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**CEES**

Centre for Ecological and Evolutionary Synthesis

**Abstracts**

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## **Organising committee**

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## Secrets of success in *Saxifraga oppositifolia*

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Ployploidy as an evolutionary mechanism in plants is particularly important in stressful environments. It has been shown that environmental stress, such as extreme climatic conditions, will enhance the production of unreduced gametes, which is usually a prerequisite for polyploidisation to occur. Polyploids are generally classified as either autopolyploids or allopolyploids. Autopolyploids have multiple chromosome sets derived from a single species while allopolyploids have a hybrid origin. Our knowledge on autopolyploidy is particularly scarce.

In this project, I have investigated consequences of autopolyploidy on phenotypic variation, with focus on reproductive strategy and reproductive output. As study system, I have used the circumpolar, arctic-alpine species *Saxifraga oppositifolia* (Saxifragaceae), in which three ploidy levels are known, diploids, triploids and tetraploids. *Saxifraga oppositifolia* thrives in a wide range of habitats, from early snow free, extremely dry ridges with long growing season, to moist snow beds with short growing season. It also shows different growth forms, which are partly associated to ploidy level and habitat. Flower production and vegetative growth clearly differ between habitats and growth forms, but how reproduction is affected by ploidy level is yet to be found. I have used five established transects around Longyearbyen, Svalbard, which cover three different habitats (ridge, heath, riverbed) to address the following questions: Have autopolyploidisation created a shift in reproductive parameters? Are polyploids more frequent in Svalbard due to a higher production of unreduced gametes?

I registered phenology twice during the growth season, collected capsules with seeds, estimated seed:capsule ratio, and tested seed germination to investigate differences in sexual reproduction related to ploidy levels and/or ecological factors. To obtain measures on vegetative investment, I collected trailing branches from plants of different ploidy levels and from various habitat types and tested the rooting ability in a rooting experiment. Pollen samples were collected and analysed with flow cytometry to obtain frequency of unreduced male gametes.

All data were further processed and analysed in R using GLM and ordinal regression. My results suggest that *S. oppositifolia* have expanded its niche to include vegetative propagation as an important factor to maintain the abundance of polyploids in Svalbard.

**(Un)safety in numbers?**

**An island study on spatial variations in plant-pollinator interactions**

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**Habitat fragmentation**, causing smaller populations, smaller patches and increased isolation, may affect reproductive success for animal pollinated plants. The general assumption state that pollinator numbers – and therefor also plant seed set – increase with increasing patch size or flower density. Yet, after a certain threshold, an increase in flower number (i.e. increasing patch size or higher flower density) will lead to *decrease* in seed set due to lower relative pollinator visitation. Hence, there may exist an optimal patch size or optimal flower density for every plant species. The aim of this study was to assess spatial variations in plant-pollinator interactions for the herbaceous plant *V. vulgaris*, and, based on the result, evaluate the plants optimal flower density.

**The focal area** included two islands in the outer Oslo fiord, southeast Norway. Specifically, I examined whether flower visitation and seed set of *V. vulgaris* varied between the islands (i.e. on area level), between populations of different flower density within the islands (i.e. on population level) and between patches of different size within the populations (i.e. on patch level). In addition, I analyzed *V. vulgaris* breeding system (i.e. the relative effect of self-pollination, optimal pollination and natural pollination on seed set). This was done by flower treatments (including bagging and hand pollination) and by a germination experiment.

**The major finding** was an interesting relationship between seed set, legitimate pollinators and plant population density. I found as expected that *V. vulgaris* seed set was higher in dense than in sparse populations for low pollinator frequencies. However, at a frequency of 0.2 (bees per flower per minute) and higher, seed set in sparse surpassed that in dense populations.

**My results show** that *V. vulgaris* optimal flower density largely depends upon pollinator frequency, and that, *given enough efficient pollinators*, reproductive success of animal pollinated plants has potential to be *higher* in sparse than in dense populations. Further, it suggests that similar proportions of pollinators to flowers may have a greater effect in sparse than in dense plant populations. The latter emphasizes the importance of maintaining viable pollinator communities in areas where conservation targeted plant species are sparse or patchily distributed.

## Effects of high-latitude light conditions on stomatal conductance and photosynthesis in white clover (*Trifolium repens*)

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Terrestrial plants play a central role in the climate system, largely due to photosynthesis and transpiration. This thesis investigates how these two processes may be influenced by the light conditions at high latitudes. Stomata are the gateways that connect the interior of plants with their surrounding atmosphere, regulating both water-loss through transpiration and uptake of CO<sub>2</sub> for photosynthesis. Opening and closure of stomata is actively regulated in response to a range of internal and environmental signals, enabling plants to balance this trade-off.

Light is a key regulator of stomatal behavior, and is central in coordinating stomatal conductance with photosynthesis. Light promotes stomatal opening indirectly, by driving photosynthesis in the leaf. Additionally, there is a direct response to blue light in the guard cells, causing opening. The direct blue-light response is more efficient than the indirect response, and is sensitive to lower irradiances. At twilight, the sun is below the horizon and only diffuse light, having a higher proportion of blue light, reaches the ground. The twilight period is extended at high latitudes. As stomatal regulation is especially sensitive to blue light, this could potentially affect stomatal movements throughout the diurnal cycle – and thus patterns of transpiration and photosynthesis – in vegetation at high latitudes.

Models of stomatal conductance currently used in Earth System Models do not consider any direct effect of blue light. Only the indirect effect of light (through photosynthesis) is included. Stomatal responses to blue light might be of higher relative importance at high latitudes, due to the extended twilight period. If so, the assumptions of stomatal conductance models might be less representative for high-latitude vegetation.

In my thesis, I investigate how an extended twilight period affects plant activity, by conducting experiments on white clover varieties originating from different latitudes. Plants of selected varieties are grown in a room mimicking high-latitude light conditions, and compared to clones grown in a control room, with light conditions corresponding to a lower latitude. Gas-exchange measurements are done throughout the diurnal cycle, and used to calculate stomatal conductance and rates of transpiration and photosynthesis. Measurements of stomatal conductance are done on all genotypes in time intervals spaced throughout the day. Moreover, gas exchange will be measured continuously for 24 hours on a subset of the genotypes. Additional measures of plant performance, including biomass increment, will also be taken. The results will be used to address how the light conditions might affect fluxes of CO<sub>2</sub> and water from vegetation at high latitudes, which is relevant in the context of Earth System Modelling.

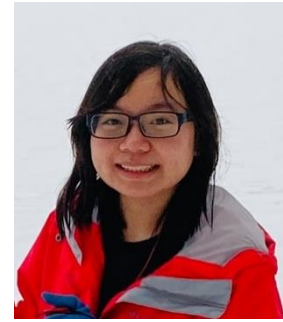
## Smaller seeds in Malagasy palms suggest unique island selection pressures

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Flowering plants' seed sizes can affect their dispersal distances, and thus their ability to colonize new habitable areas. When species enter new areas, differences in biotic and abiotic conditions result in new pressures that shape seed size evolution. Thus, comparing seed sizes in regions with species interchanges may better our understanding of the selective pressures that govern seed size evolution in these areas.

Around 35 Mya, members of the palm family (Arecaceae) dispersed from mainland Africa to Madagascar, which now contains over 200 endemic palm species. Previous comparisons of fruit sizes (a proxy for seed sizes) in mainland Africa and Madagascar have concluded that there is no significant difference in fruit sizes between the two regions. However, these studies either neglected phylogenetic information or assumed that fruit size evolution followed a Brownian motion (BM, implying trait evolution following a random walk) model without considering other models of trait change.

In our study, we compared models of palm fruit and seed size evolution using BM and Ornstein-Uhlenbeck (OU, implying trait evolution toward an optimum value) models and allowed these to have either the same or different regional parameters. We compiled fruit and seed length data from the literature for palm species in Madagascar and in mainland Africa. Using the largest available species-level palm phylogeny, we then compared the models of trait evolution given the compiled data. The best-fitting phylogenetic model – an OU model with the same evolutionary rate but different trait optima for the regions – suggests that Malagasy fruits and seeds evolve at the same speed as their mainland counterparts but that this evolution is toward optimum lengths ~30% smaller than those of mainland fruits and seeds. We conclude that differing selection pressures on Malagasy palms are responsible for smaller fruits and seeds on the island compared to the mainland. Future work will focus on investigating possible explanations for the smaller fruit and seed sizes in Madagascar, such as climatic unpredictability on the island or selection pressure from smaller-bodied vertebrate dispersers.

## How do changes in farmland affect farmland birds in Norway? Yellowhammer (*Emberiza citrinella*) is used as an example

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The population of farmland birds have been declining in Europe during the last decades. NIBIO (Norwegian Institute of Bioeconomy Research) has for the last 17 years been monitoring farmland birds and showed that the population of many of them have declined in Norway. One of these birds is the Yellowhammer (*Emberiza citrinella*).

Yellowhammer is a resident and migratory bird in Norway. They will often breed on farmlands and live by vegetation edges and thickets. They also like open areas with scattered trees and bushes. Therefore, they thrive on farmlands and depend on an active agriculture. Young fledglings get insects and other invertebrates from their parents. Nevertheless, seeds will be their most important food source throughout their life. Their nests are often found on the ground in open areas like road edges and forest edges.

Yellowhammer is Near Threatened (NT) according to the Norwegian red list. The reasons for why the Yellowhammer populations are declining have been suggested to be due to a change in their habitat. Indeed, farmland became more homogenous, vegetation edges and open spaces are disappearing, and the supply of waste grains is decreasing. Modern machines, fall plowing and burning straw have led to the decrease of grain availability. In this project, I will look how these suggested environmental changes, and other factors as temperature and geographic position are affecting the spatial habitat occupation by Yellowhammer. For this, I will use data on Yellowhammer distribution and abundance from the Norwegian monitoring program for agricultural landscapes from 130 plots, of 1 x1 km squares, in the Norwegian farmland across the country. NIBIOS 2020 report, based on the same data I am going to use, mentions that the distribution of yellowhammer in Norwegian farmland is quite stable, but their abundance is clearly declining. For the data analysis Generalized additive models (GAM) will be used.



## Anatomical constraints on venom and toxin evolution in giant centipedes

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Animal venoms are biochemical arsenals that contain a diversity of bioactive peptides and proteins that are collectively referred to as toxins. Venoms have received attention as sources of molecules with potential applications in medicine, industry, and agriculture, however they are also useful models for studying the processes of evolution across levels of biological, or phenotypic, complexity. Centipedes are predatory arthropods in the class Chilopoda (Subphylum: Myriapoda). They are nocturnal active predators, which incapacitate a variety of prey using paralyzing neurotoxins via modified appendages called forcipules. This class contains five different genera: *Scutigermorpha*, *Lithibiomorpha*, *Craterostigmomorpha*, *Geophilomorpha*, and *Scolopendromorpha*. Centipedes represents some of the oldest clusters of venomous arthropods, as the class emerged approximately 440 million years ago. Centipede venoms are also thought to evolve under physiological constraints imposed by their morphologically simple venom glands. Centipedes thereby present an opportunity to study the evolutionary interaction of morphological and molecular traits across a wide range of evolutionary time

In my master project, I am using a bioinformatic approach to determine the venom compositions of a wide set of representatives across centipede taxonomy. I will then combine this with different morphological data to test whether morphology affects the evolution of either centipede toxin or venom composition, and how the venom has evolved through the different taxa.

To date, I have determined the venom compositions of three species using bioinformatic analyses of transcriptomic and venom proteomic data. *Henicops maculatus*, *Scolopendra leata*, and currently analyzing the peptides from venom sample of the *Scolopendra polymorpha* species. As I am proceeding from one species to the other, I am updating the current database containing the previous results from other centipede venom examinations.

During the master's degree I will finish examining the existing transcriptomes from other species, which include the ones mentioned above. Furthermore, I will proceed with examining the decided species *Henia vesuviana*, also referred to as *Chaetechelyne vesuviana*. This is a small species, which is recorded to have a body length of 50mm and belongs to the genus *Geophilomorpha*. It is known that the venom glands of this species extend a third of its body length, making this an ideal species to examine in sense of morphological effects on centipede venom evolution and composition.



## **Ecosystem effects of invasive domesticated salmonids and warmer climate**

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The impact of escaped farmed Atlantic salmon on wild salmon populations has been studied in the past decades. It is now well documented that they impose a negative impact both through introgression, but also through interference competition. Yet, there is little literature on the ecosystem impact of escaped farmed salmon. Climate warming is another factor that may act synergistically with biological invasions, such as when escaped farmed salmon enters a natural ecosystem. In parallel, climate warming will affect the abiotic and biotic drivers of ecosystem functioning.

To test the prediction that impacts of escaped farmed salmon on ecosystem functioning will increase in warmer conditions, I will quantify the impact of offspring from escaped farmed salmon on the community and ecosystem levels. To do this I'm using a set-up of semi-natural stream channels with natural substrate sampled from the river Imsa.

The experiment is designed to test two factors: impact of domesticated salmon (3 levels: wild, farmed and no fish) and temperature (2 levels: current and warmed temperature). A treatment without fish is used to serve as a control to provide baseline information on ecosystem functioning. Temperature regimes are based on the predicted future climate scenarios for Norway. I have 4 replicates of wild and farmed treatments for each temperature scenario (warm and ambient). Further, 4 channels with no fish treatments who serve as control as a baseline ecosystem functioning, 2 for each temperature scenario.

In order to measure the effect on ecosystem functioning I will investigate primary production, secondary producer composition and decomposition rates. Primary production is measured using a BenthosTorch® for cyanobacteria, diatoms and green algae concentrations. A Surber sample is used at the end of the experiment for secondary production. While decomposition is measured using a setup of two mesh bags with dried leaves with and without access for invertebrates. Primary production and decomposition are measured at 3 stations in each stream channel at different times during the experiment for replicates.

The experiment aims to contribute to more knowledge about the ecological impact of farmed salmon and the interactive impacts of two human-induced stressors (invasive domesticated salmonids and climate warming).

## The distribution of Lampreys in Haldenvassdraget

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There is not a lot known about the distribution of some small-sized freshwater fish in Norway. But I wish to do something about it! Some freshwater fish is general difficult to observe, catch and identify. But what if you don't have to see the fish to find it? Enter eDNA. Instead of sampling the organism (fish), we now sample the environment (water) where the organism resides.

For my thesis I will look for the three species of Lampreys that inhabit one of Norway's largest drainage system, Haldenvassdraget. I expect to find brook lamprey (*Lampetra planeri*) and European river lamprey (*Lampetra fluviatilis*) in the entire drainage system, and Sea lamprey (*Petromyzon marinus*) in the areas closest to the coast. It will be interesting to see how far up the drainage system Brook and European river lamprey are, and how far inland the Sea lamprey will be found.

The plan is to collect eDNA samples from 45 different locations in Haldenvassdraget, all the way from Floen in Aurskog-Høland to the costal water in Halden. The samples will be analysed using both qCPR and DNA-metabarcoding on each sample. qCPR will only show the presence of lamprey species, while DNA-metabarcoding will be used to identify multiple fish species including Lampreys. By using both methods I will be able to say something about the sensitivity of the methods, and hopefully which is better suited to be used on a larger scale, such as at a national scale.

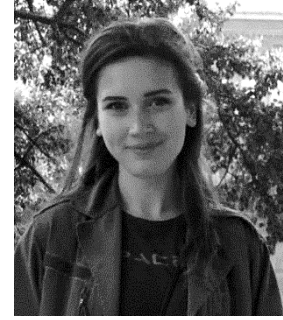
## The first whole-genome sequencing of river- and brook lamprey

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Lampreys represent one of the most primitive vertebrate lineages alive today. The group contains 41 marine and freshwater species with varying life histories and adaptations. Because of the lineage's longevity, the lamprey genome has been of interest in several previous evolutionary studies. While the river lamprey (*Lampetra fluviatilis*) and the brook lamprey (*Lampetra planeri*) might look similar, have ammocoete life-stages of comparable length, and share the same habitat, their life histories differ significantly. The river lamprey is a parasite and spends years as a juvenile attached to other fish, rasping at their skin. The brook lamprey is a filter feeder, that spends most of its life as a larva, sifting through detritus at the bottom of the river.

Through whole-genome sequencing, we can determine whether the river- and brook lamprey are in fact two species, or merely morphologically different ecotypes of the same species. Previous studies have shown little genetic difference between the two lampreys, raising questions about their status as two distinct species. In this project I will be assembling highly accurate long reads (Hifi reads, PacBio) from river- and brook lamprey, sourced from Åsdalsåa, in South-Eastern Norway and Hunserödsbäcken in South-Western Sweden, using HiCanu and Hifiasm. After genome assembly, I will use bioinformatic tools to compare the two genomes to each other, and to other previously assembled lamprey genomes such as the pacific- (*Entosphenus tridentatus*), sea- (*Petromyzon marinus*) and arctic lamprey (*Lethenteron camtschaticum*).

## How hydropower induced changes in temperature, quality and quantity of water influences structure and functioning of riverine biofilms

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Microbial communities are major players in the biogeochemical processes and ecosystem functioning of river networks. In river ecosystems, biofilms are the predominant form of microbial life, acting as interface layers between water and sediment and energy source at the base of the food web. Damming rivers for hydropower can have severe effects on water quality, sediment transport, nutrient cycling, habitat diversity and river biota. Despite the important role of biofilm, studies addressing the effects of hydropower on the community structure and functioning of these microbial communities are still scarce and biomonitoring tools relying on prokaryotes are still lacking. In this project we aim at screening the biofilm microbial communities living in Norwegian river systems, comparing metabarcoding and quantitative techniques such as Catalyzed reported deposition fluorescence in situ hybridization (CARD-FISH). We want to investigate the efficacy of both techniques in detecting changes in microbial community structure associated with environmental drivers. Given the extreme sensitivity of microorganisms to changes in nutrients and water quality, we also suggest a way to identify prokaryotic taxa which might be useful as freshwater bioindicators. Furthermore, we intend to analyze biofilm community structure and functioning in river systems impacted by dams for hydropower production. We will compare impacted and unimpacted river reaches by using 16S sequencing to evaluate differences in alpha and beta diversity of the biofilm communities. In addition, we will employ a proxy for organic matter to gauge breakdown rates in impacted and unimpacted reaches. The development of new prokaryotic bioindicators would benefit the ongoing effort of protecting freshwater environments and despite the benefits of hydropower as a renewable energy source, we stress the urge for studies addressing the effects of altered flow regimes on microbial communities and the key ecosystem processes they drive.

## **The use of acoustic alarms (pingers) as a mitigation tool to reduce bycatches of harbour porpoises (*Phocoena phocoena*) in commercial gillnet fisheries in Norway**

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Incidental entanglement in gillnets is the biggest threat to harbour porpoises (*Phocoena phocoena*) and many other small cetaceans all over the world, including Norway. In Norway, gillnets are set by a large fleet of about 6000 active fishing vessels, that operate in coastal waters, where harbour porpoises are also commonly found. Bycatch estimates indicate that more than 3000 porpoises are killed as bycatch in these fisheries every year, but lack of knowledge about harbour porpoise population structure and seasonal movements make it difficult to evaluate the consequences of this mortality to affected populations.

Here, I report results from field trials where we tested the effectiveness of acoustic alarms (pingers) as a mitigation tool to reduce harbour porpoise bycatches. Data was collected in high-bycatch regions and fisheries, over the course of two years. A total of 19 porpoises were bycaught, all in control nets. I conclude that pingers could theoretically reduce bycatches by 96.7%, assuming 100% compliance and ~ 0% defective pingers. I also outline a few possible scenarios for partial pinger deployments in selected fisheries, areas and seasons, and evaluate how such deployments could be expected to affect total bycatch in the context of international sustainability limits. Furthermore, I share reports from the trial participants on time costs associated with pinger use, that indicated that a typical gillnet fisher using pingers on all gillnets could expect to spend 5.5 hours of extra work per year due to pingers slowing down fishing activities in various ways.

Finally, I try to take a wider perspective and consider the outlook for pinger use as a permanent tool in the bycatch mitigation toolbox in Norway, given a recent government regulation on acoustic alarms and how these alarms have so far been received by the fishing industry.

## Starvation effects on life history traits in fluctuating vs. stable temperatures; An experimental study with *Daphnia magna*

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Dietary restriction has typically been studied at constant temperatures, but *Daphnia magna* are adapted to large daily fluctuations in temperature. The goal for this study was to find out whether starvation has more severe life history consequences in fluctuating than in constant temperatures. Individuals from two clones (genotypes) were assigned to one of two food concentrations corresponding to starvation (0.05 mg C/ind/day) and ad libitum condition (0.3 mg C/ind/day), and then assigned to a treatment of fluctuating temperatures (17°C–27°C) or constant temperature (22°C). Key life history variables were recorded. Individuals with high food level had higher juvenile molting rate, growth rate, earlier maturation and higher fecundity than the ones with the low food level. Similarly, individuals with high food level at constant temperature had higher adult molting rate, growth rate and fecundity than ones at fluctuating temperature. Individuals experiencing low food at fluctuating temperature reached maturation earlier than at constant temperature, but otherwise there was no significant effects of temperature treatment on molting rate and fecundity. The results indicate that the thermal fluctuations effects were inconsistent across food treatments.

## **Life history response to covariance between the fluctuation of temperature and food availability in *Daphnia magna***

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*D. magna* is a freshwater species of planktonic crustaceans living in a variety of habitats in mainly the Northern Hemisphere, but also scattered through the Southern Hemisphere. The effects of climate change and anthropogenic activities on freshwater systems is difficult to predict and will likely affect variably across habitats. It is therefore important to explore different species' response to several environmental eventualities and create a solid foundation from which predictions can be made. This experiment seeks to investigate the response of two *D. magna* genotypes, one originating from Sweden and one originating from Morocco, to treatments of fluctuating temperatures under limited and unlimited food conditions. 10 individuals of each genotype were subjected to one of three treatments, negative- or positive covariance between temperature and food availability and constant temperature and food availability, and followed until the release of the third clutch or termination. Due to a large proportion of males, only the Swedish genotype was used to compare the treatments. The two genotypes could be compared only through the individuals subjected to the constant treatment and males subjected to positive and negative covariance of food and temperature were compared until the age of 8 days.

Relative to those subjected to the constant treatment, individuals subjected to a positive covariance of food and temperature showed similar investment in reproductive timing and size of offspring and less investment in growth and clutch sizes. Those subjected to a negative covariance displayed a higher investment in size of offspring and less investment in growth, clutch size and reproductive timing, as well as a general trend of more variation between the individuals, in relation to both other treatments. Comparisons of the genotypes showed that the Swedish genotype had later reproductive timing than the Moroccan genotype, but otherwise relatively similar expressions. Males subjected to the positive covariance treatment had higher growth rate than those subjected to the negative covariance.



## Effects of predictability in food conditions on life history traits of *Daphnia magna*

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Variation in food availability is a key driver of ecological and evolutionary dynamics, as it affects organisms through their energy acquisition and allocation to life history traits. For *Daphnia* living in small ponds, food conditions are often variable and unpredictable, for instance through algae blooms. The life history consequences of predictability of food level variation are not well known, but theoretical predictions suggest negative effects.

In this project, life history responses of *Daphnia magna* to variable food conditions were studied using three different treatments of the algae resource: constant food level, predictable variation (alternate high or low level), and unpredictable variation (pre-determined daily level from random sequences), where both variable treatments had the same mean (equal to the constant treatment). Two clones (genotypes) of *Daphnia* were studied, one from Morocco and one from Sweden, with 10 individuals from each clone in each treatment (in total 60). The experiment lasted 18 days. Molts, eggs and offspring were noted every day for each individual. Body length was measured for the individuals three times during the experiment. In one clone many individuals were males, and few individuals reproduced, so the main results reported were molting rate and growth. The results indicated that the individuals in the constant treatment grew and developed faster than in both variable treatments, and were bigger overall. The individuals in the variable treatments had similar growth rates. Molting rate was calculated for both the juvenile and adult stage and was also higher in the constant treatment. *Daphnia magna* live in highly variable environments, yet perform better under constant food conditions, in line with theoretical predictions. These results suggest that the predictability of variation is less important than the amount of variation.

## Spatial patterns of grazing damages of red deer in agriculture

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Agricultural practices are changing all over the world putting biodiversity at risk. Changes to farming includes both extension of area and intensified use of existing areas, but also abandonment of farmland. Understanding how different land use practices affect biodiversity and ecosystems has become a key issue for conservation. However, agriculture also contribute with subsidies to wildlife in the form of high-quality food. In this way, the natural and farmed landscapes have coupled dynamics.

Red deer have shown to utilize high-nutrient grass produced in fertilized grasslands, and this grazing may remove more than half of the biomass production. The size of the Norwegian red deer (*Cervus elaphus*) population is today historically high, and the red deer locally damage agricultural crops at the west coast of Norway. Yet, we lack estimates of the level and variation of grazing pressure at broader scales.

The aim of this thesis is to measure and identify landscape level drivers of red deer grazing pressure on agricultural meadows in the county of 'Møre og Romsdal', Norway.

Field work will be conducted in the periods May-June and July-August 2021. Grazing pressure will be measured along transects following a spatially hierarchical design. I will then analyse the spatial variation in grazing pressure within the meadow, between meadows in the local area and between meadows in the larger region, and relate the variation to population density of red deer, topography, and distance to coast.

## **Lyme disease dynamics – Exploring spatial, temporal and demographic trends**

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Lyme borreliosis has been a notifiable disease in Norway since 1991. In my presentation, I will introduce the national Lyme disease patient data set collected by the Norwegian Surveillance System for Communicable Diseases (MSIS). I will describe how I am using the data to investigate Lyme disease dynamics, including seasonality and spatial distribution. I will also discuss the overlap between disease dynamics and demographics, and how demographic trends in the data can be used to gain further insight into Lyme disease ecology.

## SedaDNA metabarcoding reveals Upper Palaeolithic human plant use at Aghitu-3 Cave in the Armenian Highlands

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Plants played an integral role in prehistoric human life, providing food, medicine, raw materials and fuel. However, current knowledge about early plant use is very limited, and based on the preservation of scarce visible remains. Caves provide a unique opportunity to study past human activity, as they mitigate the full effects of the elements on the organic materials (e.g. bones, faeces and plant remains) concentrated by humans and animals. By analysing DNA preserved in cave sediments, we can identify organisms in the absence of any visible remains. This opens up new ways to study past plant use which are complementary to more traditional proxies such as pollen, which may come from plants growing far beyond the surroundings of a cave.

Aghitu-3 Cave contains a 15,000 year long record (from ~39-24,000 cal BP) of Upper Palaeolithic human settlement and environmental variability in the Armenian Highlands. Finds from the cave include stone artefacts, faunal remains, bone tools, shell beads, charcoal and pollen. We applied sedaDNA metabarcoding to the Aghitu-3 sedimentary sequence to obtain a temporal reconstruction of human plant use during the Upper Palaeolithic. Our results reveal the presence of several taxa, including those with known medicinal properties. Our sedaDNA results support and complement anthracological and palynological evidence while increasing taxonomic resolution. With this study we show that ancient DNA metabarcoding of cave sediments provides novel insights into the plant use of prehistoric humans.

## Unexpected assemblage of puffin diversity in northern Greenland

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The Atlantic puffin (*Fratercula arctica*, Linnaeus, 1789) is an iconic seabird species that has been designated as "vulnerable" to extinction globally and listed as "endangered" in Europe. Its breeding range stretches from High Arctic European Russia, Norway, Greenland, and Canada, southward to France and the USA. Puffins have been broadly classified into three subspecies, namely *F. a. grabae* (small), *F. a. arctica* (intermediate) and *F. a. naumanni* (large), along a latitudinal gradient based on size. Yet, analyzing the genomic population structure across the entirety of the puffin's breeding range we have previously demonstrated that there are, in fact, four genomic clusters, which only partially support the current division into three subspecies. The High Arctic, including Spitsbergen, Nova Zemlya, northeastern Canada and northwestern Greenland is home to the large subspecies *F. a. naumanni*. Intriguingly, preliminary studies at Thule, the most northern breeding population of puffins in the western North Atlantic, have shown that two distinct size classes of puffins are present within the same colony. Using whole genome sequencing of three individuals of each size class, the puffins at Thule were placed into the previously identified global population structure, which revealed substantial differences in assignment to formerly defined genomic clusters between the two size classes. This somewhat unexpected assemblage of the different genomic clusters in a single location at the most northern edge of the puffin breeding range not only provides a new perspective on the population structure of the Atlantic puffin and might be indicative of similar scenarios at other puffin colonies, but is also of utmost importance for local and regional conservation management in an area where environmental conditions are changing rapidly.

## **Ancient DNA analyses of Neolithic Atlantic Bluefin Tuna from Scandinavia**

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Atlantic bluefin tuna is a commercially important marine apex predator distributed across the Atlantic Ocean, from the Gulf of Mexico to the Mediterranean and the Norwegian Sea. In recent history, Atlantic bluefin tuna has experienced severe overfishing, resulting in population collapse and a listing on the IUCN red list. Humans are known to have harvested Atlantic bluefin for millennia – trap fisheries around the Mediterranean have been documented by historical sources for the past 2600 years, and archeological findings along the Skagerrak coast indicate Atlantic bluefin exploitation in Scandinavian Mesolithic and Neolithic periods. While it is known that tuna fishing has occurred for thousands of years, the impact human exploitation has had on tuna evolution and ecology remains poorly understood. Recent excavations at Jortveit, southern Norway, have produced an abundance of tuna bones dated to the Early and Middle Neolithic period (3900-2350 BCE). Producing more tuna bones than any other known location in Scandinavia, the Jortveit excavations provide a unique opportunity for a population-scale study of ancient tuna and will allow comparative analyses between ancient and modern populations. Analyses of numerous specimens revealed remarkable aDNA preservation with 100% library success and samples yielding, on average, 30% endogenous DNA. We compare whole-genome shotgun data from this ancient set of specimens to modern conspecifics, providing the oldest population scale baseline comparison of Atlantic bluefin tuna.

## Understanding the genomic structure of Atlantic cod using ancient DNA

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Long-term human exploitation is of substantial concern for wild species. Heavy exploitation can have severe consequences such as depletion of genetic diversity or significantly alter ecosystem functions. Ancient DNA (aDNA) methods can provide insights into the evolutionary potential and population demography of heavily exploited species. Atlantic cod (*Gadus morhua*), an economically important species in the North Atlantic, has experienced severe fishing pressures during the last century. Despite the dramatic population declines and collapses associated with continuous fishing activities, the extent of human impact on wild Atlantic cod populations is not entirely understood.

For one of my PhD projects, I investigate the genetic fluctuations and changes in effective population size of Atlantic cod by comparing ancient (up to 6500 BCE) to modern mitogenomes sampled across the North Atlantic Ocean. I found that Atlantic cod has high mitogenomic variation with low genetic structure. I did not detect significant loss of genetic variation on the time scale that was investigated here. Instead, I found an influence of historical demographic processes on the mitogenomic variation of Atlantic cod. These results highlight that although long-term fishing pressures have had negative consequences for the abundance of Atlantic cod, these pressures have not had an extensive impact on its mitogenomic diversity.



## Tracing the Early Origins of the Atlantic Herring Trade Using Ancient DNA

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The Atlantic herring (*Clupea harengus*) industry began over 1000 years ago in Europe as seafaring and preservation technologies were developed in conjunction with increasing urbanization across the continent. Large-scale patterns of trade between developing nations often included Atlantic herring, particularly between 1000 and 1700 C.E. Historical and archaeological accounts indicate the quantity of herring fished was comparable at some periods to the industrial herring fisheries of the early 20<sup>th</sup> century. To assess both the role of the herring trade in early urbanization and industrial trade networks and the impact of developing European nations on the marine ecosystems of the north Atlantic, I analyze DNA extracted from archaeological herring samples collected around Europe. The first 18 months of the project have been focused on sampling, lab work, and developing tools for future analysis. To date, over 100 herring bones have been processed in the dedicated ancient DNA lab at CEES. This represents 14 archaeological sites from key locations around Europe that track the rise of the proto-industrial herring fishery. Due to the unpredictability of success in recovering ancient DNA from archaeological samples, only a small subset of these will be deep-sequenced for high-coverage genomic analysis. To mitigate the loss of data associated with poor DNA recovery, I have developed a new software program that is capable of genomic assignment tests from extremely low-coverage genomic sequence data. The second half of the project will be focused on analyzing the many sequences recovered from the past 18 months of sampling and lab work, both with our newly-developed software program and with other analytic techniques.

## Past and present hybridization between Arctic and Polar cod disentangled by genome sequencing

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Interbreeding between genetically distinct species, sub-species and/or diverging populations, i.e. hybridization, has been recognized as an evolutionary force contributing to diversification and thus, adaptive radiation and speciation throughout the three of life. By taking advantage of the recent advancement within comparative and phylogenomic analyses, reconstructions of evolutionary histories – which includes reticulated networks reflecting the complexity of how species diversify and the relationship among them – are now commonplace.

Polar cod (*Boreogadus saida*; Lepechin, 1774) and Arctic cod (*Arctogadus glacialis*; Peters, 1872) represent two key species in Arctic ecosystems, known to be important prey for a range of taxa. The Polar cod is among the most ubiquitous Arctic fishes and found in a wider range of habitats than Arctic cod, which is restricted to more Arctic regions. During early life stages both are found to be associated with sea ice and show remarkable adaptation to living in colder environments. Recently, studies have provided evidence for both past and present geneflow events between these species. As sea ice in the south-eastern Barents is expected to decrease in the years to come, we hypothesize based on their shared early life history, that overlap of their spawning range(s) may increase, leading to increased hybridization events in the future. Here, we aim at using the newly generated chromosome-anchored genomes of several gadid species including Arctic and Polar cod, together with population genome sequencing data to elucidate the i) the extent of past and present introgression events and ii) how these events have impacted the evolution of the genomic architecture of both species as well as iii) their genetic diversity and thus, adaptive capacity. Studying the evolution of these fishes, their relationship, genetic adaptations, and the potential for genetic exchange is important for understanding how these species will cope with the changing environment.

## **Inversion breakpoints in Atlantic cod linkage groups- precise or imperfect breaks at the individual level?**

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Locally adapted populations within a species are genetically distinct and likely to be irreplaceable. Atlantic cod populations adapted to different lifestyles and geographic regions (i.e. environmental and ecological conditions) despite high gene flow. Certain Atlantic cod populations suffer from overexploitation resulting in population decline, while others are affected by ecosystem change due to human activities and climate change. It is therefore crucial to improve our understanding of the genetic mechanisms leading to local adaptation (and possibly speciation processes in a longer time frame) for sustainable management of genetic resources in a globally changing world. Chromosomal inversions are likely to be involved in local adaptation and have a potential for future cod-management, and they may also provide information about genes involved in behaviour biology and environmental adaptations in different cod populations. Previous studies have found an inversion on Linkage Group 1 (LG1) associated with migratory behaviour (e.g. skrei) whereas an overrepresentation of a chromosomal inversion in fjord cod and Baltic Sea cod on LG02 may be linked to adaptation to low salinity. Since chromosomal inversions lead to suppression of recombination and thus essential genes for adaptation are inherited as one unit (“supergene”), this may be an important evolutionary principle. In the ongoing Aqua Genome Project, more than 800 individual cod from across its geographical range have been full-genome sequenced. The distributions of inversion genotypes have been identified. The goal of my project is to determine if the inversion breakpoints are exactly the same or slightly variable across individuals and populations. Using a PCR and sequencing approach individuals from different cod populations will be compared around the inversion breakpoints on LG01, LG02, LG07, and LG12. We will compare and investigate genetic variation (including SNPs, STRs, CNVs) and even more complex repeats within and around the breakpoint regions.

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