and their sustainability under human impact, ultimately aiding conservation strategies as well as potential restoration activities. The design of the project and background will be presented during a poster session.

Feb 14

Molecular phylogenetics and taxonomy of the tropical lichen genus *Phyllopsora*

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The lichen genus *Phyllopsora* belongs to the family Ramalinaceae (Ascomycota) and currently comprises 71 species. Apart from a few temperate species, they grow mainly on bark in (sub-)tropical rainforests and moist woodlands. A typical growth form characterizes the genus: It forms squamules or areoles that grow on a dense hypothallus. Species identification is generally challenging and is based on ascospore morphology, vegetative dispersal units and thallus construction. Many species contain complex chemical compounds (lichen substances) whose composition is often diagnostic at the species level. Some species contain up to five different chemotypes, while about one third of the species lack lichen substances. It is often difficult to assign freshly collected material of *Phyllopsora* to any known species leaving many specimens unidentified. About 10% of all species are known from type collections only, which sometimes are 50-150 years old and in bad shape. These species are poorly understood, and it is not possible to tell if they are congruent with modern collections. Attempts are made to sequence old DNA (if the original material is rich enough). If not successful, we might select epitypes among recently collected, sequenced specimens. Recent molecular studies of the whole family have shown that the genus is not monophyletic, indicating convergent evolution of the typical growth form.

In the present study, we aim to circumscribe the true *Phyllopsora s. str.* supported by multiple sources of data (i.e. integrative taxonomy). We have collected material in Brazil, Venezuela and Sri Lanka and investigated extensive loans from various herbaria. We have generated multi-locus sequence data for as many species as possible. Our preliminary phylogenetic results corroborate previous indications that the current taxonomy is in strong need of revisionary work. Several new species are described.

Mapping the diversity of crustose lichenized and lichenicolous fungi in Norwegian rainforests

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The Norwegian boreo-nemoral and boreal rainforests are unique and internationally recognized hot-spots for biodiversity. They are listed as endangered habitats in Norway and proposed as selected habitat types according to the Nature Diversity Act. The rainforests are distributed along the Norwegian west coast from Vest-Agder to southern Troms. They are distinguished in the Norwegian forest landscape by their rich diversity of highly oceanic forest epiphytes including bryophytes and lichens, often showing subtropical and tropical affinities.

In a project funded by the Norwegian Biodiversity Information Centre, we monitor the diversity of two incompletely known functional groups of epiphytes in the boreo-nemoral and boreal rainforests: crustose lichenized and lichenicolous fungi. We monitor these groups at three levels of diversity, including methods of traditional biodiversity mapping, DNA barcoding, and metabarcoding of selected trees (pilot study). During the first year of the project, about 50% of the planned field work has been completed and the identification and barcoding of the samples has started. First results indicate a high proportion of previously unknown taxa within these forests, including at least two species of lichenicolous fungi new to science and 12 species of lichenized and lichenicolous fungi new to Norway or Scandinavia, and numerous additional finds of rare or neglected species.

In this presentation, we will talk about (1) ongoing and future activities within our research project, (2) first results, and (3) opportunities for students and researchers interested in lichens and lichenicolous fungi of the Norwegian boreo-nemoral and boreal rainforests. The latter includes a five-days ForBio course in Steinkjer planned for August 2018.

Ancient DNA to reveal the genetic history of European reindeer

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The origin and genetic history of the domestic reindeer (*Rangifer tarandus*) is controversial. Past studies of genetic diversity in Europe and Asia, based on small mitochondrial genome fragments and nuclear microsatellites, indicate there may have been up to three major domestication events in the history of reindeer husbandry. Interbreeding of domestic and wild reindeer may also obscure the genetic signature of the domestication event(s).

Using ancient specimens to provide temporal data could avoid the confounding effects of introgression from wild reindeer and may help to elucidate the history of the reindeer.

We extracted ancient DNA from a variety of well-preserved ancient European reindeer bones and teeth, built these extracts into high-throughput sequencing libraries, and performed shotgun sequencing. We report preliminary results indicating the fraction of endogenous sequences that align with an available reindeer draft genome, and the existence of DNA damage patterns authenticating the ancient origin of the DNA. We report preliminary results about changes in reindeer mitochondrial genomic diversity over the past 50,000 years.

Current extinction of mammals more than 100 times higher than during Last Glacial Maximum

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In the recent years we have been witnessing well-recorded, dramatic declines in population sizes of several mammal species and several instances of extinction, which can be attributed to a large extent to the impact of our own species. These negative trends raise concerns and worries about human impact on the natural world and about the future of biodiversity. However, in order to properly assess the magnitude and severity of the current rate of species loss, we need to understand, how many extinctions we would expect under natural conditions, including fluctuations in climate. Such information is available in the fossil record, which provides direct evidence, though incomplete, of past biodiversity. Here we use a well-curated dataset of last occurrence dates of extinct mammalian species to reconstruct the loss of Mammalian species during the past 130,000 years (130 ka), a time period with significant fluctuations in world climate. We observe a more than 1000-fold increase of extinction rates at present in relation to the base extinction rate from 130 ka ago. The rapid increase in extinction rates does not follow climatic variations but rather coincides with the accelerated population growth and expansion of our own species *Homo sapiens*. We contrast this extinction rate estimated from fossil data with species-specific extinction risk assessments provided by the IUCN (International Union for Conservation of Nature). We apply these risk assessments for modeling future extinctions. The results are alarming and show that we are entering an unprecedented extinction of mammal species, which may lead to a loss of several hundred mammalian species by the year 2100. This would equate to a further increase of extinction rates by more than one order of magnitude in comparison to the already unnaturally high extinction rate at present. However, we find that efficient conservation management has the potential to decrease future species losses significantly. While our findings concerning the magnitude of the current extinction are alarming, they also provide guidance for future policy making and conservation management decisions.

REININ project: Reindeer interactions from plants and birds to humans: balancing the odds of climate change

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Understanding how species adjust their ecology to changing environmental conditions and how this in turn affects ecosystem functioning is an essential requirement in the context of global change. Rangifer tarandus (family Cervidae), called reindeer in Eurasia and caribou in North America, is the most abundant large herbivorous species with circumpolar distribution in the northern part of the Holarctic. It is also a keystone species in the arctic ecosystems, involved in a complex network of biotic interactions including primary producers (e.g., plants, lichens, bryophytes), carnivore populations and humans, providing essential ecosystem services to indigenous peoples in terms of food, clothing, shelter and transportation. Also, reindeer husbandry is deeply rooted into indigenous peoples history and is essential for their cultural identity. Using DNA metabarcoding the aim of the REININ project is to analyze geographic, climatic and seasonal patterns of reindeer diet variation in different socio-economic settings across the Arctic – Svalbard (wild reindeer, no management, no seasonal migrations), Norway, Finnmark (semi-domesticated reindeer, long traditions), Russian Arctic (both wild and domestic reindeer, long traditions), Canada (wild populations of caribou and recently introduced reindeer herding). In collaboration with field ecologists and social scientists, we are currently: (i) Documenting variations in reindeer diet quality and composition across seasons, habitats, geographic regions, and in relation with the presence/absence of other herbivore species in the Arctic, such as geese, ptarmigan or rodents; (ii) Collecting socio-economic data and local knowledge through interviews with reindeer herders and other important stakeholders involved in the reindeer husbandry. Our final objective is the integration of ecosystem-based information with socio-economic data and local knowledge that will allow the identification of relevant governance solutions for sustainable reindeer husbandry and resilient tundra ecosystem management in the face of climate change.

Modelling trophic link distribution in a tundra arthropod community

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More than any other region, the Arctic is currently confronted with massive transformation processes due to climate change. Higher temperatures in combination with increasing precipitation are shortening flower phenology and favor expansion of shrubs. The predator community of the High Arctic is unique in structure. Here, predator groups abundant in other parts of the world (like ants and predatory ground beetles) are missing and replaced by an abundance of spiders, mainly wolf spiders (Lycosidae) and crab spiders (Thomisidae). Current and future climate change will likely affect the abundance and diversity of the key prey of spiders. At the same time, the most abundant lycosid, *Pardosa glacialis*, is experiencing a shift in body size distribution, reflected by a change in size dimorphism over the last two decades. In association with a change in spider abundance, this is likely to reflect into changes in prey choice and higher intraspecific competition. To predict how climate change may affect the prey selection and trophic role of spiders, we here use an elevation gradient in a 'space-for-time' approach. Applying a High Throughput Sequencing (HTS) approach to identifying spider gut contents, we directly establish the trophic links involving *Pardosa* along an elevation gradient representing different habitats in Zackenberg, NE-Greenland and investigated effects of prey availability (local presence and abundance), predator and prey body size and habitat characteristics on the occurrence and strength of predator-prey interactions. To achieve that, we collected prey and predator organism along three parallel elevation gradients, spanning from 19-586 m a.s.l. every week in July 2015 and additionally screened predators for invertebrate prey DNA. We found that lycosid and thomisid spiders feed on a wide spectrum of prey, particularly dipterans, and showing particularly strong interactions with prey species associated with soil and aquatic habitats. Feeding preferences and strength are directly related to elevation-dependent prey availability as well as predator body size, indicating shifts in feeding behavior with age and elevation. We conclude that feeding behavior is driven by both environmental and predator traits. Flexibility in prey choice allows optimal exploitation of prey resources suggesting high adaptive capacity under changing conditions.

Towards an integrative taxonomic revision of *Allodia* s. str. (Diptera, Mycetophilidae)

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The taxonomic expertise of the dipteran family Mycetophilidae, the true fungus gnats, has long traditions in Northern Europe, and the fungus gnat fauna is well known. This accumulated knowledge has been used to build a reference library of DNA barcodes. The library serves as an excellent basis to study large or problematic genera of fungus gnats. *Allodia* is such a genus, with its highest diversity in the northern boreal forests, still very little is known about the Nearctic species. The genus includes about 75 nominal species, split into two subgenera; *Allodia* s. str. and *Brachycampta*.

In this study, we investigate the diversity, distribution and phylogenetic relationships among Holarctic species in *Allodia* s. str. The mitochondrial CO1 and the nuclear ITS2 markers, together with morphology, are used to evaluate the delimitation of species and their distribution patterns. Hitherto, we have examined 21 of a total 40 hypothetical species (molecular operational taxonomic units), suggested by the BIN system in The Barcode of Life Database (BOLD).

The results suggests several patterns of trans-Palaeartic and circumpolar species distributions. Most of the hypothetical species are supported by morphology and differences in ITS2 sequences. Additionally, several of the species with a Palaeartic distribution have closely related sister species in the Nearctic. Approximately ten species will, based on these results, be described as new to science, most of which have a Nearctic distribution.

Molecular phylogenetics reveals unknown relationships within Empidoidea (Diptera)

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The Empidoidea is a large and morphologically diverse superfamily within the order Diptera, true flies, and its members occupy a vast array of habitats and different species groups express a great variation in life histories. The group has been subject to multiple revisions and for the last decades the internal relationships are considered unknown.

We hypothesize the evolution of this group based on molecular data, as well as discuss its diversity. We also present a phylogeny based on the mitochondrial genes COI and Cyt β and the nuclear genes CAD, EF-1 α and IDH in a Bayesian analysis. Several groups withstand testing, but we also find novel relationships in the evolutionary context and can present more thorough and stable phylogenetic hypothesis than presented before.

Our results illustrating the higher systematics of Empidoidea are more similar to previous tentative molecular studies than those based on morphological data, but several subfamilies and tribes based on morphology are corroborated. We discuss these findings, how they relate to previous studies and how some morphological characters could be plesiomorphic. We finally propose a new classification based on this molecular analysis.

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