ForBio Annual Meeting Oslo

29th November – 1st December 2021

Welcome to our ForBio Annual Meeting! This year we will meet in Oslo both in-person and online. Not only do we have the highest number of participants, but thanks to the hybrid format and an effort to travel by train as much as possible, we also have the lowest carbon footprint of any ForBio meeting. The program includes 5 keynotes, 22 talks and 12 lightning talks spread out over four half days. We will be in the Tøyen Manor House and the Oslo Climate House. All talks can be joined on Zoom. In addition the Tuesday morning session will be online only.

Organizing Committee

Quentin Mauvisseau, Natural History Museum, University of Oslo

Elisabeth Stur, NTNU University Museum, University of Trondheim

Nataliya Budaeva, University Museum of Bergen, University of Bergen

Galina Gusarova, The Arctic University Museum of Norway, UiT, Tromsø

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ForBio Annual Meeting Slack Channel

https://join.slack.com/t/forbioannualm-3851303/shared_invite/zt-yzx7f3cy-1fDKMVUXWCyqELW2kV7OCA

November 29th - Tøyen Manor House

12:00 - 13:00	Light lunch, coffee and mingling
13.00 – 13.15	Introduction and Welcome
	Hugo de Boer, Leader of ForBio, UiO
13.15 – 14.00	Keynote – Chair: **Hugo de Boer**
	Natasha de Vere, Natural History Museum of Denmark, University of Copenhagen
	DNA barcoding floras and their applications for plants, people and pollinators
Session 1	Chair : **Jesus Adrian Chimal Ballesteros**
14.00 – 14.20	**Niko Johansson**, Finnish Museum of Natural History, University of Helsinki
	Woodpeckers as potential dispersal vectors for lichens
14.20 – 14.40	Coffee Break
14.40 – 15.00	**Oliver Kersten**, Department of Biosciences, University of Oslo
	Complex population structure of the Atlantic puffin revealed by whole genome analyses
15.00 – 15.20	**Megan Gross**, Natural History Museum, University of Oslo
	Using environmental DNA to direct future isolation of short-branch microsporidia
Session 2	Chair : **Thore Koppetsch**
15.20 – 15.25	**Aurélie Boilard**, Department of Biosciences, University of Oslo
	122 000 years of fauna diversity of Nordic ecosystems explored through paleogenomics

15.25 – 15.30 **Erik Möller**, Natural History Museum, University of Oslo

Molecular phylogenetics and genus delimitation in the Rhizocarpaceae (lichenized ascomycetes) with focus on the Rhizocarpon hochstetteri-complex

15.30 – 15.35 **Hedvig Mjøen**, Natural History Museum, University of Oslo

The identity of Veratrum in Northern Norway

15.35 – 15.40 **Alberto Valero-Gracia**, Natural History Museum, University of Oslo

"InverOmics", phylogeny and evolution of Spiralia based on genomic data: a first report

15.40 – 15.50 Lightning Q&A

15.50 – 16.15 Coffee Break

16.15 – 17.00 Keynote – Chair: **Quentin Mauvisseau**

Naiara Rodriguez-Ezpeleta, AZTI, Basque Research and Technology Alliance

Modernizing marine management using innovative genomic approaches

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November 30th - Digital morning & Climate House afternoon

9.00 – 9.15 Digital mingling "You're muted", "I can't share screen", "Are you here?

Session 3 Chair: **Solveig Bua Løken**

9.15 – 9.30 **Malene Nygård**, University Museum, Norwegian University of Science and Technology

Custom hybrid capture probes enable herbarium specimen phylogenomic analysis of the sedges (Cyperaceae)

9.30 – 9.45 **Polina Borisova**, Shirshov Institute of Oceanology, Russian Academy of Sciences

Diversity of Laonice (Annelida, Spionidae) from the Arctic and the North Atlantic

9.45 – 10.00 **Anna Karolina Oliveira de Queiroz**, Natural History Museum, University of Oslo

Dietary analysis of Carangid fishes from Southeastern Brazil determined by metabarcoding

10.00 – 10.10 Coffee Break

Session 4 Chair: **Ann Evankow**

10.10 – 10:25 **Martha Everett**, Shirshov Institute of Oceanology, Russian Academy of Sciences

Molecular and morphometric analyses reveal highly underestimated diversity in Eteone (Phyllodocidae, Annelida)

10.25 – 11:40 **Jaime Morin Lagos**, University Museum, Norwegian University of Science and Technology

The most comprehensive mitogenome phylogeny of the tribe Arini (Psittacidae) with emphasis in Pyrrhura parrots

10.40 – 10:55 **Thomas Baudry**, University of Poitiers & University of French West Indies

Mapping a super-invader in a biodiversity hotspot, an eDNA-based success story

10.55 – 11.05 Coffee Break

11.05 – 11:20 **Becky Cramer**, Natural History Museum, University of Oslo

Sperm evolution in the Canary Islands chiffchaff

11.20 – 11:25 **Maonian Xu**, Faculty of Pharmaceutical Sciences, University of Iceland

Intrathalline microalgal diversity and ultrastructural features of the new lichenized Trebouxia delisei lineage (Trebouxiophyceae, Chlorophyta)

11.25 – 11:30 **Maël Grosse**, University of the Balearic Islands

Polychaetes in Norwegian ports: uncovering diversity in coastal anthropogenic environment

11.30 – 11.35 Wrap-up

12.00 – 13.00	Lunch at the Climate House
13.00 – 13:45	Keynote – Chair: **Galina Gusarova**
	Dimitar Stefanov Dimitrov, Department of Natural History, University Museum of Bergen
	Following the web of Ariadne: the quest towards understating spiders diversity
Session 5	Chair: **Aurélie Boilard**
13.45 – 14.05	**Maria Ariza Salazar**, Natural History Museum, University of Oslo
	Ground-truthing soil eDNA plant diversity assessments
14.05 – 14.25	**Gertrude Evusa**, University of Oslo
	Utility of Kalanchoe (Crassulaceae) in Kenya
14.25 – 14.40	Coffee Break
14.40 – 15.00	**Ehsan Moqanaki**, Faculty of Environmental Sciences, Norwegian University of Life Sciences
	Field determinants of PCR success in specimen identification using non-invasive DNA sampling of carnivore scats
15.00 – 15.20	**Mika Kirkhus**, Faculty of Environmental Sciences, Norwegian University of Life Sciences
	Shedding light on the hidden diversity and host specificity of tremellalean lichenicolous fungi in Norway
15.20 – 16:05	Keynote – Chair: **Nataliya Budaeva**
	Nicolas Straube, Department of Natural History, University Museum of Bergen
	Museum Collection Specimens as DNA Archives
16.05 – 16.20	Coffee Break
Session 6	Chair: **Emma Whittington**
16.20 – 16.25	**Ana Teresa Capucho**, Natural History Museum, University of Oslo
	Assessing biodiversity in the marine algae belt
16.25 – 16.30	**Fabian Kellner**, University Museum, Norwegian University of Science and Technology

Genomic consequences of historical overharvest in Svalbard reindeer

16.30 – 16.35 **Madhushri Varunjikar**, Institute of Marine Research, Bergen

Molecular phylogeny of fish and insect species using spectra comparison tool compareMS2

16.35 – 16.40 **Helene Grindeland**, Natural History Museum, University of Oslo

Accumulation of hybrid incompatibilities within two species (Arabis alpina and Cardamine hirsuta) relative to mating system and population divergence times

16.40 – 16.50 Lightning Q&A

17.00 – 20.00 Tapas mingle at the Climate House

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December 1st - Tøyen Manor House

9.00 – 9:45 Keynote – Chair: **Elisabeth Stur**

Andreas Altenburger, The Arctic University Museum of Norway

How to steal chloroplasts - lessons from the marine mixotroph Mesodinium rubrum

Session 7 Chair: **Margret Veltman**

9.45 – 10.05 **Thore Koppetsch**, Natural History Museum, University of Oslo

Determinants affecting the analysis and detection of introgression in phylogenies

10.05 – 10.25 **Anastasia Poliakova**, Tromsø University Museum - The Arctic University of Norway

Vegetation and environment history of the western Kola Peninsula reconstructed based on the sediment ancient plant DNA from the lake Imandra

10.25 – 10.40 Coffee Break

10.40 – 11.00 **Michael Matschiner**, Natural History Museum, University of Oslo

Supergene origin and maintenance in Atlantic cod

11.00 – 11:20 **Emma Whittington**, Natural History Museum, University of Oslo

Comparative Proteomics of the Perivitelline Layer – the Site of Avian Sperm-Egg Interaction

11.20 – 11:40 **Markus Fjelde**, Natural History Museum, University of Oslo

Cryptic diversity unveils unexpected challenges in the seemingly paraphyletic lichen genus Calvitimela (Lecanoromycetes, Ascomycota)

Session 8 Chair: **Maria Ariza Salazar**

11.40 – 11:45 **Dilli Rijal**, Institute of Marine Research, Tromsø

Contamination during fish sampling affects molecular diet inferences

11.45 – 11:50 **Ann Evankow**, Natural History Museum, University of Oslo

Patterns and Processes of Cryptic Species Diversity of Soil Crust Lichens of South Africa

11.50 – 11:55 **Abush Zinaw Zergabachew**, Natural History Museum, University of Oslo

Taxonomy and biogeography of the subtribe menthinae (lamiaceae), with focus on the tropical eastern African 'sky-islands'

11.55 – 12:00 **Solveig Løken**, Natural History Museum, University of Oslo

Using target capture to resolve taxon limits in Ledebouria and related genera

12.00 – 12.10 Lightning Q&A

12.10 – 13.10 Lunch at Tøyen Manor House

13.10 – 13.30 Awards and Closing

Woodpeckers as potential dispersal vectors for lichens

Niko Johansson[1*]; Ulla Kaasalainen[2]; Jouko Rikkinen[1]

[1] Finnish Museum of National History (LUOMUS), Helsinki; [2] Department of Geobiology, University of Göttingen, Göttingen; [*] E-mail: niko.johansson@helsinki.fi

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Animal-mediated dispersal has often been discussed in the context of biogeography and dispersal of lichens and fungi, but experimental evidence remains scarce. Tree-dwelling birds, such as woodpeckers, would seem to represent ideal dispersal vectors for organisms growing on standing tree trunks, such as epiphytic lichens and fungi. We have utilized bird natural history collections as a novel source of data for studying dispersal ecology of lichens. We screened freshly preserved specimens of three Finnish woodpecker species for microscopic propagules. Samples were taken from bird feet as well as chest and tail feathers. Propagules were extracted using a sonication-centrifugation protocol and the material obtained was identified using light microscopy. Diverse biological material was recovered from all specimens of all bird species, from all positions sampled. Most abundant categories of discovered biological material included lichen soredia, fungal spores and bryophyte fragments. Additionally, freshwater diatoms, bryophyte spores, algal cells, testate amoebae, rotifers, nematodes, pollen, and arthropod appendages were identified. We discuss the relevance of our findings in the context of dispersal ecology of lichens and discuss the next steps of our research: using molecular approaches to identify dispersing taxa in bird plumage.

Complex population structure of the Atlantic puffin revealed by whole genome analyses

Oliver Kersten[1]*, Bastiaan Star[1], Deborah M. Leigh[2], Tycho Anker-Nilssen[3], Hallvard Strøm[4], Jóhannis Danielsen[5], Sébastien Descamps[4], Kjell E. Erikstad[6,7], Michelle G. Fitzsimmons[8], Jérôme Fort[9], Erpur S. Hansen[10], Mike P. Harris[11], Martin Irestedt[12], Oddmund Kleven[3], Mark L. Mallory[13], Kjetill S. Jakobsen[1], Sanne Boessenkool[1]*

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[9]*Littoral, Environment et Sociétés (LIENSs), La Rochelle Université, La Rochelle, France*
[10]*South Iceland Nature Research Centre, Vestmannaeyjar, Iceland*
[11]*UK Centre for Ecology & Hydrology, Midlothian, UK*
[12]*Department for Bioinformatics and Genetics, Swedish Museum of Natural History, Stockholm, Sweden*
[13]*Department of Biology, Acadia University, Wolfville, Canada*

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The factors underlying gene flow and genomic population structure in vagile seabirds are notoriously difficult to understand due to their complex ecology with diverse dispersal barriers and extensive periods at sea. Yet, such understanding is vital for conservation management of seabirds that are globally declining at alarming rates. Here, I will present results on the population structure of the Atlantic puffin (*Fratercula arctica)* after assembling its reference genome and analyzing genome-wide resequencing data of 72 individuals from 12 colonies. I will present evidence for four large, genetically distinct clusters, isolation-by-distance between colonies within these clusters, and a secondary contact zone. These observations disagree with the current taxonomy, and show that a complex set of contemporary biotic factors impede gene flow over different spatial scales. The presented results highlight the power of whole genome data to reveal unexpected population structure in vagile marine seabirds and its value for seabird taxonomy, evolution and conservation.

Using environmental DNA to direct future isolation of short-branch microsporidia

Megan Gross[1], Lubomir Rajter[2], Frédéric Mahé[3,4], Micah Dunthorn[1]

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The classical known long-branch microsporidia are highly derived parasites of animals and some protists. Long-branch microsporidia have complex spores with the unique polar filament, with highly reduced nuclear and mitochondrial genomes, and have lost many DNA repair enzymes. One way to better understand how long-branch microsporidia evolved these characteristics, is to understand how these same characteristics evolved in the short-branch microsporidia. The short-branch microsporidia form a basal grade composed of partially characterized lineages and numerous novel environmental lineages. In order to know where we have to go for future sampling and isolation of the short-branch microsporidia, we used a new curated database of all available protistan environmental sequencing datasets of the V4 region of the SSU-rDNA locus. With the cleaned and curated molecular OTU table, we performed alpha- and beta-diversity analyses. Potential differences in the short-branch microsporidia's diversities and abundances were investigated based on their occurrence in five different biomes: freshwater, hypersaline, marine benthic, marine pelagic, and terrestrial.

122 000 years of fauna diversity of Nordic ecosystems explored through paleogenomics

Aurélie Boilard [1], Marius Robu[1], Bastiaan Star[1], Love Dalén[2], Sanne Boessenkool[1]

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Paleogenomics is a molecular approach to paleontological records allowing the analysis of past ecosystems through ancient DNA (aDNA) found in fossils and soils. The discovery of Europe's northernmost bone-rich karst cave system with sediments and bones dated up to 122ka, in Kjøpsvik (68°50'N) Northern Norway, presents a unique opportunity to study the response of arctic and boreal ecosystems to climate change during the last interglacial. The objectives of this project are to : (i) reconstruct faunal diversity and (ii) genetic diversity of mammalian populations as well as (iii) their distribution throughout the last glacial cycle over a period of 122 000 years. Metabarcoding will be used on bulk bone material (aDNA) and sediments (sedaDNA) to reconstruct the faunal diversity from excavated bone fragments. Genomic analyses based on both mitochondrial and nuclear genomes will be conducted to study historic biogeography of selected species. This study will provide new insights into mammalian diversity of high latitude ecosystems of Scandinavia throughout the last glacial cycle, and contribute to our understanding of their resilience and adaptive capabilities in the face of climate change.

Molecular phylogenetics and genus delimitation in the Rhizocarpaceae (lichenized ascomycetes) with focus on the *Rhizocarpon hochstetteri*-complex

Erik Johan Möller[1]

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The Rhizocarpaceae is a globally distributed and common family of lichenized fungi. The family consists of four genera (*Catolechia, Epilichen, Poeltinula* and *Rhizocarpon*) and c. 150 accepted species, of which all but nine belong in the genus *Rhizocarpon.* Previous molecular studies have shown that *Rhizocarpon*, as circumscribed today, may be paraphyletic with the other three genera nested. New species of *Rhizocarpon* are constantly described, suggesting there are potentially much undiscovered species diversity. My aim with this study was to provide a more natural circumscription of genera in the Rhizocarpaceae, while also investigating the *R. hochstetteri* species complex in more depth, using an integrative taxonomic approach. I have analyzed 148 Rhizocapaceae specimens phylogenetically based on three loci, both nuclear and mitochondrial, and compared the supported tree topology to morphological, anatomical, and chemical data. Obtained phylogenetic results show that there are at least four well supported clades (A—D) in the Rhizocarpaceae that do not corroborate current generic circumscriptions. Additionally, the phylogeny renders *Rhizocarpon* paraphyletic with *Poeltinula, Catolechia* and *Epilichen* nested. More specifically, *Poeltinula* is nested in the *R. hochstetteri*-complex (jointly clade A). *Epilichen scabrosus* is nested within *Catolechia* with *E. glauconigellus* as their distinct sister (jointly clade B). Representatives for the main bulk of the *Rhizocarpon* species, including the type species, form their (clades A+B) sister (clade C). *Rhizocarpon oederi* and *R. pycnocarpoides* form a sister group (clade D) to the rest of the family (clades A+B+C). I also show that the *R. hochstetteri*-complex consists of at least 11 well-separated clades, a finding that provides several insights: (1) specimen identities, (2) species limits, (3) recognition of new species, and (4) that, even though there are cases of substantial overlap, there are clear trends concerning ecology, chemistry and anatomical traits between these species.

The identity of *Veratrum* in Northern Norway

Hedvig Elisabeth Mjøen[1,3], Solveig Bua Løken[1], Charlotte Sletten Bjorå[1]

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The genus *Veratrum* (Melanthiaceae) comprises approximately 30 species from temperate and arctic North America and Eurasia. The Eurasian species *Veratrum album* L. has its main distribution in the mountainous areas of central and southern Europe and is also locally abundant in coastal areas of northeastern Finnmark, Norway. The conception of *V. album* has varied in different works and several taxa have been described as closely related species or as subspecies or varieties of *V. album*.

Veratrum album L. in northern Norway is characterized by having greenish flowers compared to the white-flowered plants of central Europe. It is unclear whether the Norwegian populations belong to the same taxon as the central European populations, as this has not been tested using molecular methods. We will present preliminary phylogenetic results based on the ITS region, which are not giving sufficient resolution to resolve the *Veratrum album* complex. We will thus perform target capture using the Angiosperm353 probe set to obtain a multi-locus data set. The aim of the project is to (1) construct a phylogeny of the genus *Veratrum, (2)* place the Norwegian taxon among its closest relatives, and (3) make a taxonomic revision of the *Veratrum album* complex with a conclusion on what name to apply for the Norwegian taxon.

"InverOmics", phylogeny and evolution of Spiralia based on genomic data: a first report

Alberto Valero-Gracia[1], Torsten Struck[1]

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The origin and evolution of Bilateria represents a core question in the Biology field. In one hypothesis, animals with a simple body organization evolve towards more complex forms several times independently; in another, animals with complicated body plans evolve towards simpler organizations by means of reductions. Support for one or the other hypotheses depends on the phylogenetic relationships within Spiralia, an animal group that includes annelids, mollusks, nemertines, platyhelminthes, and many other organism of substantial zoological interest and high ecological relevance. During this talk I will present some of the first results obtained within the frame of InvertOmics, a project in which we are dealing with some of the most incredible animals that populate the ocean realm.

Custom hybrid capture probes enable herbarium specimen phylogenomic analysis of the sedges (Cyperaceae)

Malene Nygaard[1], Mika Bendiksby[1], Vanessa C. Bieker[1], Michael D. Martin[1], Stefan Prost[2,3,4], & Eva Maria Temsch[5]

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[2] Department of Behavioural and Cognitive Biology, University of Vienna, Vienna, Austria
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Carex (Cyperaceae), also known as sedges, is the world's third largest genus of flowering plants comprising approximately 2,000 species. The majority of *Carex* species are taxonomically well-defined units. Some sections within *Carex* are, however, known for extensive intra-sectional hybridisation, which makes them taxonomically challenging. One such critical group is *Carex* section *Ceratocystis*. Previous attempts to reconstruct the phylogeny of *Ceratocystis*, based on traditional nuclear and plastid DNA sequences, have been inconclusive, typically with numerous polytomies. There are at least two likely explanations for the lack of resolution and branch support in this particular section. These include incomplete lineage sorting (ILS), given the section's relatively young age, and past and ongoing hybridisation with introgression among sympatric species. Utilization of multi-locus data has the potential of elucidating incongruities among gene trees resulting from ILS or hybridisation with introgression, or both. The modern genomic approach Hyb-seq enables targeted sequencing of thousands of nuclear exons and their flanking intronic regions. This approach is also highly suitable for degraded biological tissue (e.g., herbarium specimens), which makes available a global sampling through inter-herbarium specimen exchange agreements.

In this study, we present (1) draft genome assemblies of three representatives from the *Carex* genus, (2) transcriptome assemblies of four sedges, including one from the section *Ceratocystis*, (3) a hybrid capture probe set designed to enable studying the intrageneric relationships of *Carex* and illustrated with its application on herbarium specimens, and (4) a maximum-likelihood phylogenetic tree for a reduced representation of species belonging to section *Ceratocystis.*

Diversity of Laonice (Annelida, Spionidae) from the Arctic and the North Atlantic

Polina Borisova[1], Vasily Radashevsky[2], Viktoria Bogantes[3], Nataliya Budaeva[4]

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[2]A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences, Russia.
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[4] Department of Natural History, University Museum of Bergen, University of Bergen, Norway

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The information on genetic diversity for many annelid species from the Siberian Arctic shelf and from the deep Arctic basins is still missing. In our work, we analyze genetic diversity of *Laonice* (Annelida, Spionidae) from the Arctic and the north Atlantic waters. *Laonice* has worldwide distribution and comprises about 40 described species. *Laonice cirrata* is the type and the oldest species of the genus with very brief original description. This resulted in reporting occurrences of *L. cirrata* from all over the world from shallow to abyssal depths making *L. cirrata* one of the well known cosmopolitan annelid species. The original material was collected from the Kara and the Laptev Seas. Additional material from the Greenland, the Norwegian and the Barents Seas was examined from the invertebrate collection of the University Museum of Bergen. Moleular analysis was based on COI (180 sequences including data from BOLD) and 28S (75 sequences) markers.
In our material we found 11 MOTU, which included seven described species of *Laonice*, most with rather limited geographical and vertical ranges. One species, *Laonice irinae* sp. nov., was described during our work. Three MOTU from deep waters appeared new to science: one species from the Fram strait (1000-1500 m) and two species from the waters around Iceland (900 m and 1400-1900 m). New material of *Laonice cirrata* has been collected from its type locality - Lofoten Islands and across the whole study area. Our data show that although this species has the widest distribution in studied material,it is limited to the Arctic and the North Atlantic waters. Pacific records of *L. cirrata* known from the literature and the GenBank should be re-evaluated and subsequently re-described.

Dietary analysis of Carangid fishes from Southeastern Brazil determined by metabarcoding

Queiroz, Anna Karolina Oliveira de[1,2]; Ribas, Talita Fernanda Augusto[1]; Sales, João Bráullio de Luna[1]; De Boer, Hugo[2]; Thorbek, Lisbeth[2]; Oliveira, Renato Renison Moreira[3,4], Laux, Marcele[3]; Rosa, Fabrício dos Anjos Santa[1]; Oliveira, Guilherme Corrêa[3], Postuma, Felippe Aldert[5], Gasalla, Maria de Los Angeles[5], Ready, Jonathan[1]

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Carangid fishes are distributed worldwide in tropical and subtropical marine ecosystems and are commercially important in fisheries and aquaculture. Their role in food webs can be unclear as dietary items are poorly identified in traditional gut content analysis, though they are known to prey on pelagic and benthic species, with clupeiform fishes being important dietary items for some species. However, few studies have evaluated the diet of more than one or two species at a time. As many species may be found sympatrically, it is unknown whether carangids share food resources or show trophic segregation. Here we used metabarcoding to analyze the diet of seven carangid species caught as bycatch in the Brazilian southwest Atlantic sardine fishery. Stomachs were processed from all species sampled including four individuals of *Chloroscombrus chrysurus*, *Trachinotus carolinus* and *Selene setapinnis*; three *Oligoplites saliens* and Caranx crysos; two *Hemicaranx amblyrhynchus* and one *Caranx latus*. COI amplicons were sequenced on the Ion GeneStudio S5 system. MOTUs were defined using QIIME and Vsearch pipelines and identified by BLAST against the nucleotide reference database from GenBank and BOLD to perform taxonomic assignment. Diets are dominated by teleost fishes. All four non-fish prey items were present in the S. setapinnis diet while only two, *Penilia avirostris* and *Sagitta enflata*, found in the diet of *O. saliens* and *C. chrysurus*. Interestingly, the main prey in the *S. setapinnis* diet is *C. crysos*, suggesting possibility of predation of juveniles of closely related species as a competitive behavior in these fishes. Other members of the family Carangidae were found in diets of six of the seven species analyzed. These findings are important because they provide additional insight into the diversity of marine ecosystems, especially the poorly known diet of carangid fishes, not discoverable using traditional methods.

Molecular and morphometric analyses reveal highly underestimated diversity in *Eteone* (Phyllodocidae, Annelida)

Martha Everett[1], Glafira Kolbasova[2], Nataliya Budaeva[3], Tatiana Neretina[4]

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Genetic diversity of the genus *Eteone,* Savigny, 1820 (*Phyllodocidae*) was studied using mitochondrial (COI, 16S) and nuclear (18S, H3) markers. The material was obtained mostly from the White Sea but also included specimens from the Sea of Okhotsk, the Barents Sea, the Norwegian Sea, the North Sea, the Greenland Sea, and the West coast of Africa. Our study discovered five monophyletic clades of *Eteone* from the White Sea and more than 13 clades altogether among the examined material. The morphological study revealed five morphotypes in the White Sea differing in the shape of the prostomium, parapodia, and dorsal and ventral cirri, and in the structure of the proboscis. Previously only two species of *Eteone* (*E. flava* and *E. longa*) were reported from the White Sea. The accepted morphological descriptions of *E. flava* and *E. longa* are different from the original descriptions given by Fabricius in 1780. The morphological study revealed morphotypes that fall under the original descriptions and morphotypes that fall under the accepted descriptions. The relation between *Eteone* and genera *Mysta,* Malmgren, 1865 and *Hypereteone,* Bergstrom, 1914 was investigated. *Mysta* and *Hypereteone* ended up inside the *Eteone* clade, which casts doubt on their separation. *E. picta* is nested within a paraphyletic clade of the genus *Paranaitis,* Southern, 1914 and makes a highly supported clade with *P. kosteriensis.* Our results suggest that further revision of *Eteone*, *Mysta, Hypereteone,* and *Paranaitis* utilizing genetic data should be performed in the study area and worldwide.

The most comprehensive mitogenome phylogeny of the tribe Arini (Psittacidae) with emphasis in *Pyrrhura* parrots

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The Arini tribe is considered the most diverse group of Neotropical parrots from the family Psittacidae. It comprises approximately 158 species distributed in at least 32 genera, including several charismatic species like the blue-and-yellow macaw (*Ara ararauna*). These parrots have been severely affected by habitat loss and fragmentation, climate change, and the illegal wildlife trade market. Previous molecular phylogenies of the tribe were inferred using only sparse sampling and a limited set of nuclear and mitochondrial marker sequences and therefore the evolutionary relationships between some taxa remain unclear. The increasing accessibility and development of next-generation sequencing (NGS) technologies facilitates large data sets of genomic data that can be used to retrieve highly supported phylogenies. Recent efforts have made publicly available genomic data of some neotropical parrots, particularly the mitochondrial genome. However, despite being the most specious genus within the tribe, *Pyrrhura* has been largely ignored. In this talk, I introduce the results from low-coverage whole-genome shotgun sequencing from which we obtained mitochondrial genome sequences of 48 *Pyrrhura* samples, representing 22 of 31 *Pyrrhura* species. Together with all publicly available mitogenome sequences, the generated dataset was used to infer the most comprehensive mitogenome-based phylogeny of the tribe Arini. The obtained phylogeny showed more resolved clades and higher support than in previous studies of Arini and *Pyrrhura*. In the future, we aim to obtain sequences from missing taxa and to include nuclear sequences in the analysis.

Mapping a super-invader in a biodiversity hotspot, an eDNA-based success story

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Human activities are leading to a global degradation of all ecosystems, thus causing a considerable erosion of their biodiversity. These ecosystems become more fragile and less resistant, for example to biological invasions, one of the main factors in the loss of biodiversity today. Hosting many endemic species, the lesser Antilles archipelago in the Caribbean is known as a biodiversity hotspot. However, recent introduction of a highly invasive species, the Australian Red Claw Crayfish (*Cherax quadricarinatus*), has led to significant threats to this fragile ecosystem. In our study, we developed, validated, and optimized a species-specific eDNA-based detection protocol targeting the 16S region of the mitochondrial gene of *C. quadricarinatus*. Our aim was to assess the crayfish distribution across Martinique Island. Our developed assay was found to be species-specific and showed a high sensitivity in laboratory, mesocosm and field conditions. We showed a significative and positive correlation between species biomass, detection probability and efficiency through mesocosm experiments. Moreover, we found that eDNA persisted up to 23 days in tropical freshwaters. We investigated a total of 83 locations spread over 53 rivers and two closed water basins using our novel eDNA assay and traditional trapping. The latter undertaken to confirm the reliability of the molecular-based detection method. Overall, we were able to detect *C. quadricarinatus* at 47 locations using eDNA detection and 28 using traditional trapping methods, all positive trapping sites were positive for eDNA. We found that eDNA-based monitoring was less time-consuming and less influenced by the crayfishes often patchy distributions, proving a more reliable tool for future large-scale surveys. The clear threat and worrying distribution of this invasive species is particularly alarming as the archipelago belongs to one of the 25 identified biodiversity hotspots on Earth.

Sperm evolution in the Canary Islands chiffchaff

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Phenotypic divergence in allopatric populations may play an important role in speciation, if that divergence then causes a barrier to heterospecific mating upon secondary contact. Understanding when allopatric populations do or do not evolve divergent phenotypes is therefore of interest. Here, we study sperm morphology diversification in allopatric populations of the Canary Islands chiffchaff (*Phylloscopus canariensis*). Sperm morphology is likely to be under substantial sexual selection, because females are thought to copulate with multiple males in a reproductive cycle, creating opportunity for sperm to compete and the female to choose among males' sperm. Sperm length may affect how effectively they are stored in the female's sperm storage tubules as well as affecting their competitive ability against sperm of other males. Despite genetic divergence between island populations, and in contrast to other passerine species where sperm has diverged among islands, sperm morphology does not differ between populations of the Canary Islands chiffchaff. We found a negative correlation between sperm total length and sperm swimming speed. Since longer total length and faster swimming speed may each be selectively advantageous under sperm competition, there may be opposing selective pressures that result in trait stasis rather than trait diversification. Chiffchaffs belong to a phylogenetic family showing relatively slow sperm evolution currently, such that there may be other constraints on sperm evolution in this clade. In the absence of sperm divergence, we may expect that sperm-female interactions will not represent a barrier to hybridization if the populations come into secondary contact.

Intrathalline microalgal diversity and ultrastructural features of the new lichenized *Trebouxia delisei* lineage (Trebouxiophyceae, Chlorophyta)

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A new lichenized algal lineage of the genus *Trebouxia* was recently reported with phylogenetic analyses (i.e. *T. delisei* lineage), which shows a specific association to the lichenized fungus *Cetrariella delisei*. This study aimed to formally describe taxa in this lineage with ultrastructural investigations, and to explore the intrathalline microalgal diversity associated with *C. delisei* using algal metabarcoding. Using transmission electron microscopy, we found that taxa of this lineage do not contain a real pyrenoid and the pyrenoglobuli are dispersed between the thylakoids in the chloroplast, which are characteristic ultrastructural features. Algal metabarcoding revealed the complexity of microalgal composition, and there can be as many as three major *Trebouxia* OTUs coexisting, followed by minor ones. Microalgal composition does not show a geographic pattern. Even though two intraspecific *C. delisei* clades were found in Iceland, each clade does not show any pattern in microalgal composition.

Ground-truthing soil eDNA plant diversity assessments

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Given the fast pace of global biodiversity loss relative to its appraisal, fast and complete assessments have never been so urgent to counteract this trend. Recent developments in sequencing technology, bioinformatics and artificial intelligence point to DNA-based assessments as the solution for increasing the pace in which biodiversity is currently being estimated. Particularly for plant assessments, soil eDNA metabarcoding promises to overcome the shortcomings of morphology-based assessments by providing a more complete picture of the vegetation that is not limited to any season. However, knowledge about how morphology-and DNA-based plant assessments compare to each other is limited, and the spatial and temporal signals of plant DNA in the soil remain unclear. These questions are essential in the evaluation of any molecular data on biodiversity. Here we propose a calibration in space and time of eDNA-based plant identifications against morphological vegetation surveys to reveal the 'ground-truth' of soil eDNA assessments. We combine morphological identifications made in seven vegetation surveys along 30-years in one hundred $1m^2$ plots extended over a boreal forest in South of Norway with eDNA metabarcoding using chloroplast trnL (UUA) intron p6 loop from soil samples collected at the same plots on the year of the last vegetation survey. We found that soil eDNA compared best with the last vegetation survey for both vascular and non-vascular plants and detected about 61- 73% and 12- 20% of the diversity registered in each vegetation survey, respectively. Taxa occurring only at one vegetation survey were also detected by soil eDNA, with signals from up to 30 years ago. The taxa which remained undetected by soil eDNA were less abundant than those detected. In addition, soil eDNA detected taxa registered in other plots and within the study area. Our study demonstrates that soil eDNA assessments detects past and present plant diversity at a local scale and therefore offers new avenues for biodiversity assessment.

Utility of Kalanchoe (Crassulaceae) in Kenya

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The genus Kalanchoe (Crassulaceae) has about 150 species of succulent shrubs and perennial, annual or biennial herbs native to tropical Africa with most of its distribution in tropical southern Africa and Madagascar. The plants are cultivated as ornamental house or garden plants. A small percentage of Kalanchoe have their utility known, which makes it impossible for them to have priority in management and conservation plans. Utility data of Kalanchoe species in Kenya was obtained from informants of varied experience in different parts of the country, between August 2019 and December 2020, using interviews and semi-structured questionnaires. Simple random sampling method was used to sample plants from populations in regions where they are distributed following plant collecting guidelines. Utility data was analyzed using PAST (4.05) software and Microsoft excel using descriptive statistics. Use value (UV), frequency of citation (FC), relative frequency of citation (RFC), Informants consensus factor (ICF), citation and use percentages were computed. The results revealed that the general uses of Kalanchoe species in Kenya include treatment of sprained leg or hand, swollen body and body parts, skin infections and wounds, respiratory system infections, gastrointestinal problems, relieving pain, cleansing the blood and against most microbial infections in human and poultry. Kalanchoe prittiwitzii, Kalanchoe densiflora, K. lateritia, K. crenata, K. marmorata and K. lanceolata were cited as the most used species of Kalanchoe in Kenya. Kalanchoe plants are threatened with overexploitation due to increased human population; habitat fragmentation and destruction due to agricultural practices, construction, deforestation, leasing of forested land to locals for cultivation, cutting and burning of bushes, new generation and modern cultures/societies being ignorant of the value of the plants and herbalists are giving up. There is urgent need for sustainable utilization, proper conservation and protection of threatened species of Kalanchoe in Kenya.

Field determinants of PCR success in specimen identification using non-invasive DNA sampling of carnivore scats

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Non-invasive DNA sampling is one of the most common techniques in survey and monitoring of terrestrial carnivores. Given the vast resources required to obtain usable environmental DNA (eDNA) under natural field conditions, pilot studies are crucial to understand the trade-offs for optimizing the sampling effort in presence of factors influencing the quality and quantity of eDNA in scats. Using data from a baseline survey of carnivores across the Southern Caucasus, we explore (1) the impact of field conditions on eDNA amplification successes and genotyping errors for carnivore fecal samples; and (2) factors affecting the accuracy of carnivore scat identification by field biologists in the absence of genetic tools. First, we evaluated the environmental predictors of mitochondrial DNA amplification and sequencing success from the field-collected carnivore scats. For the putative brown bear (*Ursus arctos*) samples, we further tested for the field and locus-specific variables influencing the genotyping success and errors of nuclear DNA using eight microsatellites. Second, using these empirical results, we compared the specimen identification of scats by surveyors to those of eDNA. We revealed some of the environmental factors influencing the DNA amplification successes and genotyping errors, but their impact varied among the mitochondrial and microsatellite loci. Field identification of scats was accurate for large carnivores, but both false positive and false negative errors were high for the co-occurring mesocarnivores. We make recommendations for future eDNA surveys of the carnivore community in the study system.

Shedding light on the hidden diversity and host specificity of tremellalean lichenicolous fungi in Norway

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Many species of the genus *Tremella* are known to live associated to lichens as lichen-inhabiting (lichenicolous) fungi. They have a dimorphic life cycle, including a haploid unicellular yeast stage and a dikaryotic filamentous stage. Lichenicolous fungi with only the unicellular yeast stage present are asymptomatic, as they lack visible symptoms or fruiting bodies, making them hard to detect. Currently, there are no studies related to lichenicolous *Tremella* in Norway. Furthermore, there is limited information on distribution, ecology, and conservation status of Norwegian lichenicolous fungi. DNA based methods have been essential in assessing the diversity and taxonomic affiliation of lichenicolous fungi. Suspicions of hidden diversity within *Tremella* arose when diverse contaminant ITS sequences of *Tremella* were obtained from healthy looking species of the Pertusariaceae. Only one lichenicolus *Tremella* species residing in species of the Pertusariaceae has been described, namely *Tremella pertusariae*.

Through this project, I will (1) assess the hidden *Tremella* diversity in asymptomatic thalli in *Pertusaria*, 2) study the diversity and distribution of lichenicolous *Tremella* fungi residing in species of *Pertusaria* in Norway, and (3) investigate the specificity of lichenicolous *Tremella* to species of *Pertusaria*. I will use high-throughput amplicon sequencing, targeting three nuclear DNA ribosomal markers (nSSU, nITS, and nLSU), on samples collected from various locations in Norway. This should allow detection of yeast stage *Tremella* in asymptomatic thalli, even when only few cells are present. I will use DADA2 to get high-resolution sample inference from Illumina amplicon data. Preliminary PCR results show that a minimum of 20-30% of 196 samples of asymptomatic thalli of *Pertusaria* contain DNA of *Tremella.*

Using target capture to resolve taxon limits in *Ledebouria* and related genera

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In this integrative systematic study, we are focusing on three closely related monocot genera: *Drimiopsis*, *Ledebouria* and *Resnova* (Asparagaceae, Scilloideae). Due to the scarcity of phylogenetically informative characters, both morphological and molecular, taxon delimitation in this clade has historically been challenging. The three genera together constitute a well-supported monophyletic group, yet the relationships within the clade remain poorly resolved. Preliminary results suggest a paraphyletic *Ledebouria*, with *Drimiopsis* and *Resnova* as sisters to one *Ledebouria* clade each. In addition, there seems to be little correlation between the distribution of morphological character states and the preliminary molecular phylogenies. A more integrative systematic approach, where an expanded set of morphological characters are evaluated in the light of a resolved phylogeny is therefore needed to understand the evolutionary history of this clade.

To obtain a resolved phylogeny for the clade, all the way down to species level, we have applied a target sequence capture approach. Using the Angiosperms353 probe set, we expect to obtain a multi-locus data set that, along with a broad geographical sampling, will provide the basis for inferring a more natural classification at all levels of the target group. To help taxon identification in the field, we hope the resolved phylogeny will provide the framework needed to identify a set of phylogenetically informative morphological characters. We will present our preliminary phylogenetic results and discuss the utility of the Angiosperms353 probe set.

Genomic consequences of historical overharvest in Svalbard reindeer

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The Svalbard reindeer (*Rangifer tarandus platyrhynchus)* is a high arctic subspecies endemic to the Norwegian Svalbard archipelago. Due to human-induced hunting over several centuries, the subspecies was driven to near extinction, and it disappeared from most of the archipelago. Following its legal protection in 1925, the population managed to recover in number and reclaim parts of its former range. However, previous studies of the consequences of overhunting on their genetic diversity have only utilized contemporary samples and thus may show an incomplete picture of the genetic consequences, potentially overlooking lineages which died out. We hypothesize that the gene pool went through a severe bottleneck, and that the populations therefore have reduced fitness when adapting to future challenges such as climate change. This is problematic because the decrease in seasonal sea-ice cover caused by climate change will further isolate populations. Here we use a combination of ancient (n=5), historic (n=6), and contemporary (n=82, from a unpublished reference panel) Svalbard reindeer whole-genome sequences to study the changes in genetic diversity prior to (3600 – 400 years BP), during (400-100 yrs BP), and after (<100 yrs BP) the period of overhunting by humans. Our very preliminary results show that there was a population turnover during/following the sharp population decline and subsequent recovery. Admixture analysis shows that populations are more strongly structured following the bottleneck. Heterozygosity is slightly decreased in modern populations, suggesting elevated inbreeding.

Molecular phylogeny of fish and insect species using spectra comparison tool compareMS2

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Large-scale scale molecular phylogenetics in the modern world is usually performed using DNA barcoding or whole genome sequencing and alignment. However, tandem mass spectrometry-based proteomics can also be used in molecular phylogenetics. Tools such as compareMS2 calculate the distance matrix by comparing tandem mass spectra thereby deriving similarities and differences between the datasets used in the study. We have tested this tool in our work on non-model organisms (seven fish species and five insect species) to build molecular phylogenies using proteomics data.

For the seven fish species namely, Atlantic cod, Atlantic haddock, Nile tilapia, Northern pike, Atlantic salmon, Southern platyfish, and pangasius, a phylogenetic tree was constructed using compareMS2 where top 500 tandem mass spectra from muscle samples and fish species were separated (MassIVE dataset MSV000087017). Similarly, for the five insect species (Black soldier fly, Yellow mealworm, Lesser mealworm, House cricket, and Morio worms), compareMS2 was used to construct an insect phylogeny from proteomics datasets acquired from two different mass spectrometers, UHR-TOF mass analyzer and Thermo Fischer Scientific Orbitrap instrument. The outcome of the compareMS2 indicated the relatedness of insect species at the taxonomic level and closely related species from the same order were grouped. The obtained results from both fish and insect proteomics datasets were compared with PhyloT phylogeny (DNA-based phylogenetic software NCBI) indicating that even with 500 tandem mass spectra molecular phylogeny can be constructed. In the insect dataset, normal-flow HPLC with shorter gradient and older mass spectrometer instrument (massIVE id MSV000088034) were used for constructing phylogenetic tree indicating the robustness of the compareMS2 tool. The compareMS2 workflow is suitable for non-model organisms, samples difficult to extract high-quality DNA, and can be applied to fossils.

Accumulation of hybrid incompatibilities within two species (*Arabis alpina* and *Cardamine hirsuta*) relative to mating system and population divergence times

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Accumulation of reproductive isolation (RI) is the central process leading to speciation events. However, very little is known about how fast postzygotic RI accumulates between diverging populations, and which factors influence the rate of postzygotic RI accumulation. Flowering plants show a variety of different mating systems ranging from strict outcrossing to predominant selfing. Selfing can impact the genetic structure, as restricted pollen dispersal will limit gene flow between populations. It can also potentially promote local adaptation and RI accumulation between populations. In this project we aim to 1) estimate the rate of postzygotic RI accumulation within the two species Arabis alpina and Cardamine hirsuta (Brassicaceae), by performing experimental crosses between populations and estimating population divergence time, and 2) test the hypothesis that selfing increases the rate of postzygotic RI accumulation by estimating selfing rates in the parental populations. This will be addressed by sowing out seeds and raising parental plants from Norway, African mountains and the Mediterranean. These populations are expected to represent a range of divergence times and most likely also a range of mating systems. By performing experimental interpopulation and intrapopulation crosses between the parental plants, the two fitness-related traits of the hybrids (1) hybrid seed failure and (2) hybrid sterility, will be used to estimate postzygotic RI. Divergence time between the parental populations and their mating system (degree of selfing) will be estimated by generating genomic data by using whole genome resequencing. The results will be used to address how quickly postzygotic RI accumulates, and whether

Determinants affecting the analysis and detection of introgression in phylogenies

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The role of hybridization in the context of diversification dynamics has recently seen increasing attention as genomic studies have led to the identification of vertebrate species produced through homoploid hybridization and hybridization has been linked to some of the most explosive adaptive radiations. Moreover, recent research has made it abundantly clear that hybridization in animals is not only far more common than previously thought, but that even highly divergent species are sometimes still able to hybridize and backcross, such as fin and blue whale or the Russian sturgeon and the American paddle fish, two species that diverged over 120 million years ago. These findings raise the question whether the methods developed for detecting hybridizations are still appropriate and applicable for suchlike scenarios, due to the fact that they were originally aimed for analyses at level of populations and recently diverged species.

The reliability of these methods has been questioned when being applied to more divergent systems where the assumption of constant evolutionary rates, which is implicit in the most commonly used methods, is more likely to be violated. To test the determinants and limitations of these methods when being applied to highly divergent species, genomic data were simulated with the program Msprime. These simulations included different settings with varying degrees of rate variation, introgression, and population size. We were able to show that commonly applied statistical methods, e.g. Dsuite among others, are producing false-positive signals of gene flow between highly divergent taxa. In addition, our results indicated that the presence and effects of long branch attraction biases must be taken into account when identifying the most appropriate methodology for the detection of gene flow.

Vegetation and environment history of the western Kola Peninsula reconstructed based on the sediment ancient plant DNA from the lake Imandra

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High-resolution reconstruction of the vegetation and environment changes in the western part of Kola Peninsula (NW Russia, Murmansk Region, the eastern part of Fennoscandia) during the last ca 13.3 cal. kyr BP was performed based on the ancient plant DNA metabarcoding analysis of the sediment material from the core Co1410 retrieved from the Lake Imandra. In total, 204 taxa are identified. The resulting sequences were assigned to vascular plants (87%), bryophytes (12%), and algae (1%). About a half (111 taxa, 49%) are identified to the level of species that belong to 150 genera and 86 families. So far, this is the most diverse palaeoflora known from Late Pleistocene-Holocene for the Kola Peninsula and NW Russia.
This record stays in a good accordance with already known regional stratigraphy and allows to specify the time of initial colonization of the ground after the glacial retreated during the Bølling-Allerød warming (13,300 -13,000 cal yrs BP). Our study suggest changes from tundra with dwarf shrubs to more open grasslands with forbs associated with the Younger Dryas and with re-entering of the glaciers at ca 13,000 – 11,800 cal yrs BP. A period of open grasslands at ca 8,500 – 11,700 cal yrs BP was associated with a relative warming. The warming resulted in an increasing plant diversity during the Early Holocene, which was followed by a period where birch forests established. Mid-Holocene climatic maximum at ca 5,500 – 7,700 cal yrs BP. with the highest regional plant diversity (177) led to the spread of woody vegetation in form of mosaic and mixed coniferous and deciduous forest. High contribution of thermophilic, aquatic plants and ferns were registered during that period. During the Late Holocene (ca -70 – 5,300 cal yrs BP) modern vegetation communities established. Human impact is clearly diagnosed after 250 cal yrs BP and is indicated by the presence of *Ribes* sp., *Hypericum* sp., and *Mentha arvensis* as well as synantropic taxa, i.e. *Trifolium* sp. and *Urtica dioica*.

Supergene origin and maintenance in Atlantic cod

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Supergenes are sets of genes that are inherited as a single marker and encode complex phenotypes through their joint action. They are identified in an increasing number of organisms, yet their origins and evolution remain enigmatic. In Atlantic cod, four megabase-scale supergenes have been identified and linked to migratory lifestyle and environmental adaptations. Here, we investigate the origin and maintenance of these four supergenes through analysis of whole-genome-sequencing data, including a new long-read-based genome assembly for a non-migratory Atlantic cod individual. We corroborate that chromosomal inversions underlie all four supergenes, and show that they originated at different times between 0.40 and 1.66 million years ago. While we found no evidence for a role of gene flow in the origin of the four supergenes, we reveal gene flux between supergene haplotypes with derived and ancestral arrangements, occurring both through gene conversion and double crossover. Our results suggest that supergenes can be maintained over long timescales in the same way as hybridizing species, through the purging of introduced genetic variation.

Comparative Proteomics of the Perivitelline Layer – the Site of Avian Sperm-Egg Interaction

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The act of fertilization requires interaction between the egg and sperm. Miscommunication between the two gametes can lead to incompatibilities, loss of fertility, and failure to produce a viable zygote. As such, identifying and exploring egg and sperm proteins that interact during fertilization is of great interest to reproductive and evolutionary biologists studying speciation, reproductive isolation and barriers to gene flow. In abalone species, the sperm protein lysin interacts with the egg protein VERL to dissolve the egg membrane. These two proteins are known to be rapidly evolving (among the fastest known) and show functionally significant differentiation between closely related species. These sequence differences act to avoid heterospecific fertilization and hybridization. Immediately prior to fertilization, sperm undergo the acrosome reaction, a process in which the sperm membrane weakens and proteolytic enzymes among other molecules are released from a vesicle in the sperm head. Proteins contained within this vesicle (the acrosome) are prime candidates for sperm proteins that interact with the egg. In many taxonomic groups, the acrosome reaction can be induced *in vitro* by the introduction of molecules such as calcium. However, in birds the acrosome reaction cannot be induced in the absence of the egg membrane (the perivitelline layer). This suggests the presence of a protein or molecule in the perivitelline layer necessary for the acrosome reaction. Using a proteomics approach, we are comparing the composition of the perivitelline layer across avian species to identify proteins involved in sperm-egg interactions. Here I will present the perivitelline layer proteome of the Eurasian nuthatch (*Sitta europaea*) and common gull (*Larus canus*) in a comparative context.

Cryptic diversity unveils unexpected challenges in the seemingly paraphyletic lichen genus *Calvitimela* (Lecanoromycetes, Ascomycota)

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Molecular phylogenetics has revolutionized the taxonomy of crustose lichens and revealed an extensive amount of cryptic diversity. Resolving the relationships between genera in the crustose lichen family Tephromelataceae has proven difficult and the taxon limits within the genus *Calvitimela* are only partly understood. In this study, we tested the monophyly of *Calvitimela* and investigated phylogenetic relationships at different taxonomic levels using an integrative taxonomic approach. A global sampling of all species currently assigned to *Calvitimela* (including available holotype, isotype and lectotype material) formed the foundations for the study. Additional population sampling of *Calvitimela melaleuca* sensu lato across Norway was performed. Chemical and morphological characters were analyzed to test their diagnostic values in the genus. More than 300 sequences from five different loci (ITS, LSU, MCM7, mtSSU, TEF1-α) were produced and used, together with existing molecular data, to infer phylogenetic relationships and estimate divergence times in *Calvitimela*. Our molecular phylogenetic results show evolutionary old and deeply divergent lineages in *Calvitimela*. Morphological characters are overlapping between divergent subgenera in the genus, whereas chemical characters are informative at the level of subgenera, but largely homoplastic at species level. Moreover, the subgenus *Calvitimela* is found to constitute four distinct genetic lineages, and detailed morphological examinations of *C. melaleuca* s. lat. reveal differences between taxa previously assumed to be morphologically cryptic. Population level analyses of *C. melaleuca* s. lat. corroborate the species to be paraphyletic. Furthermore, young evolutionary ages and signs of gene tree discordance indicate a recent divergence and possibly incomplete lineage sorting in the subgenus *Calvitimela*. Phylogenetic analysis of the mtSSU suggests that the Antarctic species *C. uniseptata* belongs in *Lecania* (Ramalinaceae). We also find molecular evidence for *C. septentrionalis* being sister to *C. cuprea*. In the subgenus *Severidea*, one new grouping is recovered as a highly supported sister to *C. aglaea*. Lastly, two fertile specimens are found to be phylogenetically nested within the sorediate species *C. cuprea*. We discuss the need for an updated classification of *Calvitimela* and the role of cryptic diversity in an evolutionary context. Through generic circumscription and species delimitation we argue for a practical taxonomy in *Calvitimela*.

Contamination during fish sampling affects molecular diet inferences

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Knowledge of trophic interaction is necessary to understand dynamics of ecosystems and develop ecosystem-based management. Ecological models are being used for giving advice on the quota for fisheries. Application of such models relies on good knowledge about the trophic interactions between fish and its prey, and the key data to study these interactions must come from large scale diet analyses with good taxonomic resolution. However, visual examination of prey is laborious and may not provide the required taxonomic resolution due to poor preservation of the prey in the guts. To overcome this, molecular methods based on analyses of prey DNA in guts and feces have been increasingly used. Despite the potential of molecular diet analysis in providing unprecedented high-resolution taxonomic data, it may also produce unreliable results if the samples are contaminated by external sources of DNA. Although such biases are ubiquitous and unavoidable in molecular diet analysis, one should aim to reduce them. By considering the freshwater European whitefish (*Coregonus lavaretus*) as a tracer for sample contamination, we studied the possible route of contaminants in beaked redfish (*Sebastes mentella*) guts sampled in the Barents Sea. We used contaminant specific COI and fish specific 12S primers to perform diagnostic and metabarcoding analysis of intestine and stomach contents of fish samples that were either not cleaned, water cleaned, or bleach cleaned after contaminant treatment. The diagnostic analysis revealed clear positive effects of sample cleaning as we detected whitefish in significantly higher numbers of uncleaned samples compared to water cleaned or bleach cleaned samples. Stomachs were more susceptible to contamination than intestines and bleach cleaning not only reduced contaminant in stomachs but made all intestine samples contaminant free. Also, the metabarcoding approach detected significantly more reads of contaminants in stomach than intestine samples. Based on read composition, our study illusively shows whitefish as one of the most important food components biasing the diet inference. Our study underlines thus the importance of surface decontamination of aquatic samples to obtain reliable information on diet from molecular data.

Patterns and Processes of Cryptic Species Diversity of Soil Crust Lichens of South Africa

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Lichens are mini ecosystems of fungi and algae. Their symbiosis involves unique chemical and physiological adaptations that enable lichens to survive in diverse climates nearly everywhere on the planet. The lichen species *Psora crenata* is an important component of biological soil crust communities in arid and semi-arid regions of South Africa. Previous studies using molecular evidence suggest there are multiple evolutionary lineages within the *P. crenata* complex, which may deserve recognition at species level. Our lab group has also found 11 potentially distinct chemotype variants of *P. crenata*, sometimes with multiple chemotypes growing in the same area. In this study, we use *P. crenata* as a model to investigate the population-level molecular, chemical, and photobiont diversity of lichen species using whole genome shotgun sequencing, thin-layer chromatography and various specimens' metadata. Based on these multiple sources of evidence, we aim to delimit species and identify how different selective forces may have influenced their genomic landscape. We present initial results from a subset of samples.

Taxonomy and biogeography of the subtribe menthinae (lamiaceae), with focus on the tropical eastern African 'sky-islands'

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Subtribe Menthinae (family Lamiaceae) is a cosmopolitan group with several conflicting taxonomic treatments and attempts at delimitation of genera in this complex and species-rich plant group. Recent analysis based on nuclear and plastid DNA data found three well-supported main lineages within the subtribe: *Satureja*, *Clinopodium* and *Micromeria*. However, older treatments like in Flora of Ethiopia and Eritrea, grouped the *Satureja* and *Clinopodium* lineages in to genus *Satureja*. In my PhD project, I will re-examine the taxonomy and biogeographic history of *Micromeria* s.str. and *Clinopodium* s.l. in Tropical Africa using a combination of automated morphometric analyses, gnome skimming and RNAseq tools. Special focus is on the eastern part of the region, where species are predominantly occurring in the extremely fragmented sky islands. In 2019, we arranged extensive field expeditions to six of the highest African mountains (Simen Mts, Bale Mts, Mt Kilimanjaro, Mt Kenya, Mt Elgon and Ruwenzori Mts) and collected silica samples, herbarium vouchers and ecological data. We have also taken DNA samples from previously collected herbarium material to cover most species and the total geographic distribution of the subtribe. This study aims to 1) revise the taxonomy of the *Satureja* lineage, 2) resolve the phylogenetic relationships within this lineage, and 3) unravel the detailed biogeographic history of the species occurring in eastern Africa.

Assessing biodiversity in the marine algae belt

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The marine algae belt, more loosely interpreted, comprises kelp forests, seagrass meadows and rocky reefs with coralline red seaweeds. It is one of the most active primary producing environments in the sea and harbors a great diversity of animals including ascidians, nemerteans, entoprocts, serpulid worms, spionid worms and caprellids. The species of these groups occupy important ecological functions as herbivores, predators or filter feeding organisms and can be sessile or agile as well as solitary or colonial. Globally these taxa comprise more than 7,000 species with around 250 species documented from Norwegian waters. Despite this, the knowledge about their taxonomy and distribution in Norway is poor and in dire need of improvement. Specimens in museum collections are often quite old material, which additionally is often wrongly determined due to unresolved taxonomic issues including the high degree of cryptic species in these groups. Besides cryptic species, many of these taxa include invasive species causing high economic damage.
This recently started project, funded by ArtsDatabanken, is focusing on the occurrence and habitat preferences of the above-mentioned taxa in the marine algae belt along the Norwegian coastline. Using both morphological and molecular methods, it aims to contribute to basic biosystematics, species distribution and nature conservation in groups that are still poorly understood and challenging to study.
Fieldwork was conducted last summer in two locations: Oslofjord and Trondheim area. The Oslofjord sampling effort was carried out with the help of two students from the UiO:Life science project. First results include new records of species for both sampled locations and several high-quality barcodes (CO1 sequences) that will be uploaded to NorBOL. Revision of museum collections, species lists and popular and scientific papers will be prepared in the next months. We also hope for more exciting results following the DNA sequencing that will be carried out this autumn.

Polychaetes in Norwegian ports: uncovering diversity in coastal anthropogenic environment

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Norway is the 7th country in the world when it comes to coastline length, with 25,148 km excluding the Islands. The conservation status of Norwegian marine ecosystems is relatively good but the coastal zone is, proportionally to its dimensions, inadequately monitored, and its biological diversity is threatened by a multitude of external pressures. Marine ports represent some of the most human-influenced marine environments. The substrate is physically modified by artificial constructions and the seabed is often subject to dredging or sediment deposition. Even though most effluent discharge has been terminated in recent years by purification measures and clean-up actions, port environments are still largely polluted from previous discharges of contaminants, input of organic matter and contaminants by diffuse runoff from urban areas, road traffic and waste spills from ships and smaller vessels. Marine bristle worms (polychaetes, Annelida) are a diverse and abundant group of invertebrates that inhabit the marine floor, from the intertidal to the deep-sea and at all latitudes. Polychaetes have an important role in seafloor ecosystem functioning. They act as representatives of marine benthic communities and have been considered one of the best indicators of environmental disturbance.

To assess and map polychaete biodiversity in port environments, we sampled a variety of substrates in the ports of Trondheim, Bergen, Stavanger and Oslo, as well as smaller ports and marina along the the Norwegian coast. We combined morphological identification and metabarcoding of three different markers: COI, 16S and 28S, to study the annelid diversity of each port and marina. We assessed the conservation status of each location, studied the connectivity between the ports and discuss the use of each method in biodiversity assessments.