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Bikuben, Kristine Bonnevies hus

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Centre for Ecological and Evolutionary Synthesis

Abstracts

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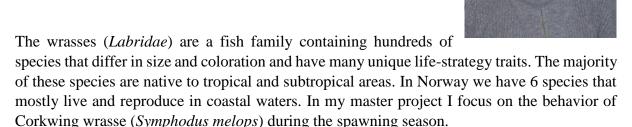
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Behavior of Corkwing wrasse during reproduction

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The wrasses (*Labridae*) are a fish family containing hundreds of species that differ in size and coloration and have many unique life-strategy traits. The majority of these species are native to tropical and subtropical areas. In Norway we have 6 species that mostly live and reproduce in coastal waters. In my master project I focus on the behavior of Corkwing wrasse (*Symphodus melops*) during the spawning season.

Territorial corkwing males build and guard the nest where they invite females to spawn. In addition, a group of males called sneakers develop female mimicry. The sneakers observe females spawning in the nest of a territorial male and then try to fertilize the eggs. In addition, egg predation from both conspecifics and other species is common. I will focus on investigating the interactions between males, how many females they spawn with and if they have any preferences to the individual they spawn with. I will also try to quantify the interactions with potential egg predators.

The gathering of data took place at IMR in Austevoll in west Norway. I identified the location of corkwing nests using snorkeling. Fish in the area were captured and tagged with PIT (Passive Integrated Transponder) tags. These tags do not require a power source; instead it is activated by an antenna that was placed around the nest. All tagged fish approaching the nest were registered by this system. I also used underwater filming, by placing video cameras aimed at the nests. The videos and the information from the PIT-antennas were later analyzed to describe spawning and fish behavior.

Right now, I work with all the data we gathered and will continue to do so. I observed around 300 marked individuals of different wrasses, where the majority were corkwing. I have data from 11 independent nests with a marked territorial male and now I work on analyzing all the data we have gotten.

The relationship between the occurrence and the bycatch rates of coastal seal in Norway

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In Norway the coastal fisheries for species such as cod (*Gadus morhua*) and monkfish (*Lophius piscatorius*) are important for many local communities. The coastal gillnet fisheries, however, may also unintentionally catch small marine mammals as incidental bycatch. This will most likely have a negative impact on the fishing gear and the handling time related to free the mammal. Not to mention the harm it causes individual seals that drown, which again may have negative consequences on population level. It is important to understand where and when such bycatches occur, to minimize these threats. Data are available about the location of grey seal (*Halichoerus grypus*) and harbor seal (*Phoca vitulina*) colonies, the spatial distribution of fishing effort, and about the reported bycatches of grey seals and harbor seals from a monitored fleet of 18-25 fishing vessels (overall length<15m). I will analyze how the bycatch rates of these coastal seals differ spatially and temporally using GIS and R. I will look for a connection between the distribution of grey and harbor seals and the probability of entanglement in gillnets. The results of the thesis could be useful to examine mitigating measures, such as time and area regulation of net fisheries, and may be of importance for the conservation of local populations of coastal seals.

Population responses to environmental variability: a simulation and comparative study

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Global climate change is likely to lead to concomitant changes in climate means, variability, and extremes, resulting in more variable and unpredictable environments for animal and plant populations. While most ecological studies have focused on shift in mean environmental conditions and its impacts on population fluctuations, we have only limited knowledge of the effects of changing variability.

Increased environmental variability is often assumed to decrease the long-term population growth rate thus being harmful for populations. However, previous theoretical and empirical studies have shown that both positive and negative effects on long-term population growth are possible.

Using the demographic databases COMADRE and COMPADRE, my postdoc project aims to investigate the effects of environmental variability on long-term population growth rates (log λ_s) across a wide range of taxa and life histories, from short-lived to long-lived species. Specifically, I examine whether vital rate response curves to an explicit environment driver could predict population responses to changes in environmental variance.

Life history responses in *Daphnia magna* to different environmental variables

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D. magna is a planktonic filter-feeding crustacean, and an ideal model species for ecological and evolutionary questions. It can reproduce clonally, making it a good choice for experiments investigating environmental effects. They mostly inhabit fresh water bodies and are widespread in the Northern Hemisphere. With more unstable and variable environmental parameters ahead, presented by climate change, it is important to test different species and system's resilience to such variability. Theoretical models suggest that the effects of increased variability on fitness can be positive or negative, depending on the curvature of the response function (Lawson et al. 2015). By applying different variables this master project group aims to investigate and quantify the life-history responses, such as juvenile growth, final size, moulting, age of maturation, clutch size, clutch size of each clutch and age at death of *D. magna* in a laboratory setting.

The project is split into four different experiments:

The first experiment will investigate effects of the fluctuating food level conditions on key life history traits of *D. magna*, in cold (10 °C) and warm (25 °C) conditions.

The second experiment will investigate life history effects in *D. magna* of fluctuating temperatures under limiting vs. unlimiting food conditions.

The third experiment will investigate life history responses to predictable and unpredictable variation in food and temperature conditions.

The fourth experiment will investigate the combined impact of maternal age and diet on offspring life history in *D. magna*.

Reference

Lawson, C.R. et al., 2015. Environmental variation and population responses to global change J. Drake, ed. *Ecology Letters*, **18**:724–736.

Ecological effects of low and declining Calcium on the key indicator species the white-throated dipper

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Acid precipitation in Scandinavia has led to low and declining Calcium levels in terrestrial and aquatic ecosystems. Acid precipitation reduces the pH in watercourses and dissolves Calcium from rock and soil. Due to the recent reduction in acid precipitation, Calcium is no longer dissolved at the same rate from rock and soil which has led to Calcium deficiency in southern Norway.

The white-throated dipper *Cinclus cinclus* (hereafter dipper) is a key indicator for clean freshwater ecosystems at higher trophic levels, due to its narrow selection of freshwater foods. The dipper prey almost exclusively on mayfly-, caddis - and stonefly larvae, and these larvae are therefore the bird's main source of Calcium for eggshell formation and presumably one of the reasons why the dipper makes unsuccessful breeding attempts. The dipper is therefore likely not directly affected by acidification, but indirectly by foraging at lower trophic levels.

To study the ecological effect of low Calcium levels, it is therefore essential to assess how the Calcium levels in the river affects the dippers breeding success. Due to extinction of salmon in the river, lower parts of the dipper study system are limed. One hypothesis is therefore that areas with liming stations will have a higher breeding success than areas without liming stations, as Calcium would not be a limiting factor downstream liming stations. By sampling water at dipper territories, upstream and downstream of the lime dispensers, it is possible to investigate if there is a relationship between the amount of available Calcium and the dippers breeding success. We can then examine the indirect effect of low Calcium levels on breeding success, assessing the dipper as an indicator species also for Calcium deficiency.

Spawning variation in northeast arctic haddock in the years 2000–2017

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In this thesis I will investigate variations in annual mean latitude of spawning of the North-east Arctic (NEA) haddock (*Melanogrammus aeglefinus*) along the Norwegian coast. For this purpose, I have used commercial landing data from the Norwegian directorate of fisheries. The mean latitude of haddock spawning ground have been calculated from the latitude and biomass information of each individual landing, based on selected landings from the spawning grounds and within the spawning period. In addition, the variations in the mean latitude of spawning has been compared with temperature data from the KOLA section as gathered by Russian Federal Research Institute Of Fisheries and Oceanography (VNIRO), spawning stock biomass (SSB) from the 2018 International Council for the Exploration of the Sea (ICES) Arctic fisheries working group (AFWG) report, mean weight of spawners (which have been calculated based on weight at age, numbers at age and proportion mature at age from the same ICES report) and mean latitude of landings. A correlation between SSB and spawning location was found, a larger SSB resulted in a more northerly distribution. There was also a correlation between mean latitude of spawning and temperature in the Barents Sea in the moths prior to spawning with a higher temperature also correlated with a higher mean latitude of spawning. The results were tested through a linear model, a stepwise model selection, and an AICc and found to be statistically significant.

Fisheries dynamics with incomplete ecological understanding
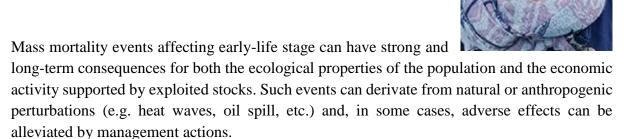
Evelyn Strombom

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Fish stocks go through boom and bust cycles. Fishing pressure is one factor we have relative control over that we know can bring these systems to criticality. We balance maximizing economic value, livelihoods and food security with uncertain systems dynamics, ecosystem pressures from other industries, and the risk that if we harvest too much, fishery collapse can be hard to recover from. What is the cost of not understanding the full ecosystem dynamics, in setting TAC or for direct ecosystem users, the fishers? I introduce two topics I will focus on while at CEES this Winter and Spring. First, I will use surveys of Lofoten fishers to obtain measures of system understanding and potential links to harvest decision-making, exploring correlations between mental accounting and risk aversion-- an important aspect in adapting to change. Second, I will use variations of standard dynamic bioeconomic optimization approaches to explore how harvest decisions that are made with knowledge of the abundance of a single species and an assumed growth function, but embedded in an unknown basic food web, can lead to unexpected results. I will also investigate ecological circumstances where decision-making with limited knowledge can suffice to maintain harvests or may even approximate optimal harvesting. Complex systems such as fisheries may always defy complete understanding. My work aims to reduce social unknowns and increase our certainty about possible futures.

An evaluation of management strategies to buffer the effect of mass mortality in early life stages of fish

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Mass mortality events affecting early-life stage can have strong and long-term consequences for both the ecological properties of the population and the economic activity supported by exploited stocks. Such events can derivate from natural or anthropogenic perturbations (e.g. heat waves, oil spill, etc.) and, in some cases, adverse effects can be alleviated by management actions.

The present work focuses on Northeast Arctic cod (Gadus morhua), which is a fish stock of high economic value. Cod individuals are recruited to the fishery around the age of 4 which gives a window of opportunity, between a potential eggs or larval mass-mortality event and the noticeable effects on catches when this weakened cohort recruit, to take actions to mitigate adverse effects. In order to assess the effects of mitigation strategies we employed a hindcasting approach and simulated scenarios of mass mortality on cod eggs and larvae followed by fishing reductions of different duration (from 1 to ten years) and intensity (from no reduction up to total ban). We used the Bayesian parameter estimates from a life cycle model for Northeast Arctic cod and compared the distribution of catches and their inter-annual variance over a period of ten years after the disturbance. By accounting for the inaccuracy of the observations and stochasticity in the population dynamics, this approach allows to quantify the range of potential effects that arise by reducing fishing pressure. Our results demonstrate that severe fishing reductions always lead to an important increase of the catches during the 10 years following the mass mortality events, however it also led to an increase in the year to year variability of the catch. Intermediate duration and intensity of fishing reduction allows to obtain a more sustainable situation, inducing less variability in the catches. The smaller fishing reduction required to counter the effects of mass mortality events on catches differs between years according mainly to the spawning stock biomass and the age structure of the population. Those results demonstrate the potential benefits of an adaptive approach to fisheries management.

Effects of temperature and sea ice on phytoplankton bloom dynamics in the Barents Sea

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Variations in physical conditions caused by climate change are likely to have large influences on marine organisms including phytoplankton. We here investigated associations between satellite derived chlorophyll data from the Barents Sea and two key abiotic factors sea surface temperature and sea ice concentration. Specifically, we investigated how climate variability, through the measured physical factors, associated with phytoplankton phenology between 1998 and 2014. Associations between sea surface temperature and phytoplankton bloom dynamics differed depending on the area. Spring phytoplankton bloom was earlier and had a higher magnitude in warm compared to cold years in the northern part of the Barents Sea, but there were no significant associations in the southern part. In the seasonally ice-covered region, the association between the timing of the sea ice retreat and the phytoplankton peak is nonlinear: sea-ice retreat time before mid-May was not associated with bloom timing whereas the phytoplankton bloom occurred before or immediately following the ice-retreat when the ice retreated after mid-May. Although drivers that are relatively constant across years, such as insolation, probably influenced the spatial gradient in Chl *a*, a space-for-time substitution captured the predicted effects of sea ice retreat on the timing and magnitude of the phytoplankton bloom quite well.

Match-mismatch dynamics between *Calanus finmarchicus* and *Gadus morhua* in the Norwegian-Barents Seas system

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One key process affecting recruitment (when the fish enter the fishery) variability is the spatio-temporal overlap between prey and predator (match-mismatch hypothesis, MMH). The Northeast Arctic cod *Gadus morhua* and its dominant prey, the *Calanus finmarchicus* copepod, have long been studied in the Norwegian-Barents Seas system. However, the mechanistic explanation of how cod survival is affected by MMH dynamics remains unclear. Most MMH studies focus on either the time synchrony or the spatial overlap between trophic levels.

Here, we use *C. finmarchicus* and *G. morhua* larvae data collected in the Norwegian-Barents Seas via ichthyoplankton surveys from 1959 through 1992. To assess the effect of the predator-prey relationship on the predator survival at age 3 (a measure of recruitment), we develop a metric of predator-prey overlap by using spatio-temporal statistical models. We then compare its interannual variability with the predator abundance at recruitment (3 years of age) to assess how MMH dynamics explain the survival of cod during the early life stages before recruitment to the fisheries.

We find that the amount of overlap between cod larvae (11-15 mm) and their prey explains 29 % of cod recruitment variability. Positive correlations between predator-prey overlap and subsequent recruitment are also found for predators of 6-10 and 16-20 mm, but not for 21+ mm. This improved predator-prey overlap metric is thus 1) useful to better understand how predator-prey dynamics at early life stages of fish impact the survival of later stages; and 2) a valuable tool for assessing the state of an ecosystem.

Long-term patterns of evolution and demography histories in Atlantic cod investigated using ancient DNA

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Atlantic cod (*Gadus morhua*) is economically one of the most important species in the Northern hemisphere. Historic exploitation of this species dates back millennia, providing wealth to the economies of the coastal communities when fish was abundant. Yet, this long exploitation history makes it difficult to quantify the extent of human impact since prehistoric times.
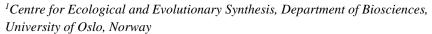
In this study, we analyze samples obtained from archaeological excavations dating up to 6000 years old using whole genome sequencing approaches. Demographic and evolutionary patterns of Atlantic cod in northern and eastern Europe will be studied comparing both mitochondrial and nuclear ancient and modern DNA to determine how genetic structure, population size and migration patterns have changed over time and how these changes are associated with environmental variation and anthropogenic pressures. We focus on identifying the origin and growth of fishing trade-routes along with patterns of diversification in order to understand the history of expanding fisheries and their impact on cod populations. This study will provide a long-term genomic perspective for Atlantic cod, with implications for fishing strategies and management measures to minimize genetic and demographic impact.

The Sheep Saga: Archaeogenomics of Viking Age sheep in the North Atlantic

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Sheep were vital to subsistence in the North Atlantic and provided milk and meat for food and wool and skins for clothing. In fact, the sails of Viking ships were made of sheep wool, enabling the settlement of the islands of the North Atlantic, the Faroes, Iceland and Greenland by the Norse. Sheep bones are frequent finds in archaeological excavations in the region but despite the importance and ubiquity of sheep in the region it is poorly understood where the sheep came from and how people have shaped their genetics over the past 1000 years.

We have sampled over 80 sheep bones from Viking Age to medieval excavations in Iceland, Greenland, the Faroe Islands, Norway and the UK and have obtained whole genome sequences of 27 ancient sheep. In addition, we have sequenced genomes from modern Icelandic, Faroese and Norwegian sheep breeds. By comparing our ancient and modern genome data to published sheep genomes we are studying the settlement pattern of sheep in the North Atlantic and the development of local breeds over the past 1000 years. The observed genomic structure reveals connections between ancient sheep in different geographical regions in the North Atlantic and the effects of founder events and genetic drift in isolated island populations. Moreover, we observe a distinct loss of genomic diversity in modern breeds, likely resulting from intensive breeding during past centuries.

Genomic population structure of the Atlantic Puffin – insights into the species' taxonomy

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The status of many of the world's seabirds has deteriorated substantially over the last decades. Similarly, most populations of the Atlantic puffin (*Fratercula arctica*) have been declining, and the species has recently been listed as "endangered" in Europe. Despite this species' cultural and economic importance, a genetic characterization of its populations, which would enhance an effective implementation of conservation strategies, is absent. Even basic taxonomy within the species remains unresolved due to the lack of genetic data, and classification into subspecies is purely based on clinal changes in morphology. Here, we assembled the first reference genome of the Atlantic puffin using 10xGenomics and provide an initial assessment of the genomic variation of *F. arctica* throughout its breeding range. Using genome re-sequencing of 76 individuals from 13 colonies, analyses of the nuclear genomes revealed groupings of colonies into multiple clusters, which only partially support the current division into three subspecies. Analyses of the mitogenomes unveiled a high degree of mito-nuclear discordance, with no substantial population structure and high mitogenomic diversity. Overall, this study provides an unprecedented perspective of the genomic population structure of the Atlantic puffin and offers a foundation to resolve the taxonomy of the species, which is of utmost importance for conservation management. The results of this study are also a starting point for more detailed population analyses across the puffin's range using fine-scale genomics combined with an improved reference genome.
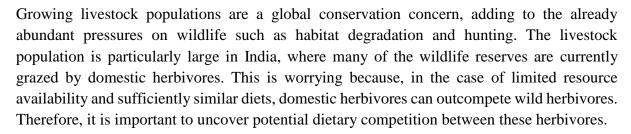
Dietary competition between wild and domestic herbivores in a wildlife sanctuary

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Growing livestock populations are a global conservation concern, adding to the already abundant pressures on wildlife such as habitat degradation and hunting. The livestock population is particularly large in India, where many of the wildlife reserves are currently grazed by domestic herbivores. This is worrying because, in the case of limited resource availability and sufficiently similar diets, domestic herbivores can outcompete wild herbivores. Therefore, it is important to uncover potential dietary competition between these herbivores.

Much of what we currently know about herbivore diet is based on traditional methods, generally using anatomical features of digested diet items, which is time-consuming, and identification can be ambiguous. Advances in DNA metabarcoding have made it possible to obtain more detailed information, and we applied this technique here to reconstruct the diet of wild and domestic herbivores in the Malai Mahadeswa wildlife sanctuary, southern India. Faecal samples were collected from a range of different herbivores living in the area, including elephants, cattle, goats, deer and macaques. We confirmed the herbivore species based on the herbivore DNA present in the samples, and used universal plant primer pair trnL g,h to amplify the plant DNA for analysing the dietary composition.

Reconstruction of the dietary niche partitioning between wild and domestic herbivores is crucial for uncovering potential food competition. With increasing pressures on wildlife from a range of different factors, DNA metabarcoding of faecal samples proves to be an effective non-invasive method providing a wealth of information that could prove vital for biodiversity conservation in wildlife sanctuaries.

The functional relevance of genic short tandem repeats in wild populations of *Arabidopsis thaliana* and *Gadus morhua*

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Repeat expansions in short tandem repeats (STRs) are mostly known for causing disease due to disruption of gene function and/or protein function. A famous example is an exonic 'CAG'-expansion in the huntingtin gene, which can cause Huntington's disease. However, the current knowledge regarding the extent and functional relevance of non-toxic STR polymorphisms is limited. In this PhD project, we address the hypothesis that STR polymorphisms serve to 'fine tune' gene and/or protein function. So far, we have explored in silico methods to quantify population-level length variation in short tandem repeats, using resequencing data of the small weed Arabidopsis thaliana and *Gadus morhua.* We used the Arabidopsis STR genotype data to explore the relationship between the local habitat and STR polymorphisms. We found that STR loci associated to the local habitat are more conserved and enriched in protein coding genes, and especially in predicted binding sites. In Atlantic cod, we are currently examining protein coding STR polymorphisms in subpopulations along a steep salinity cline.

An analysis of the Atlantic cod transcriptome

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The genome of Atlantic cod was published in 2011. Later, a second assembly has been published and a third has been made public. In addition, the transcriptome of Atlantic cod has been sequenced. Mapping of a transcriptome against the genome assembly, showed that many transcripts do not align to the genome at all, and other only have a partial mapping. This is the background for my research, and the aim is to find out what these transcripts are, why they do not map and if they have any common features.

Compared to other species, the Atlantic cod genome have a much higher density of short tandem repeats (STRs). Our hypothesis is that STRs affect the mapping of the transcripts to the genome. My results show that there are more than twice as much bp/Mbp in STRs, in the transcripts that do not map to the genome, compared to the total transcriptome. This gives an indication that the STRs play a role in why they do not map. I will go further into these results and do statistical estimations on questions such as where in the transcripts the majority of STRs are located, and if any particular kind of STRs are more likely to occur in certain regions.

I have done a gene ontology enrichment analysis on transcripts not mapping, to analyze if the annotated genes have some common functional characteristics. The analysis shows no gene ontology enrichment among these transcripts. By using a genome browser, I have added tracks of transcripts where only parts of them map to the sequenced genome, and tracks that show gaps and STRs in the genome. This can give an indication of the reason for why the transcripts do not map. I have annotated all transcripts, so that for transcripts that do not map I can find the corresponding region (the syntetic region) in other fish species. The results show that there are some genes annotated in the transcripts, that are conserved among other fish species, but not annotated and not found in the Atlantic cod genome. However, my research shows that there are some contaminations in the sequenced transcriptome, which can explain why the transcripts do not map to the genome of Atlantic cod.
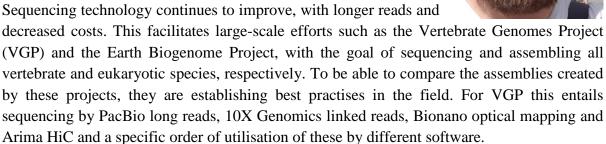
My research will contribute to the research on the evolution of STRs in Atlantic cod, and what role they have in the genome.

Current best practises in whole genome sequencing and assembly with emphasis on codfishes

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Sequencing technology continues to improve, with longer reads and decreased costs. This facilitates large-scale efforts such as the Vertebrate Genomes Project (VGP) and the Earth Biogenome Project, with the goal of sequencing and assembling all vertebrate and eukaryotic species, respectively. To be able to compare the assemblies created by these projects, they are establishing best practises in the field. For VGP this entails sequencing by PacBio long reads, 10X Genomics linked reads, Bionano optical mapping and Arima HiC and a specific order of utilisation of these by different software.

VGP is already creating assemblies for a diverse set of vertebrates that contain chromosome-length sequences with few gaps, both improving on available assemblies and making public assemblies for new species. This will change the way many biologists work.

Here, I will go through the example of Atlantic cod that has been sequenced and assembled through the VGP and compare to in-house projects of different codfishes. The codfishes contain substantial amounts of short tandem repeats and this can impede both sequencing and assembly of these genomes, and I will talk about preliminary results characterising these.

Genetic population structure of Atlantic haddock

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The evolutionary relationship of venom toxins and venom gland anatomy of the giant centipede (family *Scolopendridae*)

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A key question in evolutionary biology is how traits affect each other's ability to evolve. However, the reciprocal evolutionary relationship between traits at different phenotypic levels – i.e. different levels of cellular organization post gene-translation – remains largely unknown. The venoms of centipedes are an interesting model for trying to understand this question, because of the hypothesized relationship between venom gland cellular complexity and molecular diversity of the venom. The project will focus on the evolutionary drivers of and constraints on centipede venom, with a focus on the family Scolopendridae. In particular, it will examine how the anatomy of the centipede venom glands may have acted as a constraint on the molecular evolution of the toxins contained in their venom. Centipedes are uniquely suited to studying the potential effect of morphology on toxin molecular evolution. The centipede venom gland is essentially a composite gland that consists of numerous glandular units that each includes two secretory cells, and that are connected through a valve-like pore to a chitinous duct. This constant ratio of number of pores to secretory cells makes the counting of pores a practical way of estimating the number of secretory cells contained in the gland, which is thought to present a potential limitation on toxin evolution. We will use phylogenetic comparative methods to investigate hypotheses of adaption and constraint on the evolutionary relationship between morphology (number of secretory cells) and venom complexity. The end objective is to have investigated hypotheses of adaption and to better understand the evolution of toxins.

Environmental and genetic factors affecting endosperm based post-zygotic hybridization barriers

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There are several important mechanisms for successful hybrid development after double fertilization of the female gametophyte, one being endosperm development. The endosperm develops initially as a syncytium and will, at a distinct developmental stage, cellularize, supporting the developing embryo in the seed by providing nutrients and serving as a protective layer. An increasing amount of examinations of hybrid seeds from varying angiosperm taxa, show that the embryo is arrested in its development when the endosperm has either precocious or failed cellularization, causing a lethal phenotype. Research has shown that the correct genomic dosage within the triploid endosperm is essential for its proper development, with an excess of maternal or paternal contribution causing precocious or impaired cellularization, respectively. Imprinted genes contribute to the genomic dosage, by silencing either the maternal or paternal allele and studies show a low conservation on imprinted genes between plant species. The low conservation of imprinted genes, together with differences in ploidy are the main means for causing imbalance in the genomic dosage in the hybrid offspring. The low conservation of imprinted genes can increase differences in the genomic dosage between species, resulting in a stronger hybridization barrier. Ploidy is also an important factor for a balanced genomic dosage in the hybrid, and either increasing or decreasing the ploidy in one of the parental species, can contribute to successful hybridization. An imbalance in the genomic dosage can mainly be caused by either differences in ploidy or imprinting in the maternal and paternal counterpart. Studies on imprinted genes show a low conservation between plant species, contributing to hybridization barriers. Imprinted genes are often in close proximity of transposable elements (TEs) and epigenetic modifications on TEs are often disturbed when exposed to increased temperatures. In addition, temperature changes have been shown to affect endosperm cellularization in rice and endosperm based post-zygotic hybridization barriers in *Arabidopsis thaliana* and *Arabidopsis arenosa*. The main goal of my thesis is to elucidate the temperature effect on endosperm-based post-zygotic hybridization barriers and whether increased temperature changes the imprinting pattern, and potentially reverses the lethal phenotype. This knowledge will contribute to further elucidate the role of imprinting in seed development, and can also potentially be used to bypass hybridization barriers.

The molecular basis of postzygotic hybridization barriers in *Arabidopsis*

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Different plant species can easily be crossed by applying pollen to stigmas. The result of successful fertilization can then be divided into germinating and aborted hybrid seeds. The first usually frustrates the botanist and the second the farmer. Surprisingly this observation has been linked in many cases (Tomato, rice, castor bean, *Arabidopsis*, and *Capsella*) to aberrant development of a simple nutrition tissue surrounding the embryo called the endosperm. Embryos extracted from the arrested seed develop, grow, and flower normally. The endosperm is often triploid, containing one paternal and two maternal genomes. However, epigenetic regulation set up during pollen and female gametophyte development overcome this unequal dose by restricting expression to maternal or paternal alleles, also known as genetic imprinting. Extensive studies on interspecies, together with interploidy crosses, now suspect imprinting to be the underlying molecular basis of these hybridization barriers (*1-4*). While their reasoning is comprehensive and spans from detailed phenotypic description, gene expression to reciprocal rescues of mutants, a complete systematic approach with genome-wide expression analysis is missing. This is where the MOLBAR project started and successfully established, described, and accomplished a complete crossing scheme between *Arabidopsis arenosa* and *Arabidopsis lyrata* (*5*). I will present preliminary results of our transcriptomic approach to uncover and map the molecular pathways underlying this hybridization barrier.

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Seed-based hybridization barriers in *Cochlearia*

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The speciation process of sister lineages is dependent upon the development of reproductive isolation over evolutionary time. Still, mechanistic drivers of reproductive isolation remain largely unknown, especially in regards to postzygotic barriers. In *Arabidopsis*, an endosperm-based hybridization barrier has been described and similar barriers have shown to be present in other plant genera. Interestingly, the barrier can be bypassed by increasing the ploidy of one of the hybridizing parents. To gain a better understanding of reproductive isolation, we investigate postzygotic hybridisation barriers in the Brassicaceae genus *Cochlearia*. *Cochlearia* species hybridize within and between karyotypes and ploidies in nature and forms a fascinating model for hybridization studies. A crossing scheme involving two diploid (2n=12, 14), one tetraploid (2n=24), one hexaploid (2n=42) and one octoploid (2n=48) species has been carried out. Investigations of developing and mature hybrid seeds indicate that maternal and paternal background has phenotypic effects on the developing seeds, mainly in the form of affecting seed size, shape and seed coat pigmentation. Further, in depth differential interference contrast (DIC) light microscopy stacks of developing three-week-old hybrid seeds indicate that seed development is affected in interspecies crosses. For example, certain cross combinations appear to facilitate embryonal developmental arrest and other cross combinations show a paternally influenced seed size phenotype.

Many MADS-box type I transcription factors have an endosperm specific expression profile during seed development and have been described for many species. We performed a gene expression analysis in early and later stages of *Cochlearia* seed development, which indicates that MADS-box genes are abundant. Moving onwards, we intend to explore the temporal expression pattern of homologous MADS-box genes in early and later stages of *Cochlearia* seed development in comparison to known expression profiles in *Arabidopsis thaliana*.
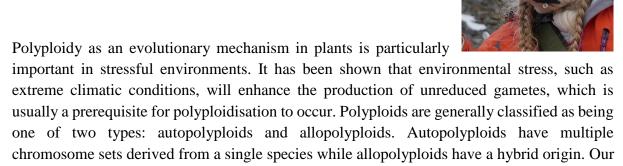
Secrets of success in *Saxifraga oppositifolia*

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Polyploidy 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 being one of two types: autopolyploids and 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 aim to investigate consequences of autopolyploidy on phenotypic variation, with focus on reproductive strategy and reproductive output. As study system, I will use the circumpolar, arctic-alpine species *Saxifraga oppositifolia* (Saxifragaceae), in which two main ploidy levels are known, diploids 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 connected to ploidy levels and habitat. Differences in flower production and vegetative growth differ clearly between habitats and growth forms, but how reproduction is varying between ploidy levels is not known. I will use five establish transects near Longyearbyen, Svalbard, covering three different habitats where *S. oppositifolia* is growing (gravel, heath, river-bed). I will collect data related to both sexual and vegetative reproduction within different ploidy levels and habitats to address the following question: Have autopolyploidisation created a shift in reproductive parameters?

More specifically, to investigate investment in sexual reproduction, number of flowers, capsules and seeds will be counted/estimated for plants with different ploidy levels. To obtain measures on vegetative investment, trailing branches of different plants will be sampled to test the rooting ability between ploidy levels. Lastly, to estimate how the frequency of unreduced gametes varies between ploidy levels, pollen from bursted anthers will be collected and analysed by flow cytometry.
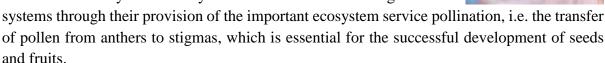
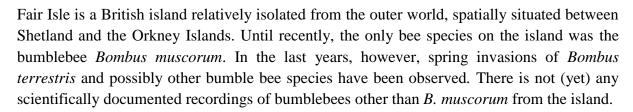# Effect of invasive bumblebee in Fair Isle

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Bee species are recognized as some of the most important organisms of the world's ecosystems. They assist both natural and agricultural systems through their provision of the important ecosystem service pollination, i.e. the transfer of pollen from anthers to stigmas, which is essential for the successful development of seeds and fruits.

Fair Isle is a British island relatively isolated from the outer world, spatially situated between Shetland and the Orkney Islands. Until recently, the only bee species on the island was the bumblebee *Bombus muscorum*. In the last years, however, spring invasions of *Bombus terrestris* and possibly other bumble bee species have been observed. There is not (yet) any scientifically documented recordings of bumblebees other than *B. muscorum* from the island.

Invasive species and their impact on native flora and fauna is acknowledged as one of the major threats to biodiversity. *Bombus terrestris* was in the 1980s recognized as an efficient tomato pollinator, and hence farmed for agricultural purposes. Due to its superior competitive ability, *B. terrestris* has spread to ranges far from their native habitats. Previous studies have shown that they in a negative way affect both local fauna by competition, and flora by "nectar-robbing" and hence inefficient pollination.

Due to its isolation, Fair Isle is an ideal place to monitor changes in the biota. Being hypothesized to be in an early stage of an invasion, it also bears an intrinsic ecological interest in itself, islands in several cases being home to endemic species (Fair Isle being no exception). In this study, my main goal will be to investigate the presence both of the native bumblebee *Bombus muscorum* and the possibly invasive species *B. terrestris*, *B. lucorum* and/ or *B. magnus*, and their effect on the native flora. I will also assess the potential competitive interactions between the native bumble bee species and the aliens.

The distribution of insect pollinators in an oil palm plantation

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The increased global demand for palm oil causes decreases in tropical rainforest cover due to expansions of oil palm fields. Oil palm plantations cover approximately 10% of the world´s permanent croplands, with Indonesia accounting for more than 53% (33.5 Mt) of global palm oil production. Oil palm is one of the world's most rapidly expanding crops and there continues to be an increase in vegetable oil and biofuel demands. Expansion of agricultural monocultures negatively affects all aspects of biodiversity including insects. Insects are the most important pollinator for tropical plant species, pollinating approximately 98-99% of all plants in this biome.

The oil palm company, PT Austindo Nusantara Jaya, is relatively conservation minded. One of the company`s goals is to keep patches of so called "high conservation value forest" left inside the plantation. This study focused on one of their plantations, a 16,620 hectares area in Ketapang, West Kalimantan, Indonesia, run by PT Kayung Agro Lestari (KAL) that contains several small patches of "close to native forest". The aim of the study is to assess whether there is an increase in pollinator density and diversity in relation to forest patch proximity. I collected pollinators (bees) by use of pan traps placed at understory vegetation height from June to October 2017. I established four transects starting at two forest patches and collections from these were compared to collections from two control sites situated more than 1 km from any forest. The data collected in this study should allow managers to make more informed decisions concerning insect pollinator conservation in relation to oil palm plantation establishment, management and development.

Some preliminary results will be presented.

Differential gene expression between commensal and non-commensal Passer sparrows

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In this project I will study differential gene expression through RNA transcription between individuals of commensal and non-commensal Eurasian sparrow species. The study species are House, Italian and Spanish sparrows. The house sparrow Passer domesticus is commensal, while the Spanish sparrow Passer hispaniolensis is a non-commensal species. The Italian sparrow Passer italiae is a hybrid species of the Spanish and House sparrow, and although its genome has almost equal contributions from both parent species, it actually shows an ecological similarity to one of its parent species, P. domesticus and is also commensal. One goal of the study is to see if the adaptations to human activity in commensal species have caused any changes in gene expression compared to the non-commensal species P. hispaniolensis. This may reveal the genes responsible for the evolution of human dependency in commensal sparrows.

This project calls for RNA sequencing as we want to understand how the same genes are expressed differently between the different species, as quite similar genomes might give substantially different individuals, all depending on the regulation and transcription of the genes. I will then map and analyse these RNA transcripts. DNA mapping and de novo assembly are two methods I will use to quantify the gene expression.

Winter distribution of small rodents in relation to snow properties and vegetation type at Finse, Norway

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In alpine regions, small rodent (Arvicolinae) cycles have been shown to dampen. Several studies suggest that changes in winter climate might be responsible for the changes in rodent population dynamics. However, we lack detailed knowledge of how the rodents are distributed in relation to snow conditions and vegetation during winter. Small rodents living in alpine regions are adapted to a life under the snow during the cold, alpine winters. Climate change increase the frequency of melt-refreeze events, hence changing the snowpack conditions from soft, wet snow to hard, ice layers which limit the winter habitat available for the small rodents. In trying to gain information about the factors affecting winter distribution of the small rodents under the snow, we have been measuring different snow properties like hardness, temperature, depth and density in a 1 km x 1 km area at Finse, and used high resolution vegetation maps of the same area. Snow measurements have been carried out in February and March/April to describe snow properties both in early and late winter. After snowmelt presence and absence data were recorded every meter along multiple transect lines of 1km throughout the study area. Fecal pellets were collected for identification of the species/genus. Statistical analyses are currently undertaken to model probability of presence as a function of snow conditions and vegetation types.

Distribution and abundance of the African elephant (*Loxodonta africana*) in Chebera Churchura National Park in Ethiopia from wet season to dry season

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In the past, Ethiopia had one of the largest African savanna elephant populations in Africa. However, due to decades of habitat loss, increasing elephant-human conflict, and continuous poaching, the country has, according to the African Wildlife Foundation, lost more than 90 percent of its elephant population since 1980 – leaving only a small, estimated number of 1,500 to 2,000 individuals (2017). The largest of the remaining populations in Ethiopia is speculated to be found in Chebera Churchura National Park (CCNP), located south west in the country. Yet, no credible population or distribution estimate is available for the African savanna elephant population in CCNP. Understanding of the potential suitable habitat of the species as well as a credible population estimate is essential to ensure timely management and conservation decisions that can protect the specie from further decline. Hence, the aim of this study is to provide a reliable population estimate as well as a distribution estimate based on different habitat types of the African savanna elephant in the CCNP, in order to help guide the conservation effort of the specie. For data collection, I will use an unmanned aerial vehicle (UAV or drone) and possibly also make use of dung count transects, and the analysis will be based on occupancy modeling and other types of hierarchical models.

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The effect of season and post-fire on habitat preferences of the endangered Swayne's hartebeest (*Alcelaphus buselaphus swaynei*) in Maze National Park, Ethiopia

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Background: The availability of preferred habitats determines the spatial and temporal distribution of herbivores in savanna ecosystems. Understanding habitat preference of a targeted wildlife species is crucial for developing effective conservation strategies. Habitat preference of large grazers in connection to grass height and post-fire effect has been debated for the last century. Here, we examined the effects of season, grass height and burning on the habitat preference on Swayne's hartebeest (*Alcelaphus buselaphus swaynei*) in Maze National Park. Data for seasonal habitat selection were collected using both direct observation along established transect lines and pellet counting using permanently established plots. Every month, we measured grass height commonly preferred by Swayne's hartebeest in grassland habitat. Starting from the first week of burning, we recorded the abundance of Swayne's hartebeest in both burned and unburned grassland patches.

Results: From detected pellets, 94.3% were recorded in the grassland habitat indicating that other habitat types are less used despite their extensive cover > 50% of the Park. During wet and early dry seasons, Swayne's hartebeest exclusively preferred grassland habitat. We found that 85.2% (n=1079) and 85.3% (n=593) of individuals observed in areas with a grass height below 30 cm during wet and early dry seasons, respectively; while 70.9% (n=2,288) preferred grass height below 30 cm during the dry season. The density of Swayne's hartebeest in burned grassland area was higher than unburned grassland areas up to 150 days since burning. However, in unburned grassland areas, the density was initially low but showed increasing trend for consecutive days, reaching similar density with burned areas after 150 days since burning.

Conclusion: Swayne's hartebeest exclusively preferred grassland habitat, particularly during wet and early dry seasons, shortest available grass height in all seasons and were attracted to burned grassland areas. Our results suggested that fire played an important role in maintaining habitat quality in grassland, and that management should continue using controlled burning as a tool for the conservation of Swayne's hartebeest. However, we remain cautious of our findings given the paucity of information regarding other confounding factors and the absence of long-term data on fire disturbance.

Key words: fire, grassland habitat, grass height, habitat preference, Swayne's hartebeest

Use of spatial clusters by red deer (*Cervus elaphus*) to identify transmission hot spots in a Chronic Wasting Disease context

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The feeding of animals, intentional or unintentional, will often lead to an aggregation of wildlife. This could in turn cause increased chances of parasite- and disease transmission between animals.

In 2016, the fatal prion disease Chronic Wasting Disease was discovered in Norwegian reindeer (*Rangifer tarandus*) in the Nordfjella region. Transmission of CWD is often by environmental transmission, which is more likely to occur by animal aggregation points. After this discovery, mitigation measures were put in place to combat Chronic Wasting Disease, including a nation-wide ban on supplemental feeding of cervids, and a ban on the use of mineral licks. However, the ban of supplemental feeding may lead to an increase in unintentional feeding, such as foraging on silage left in fields. During my masters, I will try to determine whether spatial clusters of red deer are related to natural foraging, intentional, or unintentional feeding, and how the clustering depends on seasonal cycles and weather conditions. To achieve this, I will study the movement of 13 individuals of red deer (*Cervus elaphus*) fitted with GPS collars.

Use of mineral licks and supplemental feeding sites by cervids in a CWD disease transmission context

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There is an estimate of 2.4 million red deer *(Cervus elaphus)* and 30,000 reindeer in Europe. Most of these populations are extensively managed, and one such common practice in northern Europe and parts of North America is the provisioning of supplemental feeding sites during winter. It is normally associated with maintaining high densities of animals for hunting, in terms of increasing or maintaining high body weights and condition overwinter, improving reproductive performance and fertility, increasing overwinter survival, control of animal movements, and reduce levels of damage caused to agriculture, forestry or natural heritage. In some areas, mineral licks are provided for cervids, or put out for livestock which also being used by cervids.

Chronic Wasting Disease (CWD) is a contagious and lethal prion disease in cervids spreading across USA and Canada, and deer population decline due to CWD have been reported. The emergence of CWD in 2016 among wild alpine reindeer *(Rangifer tarandus)* in Nordfjella, Norway, therefore pose a serious threat to cervids potentially across the whole of Europe in a long-term perspective. The incubation time can be several months, and infected individuals are capable of transmitting the disease and contribute to environmental contamination by shedding prions in saliva, urine, feces, and through carcasses. The most likely route of infection is through oral intake. Therefore, the probability of CWD disease transmission is enhanced at sites where the frequency of behaviors such as defecating, urinating, licking and eating from the ground is increased. The mitigation measures to combat CWD in Norway involves a national wide ban on artificial mineral licks and feeding sites for cervids. Nevertheless, such mineral licks are still widely used for livestock in areas with sympatric cervids, even in the Nordfjella region where CWD was discovered. The soil near mineral licks have high concentration of prions, and they are regarded as transmission hotspots for CWD. However, the variation of how much cervids actually use feeding sites and mineral licks is not well documented, and there is very little quantitative information regarding the temporal and spatial pattern of use.

Currently, there is a rapid growing use of camera traps as a method to study and detect elusive animals and their distribution, abundance and behavior. Such methods now allow the study of supplemental feeding sites and mineral licks used by cervids, and their seasonal, temporal and spatial patterns in a CWD disease transmission context.

Flashing large mammals – do they mind?

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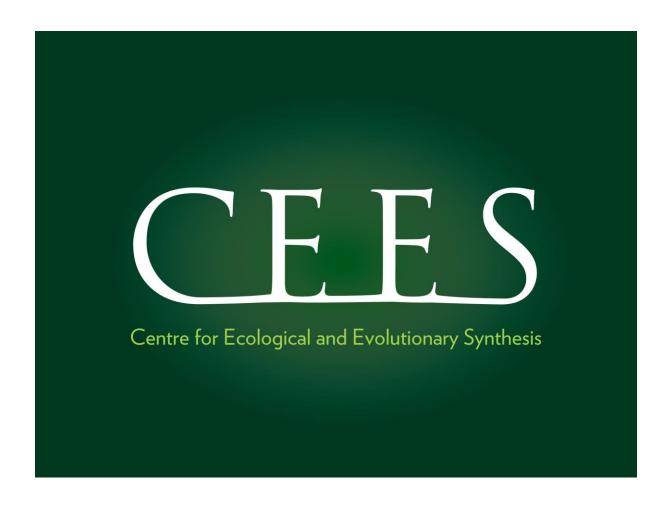
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Most mammals are nocturnal and elusive. It is therefore inherently difficult to assess their behavior and distribution by direct observation. Marking of animals with GPS or other methods can provide very detailed knowledge of use, but studies are often limited in geographic extent due to expenses and their invasive nature requiring handling of animals. Distribution of medium sized and large mammals are therefore often based on proxy data such as harvest statistics, but such methods are often quite unreliable due to variable hunter effort. In particular for large carnivores, harvest may also be low or absent for periods where management targets are not obtained. The use of camera trapping have markedly improved our ability to non-invasively quantify activity and density of many species of mammals. Camera traps have been used to estimate abundances of single species or communities. Detectability is markedly affected by placement relative to trails. There are limited number of studies for how details of the technology affect behavior and subsequent detectability of different species. In particular, some new models include flash that may affect behaviour of species differently, but this remains to be quantified.

The aim of this thesis is to provide a quantification of the distribution of large mammals, mainly red fox, roe deer and lynx, in a landscape in southern Norway from agricultural areas to more remote forest areas by aid of camera trapping. A subgoal is to assess how camera traps with and without a flash affect the behavior and subsequent detectability of the different animal species. I aim to answer:

- What is the seasonal pattern of use of a gradient of habitat from agricultural areas to forest areas in southern Norway?

- Do detectability differ depending on technology (flash) of camera traps and differently depending on species?

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